

# Sentaurus Process User Guide

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## Contents

# About This Guide

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Sentaurus Process is an advanced 1D, 2D, and 3D process simulator suitable for silicon and nonsilicon semiconductor devices. It features modern software architecture and state-of-the-art models to address current and future process technologies.

Sentaurus Process simulates all standard process simulation steps, diffusion, implantation, Monte Carlo (MC) implantation (Taurus MC or Crystal-TRIM), oxidation, etching, deposition, and silicidation. Capabilities in 3D include meshing of 3D boundary files through the MGOALS library, implantation through the Imp3D module from FhG Erlangen, mechanics (stress and strain), diffusion, a limited capability for 3D oxidation, and an interface to Sentaurus Structure Editor, which is the 3D geometry editing tool based on the ACIS solid modeling library.

Sentaurus Process uses the Alagator scripting language that allows users to solve their own diffusion equations. Alagator can be used to solve any diffusion equation including dopant, defect, impurity, and oxidant diffusion equations. Simulation of 3D diffusion is handled exactly as for 1D and 2D. Therefore, all the advanced models and user programmability available in 1D and 2D can be used in 3D. In addition, a set of built-in calibrated parameters is available with Advanced Calibration.

The main chapters are:

- [Chapter 1](#) describes how to run Sentaurus Process.
- [Chapter 2](#) presents an overview of how Sentaurus Process operates.
- [Chapter 3](#) presents the ion implantation technique used in Sentaurus Process.
- [Chapter 4](#) provides information on the dopant and defect diffusion models and parameters.
- [Chapter 5](#) describes atomistic kinetic Monte Carlo diffusion.
- [Chapter 6](#) discusses the Alagator scripting language for solving diffusion equations.
- [Chapter 7](#) provides details about using Advanced Calibration in Sentaurus Process.
- [Chapter 8](#) describes the oxidation models.
- [Chapter 9](#) describes the computation of mechanical stress.
- [Chapter 10](#) describes the mesh algorithms and meshing parameters available in Sentaurus Process.
- [Chapter 11](#) discusses etching and deposition, and other geometry manipulations available in Sentaurus Process.
- [Chapter 12](#) presents strategies for using the IC WorkBench EV Plus–TCAD Sentaurus interface.
- [Chapter 13](#) presents strategies for analysing simulation results.

## About This Guide

### Audience

- [Chapter 14](#) discusses numerics-related issues, time integration methods, and the linear solvers used in Sentaurus Process.
- [Appendix A](#) lists the available commands, including descriptions, options, and examples.

---

## Audience

This user guide is intended for users of the Sentaurus Process software package.

---

## Related Publications

For additional information about Sentaurus Process, see:

- The TCAD Sentaurus release notes, available on SolvNet (see [Accessing SolvNet on page xxxiii](#)).
- Documentation available through SolvNet at <https://solvnet.synopsys.com/DocsOnWeb>.

---

## Typographic Conventions

Convention	Explanation
< >	Angle brackets
{ }	Braces
[ ]	Brackets
( )	Parentheses
<a href="#">Blue text</a>	Identifies a cross-reference (only on the screen).
<b>Bold text</b>	Identifies a selectable icon, button, menu, or tab. It also indicates the name of a field or an option.
Courier font	Identifies text that is displayed on the screen or that the user must type. It identifies the names of files, directories, paths, parameters, keywords, and variables.
<i>Italicized text</i>	Used for emphasis, the titles of books and journals, and non-English words. It also identifies components of an equation or a formula, a placeholder, or an identifier.
<b>Menu &gt; Command</b>	Indicates a menu command, for example, <b>File &gt; New</b> (from the <b>File</b> menu, select <b>New</b> ).
NOTE:	Identifies important information.



## Customer Support

Customer support is available through SolvNet online customer support and through contacting the Synopsys support center.

---

### Accessing SolvNet

SolvNet includes an electronic knowledge base of technical articles and answers to frequently asked questions about Synopsys tools. SolvNet also gives you access to a wide range of Synopsys online services, which include downloading software, viewing documentation, and entering a call to the Synopsys support center.

To access SolvNet:

1. Go to the SolvNet Web page at <https://solvnet.synopsys.com>.
2. If prompted, enter your user name and password. (If you do not have a Synopsys user name and password, follow the instructions to register with SolvNet.)

If you need help using SolvNet, click Help on the SolvNet menu bar.

---

### Contacting Synopsys Support

If you have problems, questions, or suggestions, you can contact Synopsys support in the following ways:

- Go to the Synopsys [Global Support Centers](#) site on [www.synopsys.com](http://www.synopsys.com). There you can find e-mail addresses and telephone numbers for Synopsys support centers throughout the world.
- Go to either the Synopsys SolvNet site or the Synopsys Global Support Centers site and [open a case online](#) (Synopsys user name and password required).

---

## Contacting Your Local TCAD Support Team Directly

Send an e-mail message to:

- support-tcad-us@synopsys.com from within North America and South America.
- support-tcad-eu@synopsys.com from within Europe.
- support-tcad-ap@synopsys.com from within Asia Pacific (China, Taiwan, Singapore, Malaysia, India, Australia).
- support-tcad-kr@synopsys.com from Korea.
- support-tcad-jp@synopsys.com from Japan.

---

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Sentaurus Process is based on the 2000 and 2002 releases of FLOOPS written by Professor Mark Law and coworkers at the University of Florida. Synopsys acknowledges the contribution of Professor Law and his advice in the development of Sentaurus Process. For more information about TCAD at the University of Florida, visit <http://www.swamp.tec.ufl.edu>.

Sentaurus Process Kinetic Monte Carlo is based on DADOS written by Professor Martin Jaraiz and coworkers at the University of Valladolid, Spain. Synopsys acknowledges Professor Jaraiz' contribution and advice. For more information, visit <http://www.ele.uva.es/~simulacion/KMC.htm>.

## CHAPTER 1 Getting Started

---

*This chapter describes how to run Sentaurus Process and guides you through a series of examples.*

This chapter is not a comprehensive reference but is intended to introduce some of the more widely used features of Sentaurus Process in a realistic context. For new users, the sections [Interactive Mode on page 44](#), [Syntax for Creating Input Command Files on page 48](#), and [Creating the Structure and Initializing Data on page 69](#) would be useful to refer to while reading this chapter. For more advanced users who need to adjust model parameters, [Like Materials: Material Parameter Inheritance on page 55](#) would be useful. For the TCAD Sentaurus Tutorial and examples, go to:

```
$STROOT/tcad/$STRELEASE/Sentaurus_Training/index.html
```

where `STROOT` is an environment variable that indicates where the Synopsys TCAD distribution has been installed, and `STRELEASE` indicates the Synopsys TCAD release number.

---

## Overview

Sentaurus Process is a complete and highly flexible, multidimensional, process modeling environment. With its modern software architecture and extensive breadth of capabilities, Sentaurus Process is a state-of-the-art process simulation tool. Calibrated to a wide range of the latest experimental data using proven calibration methodology, Sentaurus Process offers unique predictive capabilities for modern silicon and nonsilicon technologies.

Sentaurus Process accepts as input a sequence of commands that is either entered from standard input (that is, at the command prompt) or composed in a command file. A process flow is simulated by issuing a sequence of commands that corresponds to the individual process steps. You should place parameter settings in a separate file, which is sourced at the beginning of input files using the `source` command.

Several commands allow you to select physical models and parameters, grid strategies, and graphical output preferences if required. In addition, a special language (Alagator) allows you to describe and implement your own models and diffusion equations.

## Setting Up the Environment

The `STROOT` environment variable is the TCAD Sentaurus root directory, and you must set this variable to the installation directory of TCAD Sentaurus. The `STRELEASE` environment variable can be used to specify the release of the software to run, for example, H-2013.03. If `STRELEASE` is not set, the default version is used which is usually the last version installed.

To set the environment variables:

1. Set the TCAD Sentaurus root directory environment variable `STROOT` to the TCAD Sentaurus installation directory, for example:

```
* Add to .cshrc
setenv STROOT <Sentaurus directory>

* Add to .profile, .kshrc, or .bashrc
STROOT=<Sentaurus directory>; export STROOT
```

2. Add the `<Sentaurus directory>/bin` directory to the user path.

For example:

```
* Add to .cshrc:
set path=(<Sentaurus directory>/bin $path)

* Add to .profile, .kshrc, or .bashrc:
PATH=<Sentaurus directory>/bin:$PATH
export PATH
```

---

## Starting Sentaurus Process

You can run Sentaurus Process in either the interactive mode or batch mode. In the interactive mode, a whole process flow can be simulated by entering commands line-by-line as standard input. To start Sentaurus Process in the interactive mode, enter the following on the command line:

```
> sprocess
```

Sentaurus Process displays version and host information, followed by the Sentaurus Process command prompt. You now can enter Sentaurus Process commands at the prompt:

```
sprocess>
```

This is a flexible way of working with Sentaurus Process to test individual process steps or short sequences, but it is inconvenient for long process flows. It is more useful to compile the command sequence in a command file, which can be run in batch mode or inside Sentaurus Workbench.

To run Sentaurus Process in batch mode, load a command file when starting Sentaurus Process, for example:

```
> sprocess input.cmd
```

---

## Starting Different Versions of Sentaurus Process

You can select a specific release and version number of Sentaurus Process using the `-rel` and `-ver` options:

```
> sprocess -rel <rel_number> -ver <version_number>
```

For example:

```
> sprocess -rel G-2012.06
```

The command:

```
> sprocess -rel G-2012.06 -ver 1.2 nmos_fps.cmd
```

starts the simulation of `nmos_fps.cmd` using the 1.2 version of Release G-2012.06 as long as this version is installed.

---

## Using a Command File

As an alternative to entering Sentaurus Process commands line-by-line, the required sequence of commands can be saved to a command file, which can be written entirely by users or generated using Ligament. To save time and reduce syntax errors, you can copy and edit examples of command files in this user guide or use Ligament to create a template.

If a command file has been prepared, run Sentaurus Process by typing the command:

```
sprocess <command_filename>
```

Alternatively, you can automatically start Sentaurus Process through the Scheduler in Sentaurus Workbench. By convention, the command file name has the extension `.cmd`. (This is the convention adopted in Sentaurus Workbench.)

## 1: Getting Started

### Example: 1D Simulation

The command file is checked for correct syntax and then the commands are executed in sequence until the simulation is stopped by the command `exit` or the end of the file is reached. Since Sentaurus Process is written as an extension of the tool command language (Tcl), all Tcl commands and functionalities (such as loops, control structures, creating and evaluating variables) are available in the command files. This results in some limitations in syntax control if the command file contains complicated Tcl commands. Syntax-checking can be switched off with the command-line option `-n`, for example:

```
sprocess -n inputfile
```

Sentaurus Process ignores character strings starting with `#` (although Sentaurus Workbench interprets `#` as a special character for conditional statements). Therefore, this special character can be used to insert comments in the simulation command file.

A file with the extension `.log` is created automatically whenever Sentaurus Process is run from a command line, that is, outside the Sentaurus Workbench environment. This file contains the run-time output, which is generated by Sentaurus Process and is sent to standard output. When Sentaurus Process is run by using a command file `<root_filename>_fps.cmd`, the output file is named `<root_filename>_fps.log`.

When Sentaurus Process is run in Sentaurus Workbench, no log file is created. Instead, the file `<root_filename>_fps.out` is generated as a copy of the standard output. For a complete list of all commands, see [Appendix A on page 851](#).

---

## Example: 1D Simulation

Many widely used process and control commands are introduced in the context of a nominal 0.18  $\mu\text{m}$  n-channel MOSFET process flow. The MOSFET structure is simulated in 1D and 2D, and the processing of the isolation is excluded.

In this section, a simple 1D process simulation is performed.

---

### Defining Initial 1D Grid

The initial 1D grid is defined with the `line` command:

```
line x location=0.0 spacing= 1<nm> tag=SiTop
line x location= 10<nm> spacing= 2<nm>
line x location= 50<nm> spacing= 10<nm>
line x location=300<nm> spacing= 20<nm>
line x location=0.5<um> spacing= 50<nm>
line x location=2.0<um> spacing=0.2<um> tag=SiBottom
```

The first argument of the `line` specifies the direction of the grid. For 1D, this is always `x`.

The grid spacing is defined by pairs of the `location` and `spacing` keywords. The keyword `spacing` defines the spacing between two grid lines at the specified location. Sentaurus Process expands or compresses the grid spacing linearly in between two locations defined in the `line` command.

**NOTE** Units in Sentaurus Process can be specified explicitly by giving the units in angle brackets. For most cases, the default unit of length is micrometer. Therefore, the statements `location=2.0<um>` and `location=2.0` are equivalent. In this section, units are given explicitly.

You can label a line with the `tag` keyword for later use in the `region` command.

---

## Defining Initial Simulation Domain

The initial simulation domain is defined with the `region` command:

```
region silicon xlo=SiTop xhi=SiBottom
```

The keyword `silicon` specifies the material of the region. The keywords `xlo` and `xhi` take tags as arguments, which are defined in the `line` command.

**NOTE** For 2D and 3D, the additional keywords `ylo`, `yhi`, `zlo`, and `zhi` are used to define rectangular or cuboidal regions. In general, the initial simulation domain can consist of several regions.

---

## Initializing the Simulation

The simulation is initialized with the `init` command:

```
init concentration=1.0e15<cm-3> field=Boron
```

Here, the initial boron concentration in the silicon wafer (as defined in the previous `region` command) is set to  $10^{15} \text{ cm}^{-3}$ .

---

## Setting Up a Meshing Strategy

The initial grid is valid until the first command that changes the geometry, such as oxidation, deposition, and etching. For these steps, a remeshing strategy must be defined.

The Sentaurus Mesh meshing engine tries to preserve the initial mesh as much as possible and only modifies the mesh in the new layers and in the vicinity of the new interfaces.

To define a remeshing strategy, use:

```
pdbSet Grid SnMesh min.normal.size 0.003
pdbSet Grid SnMesh normal.growth.ratio.2d 1.4 ;# this is for 1D and 2D
```

where:

- The parameter `min.normal.size` determines the grid spacing of the first layer starting from the interface in micrometers.
- The parameter `normal.growth.ratio.2d` determines how fast the grid spacing can increase from one layer to another. This parameter is unitless.

---

## Growing Screening Oxide

The 1D process simulation is started by thermally growing a thin layer of sacrificial screening oxide:

```
gas_flow name=O2_1_N2_1 pressure=1<atm> flowO2=1.2<l/min> flowN2=1.0<l/min>
diffuse temperature=900<C> time=40<min> gas_flow=O2_1_N2_1
```

The `gas_flow` statement is used to specify the gas mixture. The name keyword defines a `gas_flow` record for later use in a `diffuse` command. The pressure of the ambient gas is set to 1 atm, and the flows of oxygen and nitrogen are set to 1.2 l/minute and 1.0 l/minute, respectively.

**NOTE** Other gas flow parameters, such as ambient gases and partial pressures, can be defined as well (see [gas\\_flow on page 901](#) for details).

The thermal oxidation step is started with the `diffuse` command. Here, the wafer is exposed to the oxidizing gases, defined in the `gas_flow` statement, for 20 minutes at an ambient temperature of 900°C.

**NOTE** More options, such as temperature ramps and numeric parameters, are available (see [Oxidation on page 603](#) for details).



Sentaurus Process prints information about the progress of the oxidation step:

```

Anneal step:      Time=40min, Ramp rate=0C/s, Temperature=900.0C
Temperature > minT. Diffusion: On  Reaction: On  Assembly: Serial
SProcess parallel assembly thread count = 1
Reaction :        0s   to   0.0001s   step   :   0.0001s   temp: 900.0C
SProcess Pardiso thread count = 1
Mechanics:        0s   to   0.0001s   step   :   0.0001s   temp: 900.0C
-----
Initializing:
-----
Initialization is done.
-----
Diffusion:        0s   to   0.0001s   step (d): 0.0001s   temp: 900.0C
Reaction :        0.0001s to 0.0001712s step   : 7.125e-05s temp: 900.0C
Mechanics:        0.0001s to 0.0001712s step   : 7.125e-05s temp: 900.0C
Diffusion:        0.0001s to 0.0001712s step (d): 7.125e-05s temp: 900.0C
Reaction : 0.0001712s to 0.0002387s step   : 6.741e-05s temp: 900.0C
Mechanics: 0.0001712s to 0.0002387s step   : 6.741e-05s temp: 900.0C
Diffusion: 0.0001712s to 0.0002387s step (d): 6.741e-05s temp: 900.0C
...
Reaction :        37.29min to          40min step   :        2.714min temp: 900.0C
Mechanics:        37.29min to          40min step   :        2.714min temp: 900.0C
Diffusion:        37.29min to          40min step (d):        2.714min temp: 900.0C

Elapsed time for diffuse 41.34s
  
```

---

## Measuring Oxide Thickness

To measure the thickness of the thermally grown oxide, use:

```

select z=1
layers
  
```

The `select` command chooses a quantity for postprocessing. Selecting 1 is a way to obtain the material thicknesses.

The `layers` command prints a list of regions with their respective top and bottom coordinates. This command also gives the integral over the selected quantity in each region. Having selected 1, the integral equals the thickness:

```

{          Top          Bottom          Integral          Material }
{ -6.178796082035e-03  3.676329713272e-03  9.855125795306e-07 Oxide }
{  3.676329713272e-03  2.000000000000e+00  1.996323670287e-04 Silicon }
  
```

Here, 3.67 nm of silicon was consumed in the thermal oxidation process, and the final oxide thickness is 9.85 nm.

**NOTE** Internally, Sentaurus Process uses centimeters (cm) as the unit for length.

Selecting boron, the output of `layers` command would look like:

```
{          Top          Bottom          Integral          Material }
{ -6.178796082035e-03  3.676329713272e-03  3.012697967871e+09 Oxide }
{  3.676329713272e-03  2.000000000000e+00  1.969873116640e+11 Silicon }
```

The integral boron concentration in the silicon layer is  $1.97 \times 10^{11} \text{ cm}^{-2} = 10^{15} \text{ cm}^{-3}$  ( $2 \times 10^{14} \text{ cm}^{-3} - 3.67 \times 10^{17} \text{ cm}^{-3}$ ), which is consistent with the specified wafer doping.

---

## Depositing Screening Oxide

A faster alternative to the simulation of the oxide growth is to deposit an oxide layer and to simulate afterwards a thermal cycle to account for the thermal budget during the oxidation. This is an efficient way to emulate the creation of the screen oxide if oxidation-enhanced diffusion (OED) and the silicon consumption during the oxidation are not important.

To deposit a 10 nm layer of screening oxide and perform a thermal cycle in an inert environment, use:

```
deposit Oxide type=isotropic thickness=10.0<nm>
diffuse temperature=900<C> time=40<min>
```

The `diffuse` command assumes an inert environment if no gas flow is specified.

When you want to omit the oxide growth but OED is not negligible, specification of a reacting ambient together with the following flag:

```
pdbSetBoolean Grid Reaction.Modify.Mesh 0
```

switches on OED without applying velocities to the mesh nodes. This is often used in three dimensions.

---

## Tcl Control Statements

Tcl constructs can be freely used in the command file of Sentaurus Process. (For an introduction to Tcl, refer to the Tool Command Language module in the TCAD Sentaurus Tutorial.)

The following code segment simulates oxidation or performs a deposition depending on the value of the Tcl variable SCREEN:

```

set SCREEN Grow
if { $SCREEN == "Grow" } {
#--- Growing screening oxide -----
gas_flow name=O2_1_N2_1 pressure=1<atm> flowO2=1.2<l/min> flowN2=1.0<l/min>
diffuse temperature=900<C> time=40<min> gas_flow=O2_1_N2_1

} else {
#--- Depositing screening oxide -----
deposit Oxide type=isotropic thickness=10.0<nm>
diffuse temperature=900<C> time=40<min>
}

```

---

## Implantation

To implant arsenic with an energy of 50 keV, a dose of  $10^{14} \text{ cm}^{-2}$ , an implant tilt of  $7^\circ$ , and a wafer rotation  $0^\circ$ , use:

```

implant Arsenic energy=50<keV> dose=1e14<cm-2> tilt=7<degree> \
rotation=0<degree>

```

Sentaurus Process reports:

```

Species          = Arsenic
Dataset          = Arsenic
Energy           = 30keV
Dose (WaferDose) = 1e+14/cm2
BeamDose         = 1.0075e+14/cm2
Tilt             = 7deg
Rotation         = 0deg
Temperature      = 300.00K
Total implant time: 0.61sec

```

```

-----
Dose in:  Silicon_1      Oxide_1      Total
           Silicon      Oxide
Boron    1.9699e+11     3.0127e+09   2.0000e+11
Arsenic  9.9703e+13     2.7722e+12   1.0247e+14
Int      9.4629e+07     7.8031e+02   1.1463e+08
Vac      8.9179e+09     1.3391e+06   8.9393e+09
ICluster 2.2353e+07     9.8551e+00   4.2353e+07
O2       1.9963e-04     2.6215e+10   3.6215e+10
B4       3.0629e-10     0.0000e+00   3.0629e-10
-----

```

## 1: Getting Started

Example: 1D Simulation

The report shows that due to the nonzero tilt angle, Sentaurus Process adapted the beam dose so that the total dose deposited on the wafer is as specified. The slice angle denotes the angle between the simulation plane and the normal to the wafer flat. By default, the simulation domain is parallel to the wafer flat.

The report shows the integrated doping concentrations for each species and region.

---

## Saving the As-Implanted Profile

To save the as-implanted profile, use:

```
SetPlxList { BTotal Arsenic_Implant }
WritePlx 1DasImpl.plx
```

The `SetPlxList` command defines which solution variables are to be saved in the `.plx` file. Here, only the total (chemical) boron and the as-implanted arsenic concentrations are saved. If the `SetPlxList` command is omitted, all available solutions are saved in the `.plx` file by default.

Besides the file name, here `1DasImpl.plx`, the `WritePlx` command also accepts a material specifier, which restricts the plot to the given material. For 2D and 3D structures, the `x`-, `y`-, or `z`-coordinates of the 1D cutline must be given.

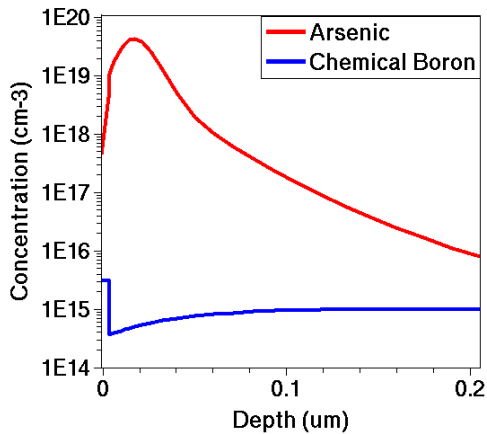


Figure 1 As-implanted arsenic profiles and background boron concentration

[Figure 1](#) shows the as-implanted arsenic profiles and the background boron concentration. The black vertical line marks the oxide–silicon interface. Note the boron depletion at the interface, which is caused by boron segregation during the oxide growth.

[Figure 1](#) is generated by loading the `.plx` file into Inspect with:

```
> inspect 1DasImpl.plx
```

---

## Thermal Annealing, Drive-in, Activation, and Screening Oxide Strip

To anneal the damage during implantation, or to drive the dopants deeper into the substrate, or to activate the implanted dopants in an inert environment, use:

```
diffuse temperature=1000<C> time=30<min>
strip Oxide

SetPlxList { BTotal BActive AsTotal AsActive }
WritePlx 1Danneal.plx
```

Here, the structure is annealed at a constant temperature of 1000°C for 30 minutes. The annealing is performed in an inert gas because no particular environment is specified.

The annealed profiles are written to the file 1Danneal.plx. The total (chemical) concentration of boron and arsenic, as well as the respective electrically active (substitutional) concentrations are saved.

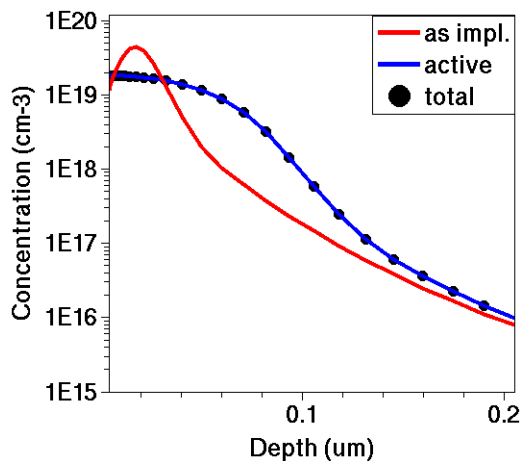


Figure 2 Comparison of as-implanted and annealed arsenic profiles

**Figure 2** compares the as-implanted and the annealed arsenic profiles. It is generated by loading both .plx files into Inspect with:

```
> inspect 1DasImpl.plx 1Danneal.plx
```

---

## Example: 2D Simulation

Many widely used process and control commands are introduced in the context of a nominal 0.18  $\mu\text{m}$  n-channel MOSFET process flow. The MOSFET structure is simulated in 2D, and the processing of the isolation is excluded. A simplified treatment is presented using only default parameters and models.

---

### Defining Initial Structure and Mesh Refinement

The command `math coord.ucs` is used to switch on the unified coordinate system (UCS). Using the UCS is recommended because the default behavior is to rotate the structure when saving and loading to the DF-ISE coordinate system. With the UCS, the structure is not rotated. Therefore, the axes in Tecplot SV match the axes in the Sentaurus Process command file. It is recommended to insert this as the first command in the command file.

The `line` command is used to:

- Define the initial size of the structure.
- Subdivide the structure.

Mesh refinement starts from the user-defined subdivisions; therefore, the specification of lines helps to compartmentalize mesh refinement. In turn, compartmentalization of the mesh prevents moving boundaries, and therefore, moving mesh refinement from affecting geometrically static areas. Whenever mesh lines move, interpolation must be used to obtain new field values, such as dopant concentrations, and this introduces errors in the simulation.

During the polysilicon reoxidation step, the oxide-silicon and oxide-polysilicon boundaries move, and this interface movement may cause mesh lines to move as shown in the following example:

```
line x location= 0.0
line x location= 3.0<nm>    ;# just deeper than reox in silicon
line x location= 10.0<um>
line y location= 0.0
line y location= 85.0<nm>   ;# just deeper than reox in poly
line y location= 0.4<um>
```

To minimize this effect, the silicon and polysilicon regions are isolated from the moving interfaces by introducing lines immediately inside the final oxide depth in both regions as shown in Figure 3.

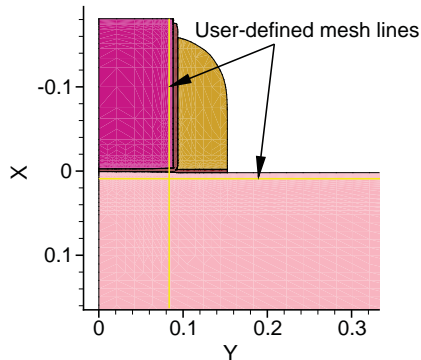


Figure 3 Final structure showing placement of user-defined lines: these lines are used to isolate silicon and polysilicon regions from boundary movement at the oxide interfaces

Sentaurus Process uses coordinate systems such that 1D, 2D, and 3D simulations are consistent. Independent of the current simulation dimension, the positive x is into the wafer; y is positive to the right, and z is positive out of the page.

**NOTE** By default, the simulation dimension is promoted only when necessary. Therefore, until a mask is introduced, the simulation remains in 1D. Similarly, when going from 2D to 3D, until a 3D mask is introduced (one that varies in the z-direction in the defined simulation domain), the simulation remains in 2D.

The initial simulation domain is defined with the `region` command. Many, if not most, simulations start with a block of silicon. The shorthand for this situation is to define a region of silicon that spans all defined lines:

```
region silicon
```

The `region` command also can be used to define a new region between specified lines. To limit the size of the region to be less than all defined lines, the lines must be given a tag with the `tag` parameter. These tags are used in the `region` command with the `xlo`, `xhi`, `ylo`, `yhi`, `zlo`, and `zhi` parameters.

Finally, the initial mesh and background doping is specified using the `init` command as follows:

```
init concentration=1.0e+15<cm-3> field=Phosphorus wafer.orient=100
```

Here, an n-doped substrate with a phosphorus concentration of  $10^{15} \text{ cm}^{-3}$  is used. The wafer orientation is set to 100, which is the default.

## 1: Getting Started

Example: 2D Simulation

Usually, localized refinement is defined by introducing refinement boxes. This strategy prevents excessive mesh that can result if mesh refinement is based solely on the `line` command (with the `spacing` parameter). Lines specified with the `line` command run the entire length (or breadth or depth) of the structure.

The refinement boxes can be inserted at any time during the simulation. The simplest form of the refinement box, used in this example, consists of minimum and maximum coordinates where the refinement box is valid and local maximum mesh spacing in the x-, y- and z-directions. A refinement box specified for a 2D simulation will be applied to 1D if it is valid for  $y = 0.0$ . Similarly a 3D refinement box will be applied if it covers  $z = 0.0$ .

The following refinement boxes specify refinement only in the x-direction for the 1D part of the simulation:

```
#--- Refinement in vertical direction -----
refinebox clear ;# remove all default refinement
refinebox min = 0          max = 50.0<nm> xrefine = {2.0<nm> 10.0<nm>}
refinebox min = 50.0<nm> max = 2.0<um> xrefine = {10.0<nm> 0.1<um> 0.2<um>}
refinebox min = 2.0<um> max = 10.0<um> xrefine = {0.2<um> 2.0<um>}
```

The other type of refinement box used in this example is the interface refinement type. Interface refinement is a graded refinement that is refined near an interface in the perpendicular direction and relaxed away from the interface. Using the `refinebox` command, you can specify interface refinement using the `interface.materials` or `interface.mat.pairs` parameter:

- Use `interface.materials` to indicate refinement will occur at all interfaces to the specified materials.
- Use `interface.mat.pairs` to choose interface refinement only at specific material interfaces.

```
#--- Interface refinement -----
refinebox interface.materials = { PolySilicon Silicon }
```

For more details on mesh refinement, see [Mesh Refinement on page 674](#).

---

## Implanting Boron

First, three sets of boron implants are performed:

```
implant Boron dose=2.0e13<cm-2> energy=200<keV> tilt=0 rotation=0
implant Boron dose=1.0e13<cm-2> energy= 80<keV> tilt=0 rotation=0
implant Boron dose=2.0e12<cm-2> energy= 25<keV> tilt=0 rotation=0
```



The first high-energy implant creates the p-well, the second medium-energy implant defines a retrograde boron profile to prevent punch-through, and the third low-energy implant is for a  $V_t$  adjustment.

---

## Growing Gate Oxide

The gate oxide is grown at a temperature of 850°C for 10 minutes in pure oxygen using:

```
diffuse temperature=850<C> time=10.0<min> O2
select z=Boron
layers
```

The `layers` command shows that the thickness of the grown oxide is 3.2 nm:

```
{           Top           Bottom           Integral           Material }
{ -2.500551327519e-03  7.862861879285e-04  1.247399405710e+10 Oxide }
{  7.862861879285e-04  1.000000000000e+01  3.197435354292e+13 Silicon }
```

For details, see [Measuring Oxide Thickness on page 7](#).

---

## Defining Polysilicon Gate

The polysilicon gate is created using:

```
deposit poly type=isotropic thickness=0.18<um>
mask name=gate_mask left=-1 right=90<nm>

etch poly type=anisotropic thickness=0.2<um> mask=gate_mask
etch oxide type=anisotropic thickness=0.1<um>
```

First, 0.18  $\mu\text{m}$  of polysilicon is deposited over the entire structure. The keyword `type=isotropic` means that the layer is grown equally in all directions, but since the simulation is in 1D, it would be the same as `type=anisotropic`.

A mask is defined to protect the gate area with the `mask` command. In this project, only half of the transistor is simulated. Therefore, the left edge of the gate mask is unimportant. In general, you should run the mask over the sides of the simulation to prevent round-off errors that could prevent complete mask coverage. The name `gate_mask` is associated with this mask for later reference.

The first `etch` command refers to the previously defined mask and, therefore, only the exposed part of the polysilicon is etched. The requested etching depth (0.2  $\mu\text{m}$ ) is larger than the deposited layer. This overetching ensures that no residual islands remain. The etching is

## 1: Getting Started

Example: 2D Simulation

specified to be anisotropic, that is, the applied mask is transferred straight down, without any undercut.

The second `etch` statement does not refer to any masks. However, the polysilicon naturally acts as a mask for this selective etching process. Again, a considerable overetching is specified.

## Working with Masks

Masks must be defined before they are used. For example, `ex_mask` blocks processing from  $-1$  to  $2\ \mu\text{m}$  and from  $4$  to  $20\ \mu\text{m}$ :

```
mask clear
mask name=ex_mask segments = { -1.0<um> 2.0<um> 4.0<um> 20.0<um> }
```

Masks can be inverted using the negative option. For example, `etch_mask` prevents processing from  $2$  to  $4\ \mu\text{m}$ :

```
mask clear
mask name=etch_mask segments = { -1.0<um> 2.0<um> 4.0<um> 20.0<um> } negative
```

Commands that use masking include `etch`, `photo`, and `deposit`.

---

## Polysilicon Reoxidation

To release stresses, a thin oxide layer is grown on the polysilicon before the spacer formation:

```
diffuse temperature=900<C> time=10.0<min> O2 pressure=0.5<atm>
```

In this step, the  $1\ \text{atm}$  default is overwritten by explicitly specifying a pressure of  $0.5\ \text{atm}$ . In all diffusion steps, Sentaurus Process automatically deposits a thin native oxide layer before starting oxidation. This layer is always present on silicon exposed to air and quickly forms on newly created interfaces.

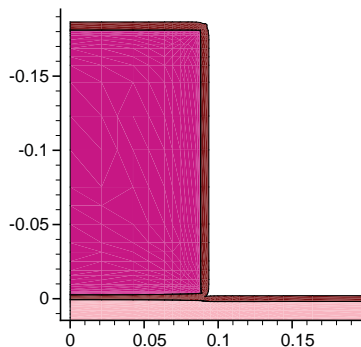


Figure 4 Polysilicon reoxidation

During oxidation, mesh movement is controlled by the TSUPREM-4 mesh library in 2D. In 1D and 3D, it is controlled by an internal moving-boundary mesh algorithm. Both of these moving-boundary algorithms perform local atomic mesh operations (element removal, edge splitting, edge flipping, and so on) which leave the rest of the mesh untouched. Mesh points are moved with the material to maintain dopant dose conservation and the dopant segregation condition at oxide–silicon and oxide–polysilicon interfaces. Figure 5 shows a close-up of the mesh after the polysilicon reoxidation step has been performed. Note that the mesh in the brown oxide layer follows the growth contours.

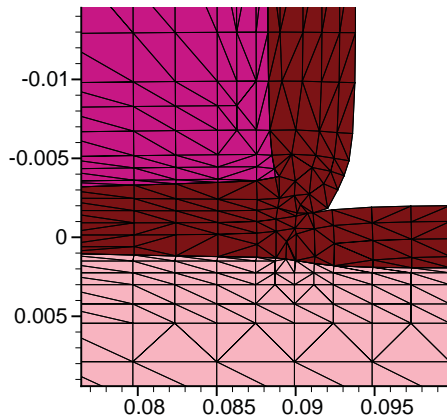


Figure 5 Mesh in thin oxide layer and in adjacent polysilicon and silicon

---

## Saving Snapshots

To save a snapshot of the current structure, the `struct` command is used. For example:

```
struct tdr= NMOS4
```

The keyword `tdr` specifies that the snapshot is saved in the TDR file format. The argument specifies the stem used for the file name. Here, the file `NMOS4_fps.tdr` is created. The figures in this section were generated from such snapshots.

For more information about the TDR format, refer to the *Sentaurus Data Explorer User Guide*.

---

## Remeshing for LDD and Halo Implants

Next, the LDD and halo implants are performed. Before that, however, the mesh must be refined to properly capture the implant. The previously defined refinement boxes specified vertical refinement with the `xrefine` parameter.

## 1: Getting Started

Example: 2D Simulation

Now, lateral refinement is required to resolve the source and drain extensions (also known as low-doped drain (LDD)) as well as the halo implants. This is accomplished by introducing a new `refinebox` command that specifies:

- Lateral refinement using the `yrefine` parameter.
- Additional vertical refinement using the `xrefine` parameter.

**NOTE** When specifying multiple overlapping refinement, the most refined specification (smallest edge length) wins.

```
refinebox silicon min= {0.0 0.045<um>} max= {0.1<um> 0.125<um>} \  
  xrefine= 0.01<um> yrefine= 0.01<um>  
grid remesh
```

The `min` and `max` keywords take x-, y-, and z-coordinates. Not all coordinates must be specified. For example, if only one number is given for minimum, it means that refinement applies to all y- and z-coordinates less than the `max` coordinate.

**NOTE** The `refinebox` command only specifies a refinement criterion, but the mesh is not changed. The `grid remesh` command forces a remesh.

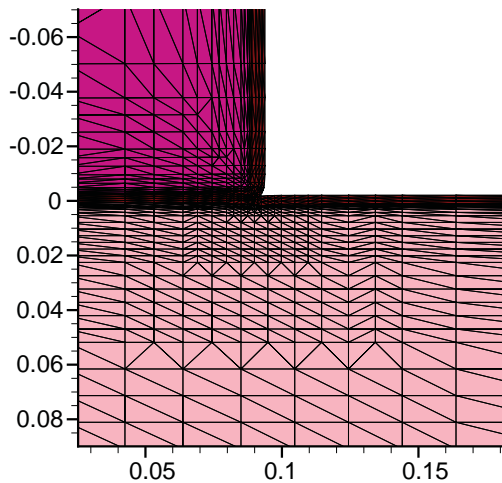


Figure 6 A combination of overlapping refinement boxes is used to define a finer mesh for LDD and halo; if multiple criteria overlap, the finest mesh specification wins

---

## Implanting LDD and Halo

The LDD and halo implants are performed using:

```
#--- LDD implantation -----  
implant Arsenic dose=4e14<cm-2> energy=10<keV> tilt=0 rotation=0  
  
#--- Halo implantation: Quad HALO implants -----  
implant Boron dose=1.0e13<cm-2> energy=20<keV> tilt=30<degree> \  
    rotation=0 mult.rot=4  
  
diffuse temperature=1050<C> time=5.0<s>
```

The LDD implant uses a high dose of  $4 \times 10^{14} \text{ cm}^{-2}$  and a relatively low energy of 10 keV. The halo is created by a quad implant using the `mult.rot` parameter, that is, the implant is performed in four steps. Each step is separated in rotation by  $360/4 = 90^\circ$  starting with the specified rotation of 0. This is performed to ensure that the boron penetrates well into the channel at the tips of the source-drain extensions. Again, a relatively high total dose of  $1 \times 10^{14} \text{ cm}^{-2}$  is used.

The implants are activated with a short thermal cycle or rapid thermal anneal (RTA).

---

## Forming Nitride Spacers

The nitride spacers are formed using:

```
#--- Nitride spacer -----  
deposit nitride type=isotropic thickness=60<nm>  
etch nitride type=anisotropic thickness=84<nm> isotropic.overetch=0.01  
etch oxide type=anisotropic thickness=10<nm>
```

First, a uniform, 60-nm thick layer of nitride is deposited over the entire structure. The keyword `type=isotropic` ensures that the growth rate of the layer is the same in all directions. Then, the nitride is etched again; however, now an anisotropic etching is used. This means that the nitride deposited on the vertical sides of the gate is not fully removed and can serve as masks for the source/drain implants. For this step, an isotropic overetch is specified. Specifying a fraction of the etch thickness, 0.01 implies a 1% isotropic component. This is needed because the oxide formed during poly oxidation has a nonvertical sidewall. Without the small `isotropic.overetch`, a small nitride residual would remain. Finally, the thin oxide layer grown during the poly reoxidation step is removed.

---

## Remeshing for Source/Drain Implants

Next the source/drain implants are performed. However, before that, the mesh is refined again.

```
refinebox silicon min= {0.04<um> 0.11<um>} max= {0.18<um> 0.4<um>} \  
  xrefine= 0.01<um> yrefine= {0.02<um> 0.05<um>} \  
grid remesh
```

This refinement box ensures that the grid is fine enough in the vertical direction to resolve the junction depth.

---

## Implanting Source/Drain

The source and drain regions are created using:

```
implant Arsenic dose=5e15<cm-2> energy=40<keV> tilt=7<degree> \  
  rotation=-90<degree> \  
diffuse temperature=1050<C> time=10.0<s>
```

To ensure a low resistivity of the source and drain regions, this implant step uses a very high dose of  $5 \times 10^{15} \text{ cm}^{-2}$ . A tilt of  $7^\circ$  is used to reduce channeling and a rotation of  $-90^\circ$  ensures that the plane of incident is parallel to the gate stack, such that the  $7^\circ$  tilt angle does not lead to asymmetry between the source and drain.

---

## Transferring to Device Simulation

To transfer from process simulation to device simulation, the possible methods are:

- The preferred and most common method is to use the internal capabilities of Sentaurus Process.
- An older method involves using Sentaurus Structure Editor and Sentaurus Mesh to add contacts to the process structure and to generate a new mesh.

In both cases:

- The structure bottom is cropped.
- The full transistor is created by reflecting about the symmetry plane.
- A new mesh is generated that is better optimized for device simulation.

If the remeshing for device simulations is performed internally, the file `NMOS_fps.tdr` can be loaded directly into Sentaurus Device.

To use the external technique after truncation and reflection, the structure is saved using:

```
struct smesh=NMOS
```

This command saves the structure and data in the file `NMOS_fps.tdr`, and the boundary in the file `NMOS_bnd.tdr`. These files can serve as input to Sentaurus Structure Editor and Sentaurus Mesh.

## Remeshing for Device Simulation

In the following example, the internal technique is used to produce a structure and mesh appropriate for device simulation. First, the structure bottom is truncated; then a new mesh strategy is introduced:

```
--Remove bottom of structure-----
transform cut location= 1.00 down

--Change refinement strategy and remesh-----
refinebox clear
line clear

pdbSet Grid Adaptive 1
pdbSet Grid AdaptiveField Refine.Abs.Error 1e37
pdbSet Grid AdaptiveField Refine.Rel.Error 1e10
pdbSet Grid AdaptiveField Refine.Target.Length 100.0
pdbSet Grid SnMesh DelaunayType boxmethod

refinebox name= Global refine.min.edge= {0.01 0.01} \
  refine.max.edge= {0.1 0.1} refine.fields= { NetActive } \
  def.max.asinhdiff= 0.5 adaptive

refinebox name= SiGOX min.normal.size= 0.2<nm> normal.growth.ratio= 1.4 \
  max.lateral.size= 5.0<nm> min= {-0.01 -0.1} max= {0.01 0.1} \
  interface.materials= {Silicon}

refinebox name= GDpn1 min= {0.0 0.04} max= {0.06 0.1} xrefine= 0.005 \
  yrefine= 0.005 silicon

refinebox name= TopActive min= {0.0 0.0} max= {0.3 0.4} \
  refine.min.edge= {0.02 0.02} refine.max.edge= {0.05 0.05} \
  refine.fields= { NetActive } def.max.asinhdiff= 0.5 \
  adaptive silicon
```

The new mesh strategy uses a combination of interface refinement, fixed boxwise refinement, and adaptive refinement on dopants.

## Contacts

Next, contacts are added to the structure using the `contact` command. These contacts are added to structure files upon writing. They are not present in the internal Sentaurus Process structure, but are added only as required when writing the structure. There are two types of contact specification:

- **Box:** For these contacts, you specify a box and a material, and all interfaces of that material that are inside the box become the contact.
- **Point:** For this contact, you specify a point inside a chosen region. The chosen region is removed, and all interfaces between the chosen region and bulk materials become part of the contact.

In the following example, only box-type contacts are used:

```
contact name= "substrate" bottom Silicon

contact name= "source" box Silicon adjacent.material=Gas \
  xlo= 0.0 xhi= 0.005 ylo= -0.4 yhi= -0.2

#--- Contacts -----
contact name= "substrate" bottom Silicon

contact name= "source" box Silicon adjacent.material= Gas \
  xlo= 0.0 xhi= 0.005 ylo= -0.4 yhi= -0.2

contact name= "drain" box Silicon adjacent.material= Gas \
  xlo= 0.0 xhi= 0.005 ylo= 0.2 yhi= 0.4

contact name= "gate" box PolySilicon xlo= -0.181 xhi= -0.05 \
  ylo= -0.088 yhi= 0.088
```

## Saving the Full Structure

To save the full structure, use:

```
struct smesh=NMOS
```



The file `NMOS_fps.tdr` is created with contacts and can be loaded into Sentaurus Device to obtain device electrical characteristics.

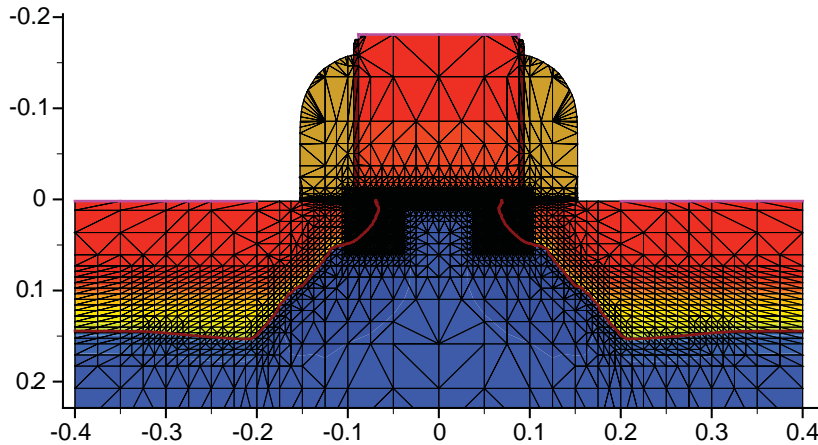


Figure 7 Final structure showing contacts and refinement appropriate for device simulation

---

## Extracting 1D Profiles

You can save 1D profiles at any point in the process flow using:

```
SetPlxList {BTotal NetActive}  
WritePlx NMOS_channel.plx y=0.0 silicon
```

as well as:

```
struct tdr=NMOS_channel.tdr y=0.0
```

For details, see [Saving the As-Implanted Profile on page 10](#).

---

## Adaptive Meshing: 2D npn Vertical BJT

A simple 2D npn vertical bipolar transistor example is introduced to show how the adaptive-meshing capabilities in Sentaurus Process can be used to ease mesh setup and allow for mesh evolution during dopant diffusion. For examples, see [2D npn Vertical Bipolar on page 38](#).

For all the applications involving long thermal diffusion steps or simulations of relatively large structures (in which doping profiles may evolve greatly), using static mesh criteria is impracticable because it requires using a fine mesh in many parts of the simulation domain. Moreover, the placement of the refinement boxes is not straightforward because often the location of gradients and junctions at the end of the thermal steps is not precisely known. For such purposes, adaptive meshing could be used. Using this feature, you only have to define

## 1: Getting Started

### Adaptive Meshing: 2D npn Vertical BJT

some refinement criteria, more or less stringent depending on the level of accuracy required. The meshing engine checks the mesh and decides automatically where, when, and if the mesh needs to be refined.

---

## Overview

Adaptive meshing can be switched on globally with:

```
pdbSet Grid Adaptive 1
```

which creates a default adaptive box covering the entire structure.

Adaptive refinement parameters can be set in the following ways:

- *Fieldwise* in the PDB with the `pdbSet` command
- *Boxwise* as parameters of the `refinebox` command
- *Materialwise*, specifying a material in a box definition
- *Regionwise*, specifying a region in a box definition

To prevent the number of mesh points from growing too large, switch off the `keep.lines` option (which is switched on by default in silicon) when using adaptive meshing:

```
refinebox !keep.lines
```

Many different refinement criteria have been implemented in Sentaurus Process for flexibility in handling different types of field and structure. For a complete list and detailed descriptions of the refinement criteria, see [Adaptive Refinement Criteria on page 680](#).

The criteria in the following example are the most commonly used and are referred to as *relative difference* and *local dose error*. Each computes the so-called desired edge length (DEL), which is defined formally as:

$$\text{DEL} = \min (l_{12} * \text{MaxError}/\text{Error})$$

where  $l_{12}$  is the length of the edge between two mesh points 1 and 2. `Error` (computed internally) is the error between points 1 and 2, and `MaxError` (set by users) is the maximum allowable error. The right-hand side of the expression is computed over all the fields that can be refined (by default, all the solution variables): the minimum value is the `DEL` for the corresponding criterion. The expression for `Error` and the name and the meaning of `MaxError` vary from criterion to criterion. For the relative difference criterion, these quantities have the form:

$$\begin{aligned} \text{Error} &= 2 * |C_1 - C_2| / (C_1 + C_2 + \text{alpha}) \\ \text{MaxError} &= R_f \end{aligned}$$

where  $C_1$  and  $C_2$  are the concentration of the field in points 1 and 2, respectively,  $R_f$  is the relative error that sets the maximum-allowed change of the field across an edge, and  $\alpha$  is the absolute error, a type of cutoff threshold below which refinement is smoothed out. They can be set in the PDB as follows:

```
pdbSet Grid Boron Refine.Abs.Error 1e15
pdbSet Grid Boron Refine.Rel.Error 0.5
```

or in the `refinebox` commands as:

```
refinebox name=Active refine.fields= {Boron Arsenic} \
  rel.error= {Boron=0.5 Arsenic=0.5} abs.error= {Boron=2e15 Arsenic=1e16} \
  Adaptive min= {-1.0 -0.1} max= {2.0 16.0}
```

For the definition of `Error` and `MaxError` for the local dose error criterion, see [Local Dose Error Criteria on page 683](#).

All the edges are compared to `DEL` to check the percentage of long edges by using the following additional parameter:

```
pdbSetDoubleArray Grid Refine.Factor {X 2.0 Y 2.0}
```

These coefficients can be set directionwise and act in the following way: An edge is defined as *long* when it is larger than `Refine.Factor*DEL` for at least one of the selected refinement criteria. When the percentage of long edges is larger than certain values, adaptive refinement is actually triggered. This value can be set as:

```
pdbSet Grid Refine.Percent 0.01
```

When adaptive meshing is switched on, it automatically affects refinement whenever a mesh is generated (such as after geometry-changing operations). During the `diffuse` command, the mesh is checked after a certain number of steps that can be separately set depending on the nature of the diffusion step:

```
pdbSet Diffuse Compute.Regrid.Steps 10 ;# during inert annealings
pdbSet Diffuse Growth.Regrid.Steps -1 ;# during oxidation and silicidation
pdbSet Diffuse Epi.Regrid.Steps -1 ;# during epitaxy
```

When the number of long edges is larger than `Refine.Percent`, remeshing is performed. The mesh quality check can be omitted by setting:

```
pdbSet Grid Refinement.Check 0
```

which can save some CPU time when performing simulations on large meshes, where the mesh checking is time consuming.

## 1: Getting Started

### Adaptive Meshing: 2D npn Vertical BJT

**NOTE** Formally, the adaptive-meshing feature consists of field-based and implant-based adaptation. There is a small difference in the way refinement criteria are applied. For details, see [Adaptive Meshing during Implantation on page 688](#) and [Interval Refinement on page 684](#). However, as the two modules use the same parameters, you do not need to define them twice.

**NOTE** Adaptive-meshing syntax to set up parameters is the same in any dimension.

The relative error criterion is effective in refining doping profiles in steep gradient regions. In the vicinity of maxima and minima, the profiles are almost flat and some loss of accuracy may occur there. Further reduction of `Rel.Error` would increase significantly the number of points in the steep slope with negligible improvements at the peaks. In that case, the max dose loss criterion can be used more effectively. This explains why the combination of these two criteria provides an optimum adaptive-remeshing strategy.

---

## Defining Initial Structure

The command `math coord.ucs` is used to switch on the unified coordinate system (UCS). Using the UCS is recommended because the default behavior is to rotate the structure when saving and loading to the DF-ISE coordinate system. With the UCS, the structure is not rotated. Therefore, the axes in Tecplot SV match the axes in the Sentaurus Process command file. It is recommended to insert this as the first command in the command file.

The `line` commands are used to compartmentalize the structure according to the meshing strategy described in the previous example:

```
line x loc= 2.0<um>
line x loc= 4.0<um>   tag=SubTop
line x loc= 6.0<um>
line x loc= 10.0<um>  tag=SubBottom
line y loc= 0.0<um>   tag=SubLeft
line y loc=1.5<um>
line y loc=2.5<um>
line y loc=8<um>
line y loc=13<um>
line y loc=22<um>
line y loc=24<um>
line y loc=30.0<um>  tag=SubRight
```

Along the x-axis, few lines are specified: the two tagged ones are needed to define the initial silicon substrate. The other two lines are defined to have uniform spacing within the box defined to refine the buried layer. Along the y-axis, more lines are defined because a coarse

initial mesh would degrade the quality of the mesh resulting from adaptation during implantation. These lines are set corresponding to the mask edges: This information is usually known to users, especially if the simulation starts from a layout, and the process flow is set up in Ligament.

---

## Adaptive Meshing Settings

As previously mentioned, adaptive parameters can be set in different ways, which lead to different refinement strategies:

```
pdbSet Grid Adaptive 1
pdbSet Grid AdaptiveField Refine.Abs.Error 1e25
pdbSet Grid AdaptiveField Refine.Rel.Error 2.0

pdbSet Grid Damage Refine.Min.Value 1e25
pdbSet Grid Damage Refine.Max.Value 1e25
pdbSet Grid Damage Refine.Target.Length 1
```

Here the following strategy is used:

- The default relative difference-type refinement is switched off by setting high values for absolute and relative errors and for the interval damage refinement.
- When parameters are set for `AdaptiveField`, they are applied to all the existing fields that can be refined.
- Actual refinement will be then controlled in specific regions by using `refineboxes`.

Three refinement boxes are defined as the structure and the process flow clearly identifies three main significant areas: buried layer, collector region, and base-emitter region:

```
refinebox name=BL refine.fields= {Antimony Phosphorus} \
  rel.error= {Antimony=0.6 Phosphorus=0.6} \
  abs.error= {Antimony=1e16 Phosphorus=1e16} Adaptive min= {2.0 -0.1} \
  max= {10.1 30.1} refine.min.edge= {0.2 0.4} max.dose.error= {Antimony=1e8} \
```

The `min` and `max` parameters set an `xy` pair of coordinates to define the extent of the box. The keyword `all` means that refinement must be applied to all materials. When using a material name, refinement is applied to the specified material only.

**NOTE** More than one adaptive type can be specified in the same box. In the `BL` box, the relative difference and local dose loss criteria are selected by specifying the parameters `rel.error` or `abs.error` and `max.dose.error`, respectively.

## 1: Getting Started

### Adaptive Meshing: 2D npn Vertical BJT

```
refinebox name=Sinker refine.fields= {Phosphorus Arsenic} \  
  rel.error= {Phosphorus=0.5 Arsenic=0.5} \  
  abs.error= {Phosphorus=5e15 Arsenic=1e16} Adaptive min= {-1.0 16} \  
  max= {2.0 30.1} refine.min.edge= {0.1 0.2}  
  
refinebox name=Active refine.fields= {Boron Arsenic} \  
  rel.error= {Boron=0.5 Arsenic=0.5} abs.error= {Boron=2e15 Arsenic=1e16} \  
  Adaptive min= {-1.0 -0.1} max= {2.0 16.0} refine.min.edge= {0.025 0.05} \  

```

The `BL` box is defined to refine the buried layer: a high level of accuracy is not required here and the values are more relaxed than in the other boxes. The `refine.min.edge` parameter adds the additional directionwise constraint not to refine edges below the specified values (units in micrometers).

The `Sinker` box is defined to refine the n-doped collector region, which contacts the buried layer. More restrictive values are used in it.

The `Active` box is used to refine the base-emitter region. Higher accuracy is required here to properly catch the base length, which all the main electrical parameters of the device are a function of:

```
pdbSet Diffuse Compute.Regrid.Steps 10  
pdbSet Grid Refine.Percent 0.01
```

According to these last two commands, the mesh is checked every 10 diffusion steps in inert annealings, and remeshing is performed if there are more than 0.01% of long edges.

---

## Buried Layer

The buried layer is obtained with high-energy and high-dose antimony implantation:

```
deposit material= {Oxide} type=isotropic time=1 rate= {0.025}  
implant Antimony dose=1.5e15<cm-2> energy=100<keV>  
etch material= {Oxide} type=anisotropic time=1 rate= {0.03}
```

Before the implantation, 25 nm of a screening oxide is deposited. After the implantation, the oxide is etched to clean the surface and to prepare it for the subsequent epi step.

---

## Epi Layer

For speed and simplicity, an epitaxial regrowth step is not performed here. Instead, a simpler deposition of a silicon layer with  $1 \times 10^{15} \text{ cm}^{-3}$  arsenic concentration is followed by a diffusion step:

```
deposit material= {Silicon} type=isotropic time=1 rate= {4.0} Arsenic \  
  concentration=1e15<cm-3>  
diffuse temp=1100<C> time=60<min> maxstep=4<min>
```

The maximum diffusion step is limited to 4 minutes to avoid having too much diffusion between two subsequent adaptive remeshing steps. An alternative would be to reduce `Compute.Regrid.Steps`, but this would lead to numerous remeshings at the beginning of the annealing when the time step is small.

The following sections describe the process steps to create sinker, base, and emitter regions. At the end of each group of steps, results are saved in TDR files.

---

## Sinker Region

This is the beginning of the 2D simulation. A 5-nm screening oxide is deposited before the phosphorus implantation to contact the buried layer. The `Sinker` mask protects the silicon area where the base will be created. The `Photo` command is used to deposit the photoresist (mask definition not shown here). The subsequent annealing is long (5 hours). For this reason, the maximum time step is allowed to increase up to 8 minutes.

[Figure 8 on page 30](#) shows the doping concentration distribution at this point of the simulation:

```
deposit material= {Oxide} type=isotropic time=1 rate= {0.05}  
photo mask=Sinker thickness=1  
  
implant Phosphorus dose=5e15<cm-2> energy=200<keV>  
strip Resist  
diffuse temp=1100<C> time=5<hr> maxstep=8<min>  
  
struct tdr=vert_npn2
```

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Adaptive Meshing: 2D npn Vertical BJT

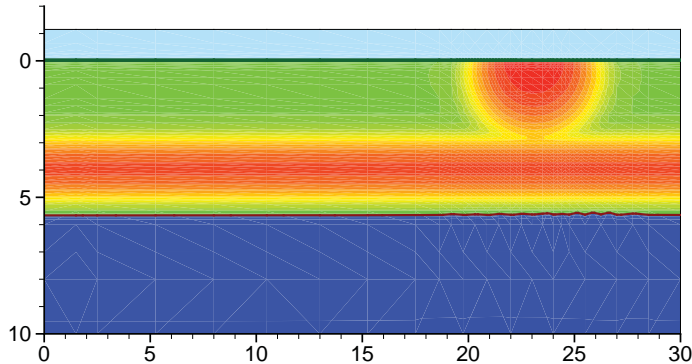


Figure 8 Doping concentration after phosphorus implantation and diffusion to contact antimony buried layer

---

## Base Region

The p-doped base region is created with a  $1 \times 10^{14} \text{ cm}^{-2}$  dose of implanted boron followed by a 35-minute inert annealing:

```
photo mask=Base thickness=1
implant Boron dose=1e14<cm-2> energy=50<keV>
strip Resist
diffuse temp=1100<C> time=35<min> maxstep=4<min>

struct tdr=vert_npn3
```

---

## Emitter Region

The highly n-doped emitter region is created with a  $5 \times 10^{15} \text{ cm}^{-2}$  dose of implanted arsenic followed by a 25-minute inert annealing. Emitter mask is designed such that arsenic is implanted also in the sinker region to increase the doping concentration at the collector contact. In addition to a TDR file, 1D profiles are extracted. [Figure 9 on page 31](#) shows the final doping distribution:

```
photo mask=Emitter thickness=1
implant Arsenic dose=5e15<cm-2> energy=55<keV> tilt=7 rotation=0
strip Resist
diffuse temp=1100<C> time=25<min> maxstep=4<min>

struct tdr=vert_npn4
```



```
SetPlxList {BTotal SbTotal AsTotal PTotal}  
WritePlx Final.plx y=5.0  
WritePlx Sinkers.plx y=23.0
```

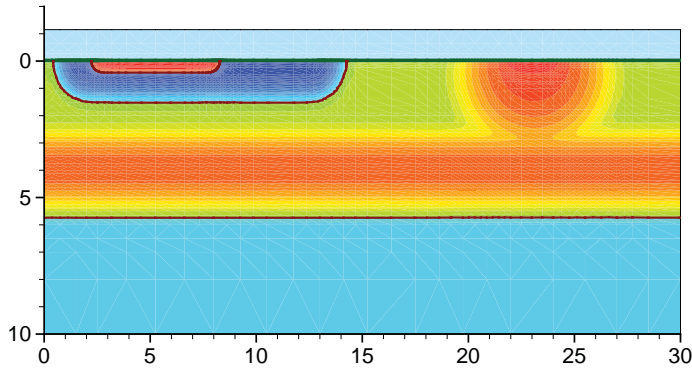


Figure 9 Final doping distribution

## Backend

The real backend steps are not simulated here. A sequence of masked etching and deposition steps are used to define emitter, base, and collector contacts:

```
etch material= {Oxide} type=anisotropic time=1 rate= {0.055} mask=Contact  
deposit material= {Aluminum} type=isotropic time=1 rate= {1.0}  
etch material= {Aluminum} type=anisotropic time=1 rate= {1.1} mask=Metal  
struct tdr=vert_npn5
```

Figure 10 shows some details of the final mesh.

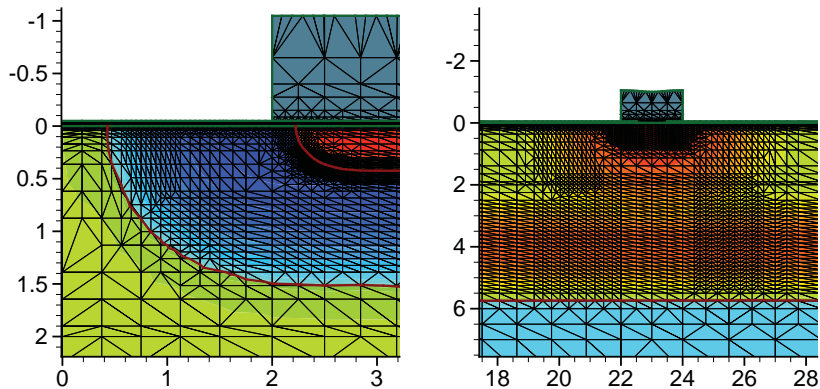


Figure 10 Details of final mesh: (left) the emitter–base region and (right) the buried layer with collector contact

## 1: Getting Started

### Full-Text Versions of Examples

The relative difference criterion refines the doping profiles, not the junctions. Obviously, if the profiles are reproduced correctly, the junctions also will be in the right place. To obtain a junction-like refinement with the relative difference criterion, set `abs.error` close to the doping level of the less-doped side of the junction. A more effective way is to select `NetDoping` as the field to be refined and apply to it the inverse hyperbolic sine (`asinh`) difference criterion (for details, see [Inverse Hyperbolic Sine \(asinh\) Difference Criteria on page 682](#)).

---

## Full-Text Versions of Examples

The following full-text versions of the examples allow convenient electronic copying of text into Sentaurus Process command files.

---

### 1D NMOS

```
# 1D Grid definition
#-----

line x location=0.0      spacing= 1<nm> tag=SiTop
line x location= 10<nm> spacing= 2<nm>
line x location= 50<nm> spacing= 10<nm>
line x location=300<nm> spacing= 20<nm>
line x location=0.5<um> spacing= 50<nm>
line x location=2.0<um> spacing=0.2<um> tag=SiBottom

# Initial simulation domain
#-----

region Silicon xlo=SiTop xhi=SiBottom

# Initialize the simulation
#-----

init concentration=1.0e15<cm-3> field=Boron

# Settings for automatic meshing in newly generated layers
#-----

mgoals min.normal.size=3<nm> max.lateral.size=0.2<um> normal.growth.ratio=1.4

set SCREEN Grow
if { $SCREEN == "Grow" } {
# Growing screening oxide
#-----
```

```
gas_flow name=O2_1_N2_1 pressure=1<atm> flowO2=1.2<l/min> flowN2=1.0<l/min>
diffuse temperature=900<C> time=40<min> gas_flow=O2_1_N2_1

# Measuring the oxide thickness
#-----
select z=1
layers

} else {
# Depositing screening oxide
#-----
deposit material= {Oxide} type=isotropic time=1.0 rate= {0.01}
diffuse temperature=900<C> time=40<min>
}

# Implanting Arsenic
#-----

implant Arsenic energy=30<keV> dose=1e14<cm-2> tilt=7<degree> \
rotation=0<degree>
# Plotting out the "as implanted" profile
#-----

SetPlxList { BTotal Arsenic_Implant }
WritePlx 1DasImpl.plx

# Thermal annealing
#-----

diffuse temperature=1000<C> time=30<min>
strip Oxide
SetPlxList { BTotal BActive AsTotal AsActive }
WritePlx 1Danneal.plx
```

---

## 2D NMOS

```
#-----
# 2D nMOSFET (0.18um technology)
#-----

math coord.ucs

pdbSet Oxide Grid perp.add.dist 1e-7

#--- Specify lines for outer boundary and to separate moving boundaries
# from the rest of the structure-----
```

## 1: Getting Started

### Full-Text Versions of Examples

```
line x location= 0.0
line x location= 3.0<nm> ;# just deeper than reox in silicon
line x location= 10.0<um>
line y location= 0.0
line y location= 85.0<nm> ;# just deeper than reox in poly
line y location= 0.4<um>

#--- Silicon substrate definition -----
region silicon

#--- Initialize the simulation -----
init concentration=1.0e+15<cm-3> field=Phosphorus

#--- Refinement in vertical direction -----
refinebox clear
refinebox min = 0 max = 50.0<nm> xrefine = {2.0<nm> 10.0<nm>}
refinebox min = 50.0<nm> max = 2.0<um> xrefine = {10.0<nm> 0.1<um> 0.2<um>}
refinebox min = 2.0<um> max = 10.0<um> xrefine = {0.2<um> 2.0<um>}

#--- Interface refinement -----
refinebox interface.materials = { PolySilicon Silicon }

#--- Sentaurus Mesh settings for automatic meshing in newly generated layers -
pdbSet Grid SnMesh min.normal.size 1.0e-3 ;# in micrometers
pdbSet Grid SnMesh normal.growth.ratio.2d 1.4 ;# used in 1D and 2D

#--- Create starting mesh from lines and refinement
grid remesh

#--- p-well, anti-punchthrough & Vt adjustment implants -----
implant Boron dose=2.0e13<cm-2> energy=200<keV> tilt=0 rotation=0
implant Boron dose=1.0e13<cm-2> energy= 80<keV> tilt=0 rotation=0
implant Boron dose=2.0e12<cm-2> energy= 25<keV> tilt=0 rotation=0

#--- p-well: RTA of channel implants -----
diffuse temperature=1050<C> time=10.0<s>

#--- Saving structure -----
struct tdr=NMOS1 FullD; # p-Well

#--- Gate oxidation -----
diffuse temperature=850<C> time=10.0<min> O2

select z=Boron
layers
struct tdr=NMOS2 FullD; # GateOx
```

```
#--- Poly gate deposition -----
deposit poly type=isotropic thickness=0.18<um>
#--- Poly gate pattern/etch -----
# MGoals settings for etch/depo
mgoals accuracy=2e-5

mask name=gate_mask segments = { -1 90<nm> }
etch poly type=anisotropic thickness=0.2<um> mask=gate_mask
etch oxide type=anisotropic thickness=0.1<um>
struct tdr=NMOS3 ; # PolyGate

#--- For graphics, first run "tecplot_sv -s:ipc" and uncomment
# the next line before running this file
# graphics on

#--- Poly reoxidation -----
diffuse temperature=900<C> time=10.0<min> O2
struct tdr=NMOS4 ; # Poly Reox

#--- LDD implantation -----
refinebox silicon min= {0.0 0.045<um>} max= {0.1<um> 0.125<um>} \
  xrefine= 0.01<um> yrefine= 0.01<um>
grid remesh

implant Arsenic dose=4e14<cm-2> energy=10<keV> tilt=0 rotation=0

SetPlxList { BTotal Arsenic_Implant }
WritePlx lDasImpl.plx y= 0.25<um>

diffuse temperature=1050<C> time=0.1<s> ; # Quick activation
struct tdr=NMOS5 ; # LDD Implant

#--- Halo implantation: Quad HALO implants -----
implant Boron dose=1.0e13<cm-2> energy=20<keV> \
  tilt=30<degree> rotation=0 mult.rot=4

#--- RTA of LDD/HALO implants -----
diffuse temperature=1050<C> time=5.0<s>
struct tdr=NMOS6 ; # Halo RTA

#--- Nitride spacer -----
deposit nitride type=isotropic thickness=60<nm>
etch nitride type=anisotropic thickness=84<nm> isotropic.overetch=0.01
etch oxide type=anisotropic thickness=10<nm>
struct tdr=NMOS7 ; # Spacer

#--- N+ implantation -----
refinebox silicon min= {0.04<um> 0.11<um>} max= {0.18<um> 0.4<um>} \
```

## 1: Getting Started

### Full-Text Versions of Examples

```
xrefine= 0.01<um> yrefine= {0.02<um> 0.05<um>}
grid remesh
implant Arsenic dose=5e15<cm-2> energy=40<keV> \
  tilt=7<degree> rotation=-90<degree>

SetPlxList { BTotal Arsenic_Implant }
WritePlx 1DasImpl2.plx y= 0.25<um>

#---- N+ implantation & final RTA -----
diffuse temperature=1050<C> time=10.0<s>
struct tdr=NMOS8 ; # S/D implants

# - 1D cross sections
SetPlxList {BTotal NetActive}
WritePlx NMOS_channel.plx y=0.0 silicon

SetPlxList {AsTotal BTotal NetActive}
WritePlx NMOS_ldd.plx y=0.1 silicon

SetPlxList {AsTotal BTotal NetActive}
WritePlx NMOS_sd.plx y=0.35 silicon

#-----#
#Transfer to device simulation
#-----#

#--Remove bottom of structure-----
transform cut location= 1.00 down

#--Change refinement strategy and remesh-----
refinebox clear
line clear

pdbSet Grid Adaptive 1
pdbSet Grid AdaptiveField Refine.Abs.Error      1e37
pdbSet Grid AdaptiveField Refine.Rel.Error      1e10
pdbSet Grid AdaptiveField Refine.Target.Length 100.0
pdbSet Grid SnMesh DelaunayType boxmethod

refinebox name= Global \
  refine.min.edge= {0.01 0.01} refine.max.edge= {0.1 0.1} \
  refine.fields= { NetActive } def.max.asinhdiff= 0.5 adaptive

refinebox name= SiGOX \
  min.normal.size= 0.2<nm> normal.growth.ratio= 1.4 \
  max.lateral.size= 5.0<nm> min= {-0.01 -0.1} max= {0.01 0.1} \
```

```
interface.materials= {Silicon}

refinebox name= GDpn1 \
  min= {0.0 0.04} max= {0.06 0.1} xrefine= 0.005 yrefine= 0.005 \
  silicon

refinebox name= TopActive \
  min= {0.0 0.0} max= {0.3 0.4} \
  refine.min.edge= {0.02 0.02} refine.max.edge= {0.05 0.05} \
  refine.fields= { NetActive } def.max.asinhdiff= 0.5 \
  adaptive silicon

grid remesh

#--- Reflect -----
transform reflect left

#--- Contacts -----
contact name= "substrate" bottom Silicon

contact name= "source" box Silicon adjacent.material= Gas \
  xlo= 0.0 xhi= 0.005 ylo= -0.4 yhi= -0.2

contact name= "drain" box Silicon adjacent.material= Gas \
  xlo= 0.0 xhi= 0.005 ylo= 0.2 yhi= 0.4

contact name= "gate" box PolySilicon \
  xlo= -0.181 xhi= -0.05 ylo= -0.088 yhi= 0.088

#--- Final -----
struct smesh=NMOS
```

---

## 2D npn Vertical Bipolar

```
# 2D NPN Vertical Bipolar Transistor
#-----

math coord.ucs

line x loc= 2.0<um>
line x loc= 4.0<um> tag=SubTop
line x loc= 6.0<um>
line x loc= 10.0<um> tag=SubBottom
line y loc= 0.0<um> tag=SubLeft
line y loc=1.5<um>
line y loc=2.5<um>
line y loc=8<um>
line y loc=13<um>
line y loc=22<um>
line y loc=24<um>
line y loc=30.0<um> tag=SubRight

# Diffuse settings to speed up simulation
#-----

pdbSet Diffuse IncreaseRatio 8.0
pdbSet Diffuse ReduceRatio 0.5

# Mesh settings
#-----

mgoals normal.growth.ratio=2.0 accuracy=2e-5 min.normal.size=10<nm> \
    max.lateral.size=30.0<um> minedge=1e-5

pdbSet Grid Adaptive 1
pdbSet Grid AdaptiveField Refine.Abs.Error 1e25
pdbSet Grid AdaptiveField Refine.Rel.Error 2.0

pdbSet Grid Damage Refine.Min.Value 1e25
pdbSet Grid Damage Refine.Max.Value 1e25
pdbSet Grid Damage Refine.Target.Length 1

pdbSet Diffuse Compute.Regrid.Steps 10

pdbSet Grid Refine.Percent 0.01

refinebox interface.mat.pairs= {Silicon Oxide}

refinebox name=BL refine.fields= {Antimony Phosphorus} \
rel.error={Antimony=0.6 Phosphorus=0.6} \
```



```

abs.error= {Antimony=1e16 Phosphorus=1e16} \
Adaptive min= "2.0 -0.1" max= "10.1 30.1" \
refine.min.edge= {0.2 0.4} max.dose.error= {Antimony=1e8}

refinebox name=Sinker refine.fields= {Phosphorus Arsenic} \
rel.error= {Phosphorus=0.5 Arsenic=0.5} \
abs.error= {Phosphorus=5e15 Arsenic=1e16} \
Adaptive min= {-1.0 16} max= {2.0 30.1} refine.min.edge= {0.1 0.2}

refinebox name=Active refine.fields= {Boron Arsenic} \
rel.error= {Boron=0.5 Arsenic=0.5} \
abs.error= {Boron=2e15 Arsenic=1e16} \
Adaptive min= {-1.0 -0.1} max= {2.0 16.0} \
refine.min.edge= {0.025 0.05}

# Masks definition
#-----

mask name=Sinker segments= {-1 22 24 35} negative
mask name=Base segments= {-1 1.5 13 35} negative
mask name=Emitter segments= {-1 2.5 8 22 24 35} negative
mask name=Contact segments= {-1 3.5 7 10 12 22.5 23.5 35}
mask name=Metal segments= {-1 2 8 9 13 22 24 35} negative

# Creating initial structure
#-----

region Silicon xlo=SubTop xhi=SubBottom ylo=SubLeft yhi=SubRight
init concentration=1e+15<cm-3> field=Boron

# Buried layer
#-----

deposit material= {Oxide} type=isotropic time=1 rate= {0.025}
implant Antimony dose=1.5e15<cm-2> energy=100<keV>
etch material= {Oxide} type=anisotropic time=1 rate= {0.03}

# Epi layer
#-----

deposit material= {Silicon} type=isotropic time=1 rate= {4.0} \
Arsenic concentration=1e15<cm-3>
diffuse temp=1100<C> time=60<min> maxstep=4<min>

struct tdr=vert_npn1

SetPlxList {BTotal SbTotal AsTotal PTotal}
WritePlx Buried.plx

```

## 1: Getting Started

### Full-Text Versions of Examples

```
# Sinker
#-----

deposit material= {Oxide} type=isotropic time=1 rate= {0.05}
photo mask=Sinker thickness=1

implant Phosphorus dose=5e15<cm-2> energy=200<keV>
strip Resist
diffuse temp=1100<C> time=5<hr> maxstep=8<min>

struct tdr=vert_npn2

# Base
#-----
photo mask=Base thickness=1
implant Boron dose=1e14<cm-2> energy=50<keV>
strip Resist
diffuse temp=1100<C> time=35<min> maxstep=4<min>

struct tdr=vert_npn3

# Emitter
#-----

photo mask=Emitter thickness=1
implant Arsenic dose=5e15<cm-2> energy=55<keV> tilt=7 rotation=0
strip Resist
diffuse temp=1100<C> time=25<min> maxstep=4<min>

struct tdr=vert_npn4

SetPlxList {BTotal SbTotal AsTotal PTotal}
WritePlx Final.plx y=5.0
WritePlx Sinker.plx y=23.0

# Back end
#-----

etch material= {Oxide} type=anisotropic time=1 rate= {0.055} mask=Contact
deposit material= {Aluminum} type=isotropic time=1 rate= {1.0}
etch material= {Aluminum} type=anisotropic time=1 rate= {1.1} mask=Metal

struct tdr=vert_npn5

exit
```

## CHAPTER 2 The Simulator Sentaurus Process

---

*This chapter provides an overview of how Sentaurus Process operates.*

The syntax and features of the command file are described, followed by an overview of the Sentaurus Process parameter database, which contains all of the model parameters and technical details regarding the running of the tool.

For new users, see [Syntax for Creating Input Command Files on page 48](#), [Creating and Loading Structures and Data on page 64](#), and [Interactive Mode on page 44](#). For advanced users who need to adjust model parameters, see [Parameter Database on page 53](#). For the TCAD Sentaurus Tutorial and examples, go to:

```
`${STROOT}/tcad/`${STRELEASE}/Sentaurus_Training/index.html
```

where `STROOT` is an environment variable that indicates where the Synopsys TCAD distribution has been installed, and `STRELEASE` indicates the Synopsys TCAD release number.

---

## Overview

To familiarize users with the different formatting used in this documentation, input commands from either a command file or the command line are presented this way:

```
sprocess -v
```

An example of output from Sentaurus Process is:

```
*****
***                               Sentaurus Process                               ***
***                               Version H-2013.03                               ***
***                               (1.5, amd64, linux)                               ***
***                               ***                                               ***
***                               Copyright (C) 1993-2002                           ***
***                               The board of regents of the University of Florida   ***
***                               Copyright (C) 1994-2013                           ***
***                               Synopsys, Inc.                                     ***
***                               ***                                               ***
*** This software and the associated documentation are confidential                 ***
*** and proprietary to Synopsys, Inc. Your use or disclosure of this               ***
*** software is subject to the terms and conditions of a written                  ***
*** license agreement between you, or your company, and Synopsys, Inc.          ***
```

## 2: The Simulator Sentaurus Process

### Interactive Graphics

```
*****
Compiled Fri Jan 25 00:56:50 PDT 2013 on tcadamd12

Started at: Wed Jan 16 09:44:59 2013 (PDT)
User name: iavci
Host name: tcadintell
PID: 12010
Architecture: x86_64
Operating system: Linux rel. 2.6.9-55.ELsmp ver. #1 SMP Fri Apr 20 16:36:54 EDT
2007
```

---

## Interactive Graphics

There are two options for interactive graphics in Sentaurus Process:

- An X-Windows-based graphical display (which will be phased out in future releases)
- An interface to Tecplot SV (which will eventually replace the X-Windows display)

The interface of Tecplot SV is available on all platforms and can be used in 1D, 2D, and 3D. The interface can be started with the simple command `graphics on`. The X-Windows-based viewer is launched with either the `plot.1d` or `plot.2d` command (see [plot.1d on page 1011](#) and [plot.2d on page 1013](#)). When the `graphics` command is used, graphical updating is performed automatically.

The Sentaurus Process–Tecplot SV interface is designed to minimize the effects of the start-up time of Tecplot SV. The usual mode of operation is to have one Tecplot SV window, which has interprocess communication (IPC) enabled, and to start and stop Sentaurus Process many times.

Because of the variability in user environments, automated start-up of Tecplot SV from inside Sentaurus Process is not reliable. Therefore, to use the Sentaurus Process–Tecplot SV interface, you must first start an IPC-enabled Tecplot SV from the UNIX command line before starting the Sentaurus Process–Tecplot SV interface from within Sentaurus Process. To start an IPC-enabled Tecplot SV, issue the following from the UNIX command line:

```
unix> tecplot_sv -s:ipc
```

Each time Sentaurus Process is started, it connects to the Tecplot SV window opened by the above command and creates a new frame where the graphical output is sent. The name of the frame contains the process ID, the user name, and the name of the computer where Sentaurus Process is run.

**NOTE** It is not necessary that the computer where Tecplot SV is launched is the same as the computer where Sentaurus Process is run, but the home directory of the user should be the same on both computers (using NFS or similar networking file-sharing).

In addition, it is possible to have multiple Sentaurus Process jobs sending graphics output to a single Tecplot SV for comparing multiple simulations in real time. For more information, see [Tecplot SV User Guide, Launching or Connecting to Tecplot SV on page 13](#)).

**NOTE** There is a convenient control mechanism built into Tecplot SV located in a dialog box, which is displayed by selecting **View > Sentaurus Interface**. In the dialog box, buttons allow you to pause and continue Sentaurus Process so that the graphics can be more closely examined when the structure or data in Sentaurus Process is changing rapidly.

It is sometimes convenient to use the Sentaurus Process `fbreak` command when using the interactive graphics. This command will pause Sentaurus Process in the input command file where the `fbreak` command occurs, allowing adjustments to be made to the display settings such as mesh on or off, selection of field to view, and range of color scale. The `fbreak` command puts Sentaurus Process into interactive mode and the command prompt `'sprocess>'` appears in the terminal window from which Sentaurus Process was run. After adjustments to the graphics have been made, the command `fcontinue` can be entered, which will resume Sentaurus Process execution.

In Sentaurus Workbench or batch mode (that is, `sprocess -u` or `sprocess -b`), the commands `fbreak` and `fcontinue` have no effect. Therefore, these commands can be placed in a Sentaurus Workbench project.

---

## Command-Line Options

[Table 1](#) lists the command-line options that are available in Sentaurus Process.

Table 1 Command-line options

Option	Short name	Function
<code>--batchMode</code>	<code>-b</code>	Switch off graphics.
<code>--diff</code>	NA	Diff mode. To see differences in data and Sentaurus Process parameter settings between two TDR files. Interpolation is used to compare results from different meshes. Usage: <code>sprocess --diff &lt;file1&gt; &lt;file2&gt;</code> where <code>&lt;file1&gt;</code> and <code>&lt;file2&gt;</code> are TDR files.

## 2: The Simulator Sentaurus Process

### Command-Line Options

Table 1 Command-line options

Option	Short name	Function
--FastMode	-f	Generate structure, no diffusion, no Monte Carlo implantation, no partial differential equation (PDE) solve, and so on.
--GENESISeMode	-u	Switch off log file creation.
--home <directory>	-o <directory>	Set SPHOME to <directory>.
--noSyntaxCheck	-n	Switch off syntax check.
--pdb	-p	Run Parameter Database Browser showing parameters as they are set during run-time. Include default parameters and parameters from the input command file if specified.
--ponly		Same as --pdb, but only shows parameters set in input command file; does not show default parameters.
--quickSyntaxCheck	-q	Only check syntax of branches that are true.
--syntaxCheckOnly	-s	Only check syntax, no execution.
NA	-v	Print header with version number.
NA	-h	Print use and command-line options.
NA	-x	Test floating-point exception handling.
NA	-X	Switch off floating-point exception catching.

---

## Interactive Mode

Sentaurus Process runs in interactive mode if no command file is given. In this mode, commands can be entered (at the command prompt) line-by-line and are executed immediately.

It is useful to run Sentaurus Process in the interactive mode for the following reasons:

- When debugging Tcl code, the program does not quit if a Tcl error is found. The error is displayed and you are prompted again for input. You can source a command file repeatedly if required.
- To easily obtain `pdb` parameter names and defaults with the `pdbGet` command.
- To print the list of built-in functions with the `help` command, and to print the list of Tcl procedures with the `info procs` command.
- To obtain command parameter names and defaults for any built-in command by using the `params` flag available in all built-in functions.

Another use of the interactive mode is to pause the simulation using the `fbreak` command. When the simulation is paused in interactive mode, the state of the simulator can be queried

using a number of commands including `grid`, `mater`, `select`, and so on. Pausing the simulation can also be useful when using interactive graphics as described in [Interactive Graphics on page 42](#).

---

## Fast Mode

When working on a new process flow, it is particularly useful to run Sentaurus Process a few times using the fast mode (`-f` command-line option). Developing a new process flow can be complex, involving many `etch`, `deposit`, and `photo` steps, some with masks; sometimes adjustments are required. In the fast mode, all diffusion, Monte Carlo implantation, and 3D remeshing commands are ignored. Only process commands for structure generation and analysis are performed. In this mode, when in three dimensions, all `struct` commands will only write a boundary into the TDR file, since the simulation mesh is not synchronized with the modified structure.

---

## Terminating Execution

You can terminate a running Sentaurus Process job in several ways. In some cases, the termination will take time or will fail for other reasons. The most fail-safe method is to use the UNIX command:

```
kill -9 <process_id>
```

where `<process_id>` is the process ID number of the running Sentaurus Process job which can be obtained with the UNIX `ps` command. This sends a signal `SIGKILL` to the corresponding Sentaurus Process job, which will cause the job to terminate immediately.

If Sentaurus Process is run directly from a UNIX shell, usually you can terminate the run by using shortcut keys. The key sequence is interpreted by the shell command, which sends a signal to the job in the foreground. Usually, `Ctrl+C` sends a `SIGINT` signal and `Ctrl+\` (backslash) sends a `SIGQUIT` signal. The running Sentaurus Process job catches all `SIGINT` signals and waits for three signals to be caught (in case it was typed accidentally) before terminating itself. However, Sentaurus Process does not catch the `SIGQUIT` signal, so this signal will typically cause Sentaurus Process to terminate immediately.

Because the exact behavior may depend on your UNIX shell, the operating system, and the local configuration, refer to the manual for the UNIX shell you are running or contact your local systems administrator for more information.

---

## Environment Variables

The Sentaurus Process binary relies on a number of supporting files found using the environment variables `SPHOME` and `SCHOME`. To change default models and parameters without modifying the installed Sentaurus Process files, copy the default `SPHOME` and `SCHOME` directories and set the environment variables (`SPHOME` and `SCHOME`) to the location of the modified directories.

By default, `SPHOME` and `SCHOME` are set based on the Synopsys standard environment variables `STROOT` and `STRELEASE`, and by the version number of Sentaurus Process using:

```
SPHOME = $STROOT/tcad/$STRELEASE/lib/sprocess-<version number>
SCHOME = $STROOT/tcad/$STRELEASE/lib/score-<version number>
```

The `SPHOME` directory has two major subdirectories, `TclLib` and `ImpLib`, where:

- The directory `$SPHOME/TclLib` contains all the default model selections in a file `SPROCESS.models`.
- The Tcl files are located in directory `$SPHOME/TclLib` and `$SCHOME/TclLib`.
- The subdirectory `$SCHOME/Params` contains the Sentaurus Process parameter database (see [Parameter Database on page 53](#)).
- The subdirectory `$SPHOME/ImpLib` contains all the implant tables.

---

## File Types Used in Sentaurus Process

The main file types used in Sentaurus Process are:

- Sentaurus Process command file (`*.cmd`)

This file, which is the main input file type for Sentaurus Process, contains all the process steps and can be edited. It is referred to as the *command file* or *input file*.

- Log file (`*.log`)

This file is generated by Sentaurus Process during a run. It contains information about each processing step, and the models and values of physical parameters used in it. The amount of information written to the log file can be controlled by the `info` parameter, which is available in nearly every command and the global default `info` level, 0, can be changed with `pdbSet InfoDefault <level>`. The higher the `info` level, the more information is logged, but it is not recommended to use `<level> > 2` for normal use because many normally unnecessary operations are performed for higher `info` levels which can slow execution.



- TDR boundary file (`*_bnd.tdr`)

This format stores the boundaries of the structure without the bulk mesh or fields. This file can be used as the structure file for the meshing engine Sentaurus Mesh and can be loaded into Tecplot SV for viewing. The name of a TDR boundary file can be specified in the `tdr` parameter of the `init` command of Sentaurus Process, and then the loaded boundary will be meshed using the MGOALS meshing library.

- TDR grid and doping file (`*_fps.tdr`)

TDR files can be used to split and restart a simulation. Such restart files are saved in the `struct tdr=filename` command because restarting requires interface data, parameter and command settings, mesh ordering information as well as bulk grid and data. If either `!pdb` or `!interfaces` is specified in the `struct` command, the TDR file will not be suitable for restarting. The TDR file can be loaded into Sentaurus Process in the `init` command, but the results of the subsequent simulation steps might differ in the simulation with the split and restart compared to a simulation of the entire flow in one attempt. TDR files store the following types of information:

- Geometry of the device and the grid.
- Distribution of doping and other datasets in the device.
- The internal structure of the mesh in Sentaurus Process required to restore the simulation mesh to the same state in memory that is present at the time of saving the file. Restart files store coordinates and field values without scaling them to DF-ISE units; files that cannot be restarted store coordinates and field values scaled to DF-ISE units.
- Finally, by default, Sentaurus Process stores all changes to the parameter database made after initial loading the database and all commands that create objects later referenced, such as refinement boxes and masks in the TDR file. A TDR file can be either reloaded into Sentaurus Process to continue the simulation or be loaded into Tecplot SV for visualization.

The parameter settings stored in a TDR file can be viewed using `pdbBrowser -nopdb -tdr <tdrfile>` (see [Viewing Parameters Stored in TDR Files on page 63](#) for details).

For more information about the TDR file format, refer to the *Sentaurus Data Explorer User Guide*.

- DF-ISE doping and refinement file (`*_msh.cmd`)

This file stores doping and mesh refinement commands and, along with the boundary file, it is used as input for the Synopsys meshing engines. This file is usually saved by the user at the end of a simulation.

- DF-ISE file (\*.plx)

This DF-ISE file format is used for saving 1D distributions of the doping concentration or other fields in a specified 1D cross section. This file can be viewed by loading it into Inspect.

---

## Syntax for Creating Input Command Files

This section is intended for users who want to create input command files manually, that is, outside of the Ligament environment. It is important to remember that Sentaurus Process is written as an extension of the tool command language (Tcl). This means that the full capability and features of Tcl are available in the input command files as well as the interactive mode of Sentaurus Process.

Standard Tcl syntax must be followed; for example, a hash symbol (#) at the beginning of a line denotes a comment and the dollar sign (\$) is used to obtain the value of a variable. Major features of Tcl include `for` loops, `while` loops, and `if then else` structures, `switch` statements, file input and output, sourcing external files, and defining procedures (functions). Variables can be numbers, strings, lists, or arrays. Refer to the literature for more information [1].

Before execution of the command file takes place, the syntax of the file is checked. This is accomplished by first modifying the command file so that all branches of control structures such as `if`, `then else`, and `switch` commands are executed. In addition, a special flag is set so that no structure operations or operations that depend on the structure are performed. This allows the syntax check to run quickly, but thoroughly. Sometimes, the modifications made to the command file during syntax checking interfere with the definition or redefinition of Tcl variables, generating a false syntax error. In these cases, switch off syntax checking for part of a command file using the special `CHECKOFF` and `CHECKON` commands:

```
# Skip syntax check for part of command file
# The CHECKOFF/CHECKON commands must start at the beginning of the line
# and be the only command on the line
CHECKOFF
if { $mode } {
    array set arr $list1
} else {
    set arr $list2    ;# error only if both branches are executed
}
CHECKON
# further commands are syntax checked
```

## Tcl Input

Sentaurus Process has been designed to optimize the use of the Tcl. Some examples of this interaction include:

- Command parameter values are evaluated with Tcl. For example, `expr` can appear in the value of an expression, that is, `parameter=[expr $pp/10.0]` is valid Sentaurus Process syntax. This particular expression sets the parameter `parameter` to the value of `pp/10` if the Tcl variable `pp` was previously defined with the Tcl `set` command.
- Tcl expressions may appear in model parameter values in the parameter database. In some cases, Sentaurus Process parameters are set with Tcl commands to be a function of other parameters.
- Sentaurus Process contains many callback procedures, which can be redefined by users to provide flexibility. For example, a callback procedure is used to initialize defects after implantation.
- Many modular built-in functions are available for postprocessing, which can be combined into a Tcl script to create powerful analytic tools.
- There are special Sentaurus Process versions of `set` (`fset`) and `proc` (`fproc`), which are stored in TDR files. When simulations are restarted using a TDR file, the settings given by `fset` and `fproc` from the previous simulation will be available.

Other syntax rules to consider when writing input command files are:

- One command is entered on one line only. There are two exceptions to this rule:
  - A backslash (`\`) is used to extend a command on to multiple lines if it appears as the last character on the line.
  - If there is an opening brace, Tcl will assume the command has not finished until the line containing the matching closing brace.
- Command parameters have the following form:
  - Boolean parameters are true if the name appears on the line. They are false if they are preceded by an exclamation mark (`!`).
  - Parameters that are of type *integer* or *floating point* must appear as `parameter=value` pairs.
  - String parameters are enclosed, in general, in double quotation marks (`" "`), for example, `parameter="string value"`.
  - Lists can appear enclosed in double quotation marks or braces, for example, `parameter= { item1 item2 ... }` or `parameter= " item1 item2 ..."`. It is necessary to have a space between the equal sign and the opening brace.

## 2: The Simulator Sentaurus Process

### Syntax for Creating Input Command Files

**NOTE** It is important to separate the equal sign from the parameter value by a space because Tcl delimiters such as ‘”’ and ‘{’ are ignored if they appear in the middle of a string. Sentaurus Process can handle *no space* between an equal sign and a double quotation mark, but it cannot correct the case where there is *no space* between an equal sign and an opening brace.

---

## Material Specification

Materials are specified the same way for all commands that require a material parameter. For a bulk material, specify only one material. For an interface material, specify two materials: one with a slash (/) and one without a slash.

Some examples are:

```
oxide           ;# This command applies to oxide.
silicon /oxide  ;# This command applies to the Si-SiO2 interface
```

The complete list of materials available can be found in the file:

```
$STROOT/tcad/$STRELEASE/lib/score-<version number>/TclLib/tcl/Mater.tcl
```

In that file, the lines that contain `mater` add create a material. For more information about creating new materials, see [mater on page 982](#).

**NOTE** Materials present in the `Mater.tcl` file do not necessarily have parameters in the parameter database. Attention must be paid to initializing parameters for a new material.

---

## Aliases

Sentaurus Process allows more control over the names of command parameters and abbreviations of parameter names. These *aliases* only apply to parameters of built-in Sentaurus Process commands, and the `pdbSet` and `pdbGet` family of commands.

This permits clarity and uniformity to commonly used names. Another benefit is that it is easier to maintain backward compatibility for parameter names while not restricting future parameter names that could conflict with common abbreviations (that is, *V* could refer to either *vacancy* or *void*).

An explicit list of allowed aliases is maintained in the `$SCORE/TclLib` directory (see [Environment Variables on page 46](#) for information about how the location of the `TclLib`

directory is determined). The `alias` command is used to view and extend the list of allowed aliases.

To print the list of aliases:

```
sprocess> alias -list
```

To view the alias of a parameter name, for example, `Vac`:

```
sprocess> alias Vac  
Vacancy
```

If an alias does not exist, the same parameter name is returned:

```
sprocess> alias NotAParam  
NotAParam
```

To create a new alias for a parameter name, for example, the alias `vaca` for the parameter `Vacancy`:

```
sprocess> alias Vaca  
Vaca  
sprocess> alias Vaca Vacancy  
sprocess> alias Vaca  
Vacancy
```

---

## Default Simulator Settings: SPROCESS.models File

Sentaurus Process starts a simulation by reading the `SPROCESS.models` file in the `$SPHOME/TclLib` directory. This file defines various default parameters and directories used during the simulation such as setting:

- The path for Tcl library files
- The path for Advanced Calibration Tcl library files
- The path for implant tables
- Default material names
- The `math` parameters for 1D, 2D, and 3D oxidation and diffusion simulations
- Default solution names
- Default diffusion callback procedures
- Default oxidation or silicidation reactions
- Default oxidation or silicidation solution callback procedures
- Default epitaxial growth callback procedures

## 2: The Simulator Sentaurus Process

### Compatibility with Previous Releases

The `SPROCESS.models` file is read once at the beginning of the simulation. You can override any of the default parameters after the file is read.

---

## Compatibility with Previous Releases

Occasionally, the default parameter and model settings change in Sentaurus Process to ensure that the default behavior gives robust, accurate, and computationally efficient results on current production technologies. Usually, when new models and algorithms are developed, they are optional. After some experience is gained, the default can be changed to take advantage of the new model or algorithm.

The old model and algorithm settings are collected into a file for each release and are available so that you can recover results from previous releases. Each file contains only those parameter changes that occurred for that particular release, so that if the release specified in the `Compatibility` command is older than the most recent release, the most recent release parameters are set first, followed by older releases in reverse chronological order.

For example, the command `Compatibility E-2010.12` issued for Version H-2013.03 will first apply parameters consistent with G-2012.06, then parameters consistent with F-2011.09, and finally parameters consistent with E-2010.12. Aliases are available for the release name so you do not need to know the release foundation letter. For example, `2011.09` can be used instead of `F-2011.09`.

The files with the compatibility parameter settings are stored in `$STROOT/tcad/$STRELEASE/lib/sprocess/TclLib/Compatibility`. These files are a useful list of all default parameter changes for each release.

**NOTE** As a result of the repair of code flaws and because of numeric accuracy limitations, exact reproduction of results from previous releases is not always possible.

**NOTE** If the `Compatibility` command is used, it should be the first command in an input file so that all subsequent commands that depend on the defaults take into account the compatibility setting.

For example:

```
# Apply defaults of the 2011.09 release (first line of input file)
Compatibility 2011.09
```

**NOTE** Default parameter and algorithm settings of the tools Sentaurus Mesh, Sentaurus Structure Editor, and the MGOALS library are not changed by the `Compatibility` command. For MGOALS library backwards compatibility, see [Summary of MGOALS Etching and Deposition Algorithms on page 759](#). To obtain backwards compatible default parameters and settings for Sentaurus Mesh and Sentaurus Structure Editor, see the backwards compatibility mechanisms described for those tools in the corresponding manual sections.

---

## Parameter Database

The Sentaurus Process parameter database stores all Sentaurus Process material and model parameters as well as global information needed for save and reload capabilities. There is a hierarchical directory tree inside the `Params` directory, which stores the default values. (To locate the `Params` directory, see [Environment Variables on page 46](#).)

Data is retrieved by using the `pdbGet` command and is set by using the `pdbSet` command. The `pdbGet` and `pdbSet` commands are checked for correctness of syntax and they print the allowed parameter names if a mistake is made. These commands are used to obtain and set all types of data stored in the database: Boolean, string, double, double array, and switch.

The higher level `pdbSet` and `pdbGet` commands call lower-level type-specific commands (`pdbGetSwitchString`, `pdbGetDoubleArray`, `pdbGetString`, `pdbGetDouble`, `pdbGetSwitch`, `pdbGetBoolean`, `pdbSetDoubleArray`, `pdbSetString`, `pdbSetBoolean`, `pdbSetDouble`, and `pdbSetSwitch`) that are not checked for errors and, therefore, are not recommended for typical use. These commands have a slight performance advantage and are used internally.

You can set some parameters in a region-specific manner. Regions can be named with the `region` and `deposit` commands and, if region-specific parameters exist, they will override the material-specific parameters if any. However, there are many circumstances where this will not give the desired behavior. In that case, you must create a new material that inherits its parameters from an existing material. Then, you must change the material properties of the new material as needed. For more information, see [Like Materials: Material Parameter Inheritance on page 55](#).

Inside the `Params` directory are subdirectories that define the highest level nodes in the database. Inside each subdirectory is a file `Info`, which contains parameters of that level. In addition, directories in the database have named files that contain parameters, which are under the node defined by the file name. For example, in the `Params` database, there is a directory called `Silicon`, which contains a file `Info`. The parameters inside `Info` are located under the `Silicon` node. As another example, inside the `Silicon` directory is another file

## 2: The Simulator Sentaurus Process

### Parameter Database

Interstitial that contains parameters under the Interstitial node, which is under the Silicon node.

Inside the files of the parameter database are commands that set database parameters. The commands have the form:

```
array set $Base { <NAME> { <TYPE> <VALUE> } }
```

where:

- <NAME> is the parameter name.
- <TYPE> is one of Boolean, String, Double, DoubleArray, or Switch.
- <VALUE> is a Tcl expression that sets the default value.

It is often necessary to enclose the <VALUE> expression in braces. Some Tcl procedures have been created to increase the usefulness of <VALUE> expressions. For example, in many places in the database, the built-in function Arrhenius is used to set the value of a parameter. Parameters that contain a Tcl function are evaluated at each diffusion time step so that temperature-dependent parameters will update correctly during a temperature ramp. It is important to remember that the Arrhenius function uses the global Tcl variable for temperature, which defaults to room temperature.

If you start Sentaurus Process and call the `pdbGet` command of a parameter that contains an Arrhenius function, it will return the value of that parameter at room temperature. The temperature can be changed with the `SetTemp` function. Subsequent calls to the Arrhenius command through `pdbGet` return values based on the given temperature. In addition, the `diffusion` command changes the global temperature for each time step, and the temperature after diffusion will be same as the temperature in the last diffusion time step.

Other functions that appear in the `pdb` parameters are `DiffLimit`, which calculates a diffusion-limited reaction rate given the diffusivity of the two reacting species, and `pdbGet*` functions, which allow parameters to be set as a function of other parameters.

For the `DoubleArray` type, a Tcl list is set that is ordered pairwise:

```
{key1 value1 key2 value2 . . . }
```

 where the parameter setting for `key1` is `value1`.

Material parameters can be stored under the known region name. To set and obtain the parameter value, use the region name instead of the material name. If the parameter is not found under the region name, it is taken from the material of that region.

Sentaurus Process writes directly to the parameter database in a number of ways. Mostly this is performed to save information for save and reload capabilities using the TDR format. Data written by the program into the parameter database is not available within the default `Params` directory or the Parameter Database Browser (PDB), but can be read using the `pdbGet` command.



For information about the TDR format, refer to the *Sentaurus Data Explorer User Guide*.

---

## Parameter Inheritance

The parameter database has a parameter inheritance feature where parameters at a certain level or node can inherit the parameters from another node at the same level. The inherited parameters can be overwritten with new values. Inheritance is indicated by the presence of a special parameter named `Like`. In one of the parameter database files, the `Like` parameter is specified as follows:

```
array set $Base {Like <Node>}
```

which means that parameters at the level of the file inherit parameters from `<Node>`, which should be another node at the same level. For example, the file:

```
Params/Silicon/Arsenic/Info
```

contains the line `array set $Base Base {Like Dopant}`, which indicates that `Arsenic in Silicon` should inherit the common parameters of all `Dopant` species in `Silicon`. Other parameters specified in that file indicate parameter settings specific to `Arsenic in Silicon`.

---

## Materials in Parameter Database

### Like Materials: Material Parameter Inheritance

The parameters of a material can be inherited from the parameters of another material using the special `Like` parameter in the PDB. When this is the case, the two materials are referred to as *like materials*. This can be used to specify different settings in different regions. First, a new material is created and made to be *like* an existing material using:

```
mater add name = <NewMat> new.like = <ExistingMat>
```

where:

- `<NewMat>` is the name of the material being created.
- `<ExistingMat>` is the name of the material whose parameters will be inherited.

**NOTE** It is important to use the `mater` command instead of directly creating the `Like` parameter because the `mater` command will make all interfaces to `<NewMat>` `Like` the appropriate interface to `<ExistingMat>`.

**NOTE** Reaction specifications, such as oxidation, silicidation, and epitaxy, are not stored in the PDB. Therefore, for a new material to react, a new reaction command must be issued (see [reaction on page 1038](#)).

## Interface Parameters

When using the PDB commands and the Alagator language, interfaces are specified as a pair of materials separated by an underscore (`_`), for example, `Gas_Oxide` and `Oxide_Silicon`. The official name follows alphabetic order, and the first letter is capitalized. However, aliases are provided that allow their order to be reversed; some shorter names are allowed; and all lowercase is generally available.

As an example of setting an interface parameter, the following command sets the numeric tolerance `Abs.Error` at the gas-silicon interface to `1e3`:

```
pdbSet Gas_Silicon Vac Abs.Error 1e3
```

---

## Regionwise Parameters and Region Name-handling

Many parameters in the parameter database can be specified regionwise including parameters related to meshing, parameters for both analytic implantation and MC implantation, and mechanics parameters. Those parameters used by Alagator as part of equations and terms, however, cannot be specified regionwise: this includes all dopant diffusion parameters and all oxidation and silicidation parameters. For the rest of the parameters, internally, the program checks if there is a regionwise specification of the parameter; if not, the materialwise specification is used.

The name of regions can be specified with the `region` command and `deposit` command; however, the name should not contain an underscore (`_`) or a period (`.`) because these characters have special meaning. During the course of the simulation, geometric operations such as etch and reflect can split regions in two. If this happens, the history of the region is maintained through its name. For example, if a region is originally named `layer1` and it is etched into two pieces, they will be named `layer1.1` and `layer1.2` according to rules given below.

These two regions will inherit the parameters of `layer1`. Furthermore, parameters for `layer1.1` and `layer1.2` also can be specified separately. If a subsequent step such as a deposit reunites `layer1.1` and `layer1.2`, the region will be given the name `layer1`. Conversely, if `layer1.1` is split into two regions, the regions will be named `layer1.1.1` and `layer1.1.2`, and so on. In this way, regionwise parameter specification is preserved for the life of the region or its parts.

The numbering of split regions is performed according to the spatial location of the pieces. The lowest point of each piece to be renamed is found (in the coordinate system of Sentaurus

Process, this would be the largest x-coordinate). To avoid numeric noise, the coordinates are compared with a specified epsilon given by `pdbGet Grid RenameDelta` (hereafter, referred to as  $RN$ ). If the x-coordinates of the pieces to be renamed are not within  $RN$  of each other, the regions are ordered from lowest to highest, that is, from the highest x-coordinate to the lowest. If any piece has its lowest coordinate within  $RN$ , its y-coordinate is compared, that is, from the lowest coordinate to the highest.

For example, in [Figure 11](#), `layer1` is split into two regions and the quantity `deltax` is less than  $RN$ , so the region on the left is given the name `layer1.1` and the region on the right is given the name `layer1.2`. If `deltax` had been greater than  $RN$ , the region on the right would have been given the name `layer1.1` because it would have been considered lower than the region on the left. Similarly, in three dimensions, first x and y are compared, and if they are both within  $RN$ , z is used for ordering, that is, from the lowest coordinate to the highest.

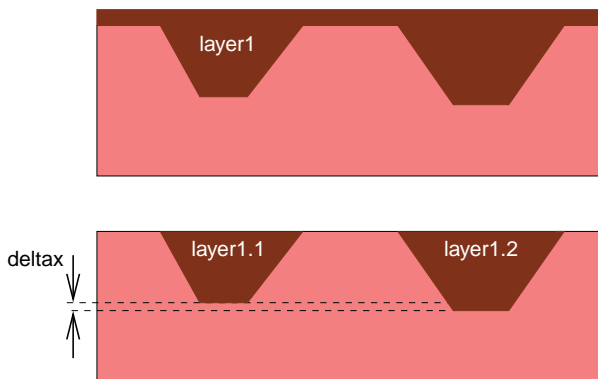


Figure 11 Illustration of region-naming rules

You can apply the above operation to the whole structure with `grid rename`. In this case, all the regions are renamed similarly to the above rules but, instead of the root being chosen by the user, all regions of the same material have the root given by the names of the materials and the extension is `_<n>` where `<n>` is the region number, for example `Silicon_1`, `Silicon_2`, and so on. This should only be used as a postprocessing step because all region-specific parameters no longer apply when the name of a region has changed.

For example, if two oxide layers are grown, one with steam (if it is the first oxide region, its name would be `Oxide_1`) and one from pure  $O_2$  (which would be `Oxide_2` if it were the second oxide region), they can have different densities. This can be considered in an MC implantation using:

```

pdbSetDouble Oxide_1 MassDensity <wet oxide density>
pdbSetDouble Oxide_2 MassDensity <dry oxide density>

```

where `<wet oxide density>` and `<dry oxide density>` would be replaced with values given in  $g/cm^3$ .

## 2: The Simulator Sentaurus Process

Viewing the Defaults: Parameter Database Browser

---

# Viewing the Defaults: Parameter Database Browser

The Parameter Database Browser (PDB) is a graphical representation of the Sentaurus Process parameter database that allows you to view and edit parameters. The PDB has three distinct areas (see [Figure 12 on page 59](#)):

- Parameter hierarchy overview in a tree structure representation.
- Parameter information in a spreadsheet representation. The columns are:
  - Parameter
  - Type
  - Value
  - Unit
  - Evaluate
  - Comment
  - Tool
  - Info Level (hidden by default)
- Graphic window to plot parameter dependence on the temperature.

The status bar has three indicators that show:

- The temperature used in temperature-dependent functions such as Arrhenius.
- The temperature point set for the x-axis.
- The x-coordinate and y-coordinate of the pointer in the graphic window.

## 2: The Simulator Sentaurus Process

### Viewing the Defaults: Parameter Database Browser

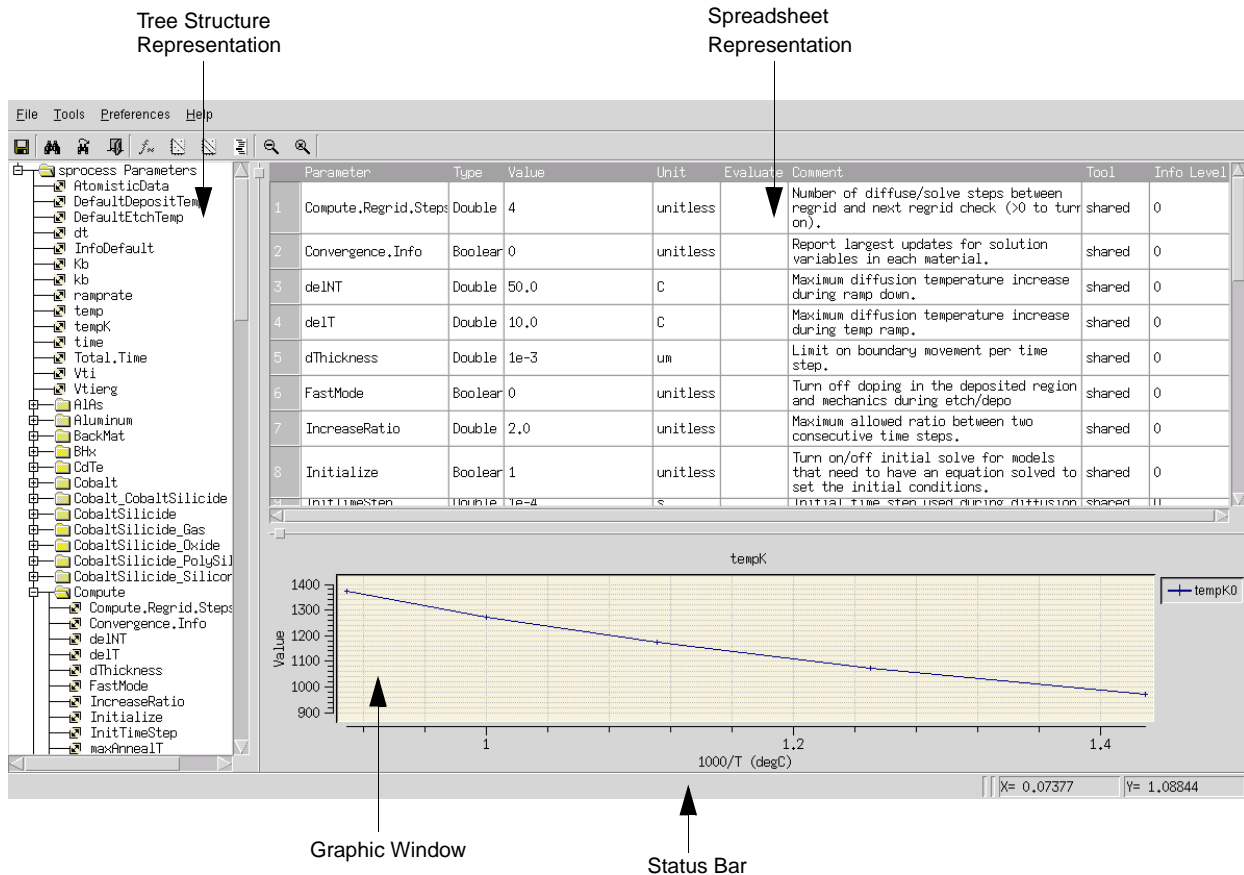


Figure 12 Parameter Database Browser

## Starting the Parameter Database Browser

To start the PDB from the command line, enter:

```
pdbBrowser
```

This searches for the database in the same location as Sentaurus Process. You can set the environment variables `SPHOME` and `SCHOME` to change the location of the parameter database for the PDB and Sentaurus Process (see [Environment Variables on page 46](#) for details). To view parameters in an input file merged with defaults, use:

```
sprocess --pdb <input command file>
```

## 2: The Simulator Sentaurus Process

Viewing the Defaults: Parameter Database Browser

or to view only the parameters specified as input in a command file, use:

```
sprocess --ponly <input command file>
```

### Browser PDB Functions

The following functions are available:

- Export Tree** Saves the whole parameter database into a specified file in the tab-delimited format. The fields of the file are **Parameter Name**, **Type**, **Value Evaluation**, **Original Value**, and **Comments**.
- Find and Find Next** Matches the pattern entered against parameter names according to the selected options. Patterns can include regular Tcl expressions. The match is highlighted when found (see [Figure 13](#)).

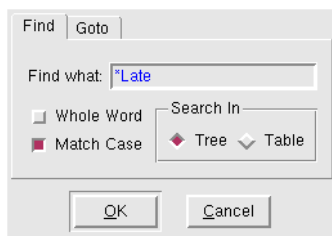


Figure 13 Find dialog box

- Goto Line** Highlights a table row or tree node that corresponds to the number entered.
- Plot** (Applies only to parameters of type *double* and *double array*.) Plots the dependency of the selected parameter on the temperature in logarithmic coordinates versus  $1/T$ . The default set of temperature values is {700.0 800.0 900.0 1000.0 1100.0}. The resulting graphs are displayed in the graphic window; otherwise, an error message is displayed.
- Plot Over** The same as **Plot** but it does not clear the graphic window of previous graphs.

**NOTE** You can zoom by dragging the mouse. To zoom out, use the middle mouse button, or click the **Zoom Out** and **Zoom Off** buttons.

**Evaluate** Evaluates the value of the selected parameter and displays the result in the Evaluate column of the table. Values can contain Tcl expressions.

**Edit** Opens the appropriate database file with an editor regardless of the user write-permissions, but the standard installation will switch off write permissions for the database. The default editor, SEdit, can be changed. The PDB Browser is updated upon file saving.

**Parameter Information** Double-clicking a nonempty table row allows you to view the corresponding parameter information in a separate window. To close the window, click the **Close** button.

**NOTE** To display a shortcut menu, right-click a parameter for plotting and evaluation in the tree and table areas.

**Arrhenius Fit** Finds the best prefactor and energy for an Arrhenius fit of a given profile, taken from the list of temperature–value pairs. The results can be plotted in the graphic window.

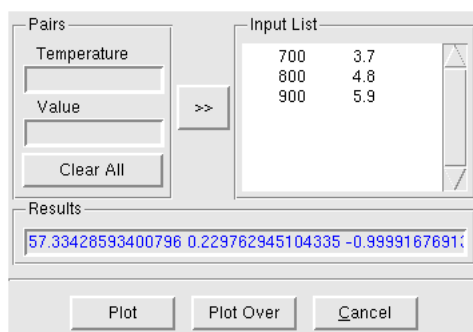


Figure 14 Arrhenius Fit dialog box

## 2: The Simulator Sentaurus Process

Viewing the Defaults: Parameter Database Browser

### PDB Preferences

The PDB allows you to reset the default settings for the following values by using the **Preferences** menu, shortcut keys, or shortcut menu of the graphic window:

#### **Preferences > Font > Family**

Changes the font family.

#### **Preferences > Font > Size**

Changes the font size.

#### **Preferences > Cursor**

Changes the style of the pointer.

#### **Preferences > Graph > Set Temperature**

The global temperature used in the temperature-dependent functions; the default is 1000.0.

#### **Preferences > Graph > Reset X Points**

The x-axis temperature point set; the default set is {700.0 800.0 900.0 1000.0 1100.0}.

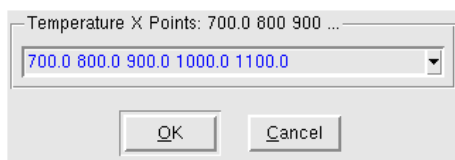


Figure 15 Reset Temperature Points dialog box

#### **Preferences > Graph > Data Point Symbol**

Node Tip: hide / show.

#### **Preferences > Info Level**

Shows or hides the Info Level column of the table.

#### **Preferences > Editor > Change Editor**

Resets the default editor.



**Preferences > Editor > Reset Update Time**

Resets the update interval.

**Preferences > Graph > X Scale**

Resets the scale to logarithmic or linear.

**Preferences > Graph > Y Scale**

Resets the scale to logarithmic or linear.

**Tools > Info Level** Chooses which parameters to display ranging from basic parameters to all parameters.

---

## Viewing Parameters Stored in TDR Files

Parameters stored in TDR files can be viewed using the `pdbBrowser` command run from the UNIX command line instead of through Sentaurus Process. By default, the PDB reads parameters from the Sentaurus Process database directory (which can be changed with the `SPHOME` and `SCHOME` environment variables). In addition, parameters stored in a TDR file can be read in using the `-tdr <filename>` option of the PDB. Parameters that appear in the database are overwritten by those contained in the TDR file, so the resultant parameter set will be the same as if Sentaurus Process had read in the file. On the other hand, it is also useful to know which parameters are only in the TDR file. To read only those parameters, the database reading can be switched off using the `-nopdb` command-line option.

For example:

```
> pdbBrowser -tdr n10_fps.tdr
```

reads the Sentaurus Process PDB and then reads parameters from `n10_fps.tdr` file overwriting values contained in the database.

For example:

```
> pdbBrowser -nopdb -tdr n10_fps.tdr
```

reads only the parameters in `n10_fps.tdr` file.

---

## Creating and Loading Structures and Data

The first step in most simulations is either to load an existing structure or to create a new one. New structures are created through a combination of the `line`, `region`, and `init` commands. The initial mesh is a tensor-product mesh where the density of lines is specified in the `line` command, and the regions are defined by specifying tags in the `line` commands and defined in the `region` command. The initial regions are always defined as axis-aligned rectangles in 2D and axis-aligned bricks in 3D.

---

## Understanding Coordinate Systems

Sentaurus Process and related tools use different coordinate systems. The most commonly encountered coordinate systems include wafer coordinates, simulation coordinates, and visualization coordinates.

### Wafer Coordinate System

The wafer coordinate system is fixed with respect to the wafer flat or notch, and is used to define the relationship of all other coordinate systems to the physical wafer. The wafer coordinate system is shown in [Figure 16](#).

The wafer x- and y-axes form a naturally oriented coordinate system when the wafer is drawn with the flat pointing down as shown in [Figure 16](#). This coordinate system is used for layout information, such as mask locations, and for setting a cutline using the `CutLine2D` command.

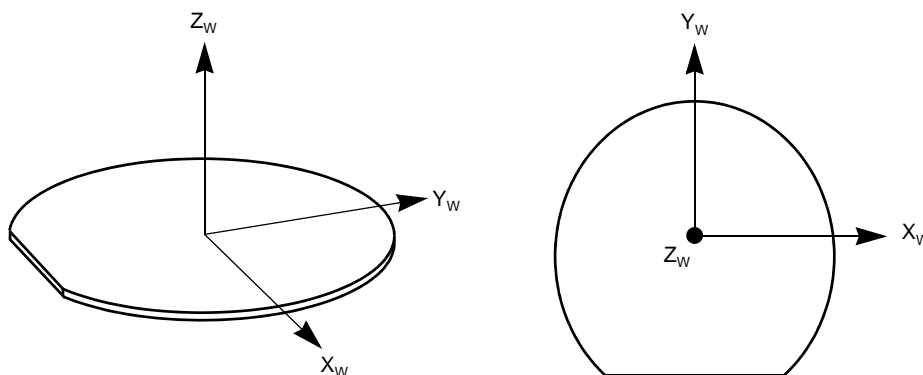


Figure 16 Wafer coordinate system

## Simulation Coordinate System (Unified Coordinate System)

The simulation coordinate system is used to define the mesh for the simulation. All coordinates that are specified with respect to the mesh are given in simulation coordinates. This includes all coordinates that are given in the Sentaurus Process command file.

The simulation coordinate system has the x-axis pointing into the wafer and the y-axis rotated with respect to the wafer y-axis. The simulation coordinate system is shown in [Figure 17](#). Simulations in 1D use only the x-axis. Simulations in 2D use only the x- and y-axes.

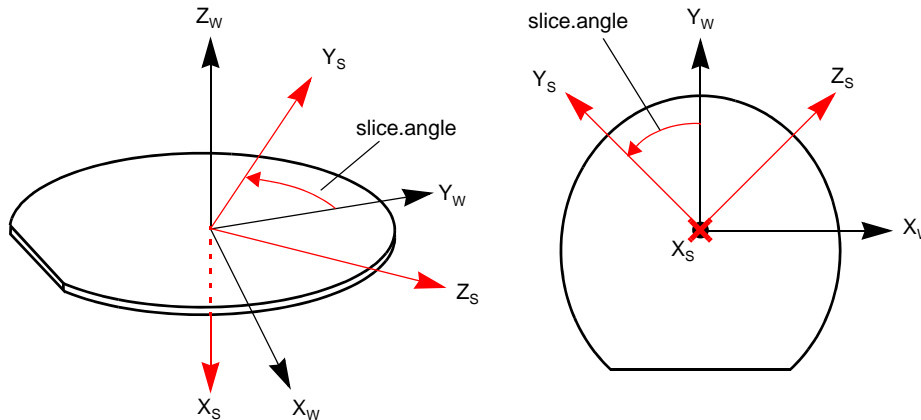


Figure 17 Simulation coordinate system (slice.angle = 45)

The rotation of the simulation axes with respect to the wafer axes is given by the `slice.angle` parameter of the `init` command. The slice angle is measured from the wafer y-axis to the simulation y-axis with positive angles counterclockwise about the wafer z-axis.

## 2: The Simulator Sentaurus Process

### Creating and Loading Structures and Data

The default value of `slice.angle` is set to  $-90^\circ$ . This causes the simulation y-axis to match the wafer x-axis, which is the usual cut direction through the layout for 2D simulations. The default simulation coordinate system is shown in [Figure 18](#).

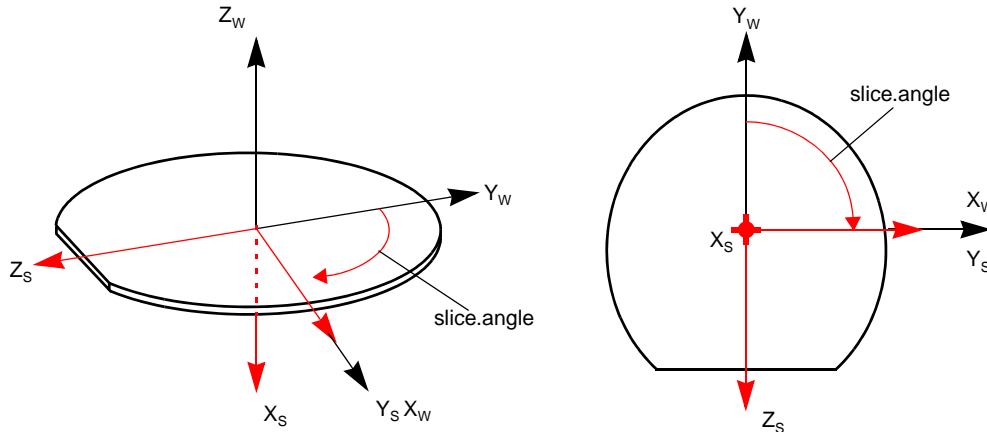


Figure 18 Default simulation coordinate system (`slice.angle = -90`)

## Visualization Coordinate Systems

Two systems can be used for visualization:

- The unified coordinate system (UCS)
- The DF-ISE coordinate system

### Unified Coordinate System

To use the UCS, specify:

```
math coord.ucs
```

This system of coordinates is explained in [Simulation Coordinate System \(Unified Coordinate System\)](#) on page 65.

**NOTE** The UCS is the recommended way of visualization and may become the default in the future.

### DF-ISE Coordinate System

The DF-ISE coordinate system is the default for visualizing TDR files. It can be set explicitly by:

```
math coord.dfise
```

The DF-ISE coordinate system is used by the DF-ISE and some TDR file formats as well as Tecplot SV. Unlike the simulation coordinate system in which the x-axis points into the wafer for 1D, 2D, and 3D, the visualization coordinate system has different axis conventions for 1D, 2D, and 3D. [Figure 19](#) shows the relationship between simulation coordinates and DF-ISE coordinates.

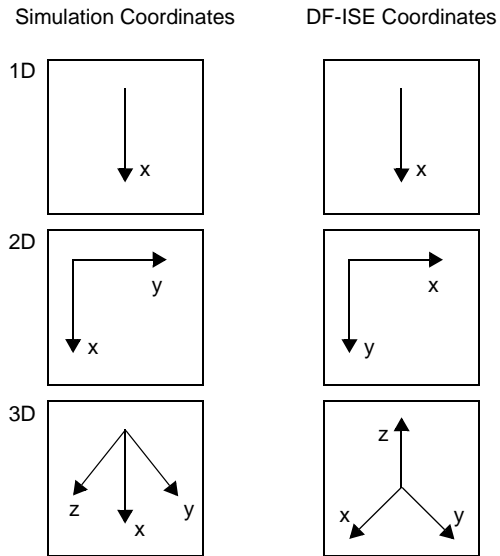


Figure 19 Simulation and DF-ISE coordinate systems

The only difference between UCS coordinates and DF-ISE coordinates is that different conventions are used to label the axes. Sentaurus Process automatically converts the axis labels when reading and writing DF-ISE or TDR files.

The relationship between DF-ISE coordinates and UCS coordinates shown in [Figure 19](#) applies to all values of `slice.angle`. In other words, the DF-ISE system is not fixed with respect to the wafer system. It always has the same rotation with respect to the wafer coordinate system as the simulation coordinate system.

[Figure 20 on page 68](#) shows the relationship between simulation coordinates and visualization coordinates.

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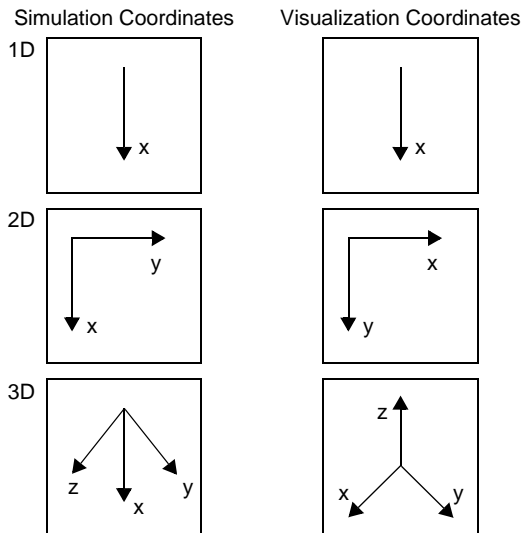


Figure 20 Simulation and visualization coordinate systems

The tensor components, for example, mechanical stresses, in 2D and 3D are the same in UCS coordinates. For a conversion table for the stress components in 2D and 3D DF-ISE coordinate systems, see [Chapter 9 on page 629](#). This also applies to other second-order symmetric tensors.

---

## Defining the Structure: The line and region Commands

The `line` and `region` commands are used together to define the structure. In the `init` command, the structure is actually formed. Care must be taken when creating a structure because there are few checks for errors.

These rules must be followed to obtain a valid structure:

- If this is not the first structure being created in a command file, the command `line clear` must be issued to remove `line` commands and stored mesh ticks.
- Line locations must be given in increasing order.
- The region boundaries are defined by tagged lines. Tagged lines are created with the `line` command where the parameter `tag` has been set (as well as the location parameter).
- At least one `region` command must be given to define the substrate.
- Regions must have a material specification, except for the `substrate` case described below.
- Regions must have the same dimensionality as the `line` commands used (that is, if line `y` is given, a 2D region is expected with `ylo` and `yhi` set).

- The `spacing` parameter is used to create lines between user-defined lines, so that not every line must be specified in the command file. Sentaurus Process smoothly grades the line density between user-defined lines to match as closely as possible the spacing at each user-defined line. In addition, there will be lines at locations given by the `location` parameter of the `line` command. By default, the `spacing` parameter is extremely large, so that if it is not set, only lines given by the `location` parameter will be in the mesh.
- The `*lo` parameter refers to the lowest coordinate value, that is, the location of the line corresponding to the `xlo` tag must be less than the coordinate corresponding to the `xhi` tag.
- The `region` command can be used to tag a region as a substrate in two ways:
  - If the region is being defined with the material name and the parameters `*hi` and `*lo`, the Boolean keyword `substrate` will tag this region as the substrate.
  - If the structure is being loaded from a previously saved file, the command:

```
region name=<region_name> substrate
```

will tag the region with `region_name` as the name of the substrate. This is the only occasion when the `region` command will be called *after* the `init` command.

Considerations when creating structures are:

- For 2D and 3D simulations, it is advantageous to create a coarse mesh in the lateral (that is, *y*- or *z*-directions) because lines created with the `line` command run all the way through the structure. Often, finer spacing in the *y*- or *z*-direction is needed near the surface; whereas, further in the bulk, a coarser spacing is required (to minimize the size of the problem).
- When MGOALS is used for etching and deposition, or meshing, it automatically creates a local refinement near interfaces that does not run the length of the structure.
- To specify refinement boxes, use the `refinebox` command. Control over the meshing parameters for MGOALS is explained in [Chapter 11 on page 709](#).

---

## Creating the Structure and Initializing Data

The `init` command is used to create the structure. If the `line` and `region` commands have been given to create a structure from the beginning, the `init` command does not require any options. It will take the structure definition and create a new structure.

Many process steps such as etching, deposition, diffusion, and implantation require a gas mesh. By default, Sentaurus Process does not add a gas mesh during the `init` command, but delays creating the gas mesh until it is needed. To add the gas mesh immediately, use the command:

```
pdbSet Grid AddGasMesh 1
```

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**NOTE** The parameter must be set before the `init` command to generate the gas mesh during the `init` command.

There are several ways to initialize fields at the time the initial structure is created from `line` and `region` commands:

- To initialize data everywhere in the structure, a field specification can be given in the `init` command.
- To initialize data in one particular region only, a field specification is given in the `region` command.

In both the `init` and `region` commands, the `field` parameter specifies the name of the data field that will be created and either the `concentration` parameter or the `resistivity` parameter is used to specify the value created. Although initialization was intended for dopants, a field with any name can be initialized with the `concentration` parameter. However, it will create a field with nodal values and, because stresses are computed on elements, it should not be used for initializing stress values (use the `stressdata` command or the `select` command for this). The `resistivity` parameter only works for fields that have the resistivity parameters set (which by default are only As, B, P, Sb, and In in silicon). The `init` command also is used to read a structure from a file. In this case, the parameter name serves as the type specification, and the value of the parameter is the file name or root name (in the case of DF-ISE), for example:

```
init dfise=file      ;# Read 'file.grd' and 'file.dat'.
                    # If not available try 'file.grd.gz' and 'file.dat.gz'
init dfise=file.grd ;# Only read a structure (no data) from 'file.grd'
                    # or 'file.grd.gz'
init tdr=file        ;# Read a geometry, data, and pdb parameters from
                    # 'file.tdr'.
init bnd=file        ;# Read a bnd file and mesh it.
```

The TDR format is used to restart a simulation by default when creating ‘splits’ in Sentaurus Workbench. This format stores all `pdb` parameter settings as well as numerous other settings coming from commands (see [Saving a Structure for Restarting the Simulation on page 74](#)).

The `bnd` parameter is used to load boundaries that are then meshed by MGOALS. In this case, the structure is meshed with the constrained Delaunay mesher, which makes use of lines coming from the `line` command.

The `init` command is used to specify the principal wafer orientation (`wafer.orient`), the lateral crystal orientation of the wafer flat or notch (`flat.orient`), and the `slice.angle` for the `implant` command, that is `angle`:

```
init wafer.orient= {<i> <j> <k>} flat.orient= {<i> <j> <k>} slice.angle=<n>
```

where `<i>`, `<j>`, and `<k>` are the crystallographic (Miller) indices. For more information about the wafer orientation and the slice angle, see [2D Coordinate System on page 89](#).



You also can set the `slice.angle` by using a 2D cutline, for example:

```
init slice.angle= [CutLine2D <x1> <y1> <x2> <y2>]
```

The first two values define the start point, and the third and fourth values define the endpoint in the wafer plane. The two points are defined in the wafer coordinate system (see [Understanding Coordinate Systems on page 64](#)).

---

## Defining the Crystal Orientation

The crystal orientation of the wafer is established by specifying the Miller indices of the wafer surface and the wafer flat. The `wafer.orient` and `flat.orient` parameters of the `init` command specify the Miller indices of the wafer z- and y-axes, respectively. The wafer surface orientation (z-axis) is set using `wafer.orient= {<i> <j> <k>}` where `<i>`, `<j>`, and `<k>` are the crystallographic (Miller) indices. The flat orientation (y-axis) can be set arbitrarily, but it must be orthogonal to the wafer surface orientation. The default surface orientation is 100 and the default flat orientation is a 110 direction for all values of `wafer.orient`.

**NOTE** The `wafer.orient` and `flat.orient` parameters of the `init` command apply to orthorhombic crystal systems only (such as silicon). For information on how to change the crystal orientation in hexagonal systems, see [MC Implantation into Silicon Carbide on page 162](#). Setting `info=2` in the `implant` command confirms user-defined settings for each region in the log file only.

[Table 2](#) lists the crystallographic directions of the wafer axes for the most common crystallographic orientations of the wafer as shown in [Figure 16 on page 64](#).

Table 2 Miller indices of wafer axes for each value of `wafer.orient`  
 (wafer axes are defined in [Figure 16](#))

Wafer orientation	$X_w$	$Y_w$	$Z_w$
100	$[1\bar{1}0]$	$[110]$	$[001]$
110	$[001]$	$[1\bar{1}0]$	$[110]$
111	$[\bar{1}\bar{1}2]$	$[1\bar{1}0]$	$[111]$

Sentaurus Process also allows you to define different crystal orientations for different regions by using the commands:

```
pdbSetDoubleArray <region_name> crystal.orient <double array>
pdbSetDoubleArray <region_name> flat.orient <double array>
```

To facilitate simulations of hybrid orientation technology (HOT), Sentaurus Process predefines three materials (`Silicon`, `Silicon110`, and `Silicon111`) for crystalline silicon. These materials have exactly the same properties, except for the default crystal orientations that are  $\langle 100 \rangle$ ,  $\langle 110 \rangle$ , and  $\langle 111 \rangle$  for `Silicon`, `Silicon110`, and `Silicon111`, respectively.

---

## Automatic Dimension Control

The maximum dimension of a simulation is determined by the specified `line` commands; `line x` commands define the extensions in the vertical direction and are required for 1D, 2D, and 3D simulations. If, in addition, `line y` commands are specified, the maximum dimension of the simulation will be at least 2D and, if also `line z` commands are specified, the maximum dimension of the simulation will be three dimensions. By default, Sentaurus Process delays the creation of a full-dimensional structure until it becomes necessary. This means that if you specify a 2D structure where all regions span the entire simulation domain in the `y`-direction, Sentaurus Process will create a 1D structure.

When a 2D or 3D mask is used in an `etch`, a `deposit`, or a `photo` command, Sentaurus Process automatically extrudes the structure and the mesh into the appropriate dimension and copies the data. This delay of creating a full-dimensional structure can be switched off in the `init` command by using the option `!DelayFullD`. To increase the dimension manually, use the `grid` command. If a 2D structure is required, that is, both the `line x` and `line y` commands but no `line z` commands have been specified, `grid 2D` or `grid FullD` will cause a 2D structure to be created.

Similarly, if `line x`, `line y`, and `line z` commands have been specified, `grid 2D` can be used to extrude a 1D structure to two dimensions, and a 1D or 2D structure is extruded to three dimensions using `grid 3D` or `grid FullD`. This functionality also can be used to increase the dimension of structures loaded from files. After the structure has been loaded, `line` commands can be issued and the dimension of the structure will increase automatically when necessary or manually using the `grid` command.

Sentaurus Process does not provide a facility to reduce the dimension of a simulation.

When structures are saved to DF-ISE files or TDR files (other than TDR restart files), the current maximum dimension as specified with `line` commands is used by default in the file. The dimension of the simulation itself is not affected. To save files in the current dimension, the `!FullD` parameter of the `struct` command can be used (see [Saving and Visualizing Structures on page 73](#)). TDR restart files are always saved in the dimension currently used in the simulation.

## Saving and Visualizing Structures

Sentaurus Process supports two file formats for reading and writing structures: TDR and the older DF-ISE. Both the TDR and DF-ISE formats allow saving the structure geometry with and without the bulk mesh and data, and with contacts. These files contain simply connected regions to operate smoothly with other Synopsys TCAD tools. One important option available for saving TDR and DF-ISE files is to omit saving gas regions because this may cause problems for other tools.

The TDR format allows for the saving and loading of geometry and data information along with `pdb` parameters. For more information about file types and standard file extensions, see [File Types Used in Sentaurus Process on page 46](#).

The TDR format is the preferred file format over the DF-ISE format. TDR files can be used to split a simulation, and restart and continue the simulation as if no file save or file load was performed. Besides the simulation grid and data, additional information is stored to facilitate such a restart. Only TDR files provide such restart capability; simulation results will differ if a simulation is performed in one contiguous run compared to saving and loading the intermediate state into `_bnd.tdr` or DF-ISE files.

Setting the parameter `math coord.<coord name>` configures whether the visualization coordinates will be identical to the simulation ones (when using `coord.ucs`) or will follow the DF-ISE criteria (when using `coord.dfise`).

When using DF-ISE, it is important to understand the difference between the simulation coordinates used by Sentaurus Process and the coordinates seen in Tecplot SV. For Sentaurus Process, the positive x-direction always points into the substrate in 1D, 2D, and 3D. TDR and Tecplot SV have different axis directions in 1D, 2D, and 3D. With `coord.dfise`, Sentaurus Process rotates the structure into the DF-ISE coordinate system when saving the structure and rotates the structure back when reading it.

[Figure 19 on page 67](#) shows the relation between the UCS and DF-ISE coordinates. The exposed surface of the substrate is oriented upwards; that is, the ‘up’ direction is always in the negative x-direction in the UCS.

To select the fields stored in TDR files, use the `SetTDRList` command. Each field name in the `SetTDRList` command is added to the list of fields, which are usually saved (if the field is present in the structure). This command also takes as arguments the macro parameters `Dopants` and `Solutions`, and their negative counterparts `!Solutions` and `!Dopants`. `Solutions` refers to variables of partial differential equations (PDEs). The solution variables must be stored in a TDR file if that file is to be used to continue a simulation. The parameter `Dopants` refers to the total and active dopant concentration fields. By default, TDR files are saved with both `Solutions` and `Dopants` names in `SetTDRList`. However, this requires

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many fields to be stored in the TDR files and, sometimes, it is more convenient to have fewer fields.

To do this, set `!Solutions` in `SetTDRList`, which unselects all fields. Then, specify the field names to be stored in the TDR file (see [SetAtomistic on page 1056](#) for saving KMC fields).

## Saving a Structure for Restarting the Simulation

When saving files using the TDR format, the current state of the parameter database is, by default, saved in the file. The parameter database contains all of the information necessary to restart a simulation including:

- Model settings
- Parameter settings
- Mesh settings from the `mgoals` command
- Refinement boxes from the `refinebox` command
- Temperature ramps from the `temp_ramp` command
- Gas flow specifications from the `gas_flow` command
- Line specifications from the `line` command
- Region specifications from the `region` command
- Reaction specifications from the `reaction` command
- Specifications for `point`, `polygon`, `polyhedron`
- Doping specifications with the `doping` command
- User materials created with the `mater` command
- Contact definitions created with the `contact` command
- Mask definitions created with the `mask` command
- Solution commands can be optionally stored using the `store` parameter of the `solution` command
- Term commands can be optionally stored using the `store` parameter of the `term` command
- Global Tcl variables can be stored with `fset`
- Tcl procedures can be stored using `fproc`

By default, when loading a TDR file, the changes in the parameter database are read in from the TDR file and are applied. For information about the TDR format, refer to the *Sentaurus Data Explorer User Guide*.

When saving a TDR file, the coordinate system used for visualization is also included in the file and is used by Tecplot SV when opening it. The visualization coordinate system can be changed using the `math pdb` command.

For the UCS, use:

```
math pdb coord.ucs
```

For the DF-ISE coordinate system, use:

```
math pdb coord.dfise
```

## Saving a Structure for Device Simulation

In general, there are three main steps to saving a structure appropriate for device simulation:

1. Define contacts.
2. Remesh the structure with appropriate refinement for device simulation.
3. Save the structure with contacts and with Delaunay weights.

Contacts are defined using the `contact` command. There are two main ways to define contacts, either:

- Using a *box* where the contact is created at the intersection of a material interface and a box.
- Using a *point* contact in which a region is specified by giving a point inside the region; then all boundaries of this region become a contact.

The contact is given a name and, if the command is executed multiple times with the same contact and the `add` parameter, the contact will include all parts specified. There are also options for creating a contact on the outer boundaries and so on. For more information, see [contact on page 861](#).

Remeshing the structure is needed to create a mesh that is better suited to device simulation. Typically, this means discarding process-based refinements, creating a very fine mesh under the channel, and refining on the p-n junction. A typical sequence of steps is:

- Clear the process mesh:

```
refinebox clear  
line clear
```

- Reset default settings for adaptive meshing:

```
pdbSet Grid AdaptiveField Refine.Abs.Error 1.e37  
pdbSet Grid AdaptiveField Refine.Rel.Error 1e10  
pdbSet Grid AdaptiveField Refine.Target 100.0
```

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- Set high-quality Delaunay meshes:

```
pdbSet Grid SnMesh DelaunayType boxmethod
```

- Set mesh spacing near interfaces:

```
mgoals min.normal.size=<n> normal.growth.ratio=<n>
```

- Set which interfaces will have interface refinement:

```
refinebox interface.materials= {Silicon}
```

- Specify adaptive refinement:

```
pdbSet Grid Adaptive 1
```

- Specify lines if necessary:

```
line y loc= $Ymin+0.001  
line z loc= $Zmin+0.001
```

- Specify refinement boxes, for example:

```
refinebox min= {<n> <n> <n>} max= {<n> <n> <n>} \  
xrefine= <n> yrefine=<n> zrefine=<n>           ;# gate refinement  
  
refinebox refine.fields=NetActive max.asinhdiff= {NetActive= 1.0} \  
refine.min.edge=<n> Silicon           ;# adaptive refinement on NetActive
```

- If using the IC WorkBench EV Plus interface, it may be useful to consider using the `icwb.refine.mask` command (see [Chapter 12 on page 795](#) and [icwb.refine.mask on page 924](#) for more information).

In these steps, <n> are coordinates or edge lengths in micrometers, and `normal.growth.ratio` is a unitless ratio.

To save the structure with contacts and to remove the gas and interfaces, it is easiest to use the command `struct smesh=<filename>`. In addition to omitting structural features not needed for device simulation, this command also chooses the minimal set of fields needed for device simulation (that is, dopants and nodal stresses).

Delaunay weights can be saved in the structure intended for device simulation by setting these parameters before generating the mesh:

```
pdbSet Grid SnMesh StoreDelaunayWeight 1  
pdbSet Grid Contact.In.Brep 1
```

The first parameter `StoreDelaunayWeight` creates the field variable `Delaunay-Voronoi weight (DelVorWeight)` that is used in the weighted box method in Sentaurus Device. The second parameter `Contact.In.Brep` switches on an experimental feature that creates contacts in the boundary representation (brep) and prevents changes to the mesh that can locally invalidate the Delaunay weight.

## Saving Doping Information in SiC and GaN for Device Simulations

Basic process simulation capabilities such as etching, deposition, and implantation with Monte Carlo are available for multicomponent materials, for example, silicon carbide (SiC) and gallium nitride (GaN). However, there are no activation models for dopants in these materials. To create active doping concentration fields that are equal to their associated total fields, when saving a file for transfer to device simulation, use the `diffuse` command with zero time, for example:

```
diffuse time=0 temperature=900
struct smesh= <file name>
```

## Saving 1D Profiles for Inspect

To store `.plx` files, use the `WritePlx` command. The command `SetPlxList` selects the fields to be stored in the `.plx` file. The command `SetPlxList` is similar to the `SetDFISEList` command, except that no fields are selected by default. Only the field names specified in `SetPlxList` are stored in the `.plx` file (see [SetPlxList on page 1060](#) and [WritePlx on page 1113](#)).

## Saving 1D TDR Files from 2D and 3D Simulations

The command `struct` also saves a 1D TDR file if the proper cutting coordinates are specified. In 2D, only one cutting coordinate is needed (either `x` or `y`; coordinate `z` makes no sense here). In 3D, the command saves the intersection of the planes specified by two cutting coordinates (for example, specifying `x` and `z` will save the `y` line containing those `x`- and `z`-coordinates). In addition to storing the mesh and data, these files save any contacts that apply at the cut point, so that the file can be loaded into Sentaurus Device for electrical analysis. This file can be visualized with Tecplot SV.

For example, in a 2D simulation, the following command:

```
struct tdr=filename y=0.5
```

picks up all the `x`-coordinates with `y=0.5` and saves them in a 1D TDR file.

In addition, in a 3D simulation, the following command:

```
struct tdr=filename x=0.2 z=0.1
```

saves the `y`-coordinates with `x=0.2` and `z=0.1` as a 1D TDR file.

For more information, see [struct on page 1086](#).

## The select Command (More 1D Saving Options)

The `select` command is a versatile command for many operations such as viewing results, postprocessing, and initializing or changing datasets. The basic command is:

```
select z=<expression>
```

where `<expression>` is an Alagator expression (see [Chapter 6 on page 559](#)). A simple example of an `<expression>` is the name of a data field such as `Potential` and `VTotals`. The value of the expression is stored in the selected field.

This selected field can be viewed with `print.data` or `print.1d`, for example, or the integrated values can be obtained using the `layers` command. The `select` command can also be used to set an existing data field or create a new data field, for example:

```
select z=1.0 name=MyDataField      ;# create a new datafield named MyDataField
                                   # and set it to 1.0 (everywhere)

select z= 0.1*Vacancy name=Void store ;# Set Void equal to 0.1*Vacancy
```

---

## Loading 1D Profiles: The profile Command

The `profile` command is used to load a 1D profile into 1D, 2D, or 3D structures. The file to be read should contain one x-coordinate data pair per line. Both linear (using the `linear` parameter) and logarithmic interpolation (default) are available. Profiles are loaded by using:

```
profile infile = file.dat name = Boron
```

Sentaurus Process reads the file `file.dat` and sets the field `Boron` accordingly.

---

## References

- [1] B. B. Welch, *Practical Programming in Tcl & Tk*, Upper Saddle River, New Jersey: Prentice Hall PTR, 3rd ed., 2000.



## CHAPTER 3 Ion Implantation

---

*The chapter presents the ion implantation technique used in Sentaurus Process.*

---

### Overview

Ion implantation is one of the most widely used processing techniques to introduce impurity atoms into semiconductor materials. In Sentaurus Process, either analytic functions or the Monte Carlo (MC) method is used to compute the distribution of implanted ions and the implantation damage. Analytic implantation models use the simple Gaussian and Pearson as well as the advanced dual Pearson functions. The implantation damage with analytic models is calculated according to the Hobler model [1]. The MC method uses a statistical approach to the calculation of the penetration of implanted ions into the target and accumulation of crystal damage based on the binary collision approximation [2].

Analytic implantation simulates the spatial distribution of the implanted ions based on the selected distribution function, which is described by moments. The distribution moments depend on the ionic species, implantation energy, dose, and tilt and rotation angles. Sets of moments for a given range of implantation parameters are provided in the form of lookup tables. Sentaurus Process can use implantation tables in the Dios format, TSUPREM-4 formats, and the Taurus Process table format. The implantation data available includes the default tables [3], the Advanced Calibration tables [4], the Taurus table set [5], and the original Tasch tables [6].

Sentaurus Process handles 1D, 2D, and 3D geometries for both analytic implantation simulations and MC simulations. The algorithms for analytic implantation are an integral part of Sentaurus Process; whereas, MC simulations are performed with the binary collision code Sentaurus MC [7] or Crystal-TRIM [8].

Analytic ion implantation is performed using the `implant` command:

```
implant <dopant> [energy=<n>] [dose=<n>] [tilt=<n>] [rotation=<n>]
```

Sentaurus Process simulates an analytic implantation step producing output such as:

```
----- implant -----
implant energy=35.00<keV> dose=1.00e.+14<cm-2> tilt=7.00<degree>
rotation=-90.00<degree> Boron
-----
Species          = Boron
```

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#### Overview

```
Dataset           = Boron
Energy            = 35keV
Dose (WaferDose) = 1e+14/cm2
BeamDose          = 1.0075e+14/cm2
Tilt              = 7deg
Tilt2D           = 7deg
Rotation         = -90deg
Slice angle      = -90deg
Temperature       = 300.00K
```

For a description of the analytic implantation mode, see [Analytic Implantation on page 90](#).

To switch from analytic implantation to MC implantation with Sentaurus MC, use the logical switch `sentaurus.mc` (or its alias `tmc`):

```
implant <dopant> [energy=<n>] [dose=<n>] [tilt=<n>] [rotation=<n>]
    [sentaurus.mc]
```

To switch from analytic implantation to MC implantation with Crystal-TRIM, use the logical switch `crystaltrim` (or its alias `ctrim`):

```
implant <dopant> [energy=<n>] [dose=<n>] [tilt=<n>] [rotation=<n>]
    [crystaltrim]
```

If the `cascades` switch is used in addition to `sentaurus.mc` or `crystaltrim`, the MC implantation is run in the full-cascade mode. For a description of Sentaurus MC and the Crystal-TRIM mode, see [Monte Carlo Implantation on page 131](#).

An external profile can be loaded using the `load.mc` switch:

```
implant <dopant> [energy=<n>] [dose=<n>] [tilt=<n>] [rotation=<n>]
    [load.mc] [file=<c>]
```

A TDR file must be specified with the `file` selector. `load.mc` works with files created by either Sentaurus MC or Crystal-TRIM. For a full description of the file-loading mode, see [Loading External Profiles on page 183](#).

The implantation energy in the `implant <dopant>` facility is given in keV by default. The implantation dose has two modes:

- The wafer dose (`WaferDose`), which refers to the expected dose in the structure after the implantation is finished. This dose is measured in ions per  $\text{cm}^2$ .
- Alternatively, the implantation dose can mean the beam dose (`BeamDose`).

In the wafer dose mode, the final implanted dose does not depend on the wafer orientation with respect to the ion beam. In the beam dose mode, the final implanted dose may change as tilt and rotation angles change. For a discussion of the meaning and implications of the tilt and rotation angles, see [Coordinate System on page 87](#). All angles are measured in degrees.

The mode of the implant dose can be specified with the following `pdb` switches:

```
pdbSet ImplantData DoseControl {Default WaferDose BeamDose}
```

The default value of `DoseControl` switch is `Default`, in which case, the mode of implant dose is chosen automatically based on the implant table format. If the currently selected implant tables are in Taurus/TSUPREM-4 format, the beam dose mode is used automatically. Otherwise, the wafer dose mode is applied. If the `DoseControl` switch is set to `WaferDose`, the wafer dose mode is used for all implantations regardless of table formats, likewise for `BeamDose`.

**NOTE** To obtain consistent results and prevent unexpected dose mode, it is strongly recommended to always set the `DoseControl` parameter at the start of command files to either `WaferDose` or `BeamDose`.

To override these global settings, use the logical switch `beam.dose` in the `implant` command:

```
implant <dopant> [dose=<n>] [beam.dose !beam.dose]
```

**NOTE** The main parameters for the implant statements `energy`, `dose`, `tilt`, and `rotation` must always be specified. Otherwise, default values are chosen that may not reflect the assumed process conditions.

In addition to `energy`, `dose`, `tilt`, and `rotation`, you can specify the implant temperature and the dose rate. Temperature and current are recognized as parameters by the format moment tables of Taurus Process.

If the structure is completely covered by photoresist, you can omit an implantation step by using the following `pdb` command:

```
pdbSet ImplantData ResistSkip 1
```

By default, it is not omitted.

The amount of information printed to the log file and displayed is controlled by the parameter `info` in the `implant` command. The value of `info` must be set to an integer value between 0 and 2. The higher the value, the more detailed information is printed to the log file and displayed. Output messages with an information level less than 3 can be easily understood by typical users.

**NOTE** Messages with `info=3` or more are better understood by users with greater knowledge of the Sentaurus Process implantation code and is reserved for debugging.

---

## Selecting Models

The implanted `species` must be a previously initialized species. To initialize an implantation species, use the `implant species=<dopant>` facility, that is:

```
implant species=<dopant> <material> [imp.table=<file>] [model] [damage]
```

**NOTE** This command does not perform an implantation step. It is distinguished from the standard use of the `implant` command by the keyword `species` (or `tables`).

Here, `dopant` can be any name, while `material` should be an initialized material (see [Material Specification on page 50](#)). To select the implantation table file, containing moments for the primary and lateral distributions, use the keyword `imp.table`. The `<model>` switch selects the implant model. The available choices are discussed in [Primary Distribution Functions on page 92](#). The following models are available:

- Gaussian distribution: `gaussian`
- Single Pearson distribution: `pearson`
- Single Pearson distribution with linear exponential tail: `pearson.s`
- Dual Pearson distribution: `dualpearson`
- External distribution: `point.response`

To switch on damage calculation, use the `damage` flag.

The following command, for example, changes the default implantation table for boron in silicon to `my_table.tab` and the implant model to `pearson`. It also switches off the damage calculation for boron in silicon:

```
implant species=Boron Silicon imp.table=my_table.tab pearson !damage
```

At the beginning of a Sentaurus Process run, all species are initialized automatically using the `implant species=<dopant>` facility.

[Table 3](#) lists the species that are supported and recognized in a Sentaurus Process run.

Table 3 Overview of default species initialized by Sentaurus Process

Atomic species	Molecular	Description
Aluminum, Antimony, Arsenic, Boron, Carbon, Fluorine, Gallium, Germanium, Indium, Nitrogen, Phosphorus, Silicon	AsH2, BF2, B10H14, B18H22, BC12, C2B10H12, C2B10H14, PH2	Used in analytic and MC implantation. Implant tables are available for atomic species and molecular BF <sub>2</sub> . For other molecular species, implantation is performed based on the tables for primary dopant species (As, B, or P).

Table 3 Overview of default species initialized by Sentaurus Process

Atomic species	Molecular	Description
Argon, Beryllium, Bromine, Cadmium, Chlorine, Helium, Hydrogen, Iodine, Iron, Krypton, Lead, Magnesium, Neon, Oxygen, Selenium, Sulfur, Tellurium, Tin, Titanium, Xenon, Zinc		No implantation tables are available. Analytic implantation will abort. Recommended for use in MC only.

You can overwrite or extend these settings at any time during a Sentaurus Process run. There are three principal ways to change the initial settings. With the previously described command, you can change the settings for *one* pair of dopant species and material. To overwrite the settings for *one* particular dopant species in *all* materials, use:

```
implant [species=<dopant>] tables=<name>
```

The <name> string selects a set of tables and model switches. Internally, Sentaurus Process executes a set of `implant species=<dopant> <material>` commands, which set the implant parameters for one pair of dopant species and material, respectively.

**NOTE** The keyword `tables=<name>` does not refer to a particular table or table name. It sets all tables and model switches for the species in all materials using a Tcl procedure.

The possible choices for <name> are discussed in [Tables on page 102](#). The following settings are available:

- Mixed dual Pearson and single Pearson tables: `Default`
- Taurus Process table set: `Taurus`
- University of Texas tables: `Tasch`
- Single Pearson tables used in Dios: `Dios`
- TSUPREM-4 native implant tables: `TSuprem4`

## Dios or Default Tables

For example, the following command changes all implant specifications for the species boron from the default to the Dios implantation tables and models:

```
implant species=Boron tables=Dios
```

If the above command is given without the keyword `species`, that is:

```
implant tables=<name>
```

### 3: Ion Implantation

#### Overview

the implant tables and model switches are overwritten for *all* species in *all* materials. The default setting for <name> is `Default` and the command:

```
implant tables=Default
```

is equivalent to the (default) initialization of all species and models at the beginning of each Sentaurus Process run.

## Taurus Tables

The command:

```
implant tables=Taurus [data.suf=<suffix>] [dam.suf=<suffix>]
```

switches to the Taurus mode. This means that Sentaurus Process uses the same moment tables as the Taurus Process implant library in TSUPREM-4. The file names for Taurus tables are conventionally named as `<ion>_in_<material>_<suffix>` and `<ion>_damage_in_<material>_<suffix>` for implant data and damage data, respectively. The default suffix is `standard` for both implant data and damage data. The optional parameters `data.suf` and `dam.suf` can be used to change the default suffix for implant data and damage data, respectively. By using different suffixes, different tables for the same species/material combination can coexist in the same directory.

In addition, if `tables=Taurus` was specified, several models are switched on that are not used by default. These models are:

- Beam dose control: `beam.dose` (see [Overview on page 79](#))
- Proportional range scaling: `range.sh` (see [Multilayer Implantations on page 109](#))
- Effective channelling suppression: `eff.channeling.suppress` (see [Screening \(Cap\) Layer-dependent Moments on page 96](#))
- Profile reshaping: `profile.reshaping` (see [Profile Reshaping on page 123](#))
- Preamorphization implants (PAI): `pai` (see [Preamorphization Implantation \(PAI\) Model on page 119](#))

**NOTE** This does not give the same results as TSUPREM-4; however, the results are similar.

## TSUPREM-4 Native Implant Tables

Sentaurus Process also can read implant tables in TSUPREM-4 native format. To select native TSUPREM-4 implant tables, use the command:

```
implant [species=<c>] tables=TSuprem4 [ts4.prefix=<c>]
```

If `species` is specified, TSUPREM-4 implant tables are applied to this particular species only. If `species` is not specified, implant tables are applied to all TSUPREM-4 supported species, which include antimony, arsenic,  $\text{BF}_2$ , boron, fluorine, indium, fluorine, and phosphorus.

The name of the TSUPREM-4 native implant table conventionally uses the species name or the species name with a prefix. Eight different implant tables in silicon are distinguished by a prefix. For example, `chboron` (which means channeling boron) is one of the boron implant tables in silicon.

The parameter `ts4.prefix` takes one of the following values: `default`, `none`, `le`, `ch`, `dual`, `ut`, `tr`, or `scr`:

- The default value is `ts4.prefix=default`, which selects TSUPREM-4 default implant tables, that is, `antimony`, `fluorine`, `chboron`, `dual.ars`, `dual.pho`, `dual.bf2`, and `tr.indium` for antimony, fluorine, boron, arsenic, phosphorus,  $\text{BF}_2$ , and indium, respectively.
- If `ts4.prefix=none`, no prefix is added, so the TSUPREM-4 implant tables (`antimony`, `boron`, and so on) are used for antimony, boron, and so on, respectively. If the corresponding table for a species in a material is not available, the default table is used.
- If `ts4.prefix=le` or `ch`, then `le<species>` or `ch<species>` tables are selected, for example, `leboron` or `chboron` for boron implantation. If the corresponding table for a species in a material is not available, the default table is used.
- If `ts4.prefix=dual`, `ut`, `tr`, or `scr`, then `<prefix>.<species>` tables are selected, for example, `dual.boron`, `ut.boron`, `tr.boron`, and `scr.boron` for boron implantation. If the corresponding table for a species in a material is not available, the default table is used.

You also can use your own TSUPREM-4 native-formatted implant tables by using the following command:

```
implant species=<dopant> <material> imp.table=<file> ts4.species=<name>  
ts4.material=<name>
```

`imp.table` specifies the file name (which should have the file-name extension `.ts4`) that contains implant moment tables in TSUPREM-4 format, such as `mys4imp0.ts4`. If the file is in the same directory where Sentaurus Process is being run, then only the name of the file is needed for `imp.table`; otherwise, the full path is required. `ts4.species` specifies the TSUPREM-4 table name for the dopant, which is one of the predefined impurity names in the implant data file. For example, in the standard `s4imp0`, the valid names for boron implant are `boron`, `leboron`, `chboron`, `ut.boron`, `tr.boron`, and `scr.boron`. `ts4.material` specifies the material name used in TSUPREM-4, which is one of the predefined material names in the implant data file. For example, in the standard `s4imp0`, the material names include `silicon`, `polysilicon`, `oxide`, `nitride`, and so on.

### 3: Ion Implantation

#### Overview

If not specified, `ts4.species` and `ts4.material` default to the species name (for example, Boron) and the material name (for example, Silicon) used in Sentaurus Process, respectively.

**NOTE** Ensure that these names match exactly the names in the TSUPREM-4 implant data file. While these names are not case sensitive, they cannot be abbreviated. For example, while `ts4.material=Polysilicon` is acceptable; `ts4.material=poly` will result in an error.

---

## Multirootation Implantation

The simulation of multirootation implantations for both the MC and analytic methods is controlled by the integer parameter `mult.rot=<n>`. If `mult.rot` is set to a number higher than 1, an implantation with a revolving ion beam is simulated. Starting with the user-defined rotation angle, Sentaurus Process performs `mult.rot` implantations with the same energy and `tilt` in one `implant` command.

The rotation angle is incremented by  $(360^\circ)/\text{mult.rot}$  and, for each implantation step, the dose is the  $1/\text{mult.rot}$ -th part of the user-specified dose.

---

## Energy Contamination Implantation

Sentaurus Process has a built-in feature for implantation with energy contamination, in which a fraction of the nominal dose has a different energy than the specified energy. To perform an energy contamination implantation, you must specify the parameter `contamination` in the `implant` command. The syntax is:

```
implant dose=<n1> energy=<n2>  
      contamination= {energy=<n3> dose.fraction=<fraction>} ...
```

Then, Sentaurus Process treats the implantation as two separate implantations in the following order:

```
implant dose=<n1*fraction> energy=<n3> ...  
implant dose=<n1*(1-fraction)> energy=<n2> ...
```



## Adaptive Meshing during Implantation

Adaptive meshing during implantation is active whenever adaptive meshing is switched on, that is, `pdbGet Grid Adaptive` returns a 1. It also can be switched on by specifying the parameter `Adaptive` in the `implant` command. For details, see [Adaptive Meshing during Implantation on page 688](#).

Since generally analytic implantation and MC implantation produce similar results, MC implantation can take advantage of this similarity for adaptive meshing. When adaptive meshing is active, MC implantation will first call analytic implantation for mesh refinement. At the end of analytic implantation, the concentration generated by the analytic implantation is discarded, while the new mesh is used for MC implantation. If the analytic implantation fails for whatever reasons (such as no implant tables for certain materials), Sentaurus Process issues a warning, and the MC implantation proceeds with the original mesh.

## Coordinate System

### Coordinates for Implantation: Tilt and Rotation Angles

Regardless of whether a simulation is 1D, 2D, or 3D, the direction of the ion beam is defined relative to the wafer coordinate system (see [Figure 16 on page 64](#)) by the values of the tilt and rotation parameters of the `implant` command. [Figure 21](#) shows the tilt and rotation angles in the wafer coordinate system.

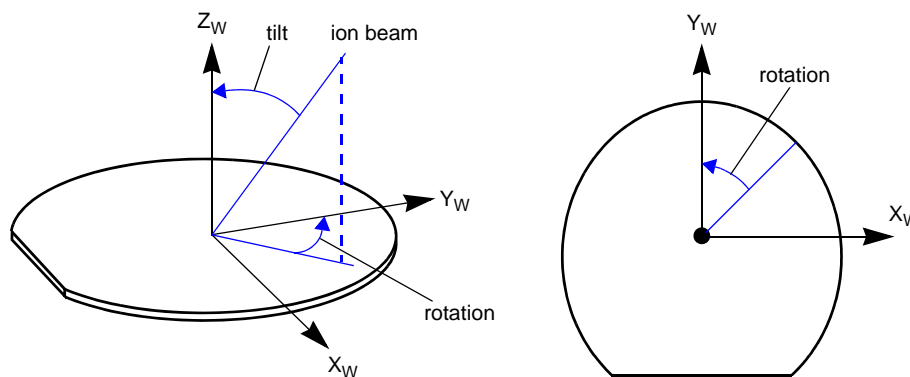


Figure 21 Tilt and rotation angles for implantation; beam angle shown corresponds to tilt = 20 and rotation = 45

The tilt and rotation angles are measured from the ion beam to the wafer z-axis and wafer y-axis, respectively. In this definition, the tilt angle is always positive, and between  $0^\circ$  (inclusive)

### 3: Ion Implantation Coordinate System

and  $90^\circ$ . However, for convenience, a negative tilt angle is allowed, and it is converted automatically to a positive tilt by adding  $180^\circ$  to the specified rotation angle. The rotation angle is positive when the beam is rotated in the clockwise direction about the wafer z-axis, and it is negative when it is counterclockwise.

Since the tilt and rotation angles are measured with respect to the wafer axes, the direction of the beam in the simulation coordinate system depends on the slice angle.

Figure 22 shows the relationship between wafer coordinates, simulation coordinates, and the beam direction.

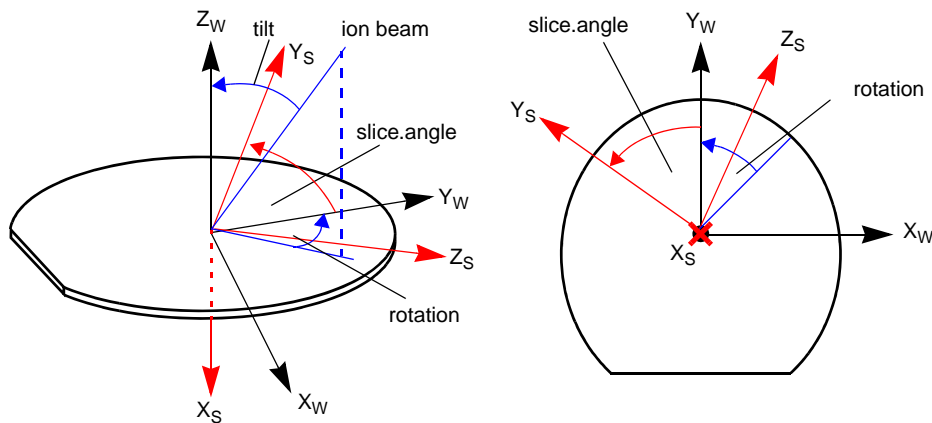


Figure 22 Tilt and rotation angles for implantation; angles shown correspond to tilt = 20, rotation = 45, and slice.angle = 60

The default values of `tilt` and `rotation` are  $7^\circ$  and  $-90^\circ$ , respectively; in other words, by default the incident ion beam is directed parallel to the wafer flat tilted away from the wafer x-axis. For the default slice angle of  $-90^\circ$ , this corresponds to an ion beam in the simulator xy plane, tilted away from the simulator y-axis. In a 2D simulation, the default ion beam comes from the left side.

Figure 23 on page 89 shows the projection into the wafer plane of the direction from which the beam strikes the wafer for `tilt` > 0 and various rotation angles.

The default simulation coordinate system (`slice.angle` = -90) is also shown.

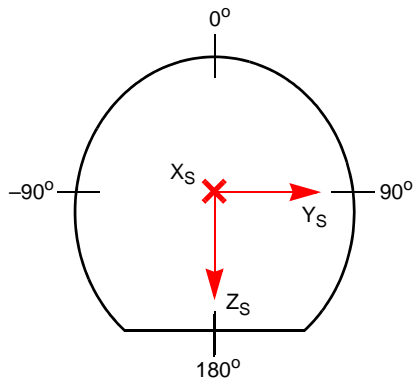


Figure 23 Implant rotation directions for positive tilt

Figure 24 shows clearly that the orientations shown in Figure 23 are consistent with the conventions defined in Figure 21 on page 87. A rotation of  $90^\circ$  corresponds to rotating the wafer a quarter turn counterclockwise.

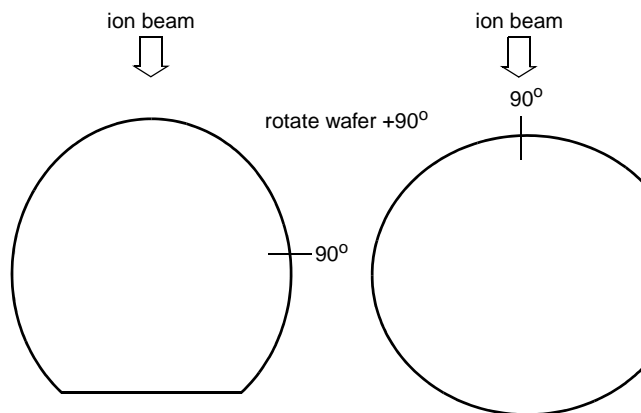


Figure 24 Rotating wafer and fixed beam direction

---

## 2D Coordinate System

In a 2D simulation, the orientation of the 2D simulation plane with respect to the wafer coordinate system must be defined. The angle between the 2D simulation plane and the y-axis is set by the `slice.angle`. The default value is  $-90^\circ$ , which orients the 2D simulation plane parallel to the wafer flat. The transformed y-axis ( $y_s$ ) is the y-axis in the 2D simulation plane.

### 3: Ion Implantation

#### Analytic Implantation

There are two ways to set `slice.angle` in the `init` command:

- To set directly, use:

```
init slice.angle=<n>
```

- To set by specifying a 2D cutline, use:

```
init slice.angle=[CutLine2D <x1> <y1> <x2> <y2>]
```

The `<x1>` and `<y1>` define the start point, and `<x2>` and `<y2>` define the end point in the wafer plane. The two points are in the wafer coordinate system (for more information on coordinate systems, see [Understanding Coordinate Systems on page 64](#)).

In general, the tilt projected to the 2D simulation plane is different from the `tilt` value. It is given by the geometric relation:

$$\cos(\text{tilt2D}) = \frac{\cos(\text{tilt})}{\sqrt{\cos^2(\text{tilt}) + \sin^2(\text{tilt}) \cdot \cos^2(\text{rotation} + \text{slice.angle})}} \quad (1)$$

The angle `tilt2D` can be found in the output of Sentaurus Process and can be negative depending on the rotation angle and slice angle.

The `tilt` value defines the relation between the wafer dose (`dose`), which is given at the command line by default and the dose, which would have to be specified in the beam-dose mode to obtain the same final implanted dose, that is:

$$\text{BeamDose} = \frac{\text{dose}}{\cos(\text{tilt})} \quad (2)$$

`BeamDose2D` as it appears in the Sentaurus Process output is defined using `tilt2D`, that is:

$$\text{BeamDose2D} = \frac{\text{dose}}{\cos(\text{tilt2D})} \quad (3)$$

---

## Analytic Implantation

Analytic implantation is performed using empirical point-response distributions. Point-response distributions are generated using the method of moments. The moments representing the primary and lateral point-response functions are taken from implantation tables.

For the purposes of 2D simulations based on analytic functions, an ion beam incident at the point  $(\xi, \eta)$  is assumed to generate a distribution function  $F(x, y, \xi, \eta)$ .

To calculate the concentration of the implanted species at a point  $(x, y)$  of the simulation domain, the superposition of all distribution functions of all possible points of incidence  $(\xi(s), \eta(s)) \in \Gamma_{\text{gas}}$  must be computed:

$$C(x, y) = N_d \int_{\Gamma_{\text{gas}}} F(x, y, \xi(s), \eta(s)) ds \quad (4)$$

where  $N_d$  is the total dose per exposed area and  $C(x, y)$  is the doping profile.

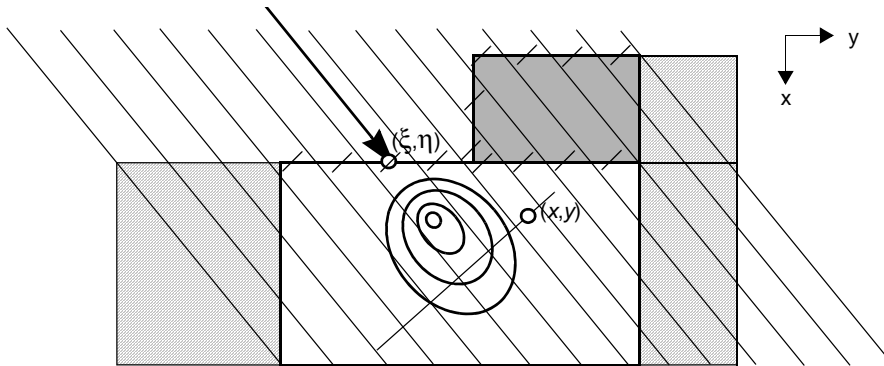


Figure 25 Point-response distribution for a particle incident at the point  $(\xi, \eta)$  at the surface; intervals are used for lateral integration at the point  $(x, y)$ ; shaded regions to left and right mark the lateral extension elements

The 2D distribution functions are always assumed to be given as a product of two 1D distribution functions orthogonal to each other: a primary distribution function  $f_p(x)$  and a lateral distribution function  $f_l(x)$ :

$$F(x, y, \xi, \eta) = f_p(x - \xi(s)) \cdot f_l(y - \eta(s)) \quad (5)$$

To perform the computation of the convolution integral in 2D, Sentaurus Process uses a set of lateral intervals perpendicular to the projected ion beam. A local 1D layer structure is computed in each interval. The spacing and width of these intervals depend on the complexity of the exposed gas surface.

In 3D, Sentaurus Process uses a slightly different algorithm. The point-response function is a 3D function. The lateral function  $f_l(x)$  is also used in the third direction:

$$F(x, y, z, \xi, \eta, \Theta) = f_p(x - \xi(s)) \cdot f_l(y - \eta(s)) \cdot f_l(z - \Theta(s)) \quad (6)$$

assuming an axially symmetric point-response function. The lateral integration is performed in the plane perpendicular to the ion beam. For each point in the lateral integration plane, again, a local 1D layer structure is computed.

---

## Primary Distribution Functions

Primary distribution functions can be set for a dopant/material combination using:

```
implant species=<dopant> <material>
  [{gaussian pearson pearson.s dualpearson point.response}]
```

The previous model selection is used if no selection for <model> is made. The primary distribution is used to represent the point-response function in 1D or the vertical point-response in 2D and 3D. Point-response functions are characterized by moments.

The first moment, the projected range  $R_p$ , is defined as:

$$R_p = \int_{-\infty}^{\infty} x \cdot f(x) \cdot dx \quad (7)$$

while the higher moments  $m_i$  are defined as:

$$m_i = \int_{-\infty}^{\infty} (x - R_p)^i \cdot f(x) \cdot dx \quad (8)$$

The standard deviation  $\sigma$ , the skewness  $\gamma$ , and the kurtosis  $\beta$  are defined as:

$$\sigma = \sqrt{m_2} \quad (9)$$

$$\gamma = \frac{m_3}{\sigma^3} \quad (10)$$

$$\beta = \frac{m_4}{\sigma^4} \quad (11)$$

### Gaussian Distribution: gaussian

$$f_p(x) = \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{(x - R_p)^2}{2\sigma^2}\right) \quad (12)$$

$$\gamma = 0 \quad (13)$$

$$\beta = 3 \quad (14)$$

## Pearson Distribution: pearson

The Pearson distributions are the solution to the following differential equations:

$$\frac{d}{dy}f(y) = \frac{y-a}{b_0+b_1 \cdot y+b_2 \cdot y^2} \cdot f(y), \quad y = x - R_p \quad (15)$$

$$\begin{aligned} a &= b_1 = -\frac{\gamma \cdot \sigma \cdot (\beta + 3)}{A} \\ b_0 &= -\frac{\sigma^2 \cdot (4\beta - 3\gamma^2)}{A} \\ b_2 &= -\frac{2\beta - 3\gamma^2 - 6}{A} \\ A &= 10\beta - 12\gamma^2 - 18 \end{aligned} \quad (16)$$

Different types of Pearson distribution are distinguished by different values of  $\gamma$  and  $\beta$ :

$$\begin{aligned} 0 < \gamma < 32 \\ \beta > \frac{48 + 39\gamma^2 + 6(\gamma^2 + 4)^{3/2}}{32 - \gamma^2} \quad \text{Type IV} \end{aligned} \quad (17)$$

$$\begin{aligned} 0 < \gamma < 32 \\ \beta = \frac{48 + 39\gamma^2 + 6(\gamma^2 + 4)^{3/2}}{32 - \gamma^2} \quad \text{Type V} \end{aligned} \quad (18)$$

$$\begin{aligned} 0 < \gamma < 32 \\ 3 + 1.5 \cdot \gamma < \beta < \frac{48 + 39\gamma^2 + 6(\gamma^2 + 4)^{3/2}}{32 - \gamma^2} \quad \text{Type VI} \end{aligned} \quad (19)$$

The Pearson–IV distribution is given by:

$$f_p(y) = K |b_2 y^2 + b_1 y + b_0|^{\frac{1}{2b_2}} \cdot \exp \left( -\frac{\frac{b_1}{b_2} + 2a}{\sqrt{4b_2 b_0 - b_1^2}} \operatorname{atan} \left( \frac{2b_2 y + b_1}{\sqrt{4b_2 b_0 - b_1^2}} \right) \right) \quad (20)$$

Sentaurus Process automatically switches between the Pearson–IV, Pearson–V, and Pearson–VI distribution functions depending on the conditions for  $\gamma$  and  $\beta$  given in [Eq. 17](#) to [Eq. 19](#). The factor  $K$  is chosen to fulfill the normalization condition:

$$\int_{-\infty}^{\infty} f_p(x) dx = 1 \quad (21)$$

## Pearson Distribution with Linear Exponential Tail: pearson.s

A linear exponential tail is added to the Pearson distribution. This is performed in an attempt to describe more accurately the profile tails for some implantations, that is:

$$f_p(x) = \begin{cases} P_p(x), & 0 \leq x < x_{max} \\ P_v(x), & x_{max} < x \leq x_a \\ P_l(x), & x_a \leq x < \infty \end{cases} \quad (22)$$

where  $P_p$  is the Pearson distribution,  $P_v$  is a transition function, and  $P_l$  is the exponential tail.

The decay length of the exponential tail is give by the parameter  $l_{exp}$  :

$$\begin{aligned} x_{max}: \quad P_{max} &:= P_p(x_{max}) = \max P_p(x) \\ x_a \geq x_{max}: \quad P_a &:= P_p(x_a) = \frac{1}{2} P_p(x_{max}) \\ P_v(x) &= P_p(x_{max}) \cdot \exp(A_1(x-x_{max})^2 + B(x-x_{max})^3) \\ P_l(x) &= P_p(x) + \frac{x-x_{max}}{l_{exp}} \cdot P_p(x_{max}) \cdot \exp\left(-\frac{x-x_{max}}{l_{exp}}\right) \end{aligned} \quad (23)$$

The constants  $A_1$  and  $B$  are computed from the continuity conditions:

$$P_l(x_a) = P_v(x_a) \quad (24)$$

and:

$$\begin{aligned} \frac{d}{dx}P_l(x)|_{x_a} &= \frac{d}{dx}P_v(x)|_{x_a} =: P'_a \\ A_1 &= \frac{3 \ln \frac{P_a}{P_{max}}}{(x_a - x_{max})^2} - \frac{P'_a}{P_a(x_a - x_{max})} \\ B &= \frac{-2 \ln \frac{P_a}{P_{max}}}{(x_a - x_{max})^3} + \frac{P'_a}{P_a(x_a - x_{max})^2} \end{aligned} \quad (25)$$

**NOTE** Exponential tail distributions are available with the Dios tables. However, care is required when using the exponential tail for implantation with large tilt angles. The  $l_{exp}$ -fit in these tables was performed for a standard  $7^\circ$  tilt in amorphous materials and does not apply to large tilt angles or strong channeling conditions.



## Dual Pearson Distribution: dualpearson

The most advanced primary distributions are available with the dual Pearson function [9], which can be chosen with the switch `dualpearson`. The dual Pearson model includes a superposition of two Pearson functions:

$$f_p(x) = \text{ratio} \cdot f_{\text{head}}(x) + (1 - \text{ratio}) \cdot f_{\text{tail}}(x) \quad (26)$$

The head and tail functions are two independent Pearson functions. The head function accounts for the profile of ions that do not channel (nonchanneling or amorphous part). The tail function accounts for the channeled ions that form the characteristic tail in the implantation profile.

A `dualpearson` function is characterized by nine parameters: the two sets of four Pearson parameters and the ratio between the amorphous and channeling doses. These parameters are usually taken from moment table files.

You can set the individual moments directly in the Sentaurus Process command line, for example:

```
implant species=<dopant> <material> [rp=<n>] [stdev=<n>] [gamma=<n>]
[beta=<n>] [rp2=<n>] [stdev2=<n>] [gamma2=<n>] [beta2=<n>] [ratio=<n>]
[lat.stdev=<n>] [lat.stdev2=<n>]
```

This overwrites the parameters found in the specified implant table. Using this facility, it is also possible to force the Pearson distributions in the `dualpearson` and `pearson` models to behave like a Gaussian distribution, for example:

```
implant species=Boron Silicon pearson gamma=0 beta=3
```

The first statement sets the implantation model to a Pearson distribution. The parameters are read from the default table. The skewness and kurtosis are set according to Eq. 13 and Eq. 14, overwriting the values found in the table. This results in a Gaussian distribution for the function characterizing the amorphous part of the profile.

You can enable or disable individual moments using `<moment>.isset pdb` switches, where `<moment>` is the name of the moments such as `rp`, `stdev`, `rp2`, `stdev2`, and so on. For example:

```
pdbSetBoolean Silicon Boron rp.isset 0
```

This command would disable a user set value for `rp`.

**NOTE** All moments set at the command line are ignored after a new implant table is selected, or an implant table has been specified again using the `implant species=<species> <material> imp.file=<name>` command. In this case, the moments from this new implant table will then be used, regardless of which moments have been set previously at the command line.

## Point-Response Distribution: point.response

See [Point-Response Interface](#) on page 114.

---

## Screening (Cap) Layer-dependent Moments

Cap layer-dependent implant tables are used to describe correctly the screening of the ion beam in the structure. The implant moments in a particular region generally depend on the combined thickness of all layers above this region. The moments are parameterized with respect to the effective thickness  $t_i^{\text{cap}}$ , which is defined as:

$$t_i^{\text{cap}} = \sum_j^{j < i} t_j f_j^{\text{eff}} \quad (27)$$

that is, as the sum over the thicknesses of all layers above the current layer multiplied by corresponding efficiency factors  $f_j^{\text{eff}}$ . These factors can be set for a particular material and a species using:

```
implant species=Boron Oxide eff.caplayer.thick 1.0
```

The default value is 1 for all materials other than silicon, where it is set to zero. Therefore, silicon layers are effectively not included in the total effective cap layer thickness.

If the implant table for a specific `<material>/<species>` combination does not contain an explicit cap layer dependence, the effective channeling suppression model is used. This model suppresses the channeling tail by multiplying the channeling part in [Eq. 26](#) by a factor  $r_{\text{suppress}}$  calculated according to:

$$r_{\text{suppress}} = \frac{1}{\frac{1}{2} \cdot \frac{C(R_{p, \text{head}})}{C(R_{p, \text{head}}) + C(R_{p, \text{tail}})} + \left(\frac{\text{MinRatio}}{\sigma}\right)^{\text{Exponent}}} \quad (28)$$

where  $C(R_{p, \text{head}})$  and  $C(R_{p, \text{tail}})$  are the peak concentrations of the unscaled profile, and  $\sigma$  is defined as:

$$\sigma = \sum_i \frac{t_i}{R_{pi}} \quad (29)$$

using the values of  $R_p$  for the amorphous (head) part of the profile for all layers  $i$  above the present layer. The amorphous part of the profile is multiplied by  $1 - r_{\text{suppress}}$  to conserve the total dose.

MinRatio is the minimum value of the ratio  $\sigma$ . The parameters MinRatio and Exponent can be set in the parameter database, that is:

```
pdbSet <material> <species> MinRatio
```

```
pdbSet <material> <species> Exponent
```

The model is applied only for values of  $\sigma$  greater than MinRatio and effective cap layer thickness greater than 2.1 nm. The effective channeling suppression model can be switched on using:

```
implant species=<species> <material> [eff.channeling.suppress]
```

The model remains inactive for explicitly cap layer-dependent implant tables.

**NOTE** This model is switched off by default and is switched on in the Taurus/TSUPREM-4 mode.

---

## Lateral Straggle

The lateral straggling of the distribution of implanted ions is specified by defining a lateral distribution function, which is a Gaussian distribution with a lateral standard deviation  $\sigma_l$ :

$$f_l(x, y) = \frac{1}{\sqrt{2\pi} \sigma_l(x)} \exp\left(-\frac{y^2}{2\sigma_l^2(x)}\right) \quad (30)$$

In general, the lateral standard deviation depends on the vertical depth of the profile. The depth dependence can be switched on or off for a particular combination of dopant species and material using the flag `depth.dependent`:

```
implant species=<dopant> <material> [depth.dependent]
```

### 3: Ion Implantation

Analytic Implantation

The lateral standard deviation can also be set in the command line using the keyword `lat.stdev`:

```
implant species=<dopant> <material> [lat.stdev=<n>] [lat.stdev2=<n>]
```

where `lat.stdev2` sets the lateral standard deviation for the tail function. If either `lat.stdev` or `lat.stdev2` is set, Sentaurus Process switches to the depth-independent lateral straggling. All `depth.dependent` switches are ignored in this case.

An additional scaling factor for both the depth-dependent and depth-independent lateral standard deviation can be used to vary the lateral straggling:

```
implant species=<dopant> <material> [lat.scale=<n>] [lat.scale2=<n>]
```

## Depth-dependent Lateral Straggle: Sentaurus Process Formulation

If a TSUPREM-3-compatible implantation table is used (`.s3`), the depth-dependent lateral standard deviation is calculated according to:

$$\sigma_l(x) = \text{lstdev} \cdot \exp\left(-\frac{x}{\text{lstdev} \cdot \text{lv}}\right) \quad (31)$$

where `lstdev` and `lv` are parameters taken from the implantation table. There are two independent sets of parameters for the two Pearson functions in the `dualpearson` model. This formulation also is used with the `Tasch` implantation tables.

## Depth-dependent Lateral Straggle: Dios Formulation

If a Dios-compatible implantation table is used, the depth-dependent lateral standard deviation is calculated using a vector of five parameters  $p_1, p_2, \dots, p_5$ . The following formula is applied [10]:

$$\sigma_l(x) = \text{stdev} \max \left( 0.01, \frac{\log\left(\exp\left(p_1 \cdot \left(\frac{p_2 \cdot x}{R_p} + p_3\right)\right) + \exp\left(p_1 \cdot \left(\frac{p_4 \cdot x}{R_p} + p_5\right)\right)\right)}{p_1} \right) \quad (32)$$

There is only one set of these parameters in each table entry. In the case of the `dualpearson` implant model (see Eq. 32), the same set of parameters  $p_1, p_2, \dots, p_5$  together with the standard deviation of the first Pearson function described by `stdev` is applied to both the amorphous and the channeling part of the distribution.

## Depth-dependent Lateral Straggle: Taurus Formulation

If a TSUPREM-4/Taurus-compatible implantation table is used, the depth-dependent lateral standard deviation is calculated using two parameters:

$$\sigma_l(x) = \sigma_0 \cdot \left(1 + \Delta\sigma \left(\frac{x}{R_p} - 1\right)\right) \quad (33)$$

The depth-independent standard deviation  $\sigma_0$  and the depth-dependent slope  $\Delta\sigma$  are read from the moment table.

This formulation is compatible with the Dios formulation (see [Depth-dependent Lateral Straggle: Dios Formulation](#)) for the following conditions:  $p4 = 0$ ,  $p1 \cdot p5 = -\infty$ . The remaining parameters can be translated as follows:

$$\begin{aligned} \sigma_0 &= \text{stdev} \cdot (p2 + p3) \\ \Delta\sigma &= p2 / (p2 + p3) \end{aligned} \quad (34)$$

---

## Analytic Damage: Hobler Model

The damage distribution is calculated using [Eq. 32](#) and [Eq. 5, p. 91](#). The primary and lateral distribution functions are taken from the literature [10]. The primary function consists of a Gaussian function and an exponential tail, joined continuously with continuous first derivatives. The distribution is normalized. The normalization factors are  $c_1$  and  $c_2$ , and  $N_{\text{vac}}$  is the number of Frenkel defects per ion.

Three types of primary function are distinguished:

- Type 0

A simple Gaussian distribution with the primary range  $R_p$  and the standard deviation  $\sigma$ :

$$f_p(x) = N_{\text{vac}} c_1 \exp\left(-\frac{(x - R_p)^2}{2\sigma^2}\right) \quad (35)$$

- Type 1

For light ion species:

$$f_p(x) = \begin{cases} N_{\text{vac}} c_1 \exp\left(\frac{x}{l}\right), & x \leq x_0 \\ N_{\text{vac}} c_2 \exp\left(-\frac{(x - R_p)^2}{2\sigma^2}\right), & x > x_0 \end{cases} \quad (36)$$

### 3: Ion Implantation

Analytic Implantation

where  $l$  is the decay length of the exponential function. The joining point  $x_0$  is calculated by:

$$x_0 = R_p - \frac{\sigma^2}{l} \quad (37)$$

- Type 2

For heavier ions, the exponential tail is directed towards the bulk:

$$f_p(x) = \begin{cases} N_{\text{vac}}c_2 \exp\left(-\frac{(x-R_p)^2}{2\sigma^2}\right), & x \leq x_0 \\ N_{\text{vac}}c_1 \exp\left(-\frac{x}{l}\right), & x > x_0 \end{cases} \quad (38)$$

In this model, four parameters  $R_p$ ,  $\sigma$ ,  $l$ , and  $N_{\text{vac}}$  are required. These parameters were obtained by MC simulations between 1 keV and 300 keV. If damage calculation is switched on, that is, if:

```
implant species=<dopant> damage
```

has been set, Sentaurus Process generates these parameters using an internal lookup table, which contains the original data available for boron, BF<sub>2</sub>, phosphorus, arsenic, and antimony in silicon.

**NOTE** For some other species, the parameters of these original species are used that are closest with respect to the atomic number in the periodic table of elements. Nitrogen uses the boron parameters. Silicon and aluminum use the phosphorus parameters. Germanium and gallium use the arsenic parameters, and indium uses the antimony parameters. Damage calculation is automatically switched off for any other species.

Type 0 is used for boron at energies  $E < 20$  keV, phosphorus at  $E < 55$  keV, and arsenic at  $E > 170$  keV. Type 1 is applied to boron and phosphorus elsewhere, and Type 2 is applied to arsenic at energies below 170 keV and antimony at all energies.

The lateral distribution is modeled using [Eq. 32](#). The five lateral parameters  $p_1$ ,  $p_2$ , ...,  $p_5$  are provided in the internal lookup table.

An alternative to the internal lookup table is to load a table file similar to the implant tables. The keyword for this is `dam.table`:

```
implant species=<dopant> <material> [dam.table=<name>]
```

This overwrites the internal lookup table for the above mentioned species using the parameters from the table instead. In addition, it enables damage calculation for species other than the original ones.

---

## Datasets

Several datasets are used to store the as-implanted profile and the implantation damage. Point-defect profiles are created at the end of the implantation step. Datasets with the ending `_Implant` contain profiles generated during subsequent implant steps. These datasets are deleted at the beginning of the next `diffuse` step.

Table 4 Datasets used in analytic implantation step

Dataset	Description
Damage	Accumulative damage (damage history). At the end of an <code>implant</code> step, the <code>Damage_LastImp</code> concentration is added using <code>Dfactor</code> . This dataset is deleted by the <code>diffuse</code> command.
Damage_LastImp	Damage created during the last <code>implant</code> step. This dataset is deleted at the end of the <code>implant</code> step.
<dopant>	Accumulative density of the dopant concentration. At the end of an <code>implant</code> step, the <code>&lt;dopant&gt;_LastImp</code> concentration is added to <code>&lt;dopant&gt;</code> .
<dopant>_Implant	Accumulative density of the dopant concentration. At the end of an <code>implant</code> step, the <code>&lt;dopant&gt;_LastImp</code> concentration is added to <code>&lt;dopant&gt;_Implant</code> . This dataset is deleted by the <code>diffuse</code> command.
<dopant>_LastImp	As-implanted dopant concentration that contains the profile generated during the last <code>implant</code> step. This dataset is deleted at the end of the <code>implant</code> step.
Int_Implant	Accumulative interstitial profile updated at the end of an <code>implant</code> step.
Vac_Implant	Accumulative vacancy profile updated at the end of an <code>implant</code> step.
Int<component>_Implant	Accumulative interstitial profiles in multicomponent material with <code>DistinctDefects</code> set to true, where <code>&lt;component&gt;</code> is the component of the composition of the material. For example, in SiC, interstitial profiles include <code>IntSilicon_Implant</code> and <code>IntCarbon_Implant</code> .
Vac<component>_Implant	Accumulative vacancy profiles in multicomponent material with <code>DistinctDefects</code> set to true, where <code>&lt;component&gt;</code> is the component of the composition of the material. For example, in SiC, interstitial profiles include <code>VacSilicon_Implant</code> and <code>VacCarbon_Implant</code> .

## Tables

### Implantation Table Library

The implantation table library is located at `$SPHOME/ImpLib/`.

#### Dios Tables

The subdirectory `Dios/` contains the tables used by default in Dios. These tables can be made the default tables for all species in Sentaurus Process by using:

```
implant tables=Dios
```

For arsenic, antimony, phosphorus, indium, germanium, gallium, nitrogen, and aluminum, the data in these tables are taken from the literature [3]. The values for boron are obtained from simulations with the 1D process simulator TESIM [11]. The values for energies  $\geq 1$  MeV are taken from the literature [2]. These tables provide moments that can be used with the Gaussian and Pearson implantation models.

#### Taurus Tables

The directory `Taurus/` contains the Taurus Process implant tables for boron,  $\text{BF}_2$ , phosphorus, germanium, indium, antimony, and arsenic. To select these tables as the default, use the keyword `Taurus`:

```
implant tables=Taurus
```

The tables contain calibrated data from sub-keV to above 10 MeV. The calibration was performed using both SIMS data and Taurus MC calculations [5].

#### Default Tables

The directory `Default/` contains tables extracted from MC simulations with Crystal-TRIM [4], which are tabulated in DIOS format. The data are available for arsenic, antimony,  $\text{BF}_2$ , boron, phosphorus, indium, and germanium in silicon, polysilicon, oxide, and nitride.

These tables provide moments that can be used with all implantation models including the `dualpearson` model. For silicon, dual Pearson moments are available that depend on energy, tilt, dose, and cap-layer thickness. For polysilicon, oxide, and nitride, single Pearson moments are available that depend on energy and tilt only.

The tables cover different energy ranges. The tilt angles range from  $0^\circ$  to  $60^\circ$ , and the oxide thickness ranges from 0 nm to 100 nm. There are tables for low, medium, and high doses for all species except germanium where only one table for a medium to high dose is available.



Sentaurus Process selects the correct table depending on the implant dose. These tables constitute most of the default tables used in Sentaurus Process.

The default tables used in Sentaurus Process are selected by using the command:

```
implant tables=Default
```

This implant command not only selects the tables from the `Default/` directory for arsenic, antimony,  $\text{BF}_2$ , boron, phosphorus, indium, and germanium in silicon, polysilicon, oxide, and nitride, but also selects the tables from the `Taurus/` directory for carbon, fluorine, and germanium in silicon, polysilicon, oxide, and nitride (see [Table 5](#)). For all other species and materials, the respective `Dios` tables are used.

Table 5 Default tables

Species	Table file	Energy range [keV]
Arsenic	<material>As_1e12-5e13.tab <material>As_1e13-8e14.tab <material>As_2e14-6e15.tab	0.5–400
Antimony	<material>Sb_1e12-5e13.tab <material>Sb_1e13-5e14.tab <material>Sb_2e14-1e16.tab	1.5–600
$\text{BF}_2$	<material>BF2_1e12-5e13.tab <material>BF2_1e13-8e14.tab <material>BF2_2e14-6e15.tab	0.5–400
Boron	<material>B_1e12-4e13.tab <material>B_1e13-6e14.tab <material>B_16e13-8e15.tab	0.2–517 (silicon) 0.2–480 (other materials)
Carbon	carbon_in_<material>_standard	0.2–400
Fluorine	fluorine_in_<material>_standard	0.2–400
Germanium	germanium_in_<material>_2007	0.6–800
Indium	<material>In_1e12-4e13.tab <material>In_1e13-6e14.tab <material>In_16e13-8e15.tab	1–400
Phosphorus	<material>P_1e12-4e13.tab <material>P_1e13-6e14.tab <material>P_16e13-8e15.tab	0.3–400 0.12–3000 (10.0 upgrade)

**NOTE** Outside the specified range, the `Default` implant tables may fall back to the `Dios` tables. Therefore, near the boundaries of the `Default` tables, inconsistent results may occur.

## Tasch Tables

The directory `Tasch/` contains the University of Texas (UT) implant tables for boron,  $\text{BF}_2$ , phosphorus, and arsenic in silicon [12]. For all other materials and species, single Pearson tables are available. The tables can be selected to be the default by using the keyword `Tasch`:

```
implant tables=Tasch
```

The tables cover different energy ranges. The boron table `ibout1.s3` contains cap layer-dependent implantation moments valid for thicknesses between 1.5–40 nm. The moments in all other tables are cap-layer independent.

Table 6 Tasch tables

Species	Table file	Energy range [keV]
Arsenic	<code>iasut0.s3</code>	7–180
$\text{BF}_2$	<code>ibfut0.s3</code>	0.5–65
Boron	<code>ibout0.s3</code> <code>ibout1.s3</code>	0.5–80 15–80
Phosphorus	<code>iphut0.s3</code>	15–180

The valid range for the tilt is  $0^\circ$  to  $10^\circ$  and, for the rotation, the range is  $0^\circ$  to  $45^\circ$ . These tables provide data to be used with all implant models.

The single Pearson tables provide only energy-dependent data covering the range between 10 keV and 1000 keV.

## TSuprem4 Tables

The directory `TSuprem4/` contains the TSUPREM-4 native implant tables, `s4imp0.ts4`, for boron,  $\text{BF}_2$ , phosphorus, indium, antimony, and arsenic. To select these tables as the default, use the keyword `TSuprem4` with an optional prefix:

```
implant tables=TSuprem4 [ts4.prefix=<c>]
```

These tables contain the original implant moments of TSUPREM-4.

## File Formats

Sentaurus Process handles a variety of table formats. The table format of the implantation table is automatically recognized by Sentaurus Process from the file extension.

### Single-Pearson Table File Format: <file>.sp

This format provides the simplest table format that can be used with Sentaurus Process. It contains energy-dependent entries for the moments to be used with the (single) pearson or gaussian model.

**NOTE** These tables cannot be used with the dualpearson model.

The format of the table entries is:

```
*
energy rp stdev gamma beta lat.stdev
```

There is no dependence of the moments on dose, tilt, rotation, or cap layer thickness. Lines with an asterisk in the first column are treated as comment lines. Missing or incomplete blocks are not properly read when the file is parsed.

### SUPREM-III Table File Format: <file>.s3

This format allows the handling of energy, dose, tilt, rotation, and cap-layer thickness-dependent dual Pearson moments. A SUPREM-III implant table file consists of two sections: one for the primary moments and one for lateral moments. Both sections start with a header, which contains the parameter range covered by the table.

The header is organized as follows:

```
*Energies:
  NumberOfEnergies energy1 energy2 ...
*Tilts:
  NumberOfTilts tilt1 tilt2 ...
*Rotations:
  NumberOfRotations rotation1 rotation2 ...
*Doses:
  NumberOfDoses dose1 dose2 ...
*Thickness:
  NumberOfThickness thickness1 thickness2 ...
```

**NOTE** The order of these entries must not be changed.

Lines with an asterisk in the first column are treated as comment lines. A table entry for a particular combination of lookup parameters has the format:

```
*
rp stdev gamma beta rp2 stdev2 gamma2 beta2 ratio1
rp stdev gamma beta rp2 stdev2 gamma2 beta2 ratio2
...
rp stdev gamma beta rp2 stdev2 gamma2 beta2 ratio<NumberOfDoses>
```

### 3: Ion Implantation

Analytic Implantation

Each line contains eight `dualpearson` moments and the ratio as defined in [Eq. 26, p. 95](#). The entries are ordered increasingly with respect to cap layer thickness, energy, tilt, and rotation.

**NOTE** There is no automatic check of the ordering of the table entries.

The tables are for one species/material combination only. The cap-layer thickness, `rp`, `rp2`, `stdev`, and `stdev2` should be given in micrometers and the angles, in degrees. The energy values must be specified in keV. No units must be specified in the tables.

The lateral part is organized in the same manner. Corresponding to the header information, the entries are ordered in the same manner as in the primary part. Each entry has the format:

```
*  
<void> lstdev lv lstdev2 lv2
```

The first item is `void` and can be used for information purposes. The parameters are used in [Eq. 31, p. 98](#) to calculate the depth-dependent lateral standard deviation. The units for `lstdev` and `lstdev2` are micrometers, whereas `lv` and `lv2` are unitless.

#### Dios Table File Format: `<file>.tab`

The Dios table file format for implantation data files allows for dependencies on energy, dose, tilt, rotation, and the cap-layer thickness. It provides the primary moments for all implantation models including the `dualpearson` model. Parameters for depth-dependent lateral straggling are available as well. The format of the table entries is:

```
# Look up parameters  
material species thickness rotation tilt energy NumberOfFunctions  
  NumberOfDoses  
# Primary moments  
rp stdev <void> gamma beta lexp <void>  
rp2 stdev2 <void> gamma2 beta2 lexp2 <void>  
# Channeling table  
dose ChannelingDose  
dose ChannelingDose  
...  
# Lateral straggling  
p1 p2 p3 p4 p5
```

Lines with a `#` character in the first column are treated as comment lines. Missing or incomplete blocks are not read properly when the file is parsed.

The first block contains entries for the material and species names, cap-layer thickness, rotation angle, tilt angle, and energy. The `NumberOfFunctions` defines the number of components of the primary distribution function. A maximum of two functions are allowed. `NumberOfDoses` defines the number of entries in the channeling table. Each entry consists of a dose and the corresponding channeling dose. All doses are expected to be positive.

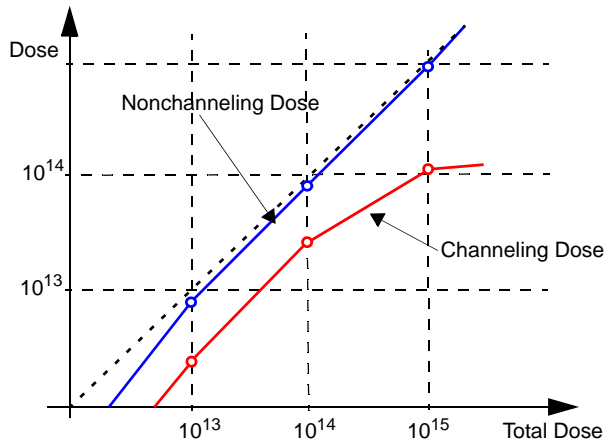


Figure 26 Piecewise linear nonchanneling and channeling dose for a dual Pearson profile as represented in default channeling table

The ratio between the amorphous part and channeling part in Eq. 26, p. 95 is calculated from this channeling table:

$$\text{ratio} = 1 - \frac{\text{ChannelingDose}}{\text{dose}} \quad (39)$$

The value for ChannelingDose is interpolated linearly using the value of the implant Dose.

The second block contains the moments for all the components of the primary distribution function. Parameters, which by definition do not exist for the function the set describes, are ignored.

**NOTE** Some entries are always ignored since they are not used in the implant models of Sentaurus Process. For example, the last moment entry (<void>) is always disregarded.

The third block contains the channeling table ordered with increasing dose, and the fourth block contains parameters for the depth-dependent lateral straggling.

**NOTE** The entries must be increasingly ordered with respect to the cap-layer thickness, rotation, tilt, and energy, so that the values for various energies (but the same other three parameters) follow each other. All data entries for the same material-dopant combination should follow each other with no interruption by entries for another material-dopant combination. The cap-layer thickness,  $r_p$ ,  $r_{p2}$ ,  $stdev$ , and  $stdev2$  should be given in micrometers and the angles, in degrees. The energy values must be specified in keV. No units must be specified in the tables.

### **Damage Table File Format: <file>.dam**

The damage tables for the Hobler damage model are similar to the Dios table file format, which allows for dependencies on energy, tilt, and rotation. The Hobler damage model table provides the primary moments for the damage model. Moments for depth-dependent lateral straggling are available as well. The format of the table entries is:

```
# Look up parameters
material species rotation tilt energy
# Primary moments
rp stdev decay nvac type
# Lateral straggling
p1 p2 p3 p4 p5
```

The syntax is the same as for the Dios table format. The item `decay` refers to the parameter  $l$ , and the item `nvac` refers to the parameter  $N_{vac}$  in [Analytic Damage: Hobler Model on page 99](#). The item `type` refers to the type of Hobler model.

### **Taurus Table Format: <file>**

The Taurus table format, which is the most general table format used in Sentaurus Process, handles data for all implant and damage models. Implant table files in the Taurus format have no file extension; that is, an implant table file without a file extension is considered to be in the Taurus format. It contains a file header and a block of numeric data. The file header consists of a list of names of the implant conditions. The names should be lowercase only. The following names are recognized:

```
energy tilt rotation dose screen temperature current
```

The sequence of these names can be arbitrary. Some names from this list can be omitted. The following units should be used for the implant conditions:

```
energy, [keV]
tilt, [degrees]
rotation, [degrees]
dose, [cm-2]
screen, [um]
temperature, [K]
current, [mA/cm2]
```

The numeric data consists of an arbitrary number of lines that form the lookup tables for implant conditions and implant moments. Each line should contain a list of numeric values for the implant conditions followed by the implant moments. The numeric values should be separated by space.

The number of the numeric values should be the same on each line. There should be at least  $n+4$  values per line for a gaussian profile,  $n+6$  values per line for a pearson profile, and  $n+13$  values per line for a dualpearson profile, where  $n$  is the number of the implant conditions specified in the file header.

The sequence of implant conditions should correspond exactly to the sequence of implant condition names in the file header. The sequence of the implant moments in one line is fixed as follows:

```
Gaussian:      rp stdev lat.stdev lat.slope
Pearson:       gamma beta
Dual Pearson:  rp2 stdev2 lat.stdev2 lat.slope2 gamma2 beta2 ratio
```

Any line that starts with a double slash `//` is considered a comment and is omitted. Always put the double slash at the first position in the line.

If the requested set of implant conditions does not have an exact match in the lookup table, a multidimensional linear interpolation is used. If a requested implant condition extends beyond the range of the lookup table, the closest value from the lookup table is used.

If the lookup table contains several lines with identical sets of the implant conditions, only the last set is used, and all the previous lines are discarded.

If a table contains data for the Hobler damage model, the following sequence of moments is used:

```
rp stdev lat.stdev lat.slope gamma beta decay nvac
```

---

## Multilayer Implantations

Point-response functions are valid only for a single material layer. For multiple layers of different materials, the point-response functions must be combined in a way that corrects the effect of the different stopping power in the covering layers. This must be performed for each lateral interval taking into account the local layer sequence parallel to the ion beam. Two algorithms are available in Sentaurus Process: numerical range scaling (NRS) [13] and dose-matching [12]. Both algorithms calculate a shift  $\delta_i$  applied to the primary point-response function. Sentaurus Process also provides an option `no`, which switches off the matching. In this case,  $\delta_i$  is set to zero in all layers.

The matching algorithm can be selected globally by using the command:

```
pdbSet ImplantData MatchControl { no | range | dose }
```

### 3: Ion Implantation

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The default value of `MatchControl` is `range`. In addition, you can select locally the matching algorithm with the keyword `match` in each `implant` command:

```
implant <dopant> [match={no range dose}]
```

The locally selected algorithm overwrites the one globally set in the PDB.

The NRS algorithm accounts for the different stopping power in different materials using the ratio of the projected ranges of the materials.

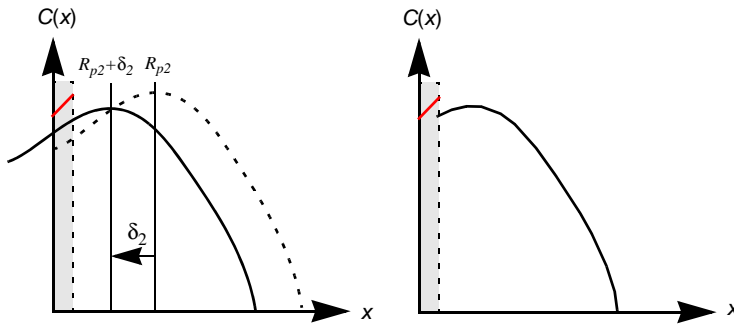


Figure 27 NRS algorithm: the point-response function in the second material is shifted and rescaled (*left*) due to existence of a layer with different stopping power (shaded region); the new profile is combined from the point response in the first layer and shifted point response in the second layer (*right*).

The shift in the  $i$ -th layer is calculated according to:

$$\delta_i = \sum_{j=1}^{j < i} t_j \left( 1 - \frac{R_{pi}}{R_{pj}} \right) \quad (40)$$

where  $t_j = d_j - d_{j-1}$  represents the thickness of the  $j$ -th layer. The profiles are matched according to:

$$C(x) = \begin{cases} f_{p1}(x) & \text{for } 0 < x < d_1 \\ \alpha_i \cdot f_{pi}(x - \delta_i) & \text{for } d_{i-1} < x < d_i \end{cases} \quad (41)$$

where  $\alpha_i$  is a rescaling factor that satisfies the normalization condition. The point-response function in the first layer is always used without a shift.

The *proportional range shift model* is used to shift the channeling portion of the implant profile independent of the amorphous part. To calculate the shift of the channeling part, the shift of the amorphous part is scaled by the ratio of the channeling range and the amorphous range:

$$\delta_{i, \text{tail}} = \delta_{i, \text{head}} \frac{R_{pi, \text{tail}}}{R_{pi, \text{head}}} \quad (42)$$



The proportional range scaling can be switched on with:

```
implant <species> [range.sh]
```

The default setting for this model is off. In the Taurus/TSUPREM-4 mode, the switch is set to on.

The dose-matching algorithm can be selected with the option `dose`. The shift  $\delta_i$  is calculated according to the dose accumulated in the above layers:

$$\delta_i = d_i - d_{\text{eff}}$$

$$D_{\text{sofar}} = \int_0^{d_{\text{eff}}} f_p(x) dx \quad (43)$$

where  $d_i$  is the position of the top of the  $i$ -th layer. The dose  $D_{\text{sofar}}$  is the integral over the primary point-response function.

## Lateral Integration

### Local Layer Structure in 2D

Local 1D layer structures are defined for a set of lateral intervals. These lateral intervals are chosen perpendicular to the projection of the ion beam into the simulation plane as shown in [Figure 28 on page 113](#).

The width of the lateral intervals is controlled by several parameters set in the parameter database. The default values can be changed by using:

```
pdbSet ImplantData LateralGridSpacing <n>
pdbSet ImplantData VerticalGridSpacing <n>
```

Starting from an initial grid, the intervals are bisected until a certain limit is reached. This limit is set by `LateralGridSpacing`, which has the default value of  $0.01 \mu\text{m}$ . Then, the intervals are bisected again until a certain vertical limit is reached. This limit is set by `VerticalGridSpacing` with the default value of  $0.01 \mu\text{m}$ .

The lateral integration is limited to a certain range of intervals to the left and right of a mesh node. This integration range depends on the maximum lateral standard deviation applied to the structure.

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Control over the lateral integration is possible by setting the number of lateral standard deviations used to set the integration range:

$$C(x, y) = \int_{y - N\sigma_{l, \max}}^{y + N\sigma_{l, \max}} f_p(x) f_l(x, y') dy' \quad (44)$$

The value of  $N$  can be set by using:

```
pdbSet ImplantData NumLateralStdev <n>
```

The default value is 5, which means that the total lateral integration width is  $10 \sigma_{l, \max}$ .

In 3D, the integration is performed over a square grid in the plane perpendicular to the ion beam. The grid is centered about a mesh node. It has a fixed size and resolution. The size is controlled by the parameter:

```
pdbSet ImplantData NumLateralStdev3D <n>
```

having the same meaning as the corresponding 2D parameter. The default value is 3.5. Each interval is subdivided by a certain number of grid points. The subdivision can be set by using:

```
pdbSet ImplantData NumGridPoints3D <n>
```

so that the total number of grid points is:

$$(2 \cdot \text{NumLateralStdev3D} \cdot \text{NumGridPoints3D})^2 \quad (45)$$

The default value for `NumGridPoints3D` is 4. Therefore, the total number of grid points is 784. The size of the integration grid is the parameter that limits the time performance of analytic implantation in 3D.

The lateral intervals are expanded by a certain amount over the left and right boundaries of the 2D device to ensure flat profiles on the left and right sides. This extension depends on the implantation `tilt` and the maximum lateral standard deviation. The maximum extension can be controlled from the parameter database. The value can be changed by using:

```
pdbSet ImplantData MaxLateralExtension <n>
```

The default is set to  $1.5 \mu\text{m}$ . A similar extension is applied in three dimensions.

## Primary Direction and Scaling

The interpretation of the range and lateral range parameters depends on the value of the implantation parameter `primary`. This can be set by using:

```
implant <dopant> [primary={beam wafer}]
```

The option `beam` switches to the beam projection mode. In this case, the primary moments are applied along the projection of the ion beam onto the simulation plane, and the lateral integration is performed perpendicular to the projection of the ion beam. This is the default mode in Sentaurus Process. The option `wafer` switches to the wafer normal mode. Here, the primary distribution function and the moments are interpreted orthogonally to the wafer surface.

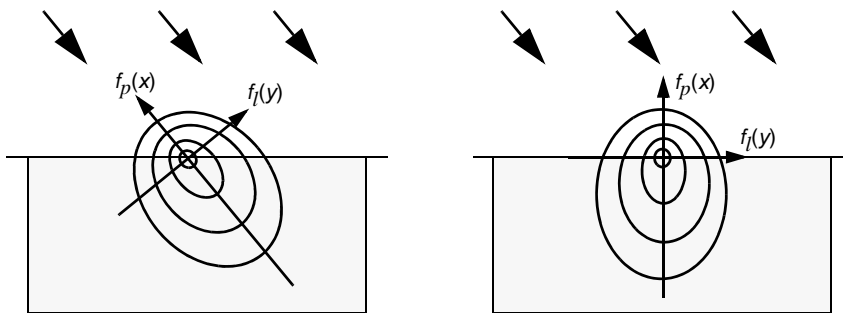


Figure 28 Beam projection mode (*left*) and wafer normal mode (*right*) for analytic implantation

An implant table can be declared angle-dependent or angle-independent by using:

```
implant species=<dopant> [angle.dependent]
```

Tilt-dependent and rotation-dependent data values extracted from SIMS measurements, or user-specified range parameters are assumed to be angle dependent. On the other hand, theoretical range parameters, such as those calculated by LSS theory, are assumed to be angle independent.

For the same pair of `tilt` and `rotation` parameters, different projected tilt angles can be observed in the 2D simulation plane. This angle is called `tilt2D` and depends on both `rotation` and `slice.angle`. Profiles in quasi-1D parts of the structure away from mask edges depend on the choice of `slice.angle`. Exactly the same 1D profiles can be observed only for symmetric primary distribution functions like the ones used in the Gaussian model and only if the primary and lateral standard deviations have the same value.

To ensure, at least approximately, that the same depth profiles are obtained for different rotation angles, and for different dimensions, the range parameters for the primary distribution function

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#### Analytic Implantation

are scaled depending on `tilt` (for 1D and 3D), or `tilt2D` (for 2D). For example, the projected range  $R_p$  is scaled as follows:

$$R_p' = R_p \cdot s_r \quad (46)$$

For tilt implants, the integrated dopant profile depends on not only the primary range parameters ( $R_p$ ,  $\sigma_p$ , and so on), but also the lateral straggling ( $\sigma_l$ ). To ensure that the same depth profiles are obtained approximately for different rotation angles, and for different dimensions, the primary standard deviation is scaled as follows:

$$\sigma_p' = \sqrt{s_r^2 \cdot \sigma_p^2 + (1 - s_r^2) \cdot \sigma_l^2} \quad (47)$$

Note that if the ratio  $\sigma_l/\sigma_p$  is too large, the scaling of the primary standard deviation may not be possible. In such a case, Sentaurus Process issues a warning message and continues by assuming  $\sigma_p' = \sigma_p$ .

The scaling factor  $s_r$ , which is used to scale  $R_p$  and  $\sigma_p$ , is selected with respect to the values of `primary` and `angle.dependent`, as shown in [Table 7](#).

Table 7 Scaling factor for the primary range

Dimension	primary	!angle.dependent	angle.dependent
1D	wafer	$s_r = \cos(\text{tilt})$	$s_r = 1$
	beam	$s_r = \cos(\text{tilt})$	$s_r = 1$
2D	wafer	$s_r = \cos(\text{tilt})$	$s_r = 1$
	beam	$s_r = \frac{\cos(\text{tilt})}{\cos(\text{tilt2D})}$	$s_r = \frac{1}{\cos(\text{tilt2D})}$
3D	wafer	$s_r = \cos(\text{tilt})$	$s_r = 1$
	beam	$s_r = 1$	$s_r = \frac{1}{\cos(\text{tilt})}$

---

## Point-Response Interface

This feature allows the use of externally generated point responses in analytic implantation. As an alternative to using implant tables, it replaces the moment-based point-response distributions. Only 1D primary distributions can be loaded with Sentaurus Process.

To use the point-response interface, the implant model must be changed to `point.response`, that is:

```
implant spec=<dopant> <material> point.response file=<name> y.position=<n>
```

To revert to the moment-based point-response distribution, switch to one of the analytic implantation functions, that is, to switch to the dual Pearson model for boron in silicon:

```
implant spec=Boron Silicon dualpearson
```

The default table setting can be used again since it has not been overwritten by the `point.response` flag.

The external primary distribution function and the damage are read from a `plx` file. A separate file can be selected for each dopant–material combination with the `file` selector and the above command.

The 1D MC implantation run is started to generate the data if the file is not found. This run is fully automated. The MC implantation model can be chosen by using the following command:

```
pdbSet MCImplant model {sentaurus.mc | crystaltrim}
```

The default MC model is `sentaurus.mc`. The 1D layer structure for this run consists of an oxide layer on top and a layer of the specified material. The thickness of the oxide layer is chosen as the total effective overlayer thickness at some point of reference at the gas surface of the structure. The position of this point at the y-axis is specified with the `y.position` parameter.

The integration routine treats the data as a continuous set to be used in the material as specified. In the convolution integral computation, the zero of the x-axis is locally matched to the surface of the structure.

The initial damage for the MC implantation simulation is taken from the damage already present in the device along a line starting from the surface at the `y.position` normal to the wafer surface.

The external profiles are interpreted as taken normal to the wafer surface. Therefore, the direction of the primary distribution should be switched from `beam` to `wafer` (see [Primary Direction and Scaling on page 113](#)). In addition, the multilayer matching method should be set to dose-matching (see [Multilayer Implantations on page 109](#)), that is:

```
implant <dopant> primary=wafer match=dose
```

The value for the primary range  $R_p$  is taken from the implant table if `match=range` is set.

---

## Analytic Damage and Point-Defect Calculation

The analytic implantation facility can generate damage profiles that are stored in the dataset `Damage` and interstitial and vacancy profiles that are stored in the datasets `Int_Implant` and `Vac_Implant`, respectively.

## Implantation Damage

The damage to the crystal is calculated on the basis of analytic damage models. Sentaurus Process calculates the damage using the model by Hobler and Selberherr [1]. Damage calculation for a species in a material can be switched on using the logical switch `damage`:

```
implant species=<dopant> <material> [damage]
```

A damage profile is calculated if the `damage` switch is set and the moments are found in the internal lookup table. Sentaurus Process can use the moments provided by Hobler [1] as described in [Analytic Damage: Hobler Model on page 99](#). At the end of an implantation step, the damage for this step is added to the Damage profile (damage history) using the `Dfactor`:

$$\text{Damage} += \text{Dfactor} \cdot \text{Damage\_LastImp} \quad (48)$$

The default value for the `Dfactor` is 1, and it can be changed in the parameter database or at the `implant` command line.

## Point-Defect Calculation

### Elemental Materials

The interstitial and vacancy profiles are calculated in a postprocessing step at the end of the `implant` command. The model used to calculate point defects is selected with the `defect.model` selector:

```
implant <dopant> [defect.model= {plus.one | effective.plus.n |  
frenkel.pair | user.defined}]
```

The `plus.one` switch selects the '+1' model to calculate the interstitial and vacancy profiles from the as-implanted profile at a particular implantation step `<dopant>_LastImp`:

$$\begin{aligned} \text{Int\_Implant} &+= \text{IFactor} \cdot \text{<dopant>_LastImp} \\ \text{Vac\_Implant} &+= \text{VFactor} \cdot \text{<dopant>_LastImp} \end{aligned} \quad (49)$$

where `IFactor` and `VFactor` are material-dependent factors that can be set in the parameter database. For example, for boron in silicon, this is performed by using:

```
pdbSet Silicon Boron IFactor <n>
```

The internal default values are 1 for `IFactor` and zero for `VFactor`. This is motivated by a simple lattice site balance argument: for each dopant atom that is assumed after implantation on a lattice site, one free interstitial is produced. The global values for `IFactor` and `VFactor` can be overwritten at the `implant` command line:

```
implant <dopant> <material> [ifactor=<n>] [vfactor=<n>]
```

The `effective.plus.n` model dynamically calculates an `NFactor` using an energy-dependent and a dose-dependent fitting formula after Hobler [14]. The `NFactor` replaces the `IFactor` in Eq. 49. This '+n' model provides an improved way to calculate the interstitial profile for heavy ions and low implant doses. Under these implant conditions, the `NFactor` can significantly deviate from one [14].

A third model can be chosen with the selector `frenkel.pair`. Here, the interstitial and vacancy profiles are calculated from the damage and dopant profiles resulting from the last implantation step:

$$\begin{aligned} \text{Int\_Implant} &+= \text{FPIFactor} \cdot \text{Damage\_LastImp} + \text{IFactor} \cdot \langle \text{dopant} \rangle \_ \text{LastImp} \\ \text{Vac\_Implant} &+= \text{FPVFactor} \cdot \text{Damage\_LastImp} \end{aligned} \quad (50)$$

where `<dopant>_LastImp` term accounts for the extra interstitials coming from substituted dopants. `FPIFactor` and `FPVFactor` can be set in the parameter database, and can be overwritten by parameters `fp.ifactor` and `fp.vfactor` at the `implant` command line.

If `crit.dose` is defined, the given value of `IFactor` in the `plus.one` and `damage` models for point defects is taken from:

$$\text{IFactor} = \text{IFactor} \cdot \min\left(1, \frac{\text{crit.dose}}{\text{dose}}\right) \quad (51)$$

The `user.defined` switch allows you to define your own algorithms to calculate interstitial and vacancy profiles. It is expected that users will define the algorithm in the `UserPointDefectModel` procedure. For example:

```
proc UserPointDefectModel { Species Name Energy Dose Model IFactor \
    VFactor CDose } {
    ...
}
```

where `Species` is the name of the implanted species; `Name` is the name of the dopant; `Energy` is the implant energy; `Dose` is the implant dose; `Model` is the implant model (for example, `tables` or `sentaurus.mc` or `crystaltrim`); `IFactor` and `VFactor` are the interstitial and vacancy factors; and `CDose` is the critical dose.

## Multicomponent Materials

In multicomponent materials, such as silicon carbide (SiC), the material is composed of different types of atom. When an impurity is implanted into SiC, both silicon and carbon lattice atoms can be displaced, thereby forming silicon interstitials or carbon interstitials, and leaving behind silicon-site or carbon-site vacancies. Instead of classifying them together as interstitials or vacancies, as in silicon, Sentaurus Process provides a mechanism to distinguish different types of interstitial or vacancy.

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To generate distinct types of point defect in multiple-component materials, you must switch on the `DistinctDefects` flag, for example:

```
pdbSetBoolean SiliconCarbide DistinctDefects 1
```

By default, this flag is true for SiC but false for other materials. As a result, instead of `Int_Implant` and `Vac_Implant`, the generated point-defect datasets in SiC are `IntSilicon_Implant`, `IntCarbon_Implant`, `VacSilicon_Implant`, and `VacCarbon_Implant`.

In this model, the total point-defect concentration is computed in the same way as the elemental material. The implantation parameters `defect.model`, `ifactor`, `vfactor`, `fp.ifactor`, and `fp.vfactor` in the `implant` command still work. `ifactor` and `vfactor` are scaling factors for interstitial profiles and vacancy profiles, respectively, in the `plus.one` defect model; while `fp.ifactor` and `fp.vfactor` are scaling factors for interstitial profiles and vacancy profiles, respectively, in the `frenkel.pair` defect model. The same Tcl procedure `CalcPlusNFactor` calculates automatically the plus factors for the `effective.plus.n` defect model.

Then, the individual point-defect concentration is computed by multiplying the total point-defect concentration by the fraction of each component. The fraction of each component is, by default, their stoichiometric weight, but it can be changed in the parameter database with the parameters `IFactor.Fraction` and `VFactor.Fraction`. For example, in SiC:

```
pdbSet SiC Composition Component0 IFactor.Fraction <n>
pdbSet SiC Composition Component1 IFactor.Fraction <n>
pdbSet SiC Composition Component0 VFactor.Fraction <n>
pdbSet SiC Composition Component1 VFactor.Fraction <n>
```

---

## Backscattering Algorithm

During the implantation, some particles may be backscattered and lost to the ambient. Analytic implantation accounts for this effect by assuming that the portion of the distribution which sticks out of the structure is backscattered from the surface, resulting in less dose implanted in the structure. This backscattering model – the TS4 backscattering model – is switched off by default. To switch on the model, either specify the logical switch `ts4.backscattering` in the `implant` command or use the global switch:

```
pdbSet ImplantData TS4Backscattering 1
```

In addition to the TS4 backscattering model, Sentaurus Process uses an advanced integration algorithm that accounts for particles backscattered from the surface. The lateral integration for a mesh node also is performed over 1D intervals above the surface. The point response is taken from the surface layer. The contributions from backscattered ions make a difference in the profile of vertical mask edges. The mask example in [Figure 29](#) illustrates the difference.



The backscattering algorithm is switched on by default. To switch off the algorithm, use either the logical switch `!backscattering` in the `implant` command, or use the global switch:

```
pdbSet ImplantData Backscattering 0
```

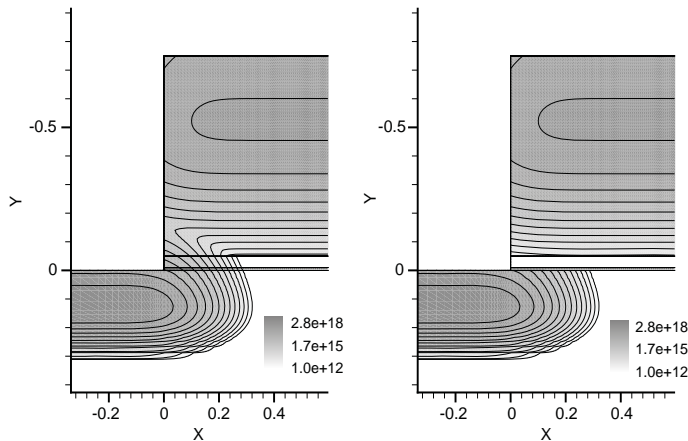


Figure 29 Boron implantation at a vertical mask edge (*left*) with backscattering and (*right*) without backscattering; tilt angle is  $0^{\circ}$  and energy is 35 keV

---

## Multiple Implantation Steps

### Preamorphization Implantation (PAI) Model

A structure already has implantation-related damage by the time an implantation is performed. This damage contributes to the suppression of the channeling tail. This applies to a series of implantations performed without intermediate anneals. In this case, an equivalent amorphous thickness is extracted as:

$$t_{i, \text{eqv}} = \frac{1}{\text{PAIThreshold}} \sum_{j \leq i} \int_{x_j} \text{Damage} dx \quad (52)$$

where `Damage` denotes the preexisting implant damage in terms of Frenkel pairs and `PAIThreshold` is a normalization parameter that can be specified in the parameter database:

```
pdbSet <material> <species> PAIThreshold <n>
```

The extracted equivalent amorphous thickness is added to the total amorphous layer thickness. If the implant table contains screen (cap) layer-dependent data, the total amorphous thickness is used as a parameter to select the implant moments as described in [Screening \(Cap\) Layer-](#)

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[dependent Moments on page 96](#). Otherwise, the profile reshaping model and the effective channeling suppression model are used.

The integral over the preamorphizing damage assumes periodic boundary conditions for the structure in 2D.

The PAI model can be switched on using:

```
implant <species> energy=<n> dose=<n> pai
```

**NOTE** The switch is off by default. The model is switched on for the Taurus implant tables.

## Coimplant Model

The fraction of the ions described by the second Pearson function is taken from implantation tables, which have been created for single ion implantation steps. This treatment is acceptable only for low-dose implantations, which create little crystal damage, but leads to a severe overestimation of the ion channeling in successive implantations with medium and high doses.

Without a thermal annealing step in between several ion implantations, the crystal damage of the first implantations remains present and reduces the ion channeling of the subsequent implantations. The channeling tail is lowered. Besides the PAI model as previously mentioned, analytic implantation provides the Coimplant (CI) model, which also takes this effect into account. In contrast to the PAI model in which the implant moments are modified locally for each cutline during the integration, the CI model modifies the channeling ratio globally for each implant. The CI model is switched on using the command:

```
pdbSetBoolean ImplantData UseCoImplant 1
```

The CI model is switched on by default.

**NOTE** The CI model is active only for `Default` implant tables, and does not affect any other implant tables.

The CI model considers damage produced by analytic or MC implantation steps. The damage information is used in subsequent analytic implantation steps to estimate the channeling ratio.

Using a least-square fit, an equivalent dose  $D^{eq}$  is calculated. This dose is chosen as the dose that would give the same amount of damage in one implant step (using the present species and implant conditions) as the preexisting damage, that is:

$$\int (\text{damage}[D^{eq}(x)] - \text{damage}_{\text{preexist}})^2 dx = \min \quad (53)$$

This is used to calculate the channeling dose  $D_c^{\text{new}}$  from the total channeling dose and the equivalent channeling dose, that is:

$$D_c^{\text{new}} = D_c^{\text{total}} - D_c^{\text{eq}} \quad (54)$$

The channeling dose is calculated from the total dose using the differential channeling dose technique (see Figure 30).  $D_c^{\text{total}}$  is the channeling dose corresponding to an implantation of  $D_c^{\text{eq}} + D_c^{\text{new}}$  into undamaged silicon.

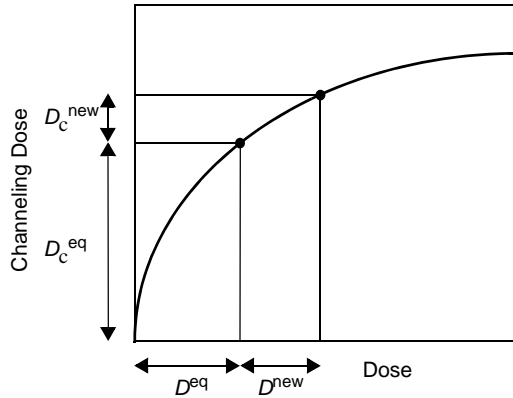


Figure 30 Channeling dose as a function of dose

In Figure 30, due to the creation of damage during implantation, the number of channeling ions increases sublinearly with the total ion dose, and eventually saturates at very high total doses. The damage from previous implantations is set equivalent to a dose  $D_c^{\text{eq}}$ . The dose of the additional implantation is shifted and, consequently, the gradient  $D_c^{\text{new}}/D_c^{\text{new}}$  and, therefore, the dual Pearson ratio are reduced.

Both  $D_c^{\text{eq}}$  and  $D_c^{\text{total}}$  are stored in lookup tables. The channeling dose  $D_c^{\text{new}}$  is used to calculate the new ratio for the dualpearson model (see Primary Distribution Functions on page 92).

This simple model is very accurate for mixed species implantations and works best in cases of subsequent implantations with similar energies. The model is only available for the Default implant mode.

The simplest way to calibrate the strength of de-channeling is given by using the effective damage factor that scales the calculated equivalent dose:

```
pdbSetDouble ImplantData <species> EffDamFac <factor>
```

The default value is 1. Increased values lead to less channeling; lower values increase the channeling of the species specified.

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To calibrate the effective damage factor depending on parameters of the implantation, the following procedure must be overwritten:

```
proc CI::coimp_dosesofar_calib { species energy dose tilt rotation } {  
  switch $species {  
    Boron { set cuc <expression_for_Boron> }  
    default { set cuc 1.0 }  
  }; # end of switch  
  return $cuc  
}
```

Sometimes, it will be necessary to reset the accumulated damage field internally used by the CI model. This can be achieved by using:

```
CI::Reset
```

To save and load the accumulated damage field, use:

```
CI::Save <filename>  
CI::Load <filename>
```

The loaded damage is added to existing accumulated damage. The accumulated damage produced by any implantation history can be checked with:

```
CI::Get_Damage_pdb Accumulated_Damage
```

This returns a list containing the vector describing the damage in the wafer on a logarithmic depth scale. A zero vector means no damage history is seen by any follow-up table implantation.

For more details about the CI model, see [\[15\]](#).

You can choose the PAI or CoImplant model by using the global switch `DamageControl`:

```
pdbSet ImplantData DamageControl {Default PAI CoImplant}
```

The default value of `DamageControl` is `Default` in which the PAI model is automatically switched on when Taurus tables are used; whereas, the CI model is chosen when default tables are used. If `DamageControl` is set to `PAI`, the PAI model is active for all subsequent implantations regardless of which tables are used. If this switch is set to `CoImplant`, the CI model is used for all subsequent implantations (note that the CI model only supports default tables), and PAI is disabled even for Taurus tables.

**NOTE** Both the PAI and CI models are designed to take into account the pre-existing damage. However, the PAI model modifies the implant moments locally, while the CI model modifies the channeling ratio globally. Generally, for a complex structure, the PAI model is more accurate at the expense of longer computation time.

**NOTE** To avoid double-counting the damage effect, when the PAI model is active, the CI model is disabled automatically.

---

## Profile Reshaping

Traditionally, it is believed that the first peak of the implanted profile in monocrystalline silicon is due to random scattering and is described by the first Pearson distribution in the dual-Pearson analytic model. The second peak (or hump) of the implanted distribution is attributed to ion channeling and is described by the second Pearson distribution in the dual Pearson model.

This approach works well for implantations with tilt angles above approximately  $4^\circ$ , where the position and width of the first Pearson distribution do not change as a function of the screen oxide thickness. However, for low tilt implantations (below  $4^\circ$ ), the position and width of the first Pearson distribution changes considerably (up to 50%) with the thickness of the screen oxide.

Typically, for a low tilt implantation performed into bare silicon, the first Pearson distribution shifts deeper into the substrate and is much wider than for a similar high tilt implantation. As the screen oxide thickness increases, the projected range and the standard deviation of the first Pearson distribution relax to their respective values at high tilt angles due to reduced channeling. Physically, this means that, for a low tilt implantation, even the first peak contains a considerable number of channeled ions. To model this effect, it is necessary to reshape both Pearsons in the dual Pearson model. This profile reshaping complements the reduction in channeling fraction provided by the effective channeling suppression model.

For ions with explicit dependency on the screen oxide thickness in the implant tables, this change in shape is addressed automatically. Otherwise, a shift is added to the projected range, the standard deviation, and the lateral standard deviation of both Pearson distributions. The shift is given by:

$$\Delta_i = \left(1 - e^{-\frac{\alpha_i t}{\sigma}}\right) (MH_i - ML_i) \quad (55)$$

where:

- $\Delta_i$  is the shift for moment  $i$ .
- $\alpha_i$  is the shift factor for moment  $i$ .

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- $t$  is the cap layer thickness.
- $MH_i$  is the value of moment  $i$  at high tilt value ( $7^\circ$ ).
- $ML_i$  is the value of moment  $i$  at a given low tilt angle.
- For historical reasons,  $\sigma$  is the standard deviation of the first Pearson distribution. However, this normalization quantity can be switched to the projected range by using the command:

```
pdbSet ImplantData ProfileReshaping.Rp 1
```

The shift factor parameters of the profile reshaping model can be set in the parameter database, that is:

```
pdbSet <material> <species> RangeFactor
pdbSet <material> <species> SigmaFactor
pdbSet <material> <species> ChannelingRangeFactor
pdbSet <material> <species> ChannelingSigmaFactor
```

The value of `RangeFactor` is used when calculating the shift of the projected range; the value of `SigmaFactor` is used for both the standard deviation and the lateral standard deviation. Setting a shift factor to zero effectively switches off this model for the respective moments. Higher values of the shift factor lead to a faster transition from a low tilt profile to a high tilt profile, with increasing amorphous layer thickness. By default, the shift factors are zero in all materials except silicon.

The profile reshaping model can be switched on using:

```
implant <species> [profile.reshaping]
```

The model remains inactive for explicitly cap layer-dependent implant tables.

**NOTE** This model is switched off by default and is switched on in the Taurus/TSUPREM-4 mode.

---

## Ge-dependent Analytic Implantation

SiGe material technology is used widely in stress engineering to improve device performance (such as mobility). In addition, the depth of the source/drain junctions in  $\text{Si}_{(1-x)}\text{Ge}_{(x)}$  can be remarkably reduced with an increase of the Ge content, which results from, not only the reduced boron diffusion for PMOS source/drain, but also the reduced projected range and channeling in as-implant itself.

Since the average mass of the atomic nucleus of the target is heavier in SiGe than in pure silicon, a scattering angle from a nuclear collision is larger. In addition, SiGe has a larger electronic stopping power than silicon due to the higher electron density. Therefore, similar to

the PAI model, the Ge effect on implantation can be modeled by using similar models for profile reshaping and effective channeling suppression.

In this model, the equivalent germanium thickness is first extracted:

$$t_{\text{Ge, eqv}} = \frac{1}{\text{GeThreshold}} \int C_{\text{Ge}} dx \quad (56)$$

where  $C_{\text{Ge}}$  denotes the germanium concentration and GeThreshold is a normalization parameter that can be specified in the parameter database:

```
pdbSet <material> <species> GeThreshold <n>
```

The following formulas are then used for the projected range reduction and the standard deviation shift:

$$\Delta R_{P, \text{Ge}} = -\text{Ge.RangePreFactor} \cdot R_{P,0} \cdot \left( 1 - \exp\left(-\text{Ge.RangeFactor} \cdot \frac{t_{\text{Ge, eqv}}}{R_{P,0}}\right) \right) \quad (57)$$

$$\Delta \sigma_{\text{Ge}} = -\text{Ge.SigmaPreFactor} \cdot \sigma_{\text{Ge},0} \cdot \left( 1 - \exp\left(-\text{Ge.SigmaFactor} \cdot \frac{t_{\text{Ge, eqv}}}{R_{P,0}}\right) \right) \quad (58)$$

where:

```
Ge.RangePreFactor  
Ge.RangeFactor  
Ge.SigmaPreFactor  
Ge.SigmaFactor
```

can be specified respectively in the parameter database as:

```
pdbSet <material> <species> Ge.RangePreFactor <n>  
pdbSet <material> <species> Ge.RangeFactor <n>  
pdbSet <material> <species> Ge.SigmaPreFactor <n>  
pdbSet <material> <species> Ge.SigmaFactor <n>
```

Similar formulas also exist for the channeling projected range and channeling standard deviation shifts with the parameter names:

```
Ge.ChannelingRangePreFactor  
Ge.ChannelingRangeFactor  
Ge.ChannelingSigmaPreFactor  
Ge.ChannelingSigmaFactor
```

### 3: Ion Implantation

Analytic Implantation

Finally, the following formula is used for effective channeling suppression:

$$r_{\text{Ge}} = r_{\text{Ge},0} \cdot \left( \frac{\text{Ge.Sup.Ratio}}{\text{Ge.Sup.Ratio} + \frac{r_{\text{Ge,eqv}}}{R_{p,0}}} \right)^{\text{Ge.Sup.Exponent}} \quad (59)$$

where `Ge.Sup.Ratio` and `Ge.Sup.Exponent` can be specified in the parameter database:

```
pdbSet <material> <species> Ge.Sup.Ratio <n>
pdbSet <material> <species> Ge.Sup.Exponent <n>
```

---

## Analytic Molecular Implantation

Sentaurus Process allows implanting arbitrary molecular species (such as `BF2` and `B10H14`). The implantation can proceed with or without the implant tables for the molecular species. If implant tables are not available for the molecular species, an approximate calculation of the dopant distribution is performed based on the tables for primary dopant species. Therefore, the only requirement for molecular implantation is that the implant data tables are available for the primary dopant species (such as `B`, `As`, or `P`). The primary dopant species, for which the profile is calculated, is specified with the `dataset` parameter in the `implant` command:

```
implant species=<molecule> dataset=<dopant>
```

To switch on the damage calculation in silicon for the molecular implant, use:

```
implant species=<molecule> Silicon damage
```

In a molecule, the implant energy is shared by several atoms according to:

$$E_i = \text{energy} \cdot \frac{M_i}{\sum_j w_j M_j} \quad (60)$$

where  $E_i$  is the energy of the  $i$ -th species,  $M_i$  is the atomic mass, and  $w_j$  is the statistical weight according to the stoichiometry of the molecule. The constituent and stoichiometry of the molecule are defined in the PDB.

You can define new molecular species with `pdb` commands. For example, you can define carborane as follows:

```
pdbSetString ImplantData Carborane Atom0 Name Boron
pdbSetDouble ImplantData Carborane Atom0 StWeight 10
pdbSetString ImplantData Carborane Atom1 Name Hydrogen
pdbSetDouble ImplantData Carborane Atom1 StWeight 14
```



Then to initialize the species, use the command:

```
implant species=Carborane dataset=Boron
```

After the above two steps are performed, you can use carborane like any other predefined implant species. For example, use the following command to perform analytic implantation for carborane:

```
implant Carborane energy=10 dose=1e14
```

**NOTE** The dose specified for molecular implantation is the dose for the molecular species. In the above example, the implanted dose for carborane is  $1 \times 10^{14} \text{ cm}^{-2}$ . Therefore, the boron dose is  $1 \times 10^{15} \text{ cm}^{-2}$ , and the hydrogen dose is  $1.4 \times 10^{15} \text{ cm}^{-2}$ .

For convenience, Sentaurus Process predefines the following molecular species:  $\text{BF}_2$  (BF2),  $\text{BCl}_2$  (BC12),  $\text{B}_{10}\text{H}_{14}$  (B10H14),  $\text{B}_{18}\text{H}_{22}$  (B18H22),  $\text{C}_2\text{B}_{10}\text{H}_{14}$  (C2B10H14),  $\text{AsH}_2$  (AsH2), and  $\text{PH}_2$  (PH2).

Depending on whether the implant tables are supplied for the molecular species, analytic molecular implantation will proceed in two different ways:

- With supplied implant tables
- Without supplied implant tables

## Molecular Implantation with Supplied Implant Tables

If the implant tables are available for the molecular species (for example,  $\text{BF}_2$ ), the implantation proceeds in the same way as the atomic species; in other words, the specified energy and dose are used to look up the moments in the implant tables. No scaling is applied to energy, dose, or the resulting profiles.

The implant tables can be specified for a molecular species with the command:

```
implant species=<molecule> <material> imp.table=<file> dam.table=<file>
```

The implant data files should be placed in the current working directory or the full path to the file should be specified in `imp.table`.

## Molecular Implantation without Supplied Implant Tables

If the implant tables are not available for the molecular species, Sentaurus Process performs an approximate calculation of the dopant distribution using the implant tables for the primary dopant species. The energy  $E_i$  for the  $i$ -th species (which is assumed to be the primary dopant species) is calculated using [Eq. 60](#).

### 3: Ion Implantation

Analytic Implantation

Assuming that there are  $N_i$  dopant atoms in a molecule, the molecular implantation is equivalent to a single atomic species implantation with the energy and dose equal to  $E_i$  and  $N_i \times \text{dose}$  (where dose is the molecular dose), respectively.  $E_i$  and  $N_i \times \text{dose}$  are used for implant moments lookup. Then, the dopant distribution is calculated in the same way as atomic implant.

## Damage Calculation

If damage tables are not supplied for the molecular species, the damage also can be calculated using the internal damage tables for the primary dopant species. The Boolean parameter `FullDamage` can be used to control the amount of damage for the molecular species:

```
pdbSetBoolean ImplantData <molecule> FullDamage <bool>
```

If `FullDamage` is true, the calculated damage is multiplied by a scaling factor:

$$S_i = \frac{\sum w_j M_j}{M_i} \quad (61)$$

This damage scaling factor roughly takes into account the damage produced by all atomic species (including the primary dopant species) and is consistent with the damage calculation used in TSUPREM-4 for  $\text{BF}_2$  implantation.

---

## Performing 1D or 2D Analytic Implantation in 3D Mode

Because analytic implantation performs lateral integration differently for one, two, and three dimensions, it may result in slightly different profiles from vertical 1D cuts, even though the same implant moments are used. In addition, for a 2D structure, the vertical 1D profiles also may be different depending on the beam direction on the simulation plane or not, in other words, depending on the rotation angles.

To obtain the same results in one, two, or three dimensions, or with different rotation angles, Sentaurus Process provides an option to perform 1D or 2D implantation in 3D mode, in which case, a 1D or 2D structure will first be extruded into a pseudo-3D structure. In other words, only the surfaces and interfaces (not the bulk) will be extended in the y- or z-direction or both directions, with the boundary conditions being taken into account. In the case of PAI, damage integration is performed in a real 1D or 2D structure. Then, the lateral integration proceeds in exactly the same way as in a 3D analytic implantation. This ensures consistent results for 1D, 2D, and 3D implantation.

To switch on this option, use either the Boolean parameter `extrude` in the `implant` command or the global `pdb` switch:

```
pdbSet ImplantData Extrude 1
```

---

## Implantation on (110)/(111) Wafers Using (100) Implant Tables

The Sentaurus Process software distribution typically includes a large set of implant tables for Si(100) wafers, but it does not include any implant tables for Si(110) or Si(111) wafers. However, you sometimes need to perform process simulations on (110) or (111) wafers. Since the Si(100) implant moments cannot be used directly for Si(110) or Si(111) wafers, certain transformations of implant moments are required to use these tables for Si(110) or Si(111) wafers.

Since SIMS depth profiles are measured along the wafer normal direction, the extracted implant moments also are obtained with respect to the wafer normal direction. On the other hand, analytic implantation is usually calculated by using the beam direction as its primary direction. If the beam direction is coincidental with the normal direction, the implant moments can be used directly without modification. However, for tilt implantations, the beam direction does not coincide with the wafer normal direction. In this case, implant moments to be applied to the primary beam direction must be scaled, or transformed, to reproduce the 1D profiles in the wafer normal direction. See [Primary Direction and Scaling on page 113](#) for more details.

Essentially, the projected range  $R_p$  is scaled as follows:

$$R_p' = R_p \cdot s_r \quad (62)$$

where  $s_r$  is the scaling factor, and the primary standard deviation  $\sigma_p$  is scaled as follows:

$$\sigma_p' = \sqrt{s_r^2 \cdot \sigma_p^2 + (1 - s_r^2) \cdot \sigma_t^2} \quad (63)$$

To use Si(110) implant tables for Si(110) or Si(111) implantations, you must calculate the corresponding angles on the (100) wafers from the specified implantation angles on the (110) or (111) wafers. For typical implantations (for example, `tilt=7°`), these angles are very large.

When you know the corresponding angle on the (100) wafer, you can use [Eq. 62](#) and [Eq. 63](#) to transform  $R_p$  and  $\sigma_p$ . [Eq. 62](#) works by simple geometry consideration. [Eq. 63](#) works reasonably well for small tilt implantations and, in theory, is accurate for isotropic amorphous material. However, due to ion channeling, [Eq. 63](#) may not be good under all situations.

### 3: Ion Implantation

Analytic Implantation

Therefore, the following options for  $\sigma_p$  scaling are provided:

- Case 0 (constant):  $\sigma_p' = \sigma_p$
- Case 1 (linear):  $\sigma_p' = \sigma_p \cdot s_r$
- Case 2 (standard):  $\sigma_p' = \sqrt{s_r^2 \cdot \sigma_p^2 + (1 - s_r^2) \cdot \sigma_l^2}$

The default  $\sigma_p$  scaling is the same as the  $R_p$  scaling (linear scaling). These cases can be selected by using the command:

```
pdbSet ImplantData StdevScalingMode {0 | 1 | 2}
```

---

## Boundary Conditions and Domain Extension

Boundary conditions are needed in ion implantation simulations to account for the geometry effects (such as shadowing) and lateral scattering of the implied structure. Both of these effects require knowledge of the materials and damage concentration outside simulation domain. The required information is synthesized by the definition of the boundary conditions.

Analytic implantation uses the same syntax as MC implantation for specifying boundary conditions. It is assumed that the simulation domain is rectangular if viewed from the top and is contained between:

```
LeftBoundary and RightBoundary (y-direction)
```

and:

```
BackBoundary and FrontBoundary (z-direction)
```

You can control the size of the lateral extension using:

```
pdbSet ImplantData MaxLateralExtension <n>
```

### Extended Boundary Condition

```
pdbSet ImplantData LeftBoundary Extend  
pdbSet ImplantData RightBoundary Extend  
pdbSet ImplantData FrontBoundary Extend  
pdbSet ImplantData BackBoundary Extend
```

The simulation domain is extended artificially in the corresponding direction. This compensates for the decay of the profile at the sides of the domain. The extended structure is removed after the implant is completed. `Extend` is the default boundary condition for ion implantation.

## Reflective Boundary Condition

```
pdbSet ImplantData LeftBoundary Reflect  
pdbSet ImplantData RightBoundary Reflect  
pdbSet ImplantData FrontBoundary Reflect  
pdbSet ImplantData BackBoundary Reflect
```

In reflective boundary condition, a reflected image with respect to the domain boundary is first constructed. Depending on the boundary condition specified on the other side, the composite structure is then either extended (if the other side is extended) or repeated (if the other side is also reflective). The added structure including the reflected image is removed after the implant is completed.

## Periodic Boundary Condition

```
pdbSet ImplantData BoundaryPeriodicY 1  
pdbSet ImplantData BoundaryPeriodicZ 1
```

This switches periodicity in the left–right or front–back direction. An array of periodic images is constructed outside the simulation domain before the implant is started. These periodic images are removed after the implant is finished.

---

# Monte Carlo Implantation

---

## Running Sentaurus MC or Crystal-TRIM

Sentaurus Process is capable of the atomistic simulation of ion implantation using either the Monte Carlo (MC) simulator Sentaurus MC, which is an improved multithreaded version of Taurus MC [7], or Crystal-TRIM [8], which originated from the Transport of Ions in Matter (TRIM) code [2]. MC implantation simulates ion implantation into single-crystalline materials or into amorphous materials of arbitrary composition. In Sentaurus Process, to select MC implantation at the command line, use:

```
implant <dopant> [crystaltrim | sentaurus.mc]
```

Alternatively, to select MC implantation as the default implantation model, use a global switch:

```
pdbSet ImplantData MonteCarlo 1  
pdbSet MCImplant model [crystaltrim | sentaurus.mc]
```

When `MonteCarlo` is set to 1, Sentaurus Process performs all the implantations using one of the selected MC models (`crystaltrim` or `sentaurus.mc`).

### 3: Ion Implantation

#### Monte Carlo Implantation

**NOTE** For simplicity, you could use the alias `tmc` instead of `sentaurus.mc` or `ctrim` instead of `crystaltrim`. For example, you may initiate Sentaurus MC implant with the following command:

```
implant <dopant> energy=<n> tmc
```

Fundamental implantation parameters, such as the implantation energy and dose, and the orientation of the ion beam with respect to the substrate must be specified using `energy`, `dose`, `tilt`, and `rotation` in the same way as for analytic implantation.

To run MC implantation in a full-cascade mode or improved BCA (iBCA) damage model, use the `cascades` or `iBCA` switch:

```
implant <dopant> [ctrim | tmc] [cascades | iBCA]
```

or using a global switch:

```
pdbSet MCImplant cascades 1  
pdbSet MCImplant iBCA 1
```

In the KMC mode, to specify the dose rate of the implantation, use the `dose.rate` parameter:

```
implant <dopant> [ctrim | tmc] [cascades | iBCA] [dose.rate=<n>]
```

If `dose.rate` is specified, it is assumed to be a uniform dose rate in units of  $\text{cm}^{-2}/\text{s}$ . If it is not specified, a Tcl procedure will be called:

```
proc DoseRate {dose} { ... }
```

which returns an implantation time as a function of implantation `dose`. By default, it is a uniform dose rate; that is, `DoseRate` is a linear function of `dose`. However, you can specify any monotonic function to take into account the particular implantation equipment setup or scanning patterns.

During the implantation, pseudoparticles representing a part of the whole dose are started from the start surface, which is constructed above the target, parallel to the wafer surface. For 2D and 3D target geometries, the start surface is subdivided into segments of equal size for which the required implantation dose is accumulated. The size of these segments can be controlled by setting:

```
pdbSet MCImplant Intervals dy <n>  
pdbSet MCImplant Intervals dz <n>
```

For 1D structures, no subdivision is performed. The number of pseudoparticles that will be started per segment can be set in the parameter database or at the command line:

```
pdbSet MCImplant Particles <n>
```

or:

```
implant <dopant> [crystaltrim | sentaurus.mc] [particles=<n>]
```

The default value is 1000. Increasing this number leads to better accuracy and an increase in simulation time. Together with the sizes of the segments, this parameter determines the statistical weight of each pseudoparticle.

Launching particles are assumed to be traveling along the direction as specified by the tilt and rotation angles. However, there is usually a small angular divergence of the ion beam so that the particles form a right cone. To specify the opening angle of the cone, in which particles are assumed to be uniformly distributed, use the command:

```
pdbSet MCImplant BeamDivergence <n>
```

Parameters controlling the electronic and nuclear stopping as well as the damage accumulation are available in the parameter database (see [Parameter Database on page 53](#)). You can set these parameters in there.

If the information level is set to 1 or above, a progress report similar to the following will be shown during the progress of implant:

implanted particles	orig traject	equiv classes	active segm	repl OK	traject fail	CPU time	
						step	total
1300( 5%)	84	4	26	1216	6	0.22	0.22
2600( 10%)	170	4	26	2430	9	0.21	0.43
3900( 15%)	262	4	26	3638	16	0.21	0.64
5200( 20%)	349	4	26	4851	24	0.30	0.94
6500( 25%)	437	4	26	6063	29	0.47	1.41
7800( 30%)	523	4	26	7277	33	0.28	1.69
.....			.....				.....
22100( 85%)	1894	4	5	20206	131	3.15	7.27
23400( 90%)	2875	4	5	20525	272	5.20	12.47
24700( 95%)	3837	4	5	20863	394	4.75	17.22
24960( 96%)	4029	4	5	20931	419	0.99	18.21
25220( 97%)	4231	4	5	20989	453	1.13	19.34
25480( 98%)	4422	4	5	21058	472	0.90	20.24
25740( 99%)	4628	4	1	21112	483	0.93	21.17
26000(100%)	4888	4	0	21112	483	0.45	21.62
.....							.....

Pseudo particles:  
implanted : 26000  
lost : 0 (0%)  
Trajectories : 4888  
Equivalence classes: 4

### 3: Ion Implantation

#### Monte Carlo Implantation

where:

- `implanted particles`: The total number of pseudoparticles implanted, which is, at the end of the simulation, equal to the product of the specified number of `particles` and the total number of segments of the implant surface. This number includes both the calculated number of particles and the successfully replicated number of particles. The percentage of already finished particles is also indicated in parentheses.

**NOTE** In a multithreaded implant, the thread ID is also shown before the percentage. For example, `6500 (2: 25%)` means that thread #2 has implanted 6500 particles and finished 25%.

- `orig traject`: The original number of trajectories that are based on the physical calculations.
- `equiv classes`: The number of equivalent classes in the current structure as detected by probing ions. For more details on equivalent classes and probing ions, see [Trajectory Replication on page 174](#).
- `active segm`: The number of currently active segments of the implant surface. At the beginning of the implant, this number is equal to the total number of start segments. This number should decrease as the implant progresses. At the end of the implantation, the number becomes zero as all segments have the required implant dose and become deactivated.
- `repl traject (OK and fail)`: The number of replicated trajectories. The number of successfully replicated trajectories is shown in the `OK` column; whereas, the number of unsuccessful trajectories is shown in the `fail` column.
- `CPU time (step and total)`: This CPU time includes the time spent for the current step and the total CPU time for the current implant.

For 2D structures, the progress of an ion implantation step can be graphically viewed using the switch `ion.movie`, for example:

```
implant <dopant> [ctrim | tmc] [ion.movie]
```

---

## Structure of Target Material

MC implantation simulates the motion of energetic particles in amorphous materials and single-crystalline materials.

### Composition

For each material, the composition is set in the parameter database. The composition can be found in the `<material> -> Composition` entry. For each `<n>`-component of the material,



the entry `Component<n>` gives the name and the stoichiometric weight, for example, for GaAs:

```
GaAs -> Composition -> Component0 -> Name = Gallium
GaAs -> Composition -> Component0 -> StWeight = 1

GaAs -> Composition -> Component1 -> Name = Arsenic
GaAs -> Composition -> Component1 -> StWeight = 1
```

or for silicon nitride:

```
Nitride -> Composition -> Component0 -> Name = Silicon
Nitride -> Composition -> Component0 -> StWeight = 3

Nitride -> Composition -> Component1 -> Name = Nitrogen
Nitride -> Composition -> Component1 -> StWeight = 4
```

The composition for both single-crystalline and amorphous materials is set this way.

## Single-Crystalline Materials

### Lattice Structure

In the case of a single-crystalline material, the positions of target atoms are calculated based on the lattice type. Crystal-TRIM supports zinc-blende (`Zincblende`) lattice only, while Sentaurus MC supports several lattice types that include simple cubic (`Sc`), body-center cubic (`Bcc`), face-center cubic (`Fcc`), zinc-blende (`Zincblende`), and hexagonal (`Hexagonal`) lattices. To set the lattice type, use:

```
pdbSet <material> LatticeType [Sc | Bcc | Fcc | Zincblende | Hexagonal]
```

### Lattice Constants

To change the lattice constant defined in the parameter database, use:

```
pdbSet <material> LatticeConstant <n>
```

For all lattice types, Sentaurus MC defines different lattice constants for three different axes. To define the other two lattice constants, use:

```
pdbSet <material> LatticeConstant_b <n>
pdbSet <material> LatticeConstant_c <n>
```

If `LatticeConstant_b` and `LatticeConstant_c` are not defined, `LatticeConstant` is used for all three axes. For a hexagonal lattice, `LatticeConstant_b` should be equal to `LatticeConstant`.

## Polytypes

For hexagonal systems, there may exist many different crystal structures due to the different stacking sequence along the *c*-axis, which is perpendicular to the plane formed by three *a*-axes (*a*<sub>1</sub>, *a*<sub>2</sub>, and *a*<sub>3</sub>). This is called polytypism. Four different polytypes are supported in Sentaurus MC, and you can select them using the following command:

```
pdbSet <material> Polytype {2H 3C 4H 6H}
```

The default polytype for silicon carbide (SiC) is 4H. For more details, see [MC Implantation into Silicon Carbide on page 162](#).

## Atomic Basis

The crystal structure consists of an atomic basis attached to the lattice points. A *basis* can be a single atom or a group of atoms attached to each lattice point. In Sentaurus MC, for simple crystals (such as a single-atom basis with simple cubic, face-centered cubic, or body-centered cubic lattice and binary compounds with zinc-blende and hexagonal lattice), the undisturbed positions of the lattice sites are constructed automatically using the information of the lattice type, the polytype (if hexagonal lattice), and the lattice constants. For more complex crystal structures, the positions of basis atoms should be specified with the `pdb` parameter `BasisVector`. The units of basis vectors are lattice constants in three crystallographic axes. For example, for zinc-blende silicon, the positions of two basis silicon atoms can be specified as follows:

```
Silicon -> Composition -> Component0 -> Name = Silicon
Silicon -> Composition -> Component0 -> StWeight = 1
Silicon -> Composition -> Component0 -> BasisVector = {0 0 0 0.25 0.25 0.25}
```

For another example, NaCl has a face-centered cubic (Fcc) lattice with an atomic basis of two atoms. The positions of Na and Cl can be specified as follows:

```
NaCl -> Composition -> Component0 -> Name = Sodium
NaCl -> Composition -> Component0 -> StWeight = 1
NaCl -> Composition -> Component0 -> BasisVector = {0 0 0}

NaCl -> Composition -> Component1 -> Name = Chloride
NaCl -> Composition -> Component1 -> StWeight = 1
NaCl -> Composition -> Component1 -> BasisVector = {0.5 0.5 0.5}
```

In Crystal-TRIM, the positions of lattice sites of the basic cell are set in the parameter database in `MCImplant -> Lattice -> Zincblende -> Cell0` in the natural coordinate system of crystal. The unit is one-half of the lattice constant. The undisturbed positions of all lattice sites of an ideal zinc blende-type crystal can be obtained from the basic cell by shifting the atomic positions in the directions of the crystallographic axes. Therefore, for any given position of the projectile, only the immediate crystalline environment is generated and rebuilt every time the projectile moves out of the current crystalline cell.

The entry `MCImplant -> Lattice -> Zincblende -> Cell11` is a complementary basic cell and gives the configuration that is obtained by shifting `Cell10` by one-half of the lattice constant.

### Thermal Vibrations

The thermal vibrations of the target atoms are important for the treatment of the motion of a projectile in single-crystalline material. In MC implantation, only instantaneous thermal displacements of target atoms from their ideal lattice sites are considered.

The displacements are assumed to obey a 3D Gaussian distribution with a root-mean-square obtained by the Debye model. The Debye temperature is set in the parameter database and can be changed with:

```
pdbSet <material> DebyeTemperature <n>
```

The default Debye temperature is 519 K for silicon.

The substrate temperature for the Debye model can be set by:

```
pdbSetDouble MCImplant Temperature <n>
```

The default substrate temperature is 300 K.

### Amorphous Materials

The structure of an amorphous material is described in a simplified manner by assuming an average interatomic distance in the target material.

### Variable Mass Density

It is possible to use a dataset `MassDensity` as the mass density of an amorphous material:

```
pdbSetBoolean <material> VariableMassDensity 1
```

Using molar fractions (see [Molar Fractions on page 138](#)) is disabled in these materials.

### Polycrystalline Materials

A polycrystalline material is characterized by its crystal orientation and grain size. Crystal orientation (one of 100, 110, and 111) can be specified by using a material-specific command:

```
pdbSet <material> CrystalOrient <n>
```

### 3: Ion Implantation

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There are two different ways to change the crystallinity (Amorphous, Crystalline, and Polycrystalline) of a material. If parameter `Crystallinity` is available (which is true for polysilicon) in the PDB, use this switch to set the crystallinity, for example:

```
pdbSet PolySilicon Crystallinity Polycrystalline
```

This command makes MC implantation models consider both crystal orientation and grain size for polysilicon.

If `Crystallinity` does not exist for a material, use parameters `Amorphous` and `Granular`:

```
pdbSet <material> Amorphous 0
pdbSet PolySilicon Granular 1
```

The first command switches off the amorphous treatment, and the second command makes MC implantation models consider the grain size.

For more details on ion implantation into polysilicon, see [MC Implantation into Polysilicon on page 160](#).

## Molar Fractions

It is possible to define a compound material with a spatially-dependent molar fraction. For example, for single-crystalline silicon, the following PDB entry:

```
array set $Base {BinaryCompounds {String {
  { SiliconGermanium GeTotal "GeTotal/[pdbGetDouble Si LatticeDensity]" }
}}}
}}}
```

specifies a binary compound  $\text{Si}_{1-x}\text{Ge}_x$  with the mole fraction of Ge calculated from the germanium concentration (`GeTotal`) divided by the silicon lattice density. Due to more computational demands, a minimum Ge concentration is required to trigger MC implantation models to treat this material in a more sophisticated way. To specify this minimum concentration, use the command:

```
pdbSet Silicon SiliconGermanium.MCmin 1e20
```

If the concentration of Ge in any of the mesh elements of silicon regions exceeds  $1 \times 10^{20} \text{ cm}^{-3}$ , MC models treat silicon as a compound material. In this case, the average charge and mass of the material is calculated individually for each mesh element. The lattice constant, the nonlocal electron stopping power, and the Debye temperature are linearly interpolated based on the mole fractions. For more details, see [MC Implantation into Compound Materials with Molar Fractions on page 161](#).

## Sentaurus MC Physical Models

The Sentaurus MC implantation model, which is an improved, multithreaded version of Taurus MC, was designed to be generally accurate and predictive with minimum user calibrations for most implant conditions. It has been calibrated from sub-keV to above 10 MeV, and for different implant conditions including random implant direction,  $\langle 100 \rangle$ ,  $\langle 111 \rangle$ , and  $\langle 110 \rangle$  channeling directions, with the same set of parameters for boron, phosphorus, and arsenic implants [7]. It also is accurate for other implant species such as  $\text{BF}_2$ , F, Al, Ge, In, and Sb [7][16]. For a detailed discussion of the physical models in Sentaurus MC and an extensive comparison with experimental SIMS profiles from sub-keV to above 10 MeV and with other MC simulators, refer to the literature [7][16]. This section briefly outlines the pertinent theory and models.

The calculation used in the Sentaurus MC model assumes that ions lose energy through two processes:

- Nuclear scattering, where the nucleus of the ion elastically scatters off the nucleus of an atom in the target. This interaction is based on the binary collision theory and is described in the following section.
- Interaction of the ion with the electrons of the target atoms. This mechanism is inelastic and does not alter the direction of the motion of the ion.

Therefore, the total change in energy of the ion after the  $i$ -th collision is the sum of the nuclear energy loss  $\Delta E_n$  and the electronic energy loss  $\Delta E_e$ :

$$E_i = E_{i-1} - \Delta E_n - \Delta E_e \quad (64)$$

### Binary Collision Theory

Sentaurus MC implantation models the energy loss of nuclear collision according to the classical binary scattering theory. The basic assumption of the mechanism for the energy loss of nuclear collision is that the ion interacts with only one target atom at a time. This assumption enables the use of the binary scattering theory from classical mechanics [17].

Consider a particle of mass  $M_1$  and kinetic energy  $E_0$  approaching a stationary particle with mass  $M_2$ . The impact parameter,  $b$ , is the distance of closest approach if the particle is not deflected and gives a convenient measure of how close the collision is. After collision, the first particle deviates from its original course by an angle  $\theta$ .

### Energy Loss

It can be shown that the first particle loses kinetic energy:

$$\frac{\Delta E_n}{E_0} = \frac{4M_1M_2}{(M_1 + M_2)^2} \cos^2(bI) \quad (65)$$

where:

- $\Delta E_n$  is the energy lost by particle 1.
- $E_0$  is its energy before collision.
- $I$  is the integral.

$$I = \int_0^{s_{\max}} \frac{ds}{\sqrt{1 - \frac{V(s)}{E_r} - b^2 s^2}} \quad (66)$$

where  $s = 1/r$  is the inverse separation between the two particles.  $V(s)$  is the potential between the two particles (assumed to be repulsive), and:

$$E_r = \frac{E_0}{1 + M_1/M_2} \quad (67)$$

is the reduced energy in the center of mass coordinates.

The upper limit of the integral,  $s_{\max}$ , is the inverse distance of closest approach of the two particles and is given by the solution to the equation:

$$1 - \frac{V(s_{\max})}{E_r} - b^2 s_{\max}^2 = 0 \quad (68)$$

### Scattering Angle

The angle  $\theta$  by which particle 1 is deflected is given by:

$$\cos\theta = \frac{1 - 0.5 \left[ 1 + \frac{M_2}{M_1} \right] \Delta E_n / E_0}{\sqrt{1 - \Delta E_n / E_0}} \quad (69)$$

**NOTE** For  $\Delta E_n / E_0 \ll 1$ ,  $\theta$  approaches zero.

### Dimensionless Form

Eq. 65 to Eq. 69 are the basic equations for classical two-body scattering. The scattering integral, Eq. 66, can be cast into a dimensionless form by assuming the potential has the form:

$$V(s) = Z_1 Z_2 k_1 s g(a_u s) \quad (70)$$

where:

- $Z_1$  is the charge on particle 1.
- $Z_2$  is the charge on particle 2.
- $k_1$  is the constant.

$$k_1 = \frac{q^2}{4\pi\epsilon_0} = 14.39495 \times 10^{-7} \text{ keV}\mu\text{m} \quad (71)$$

$g(a_u s)$  is an arbitrary function of  $a_u s$ , to be defined later, and  $a_u$  is a unit of length. Taurus MC uses the so-called universal screening length [18]:

$$a_u = 0.8854 \times 10^{-4} \frac{0.529}{(Z_1^{0.23} + Z_2^{0.23})} \mu\text{m} \quad (72)$$

and a dimensionless impact parameter:

$$b_n = b/a_u \quad (73)$$

and a dimensionless energy:

$$\epsilon = \frac{a_u E_r}{Z_1 Z_2 k_1} \quad (74)$$

Using Eq. 70, Eq. 73, and Eq. 74 in the scattering integral Eq. 66 and making the substitution  $s' = a_u s$  gives:

$$I = \frac{1}{a_u} \int_0^{s'_{max}} \frac{ds'}{\sqrt{1 - s' g(s')/\epsilon - b_n^2 s'^2}} \quad (75)$$

From Eq. 65, the quantity of interest is  $\cos^2(bI)$ , which becomes:

$$\cos^2(bI) = \cos^2 \left[ b_n \int_0^{s'_{max}} \frac{ds'}{\sqrt{1 - s' g(s')/\epsilon - b_n^2 s'^2}} \right] \quad (76)$$

Therefore, using Eq. 76,  $\cos^2(bl)$  can be evaluated in terms of the dimensionless variables  $b_n$  and  $\epsilon$ , without reference to the charge or mass of a particular particle.

### Coulomb Potential

As an example of the above procedure, consider the Coulomb potential between two particles:

$$V(r) = \frac{Z_1 Z_2 k_1}{r} \quad (77)$$

or:

$$V(s) = Z_1 Z_2 k_1 s \quad (78)$$

In this case,  $g(a_u s) = 1$ . Then, from Eq. 76:

$$\cos^2(bI) = \cos^2 \left[ b_n \int_0^{s'_{max}} \frac{ds'}{\sqrt{1 - s'/\epsilon - b_n^2 s'^2}} \right] \quad (79)$$

with:

$$s'_{max} = \frac{\left( \sqrt{1 + 4b_n^2 \epsilon^2} - 1 \right)}{2\epsilon b_n^2} \quad (80)$$

from a solution of Eq. 68.

Then, the integral can be evaluated exactly, giving:

$$\cos^2(bI) = \frac{1}{1 + 4b_n^2 \epsilon^2} \quad (81)$$

For a given impact parameter  $b$  and incident energy  $E_0$ , the dimensionless  $b_n$  and  $\epsilon$  can be obtained from Eq. 73 and Eq. 74, giving  $\cos^2(bI)$  from Eq. 81. Then, the energy loss due to the collision is given by Eq. 65, and the angle at which particle 1 leaves the collision is given by Eq. 69.

### Universal Potential

For the simple form of the Coulomb potential used in the previous example, the scattering integral can be solved analytically. For more realistic interatomic potentials, however, the scattering integral cannot be evaluated analytically.



For example, the universal potential [18] that is used in Sentaurus MC is:

$$V(r) = \frac{Z_1 Z_2 k}{r} \left[ 0.18175 e^{-3.1998r/a_u} + 0.50986 e^{-0.94229r/a_u} + 0.28022 e^{-0.4029r/a_u} + 0.028171 e^{-0.20162r/a_u} \right] \quad (82)$$

An analytic solution does not exist since the upper limit of the integral in Eq. 66 is given by Eq. 68, which becomes a transcendental equation with this potential. In Taurus MC, the quantity  $\cos^2(bI)$ , in its dimensionless form (Eq. 76), is numerically integrated for a wide range of its parameters  $b_n$  and  $\varepsilon$ . These results are stored in tables. Then, at each collision,  $\cos^2(bI)$  is obtained from these tables. This scheme eliminates the need to find  $s_{\max}$  for each collision, minimizing the amount of arithmetic operations performed during the calculation of the trajectory of an ion, while retaining accuracy.

Tables for the universal potential over a wide range of energies and impact parameters are provided for immediate use in Taurus MC. These tables span the normalized energy range of  $10^{-5} \leq \varepsilon \leq 100$  and the normalized impact parameter range  $0 \leq b_n \leq 30$ . For  $\varepsilon > 100$ , the Coulombic form (Eq. 82) is used. Values of  $\varepsilon < 10^{-5}$  are not encountered for ion-atom combinations of interest at energies above the energy at which the ion is assumed to have stopped (5 eV). For values of  $b_n > 30$ , the ion is assumed to be undeflected.

### Implantation into Amorphous Materials

This section describes how the binary scattering theory of the previous section is used to calculate ion trajectories in an amorphous solid. Assume an ion with kinetic energy  $E_0$  hits a target with an angle  $\theta_0$  with respect to the target normal. The surface of the target is assumed to be at  $y = 0$ , with  $y$  increasing vertically into the target. To set the incident energy  $E_0$  in the `implant` command, use the `Energy` parameter. To specify the incident angle  $\theta_0$  in the `implant` command, use the `tilt` parameter.

Given the atomic density  $N_{\text{dens}}$  for the target material, the mean atomic separation between atoms in the target is  $1/(N_{\text{dens}})^{1/3}$ . Between scattering events, the ion is assumed to travel a distance:

$$L = 1/(N_{\text{dens}})^{1/3} \quad (83)$$

As the ion enters the target material, it approaches the first target atom with impact parameter  $b$ , defined in the previous section. The probability of finding a target atom between  $b$  and  $b + \delta b$  is given by:

$$w(b)\delta b = 2\pi N_{\text{dens}}^{2/3} b \delta b \quad (84)$$

for  $b < 1/\sqrt{\pi N_{\text{dens}}^{2/3}}$ .

### 3: Ion Implantation

#### Monte Carlo Implantation

If  $R_{\text{rand}}$  is a uniformly distributed random number between 0 and 1, the probability distribution gives:

$$b = \sqrt{\frac{R_{\text{rand}}}{\pi N_{\text{dens}}^{2/3}}} \quad (85)$$

Given the above definitions, the algorithm for calculating the energy loss through nuclear collisions experienced by the ion proceeds as follows:

- A random number between 0 and 1 is chosen.
- The normalized impact parameter for this collision is calculated from [Eq. 73](#) and [Eq. 85](#):

$$b = \frac{1}{a_u} \sqrt{\frac{R_{\text{rand}}}{\pi N_{\text{dens}}^{2/3}}} \quad (86)$$

- The ion energy,  $E_0$ , is normalized to:

$$\varepsilon = \frac{a_u E_0}{(1 + M_1/M_2) Z_1 Z_2 k_1} \quad (87)$$

from [Eq. 67, p. 140](#) and [Eq. 74, p. 141](#).

- Now, the value of  $\cos^2(bI)$  can be obtained from the tables, and [Eq. 65, p. 140](#) gives the energy loss due to nuclear scattering:

$$\Delta E_0 = \text{nucl.cor} \cdot E_0 \frac{4M_1 M_2}{(M_1 + M_2)^2} \cos^2(bI) \quad (88)$$

where `nucl.cor` is an empirical nuclear-scattering correction factor with a default value of 1.0, which can be changed in the parameter database by using:

```
pdbSetDouble <material> <dopant> nucl.cor <n>
```

This procedure is repeated for each collision event.

### Implantation into Crystalline Materials

The binary collision calculation for crystalline materials proceeds in the same way as in the amorphous case, except that the selection of the collision partners of the projectile with target atoms is conducted in a more sophisticated manner.

Instead of using the density of the target material and a random number, Sentaurus MC determines the collision partners based on the position of the projectile relative to the sites on an idealized lattice. The algorithm for selecting the collision partners is based on

MARLOWE [19]. Sentaurus MC implantation uses a sophisticated *multibody* collision algorithm to simulate the collisions of well-channeled particles, as shown in Figure 31.

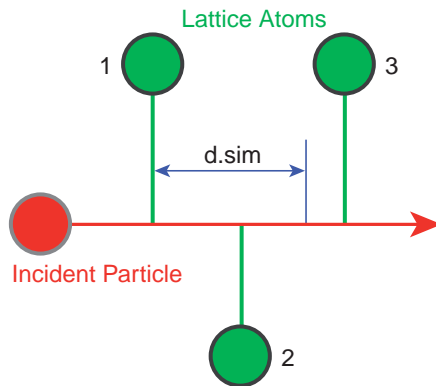


Figure 31 Illustration of “simultaneous” collision, and definition of the `d.sim` parameter

If the distance of two or more projected target atoms to the undeflected trajectory of the incident particle is less than `d.sim` (simultaneous collision distance), then the multibody collision algorithm is invoked. For example, in Figure 31, 1 and 2 are considered to be *simultaneous* collisions, but 3 is not. To change the default value of `d.sim`, use the command:

```
pdbSetDouble <material> d.sim <n>
```

The scattering events are computed for each target individually, and the final moment and energy of the incident particle are computed by applying momentum and energy conservation principles.

The simultaneous collisions are handled in the same way as for MARLOWE, except for the location of the turning point. In MARLOWE, the turning point is assumed to be the average of those of the simultaneous collision partners. In Sentaurus MC, the turning point is placed at a point determined by the collision with the minimum impact parameter. Simulations have indicated that such a scheme obtains better results for ultralow energy implantations, while it has little impact on implantation energies above 5 keV. This allows Sentaurus MC to treat the entire implantation energy range, including ultralow energy and very high energy, with the same model, in exactly the same way.

Ion channeling, which is the preferential penetration of implanted ions along crystal axes or planes, occurs naturally due to the inclusion of the crystal structure of the lattice. Both axial and planar channeling show enhanced penetrations. The effect of the `tilt` and `rotation` parameters is much more pronounced for implants into crystalline silicon than into amorphous silicon.

## Electronic Stopping Model

A moving ion loses energy by inelastic electronic processes, which include both nonlocal and local stopping power. Sentaurus MC uses the same electronic stopping model for both amorphous and crystalline materials. For each collision, the energy loss due to electronic stopping is:

$$\Delta E_e = x^{nl} \cdot \Delta E_e^{nl} + x^{loc} \cdot \Delta E_e^{loc} \quad (89)$$

$$x^{nl} + x^{loc} = 1 \quad (90)$$

$$x^{nl} = \min(\text{nloc.pre} \cdot \varepsilon^{\text{nloc.exp}}, 1) \quad (91)$$

where  $\varepsilon$  is the scaled dimensionless energy.

`nloc.pre` and `nloc.exp` are specified in the material parameter database and can be changed by using:

```
pdbSet <material> <dopant> nloc.pre <n>
pdbSet <material> <dopant> nloc.exp <n>
```

### Nonlocal Electronic Stopping

Nonlocal electronic stopping acts as the dragging (frictive) force on moving ions, which is proportional to the ion velocity and is independent of the impact parameter:

$$\Delta E_e^{nl} = L \cdot N_{\text{dens}} \cdot S_e \quad (92)$$

$$S_e = \text{LSS.pre} \cdot S_{es} \cdot \sqrt{E_m} \cdot f_{es}^{-1} \quad (93)$$

where  $L$  is the free flight path between collisions and  $E_m$  is the ion energy at the stopping power maximum.

The quantities  $S_{es}$  and  $f_{es}$  are given by [7][20]:

$$S_{es} = \frac{1.212 Z_1^{7/6} Z_2}{\left[ Z_1^{2/3} + Z_2^{2/3} \right]^{3/2} M_1^{1/2}} \quad (94)$$

$$f_{es} = \left[ \left( \frac{E_0/E_m}{\ln(E_0/E_m + E_m/E_0 + e - 2)} \right)^{\delta/2} + \left( \frac{E_m}{E_0} \right)^{\delta/2} \right]^{1/\delta} \quad (95)$$

where:

- $Z_1$  is the ion atomic number.
- $Z_2$  is the composite target atomic number.
- $e$  is the base of natural logarithm.
- $\delta = 1.425$  is a fitting parameter.

LSS.pre is specified in the material parameter database; to change it, use:

```
pdbSet <material> <dopant> LSS.pre <n>
```

### Local Electronic Stopping

Local electronic loss is a result of the electron exchange between the moving ion and the target atom, which is based on the Oen–Robinson model [21] and is dependent on the impact parameter:

$$\Delta E_e^{loc} = \frac{S_e}{2\pi a^2} \cdot \exp\left(-\frac{b}{a}\right) \quad (96)$$

$$a = f \cdot \frac{a_u}{0.3} \quad (97)$$

$$f = \text{scr.par} \cdot \frac{1.45}{Z_1^{2/5}} \quad (98)$$

where scr.par is an adjustable screening length parameter that you can change by using:

```
pdbSet <material> <dopant> scr.par <n>
```

### Damage Accumulation and Dynamic Annealing

As the ions travel through a crystalline target, they collide with the target atoms and displace many of them from their lattice sites. In the binary collision approximation (BCA) code, it is assumed that, if the transferred energy exceeds a certain threshold, the target atom is displaced and, at this lattice site, a vacancy is generated. When the displaced atom comes to rest, it is identified as an interstitial. This defect production rate can be evaluated either by the modified Kinchin–Pease formula [22] or by simulating the full cascade. Sentaurus MC provides both types of damage calculation.

## Damage Accumulation Models

The default damage model calculates the deposit energy  $E_D(x)$  for each collision, which is then converted to the number of point defects (Frenkel pairs) using the modified Kinchin–Pease formula [22]:

$$n(x) = \kappa(E_D / (2 \cdot \text{disp.thr})) \quad (99)$$

where  $\kappa = 0.8$  and  $\text{disp.thr} = 15$  eV for silicon by default.

If the `cascades` switch is specified in the `implant` command, Sentaurus MC traces all of the generated secondary recoils. After each collision, a calculation is performed to determine the trajectories of the silicon lattice atoms that are knocked from their sites in the lattice by collisions with implanted ions. A silicon atom is assumed to be knocked from its site when it absorbs an energy greater than a damage threshold `casc.dis` from a collision.

The silicon atoms freed from the lattice can, in turn, knock other atoms from their sites so that cascades of damage result. Sentaurus MC calculates the trajectories of these knock-ions with the same detail as the implanted ions. A vacancy is assumed to have formed whenever a lattice atom is knocked from its site. An interstitial is assumed to have formed whenever a silicon lattice atom that has been knocked from its site comes to rest. This damage model can be used to calculate the different profiles of interstitials and vacancies, that is, I–V separations.

`disp.thr` and `casc.dis` are specified in the material PDB and you can change them using:

```
pdbSet <material> <dopant> disp.thr <n>
pdbSet <material> <dopant> casc.dis <n>
```

## Dynamic Annealing

Not all of the defects as calculated above will survive; some of the generated defects will recombine within the cascade as well as with the preexisting defects. To achieve computational efficiency, Sentaurus MC uses a statistical approach to account for the I–V recombination in both intracascades and intercascades. The encounter probability of the projectile with interstitials also is accounted for statistically. The net increase of the defects in a local region with defect concentration  $C(x)$  is:

$$\Delta n(x) = \text{surv.rat} \cdot n(x) \cdot \left(1 - \frac{\text{sat.par} \cdot C(x)}{N_{\text{dens}}}\right) \quad (100)$$

In the cascade damage model, `surv.rat` and `sat.par` are replaced with `casc.sur` and `casc.sat`. To conserve particle numbers, interstitials and vacancies are recombined in pairs, and the model distinguishes between recoiled interstitials and recoiled lattice atoms. When an interstitial is recoiled, the local interstitial number decreases by one and no vacancy is produced. On the other hand, when a lattice atom is recoiled, a vacancy is created. However, defect recombination must be considered.

The intracascade recombination is accounted for by a factor `casc.sur`, while intercascade recombination is accounted for by a probability  $1 - (N_I/N_{\text{dens}})$ , which describes that the vacancy is not located within the capture radius of an interstitial.

When a recoil comes to rest, it is only allowed to recombine with vacancies from previous cascades, which is described by a factor  $1 - (N_v/N_{\text{dens}})$ , but not with those of the same cascade since this recombination has already been accounted for by vacancy intracascade recombination in the previous step. `surv.rat` and `casc.sur` are specified in the material PDB and you can change them using:

```
pdbSet <material> <dopant> surv.rat <n>
pdbSet <material> <dopant> casc.sur <n>
```

For light implant species, damage could saturate at certain concentrations due to the balance between defect production and dynamic annealing. Damage saturation is controlled by the parameters `sat.par` and `casc.sat` for the default damage model and cascade damage model, respectively. The default value is 1 for all implant species. Therefore, with the default parameter, the maximum damage is equal to the lattice density. If, for example, `sat.par` is set to 4.35, damage saturates at 23% of the lattice density and cannot exceed the amorphization threshold ( $1.15e22 \text{ cm}^{-3}$  by default). Therefore, the crystal will never be amorphized in this case. To change these parameters, use:

```
pdbSetDouble <material> <dopant> sat.par <n>
pdbSetDouble <material> <dopant> casc.sat <n>
```

**NOTE** For heavy species, a single cascade may amorphize the crystal. Therefore, the intracascade parameter `sat.par` may not prevent the amorphization even if it is set to a very large value.

### Damage De-Channeling

The accumulated damage has a significant effect on the destination of the subsequent ions, thereby altering the shape of the impurity profiles. This effect is known as *damage de-channeling*. Sentaurus MC handles this problem by switching from the crystalline model to the amorphous model based on the damage that has accumulated in the substrate. If the local defect concentration  $C(x)$  is greater than the amorphization threshold, this local region is assumed to be amorphized, and the amorphous collision model is used for this local region.

For the local regions with defect concentrations below the amorphization threshold, the probability of selecting the amorphous model is proportional to the local defect concentration  $C(x)$  and a random number call. The amorphous collision model is selected when:

$$R_{\text{rand}} < \text{amor.par} \cdot \frac{C(x)}{N_{\text{dens}}} \quad (101)$$

### 3: Ion Implantation

#### Monte Carlo Implantation

Increasing `amor.par` makes the profiles more like those implants into amorphous materials. For the cascade damage model, `amor.par` is replaced with `casc.amo`. The parameters `amor.par` and `casc.amo` are specified in the material PDB, and you can change them using:

```
pdbSet <material> <dopant> amor.par <n>
pdbSet <material> <dopant> casc.amo <n>
```

**NOTE** For low energy implants, due to very shallow projected ranges, the mesh near the surface should be refined to account fully for the damage de-channeling effect.

**NOTE** The amorphization process is not explicitly simulated by Sentaurus MC. However, for the MC model, by common practice, when a critical amount of damage is accumulated in a certain region, a crystal/amorphous phase transition is assumed to occur in this region. For a silicon target, this critical amorphization threshold is approximately 25% of the lattice density. Therefore, if the defect concentration reaches more than  $1.15 \times 10^{22} \text{ cm}^{-3}$  for silicon, this region is considered to be amorphized. Using this criterion, Sentaurus MC predicts the onset of amorphization and the thicknesses of the amorphous layers for high-dose implantations.

### Improved Binary Collision Approximation Damage Model

During implantation, energetic ions penetrate into the target and lose their energy through collisions with atoms and electrons. It is traditionally assumed that only energy deposited in the form of nuclear collisions contributes to damage generation; whereas, energy transfers to the electronic system are taken as inelastic losses. While energetic atoms are in the ballistic regime (that is, they have energies well above the displacement threshold `casc.dis`), they can be well simulated using binary collision approximation (BCA) algorithms. However, as their energy decreases to the thermal regime (around and below the displacement threshold), multiple interactions with target atoms become important. Molecular dynamics (MD) simulations demonstrate that energy transfers among atoms at this low-energy regime can generate amorphous pockets, thereby generating more damage than BCA models. The improved BCA (iBCA) damage model is an attempt to simulate MD simulation results within the framework of BCA.

The iBCA damage model implemented in Sentaurus MC implant is largely based on an the published article [\[23\]](#) (for the detailed physical basis of the model, refer to this article).

This section briefly describes the model, its usage, and the parameters that are accessible to users.



The procedure followed in the iBCA model is:

1. The collision phase of the cascade is simulated with the conventional BCA model.
2. The BCA simulation provides the position of Frenkel pairs generated during the cascade, the remaining energy of the recoils at the end of their trajectories, and the position and energy of all the atoms that receive any amount of energy above the minimum energy (`MinHotEnergy`). These particles are called *hot particles*.
3. At the end of the collision phase, there is a set of vacancies, interstitials, and hot particles.

Within BCA, the energy conservation principle applied to elastic binary collisions implies that the energy of the incident particle must be equal to its energy after the collision plus the recoil energy plus the energy required to take the recoil away from its lattice site.

A moving atom stops when its energy is insufficient to generate more subcascades. However, the remaining energy of the generated interstitial at the end of its trajectory can still contribute to generate more damage if low-energy interactions were modeled. To consider this effect within the iBCA model, the residual energy of each generated interstitial is equally shared with its neighboring atoms. Ballistic collision only considers the impinging atom and the closest target atom (two-body interactions); however, as energy decreases, collisions with several target atoms occur more often, and groups of energetic atoms are created as the cascade develops (many body interactions).

After this energy rearrangement, you evaluate which atoms are disordered taking into account their efficiencies:

$$eff = \frac{\rho - E_T}{D_C} \quad (102)$$

where  $\rho$  is the energy density, and  $E_T$  and  $D_C$  are the threshold energy density and damage generation cost, respectively. If the calculated efficiency of a given atom is below zero, it is not disordered.

If  $eff$  is between 0 and 1, the atom is disordered with a random probability given by its efficiency. If  $eff$  is 1 or greater, the atom is disordered and a random neighbor is disordered with the probability given by the remaining efficiency ( $eff - 1$ ) and so on.

To simulate the energy diffusion process: First, evaluate the efficiency of those atoms with the highest amount of energy in their environment. Second, repeat the process until no further energy remains to create more disordered atoms.

This scheme for damage generation can be regarded as a combination of the two traditional BCA approaches for damage description. As in the full-cascade BCA, ion and recoil trajectories are followed to generate damage at the atomic level and to provide the individual positions of Frenkel pairs, but you also must consider the energy deposited in atoms not

### 3: Ion Implantation

#### Monte Carlo Implantation

displaced by ballistic collisions. This energy is used to generate thermally disordered atoms following a scheme similar to the modified Kinchin–Pease approach. Nevertheless, since the residual deposited energies that are being considered to determine efficiencies are always at the low-energy regime, the local character of damage generation is guaranteed. In addition, the damage efficiency expression accounts for phase transformation (melting) and heat dissipation through the dependency of the parameters  $E_T$  and  $D_C$  on the number of energetic neighbors. This feature captures the nonlinear effects on damage generation due to the proximity of several energetic atoms as it occurs in molecular implants.

To activate the iBCA damage model, specify `iBCA` in the `implant` command or switch on the global switch:

```
pdbSet MCImplant iBCA 1
```

You can calibrate the iBCA damage model by changing the minimum energy for hot particles (`MinHotEnergy`) and the maximum distance for the local neighbors (`DistLocalNeighbors`):

```
pdbSet Silicon MinHotEnergy <n>
pdbSet Silicon DistLocalNeighbors <n>
```

By default, `MinHotEnergy` is 1 eV, and `DistLocalNeighbors` is 3.84e-4  $\mu\text{m}$ .

In addition, you can calibrate the model by changing the formulas for the threshold energy density (`Et_iBCA`) and the damage generation cost (`Dc_iBCA`) by modifying Tcl procedures. As noted in the article [23], the default Tcl procedures for these quantities are defined as:

```
proc Et_iBCA { ln } {
    set et [expr 11.348 * pow($ln+1, -0.837) + 0.931]
    return $et;
}

proc Dc_iBCA { ln } {
    set dc [expr 11.211*exp(-0.146*$ln + 0.00158*$ln*$ln)];
    return $dc;
}
```

where `ln` is the number of local neighbors.

**NOTE** To avoid nonphysical results, only fine-tuning of these formulas is recommended.

**NOTE** Because the iBCA damage model is substantially more CPU intensive than the cascade damage model, only low-energy implant is practical for this damage model.

## Crystal-TRIM Physical Models

Crystal-TRIM simulation is based on the binary collision approximation (BCA), which represents the motion of ions in the target material as a set of binary collisions with the target atoms [2].

BCA is valid in a wide range of projectile energies, from approximately 100 eV to many MeV. It can, therefore, be employed over the whole range of energies of interest for ion implantation. For energies below approximately 100 eV, collective interactions may play an increasingly important role and BCA may become invalid. Nevertheless, the applications of Crystal-TRIM to ultra low-energy implants lead to results that are still sufficiently good compared with experimental data.

At each collision, the projectile loses a part of its energy due to elastic nuclear scattering at target atoms and inelastic electronic interactions. The particles are assumed to come to rest if their energy is in the order of 15 eV.

### Single-Crystalline Materials

#### Nuclear Collisions and Collision Cascades

Nuclear scattering is treated by classical mechanics using a Coulomb-screened pair potential (ZBL potential [18]). If the energy transfer to the target atoms exceeds the so-called displacement threshold (approximately 15 eV for silicon), the target atom can leave its site and become displaced (primary recoil).

By default, only the trajectories of implanted ions are simulated. The number of vacancies and displaced target atoms produced at each collision is calculated approximately using the modified Kinchin–Pease formula.

A full cascade-type of simulation is performed if the keyword `cascades` is used. The trajectories of energetic recoils are calculated in the same way as for the original ions. A primary recoil with sufficiently high initial energy can generate more recoils (*collision cascade*). While both methods yield correct range profiles, only the full-cascade simulation produces physically correct profiles of vacancies and displaced atoms. However, a full-cascade simulation requires more computational time.

In single-crystalline silicon, vacancies and recoils are often identified with the vacancies and interstitials responsible for transient-enhanced diffusion (TED) of dopants. The choice of a diffusion model determines whether the full-cascade mode of Crystal-TRIM must be applied.

## Electronic Stopping

Electronic energy loss of the projectile is treated using semiempirical models.

For crystalline target materials, the loss depends on the local electronic density in the environment of the projectile. Therefore, the use of a local approach is particularly important for investigations of channeling effects in single-crystalline substrates.

A simplified local approach, the so-called modified Oen–Robinson formula [21], is used. The parameter `CEX1` describes the variation of the electron density for a projectile moving in the  $\langle 110 \rangle$  direction of the crystal, while `CEX2` does the same for any other direction. The value for `CEX1` and `CEX2` are set in the parameter database and can be changed by using:

```
pdbSet <material> <dopant> CEX1 <n>
```

The value for `CEX1` should be close to 1 or at least within the range of 0.5 and 3. The default value for `CEX2` is 2.

The automatic calibration of these parameters can be switched off individually using `AutoCEX1`, `AutoCEX2`.

## Amorphous Materials

### Nuclear Collisions

In amorphous materials, nuclear collisions are described by assuming that consecutive binary collisions are completely uncorrelated. The only structural parameter that influences nuclear scattering is the average interatomic distance in the target material, which determines the maximum free flight-path length to the next collision and the maximum impact parameter.

By default, the impact parameter is assumed to be distributed uniformly between zero and its maximum value. The free flight-path length is constant and equal to the average interatomic distance. Alternatively, a slightly different description of the structure of the amorphous material is possible using the switch `AdvancedAmorph`:

```
pdbSet <material> <dopant> AdvancedAmorph 1
```

In this case, the free flight-path length is assumed to have a half-Gaussian distribution above the interatomic distance scaled with a value of the parameter `AMAV`. The standard deviation is controlled by the parameter `AMDEV`.

The default values are  $AMAV=1$  and  $AMDEV=0$ , which correspond to setting `AdvancedAmorph 0`. The values of  $AMAV$  and  $AMDEV$  can be set in the parameter database:

```
pdbSet <material> <dopant> AMAV { <n> <n> <n> <n> }
pdbSet <material> <dopant> AMDEV { <n> <n> <n> <n> <n> <n> }
```

The set of parameters is given as an array. A pair of entries always specifies the number and the value of the parameter, that is:

```
pdbSet Silicon Boron AMAV {0 -1.25e-4 1 0.93}
```

sets the two parameters for the calculation of  $AMAV$  to  $-1.25$  and  $0.93$ , respectively.

$AMAV$  and  $AMDEV$  are made dependent on the atomic number of an implanted ion and its energy. For arsenic, boron, and phosphorus in silicon, calibrated values are available in the parameter database, and the `AdvancedAmorph` flag is set to 1. The calibration can overwrite external settings of these parameters performed with `pdbSet`. To switch off the calibration, use:

```
pdbSet Silicon Boron AutoAMAV 0
```

A similar parameter is available for  $AMDEV$ .

**NOTE** This model should not be applied to implantation energies below 10–20 keV. For low-energy implants, especially of boron, the default values lead to wrong results. You should select  $AMAV$  and  $AMDEV$  manually, where  $AMAV$  should be close to 1 and  $AMDEV$  should be a positive number.

Table 8 Values for  $AMAV$  and  $AMDEV$  used in Crystal-TRIM `AdvancedAmorph` mode

Energy [keV]	B/BF <sub>2</sub>		P		As	
	AMAV	AMDEV	AMAV	AMDEV	AMAV	AMDEV
10	0.9287	0.0275	0.8888	0.0700	0.9490	0.0400
30	0.9262	0.0141	0.8963	0.0700	0.9490	0.0400
50	0.9237	0.0113	0.9038	0.0700	0.9490	0.0400
100	0.9175	0.0088	0.9225	0.0700	0.9490	0.0400
200	0.9050	0.0000	0.9600	0.0700	0.9490	0.0400
400	0.8800	0.0000	1.0350	0.0700	0.9490	0.0400

A single-crystalline material can also be treated as amorphous by setting:

```
pdbSet <material> Amorphous 1
```

## Electronic Stopping

A nonlocal approach based on the ZBL formula [18] is used for amorphous materials. This formula uses an average density of electrons and has only one fitting parameter, `Lambda`. This factor is used for the scaling of the ion-screening length in the ZBL electronic-stopping cross section. Default values of `Lambda` are also set in the parameter database. Values of `Lambda` close to 1 (between 0.7 and 1.5) are recommended. The automatic calibration of this parameter can be switched off by using `AutoLambda`.

## Damage Buildup and Crystalline–Amorphous Transition

The damage accumulation leading to de-channeling of ions and recoils, and the subsequent crystalline–amorphous transition is described by a phenomenological model [22]. It can be completely switched off by using:

```
pdbSet Ctrim DamageAccumulation No
```

This switches off both the damage accumulation and de-channeling. During the current implant step, no additional damage will be produced and the existing predamage will have no effect. Two other model options are available.

### Full Amorphization Above a Critical Value

This model leads to full amorphization in mesh elements if the damage probability reaches a critical limit and is chosen by setting:

```
pdbSet Ctrim DamageAccumulation Full
```

Below a certain threshold described by the parameter `DCrit`, the damage probability `PD` is assumed to depend linearly on the nuclear energy deposition per atom ( $E_n$ ). The proportionality factor is `DAcc`. If `PD` is greater than this value, the volume element is completely amorphized and `PD` = 1, that is:

$$PD = \begin{cases} D_{Acc} \cdot E_n, & D_{Acc} \cdot E_n \leq D_{Crit} \\ 1, & D_{Acc} \cdot E_n > D_{Crit} \end{cases} \quad (103)$$

In most cases, `DCrit` should be less than `DAcc` to allow amorphization for high implantation doses.

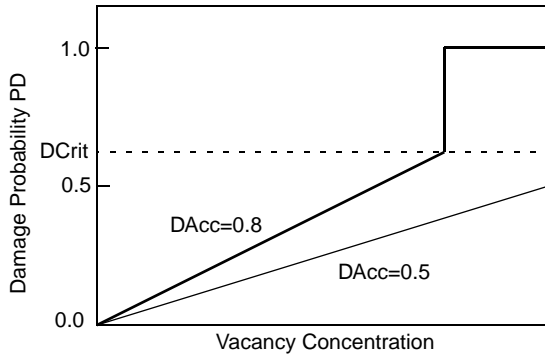


Figure 32 Onset of amorphization after reaching DCrit for two values of DAcc

### Saturation at Critical Value

```
pdbSet Ctrim DamageAccumulation Saturation
```

According to this model, below a threshold value DCrit, the damage probability PD has the same linear behavior as in the ‘full’ model, but cannot grow above DCrit:

$$PD = \begin{cases} DAcc \cdot E_n, & DAcc \cdot E_n \leq DCrit \\ DCrit, & DAcc \cdot E_n > DCrit \end{cases} \quad (104)$$

For both models, the values of the parameters DAcc and DCrit depend mainly on the atomic number of the implanted ion.

Table 9 lists values for some species. The automatic calibration for these values can be switched off using AutoDAcc and AutoDCrit.

Table 9 Values for DAcc and DCrit for most important species

	BF <sub>2</sub>	As, Ga, Ge	In, Sb, Sn	B, C, N	Al, P, Si
<b>DAcc</b>	0.15	0.3	0.3	0.1	0.2
<b>DCrit</b>	0.02	0.05	0.05	0.99	0.1

### Internal Storage Grid for Implantation Damage

By default, Crystal-TRIM stores the accumulated damage at the mesh. This makes the damage accumulation dependent on the mesh and can lead to errors if the mesh is too coarse. Typically, the amorphous boundary depends nonlocally on the mesh size closer to the surface of the structure.

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#### Monte Carlo Implantation

An internal grid can be used to accumulate and store as-implanted damage. This can be switched on by using:

```
pdbSet Ctrim UseInternalGrid 1
```

This allows for a mesh-independent storage of the damage information. You can control the grid spacing by using:

```
pdbSet Ctrim InternalGridSpacing <n>
```

In each grid cell, the accumulated as-implanted damage and the amorphization flag are stored. During postprocessing, the accumulated as-implanted damage is transferred (interpolated) from the internal grid to Sentaurus Process elements and then to Sentaurus Process nodes.

If two or more Crystal-TRIM steps directly follow each other, you can choose to leave the as-implanted damage stored on the internal grid instead of transferring it to the mesh. The switch `keepdamage.igrid` must be used within the `implant` command:

```
implant As crystaltrim keepdamage.igrid
```

The default is `!keepdamage.igrid`.

**NOTE** If `keepdamage.igrid` is used, the Sentaurus Process Damage dataset will not be incremented in the postprocessing. If the subsequent processing step is not a Crystal-TRIM implantation, the damage information will be lost.

To access the damage information, which was stored on the internal grid during the previous Crystal-TRIM implantation, the switch `predamage.igrid` (default is `!predamage.igrid`) must be used within the `implant` command: An example is:

```
# first step
# no damage post-processing, keep damage on internal grid for the following
# steps
implant As crystaltrim keepdamage.igrid

# second step
# use pre-damage on igrid from the previous step
# no damage post-processing: one more step follows
implant B crystaltrim predamage.igrid keepdamage.igrid

# third step
# use pre-damage on igrid
implant P crystaltrim predamage.igrid
```

**NOTE** It is not possible to save the information from the internal grid to a file using the `struct` command after the current Crystal-TRIM step.



## Molecular Implantations

The MC method allows for the implantation of molecular ions or atomic cluster species such as  $\text{BF}_2$ . The assumption is that the molecule immediately breaks up into its constituents upon impact on a solid surface.

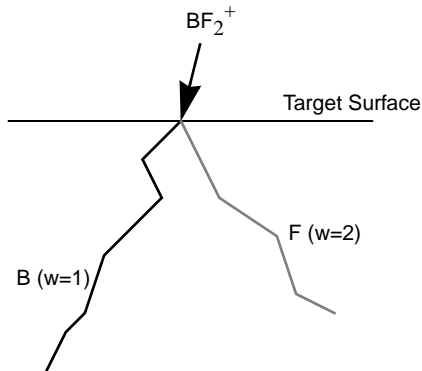


Figure 33 Schematic of molecular implantation of  $\text{BF}_2$ ; one trajectory is calculated for each atomic species,  $w$  is the weight assigned to the species

This is a valid approximation if the binding energy of the molecule is considerably smaller than the implant energy (for example, for  $\text{BF}_2$ :  $E_B \sim 9$  eV).

The implant energy is shared by several atoms according to:

$$E_i = \text{energy} \cdot \frac{M_i}{\sum_j w_j M_j} \quad (105)$$

where  $E_i$  is the energy of the  $i$ -th species,  $M_i$  is the atomic mass, and  $w_j$  is the statistical weight according to the stoichiometry of the molecule.

The constituents move as separate particles. However, particles of different species are not completely independent because of the interaction through the implantation damage.

Sentaurus Process supports several molecular species:  $\text{BF}_2$  (BF2),  $\text{BCl}_2$  (BCl2),  $\text{B}_{18}\text{H}_{22}$  (B18H22),  $\text{AsH}_2$  (AsH2), and  $\text{PH}_2$  (PH2). An implantation of  $\text{B}_{18}\text{H}_{22}$ , for example, can be performed with:

```
implant B18H22 energy=100 [ctrim | tmc]
```

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The atomic masses, statistical weights, and the molecular composition are available in the parameter database. A full molecular implantation is performed if the keyword `full.molecular` is explicitly set, that is:

```
implant <dopant> [ctrim | tmc] full.molecular
```

In this case, the trajectories for all atomic species are calculated. At the end of the simulation, datasets for each ballistic constituent of the original molecule are generated. This is the default. Only the trajectory of the significant species (B in the case of  $\text{BF}_2$ ) is calculated if `!full.molecular` is chosen.

**NOTE** This feature is available to both Sentaurus MC and Crystal-TRIM.

---

## MC Implantation into Polysilicon

Polysilicon has three states of crystallinity:

- Amorphous
- Crystalline
- Polycrystalline

By default polysilicon is considered amorphous and can be treated as a single-crystalline or polycrystalline material by using:

```
pdbSet PolySilicon Crystallinity Crystalline
pdbSet PolySilicon Crystallinity Polycrystalline
```

Crystal orientation (one of 100, 110, and 111) can be specified using the material-specific `pdb` command:

```
pdbSet PolySilicon CrystalOrient 110
```

This command sets the crystal orientation for all polysilicon regions to `<110>`.

If the crystallinity is set to `Polycrystalline`, MC implantation checks for the existence of the `GSize` dataset or `GrainSize` parameter. If neither is found, the grain model is disabled, and the material is assumed to be single crystalline. The default grain size is  $5 \times 10^{-5}$  [cm], and can be changed with the command:

```
pdbSet PolySilicon GrainSize <n>
```

or by initializing the `GSize` dataset:

```
select z=<n> name=GSize
```

The units for both `GrainSize` and `GSize` are centimeters.

The grain size also can be scaled with the `GrainFactor` parameter:

```
pdbSet PolySilicon GrainFactor <n>
```

The default `GrainFactor` is 1.

The polycrystalline model works by frequently switching between the crystal algorithm and the amorphous algorithm. The probability of switching from the crystal model to the amorphous model is determined by the accumulative path length in crystal (`pathlength`) and polycrystalline grain size (`GrainSize`). It switches from the crystal model to the amorphous model if:

$$\text{pathlength} > R_{\text{rand}} \cdot (\text{GrainFactor} \cdot \text{GrainSize}) \quad (106)$$

where  $R_{\text{rand}}$  is a random number between 0 and 1. The polycrystalline model shares the same random number sequence with other modules in MC implantation. Therefore, if the random seed is reset, the random numbers used in the polycrystalline model are changed as well.

After an amorphous collision is processed, the `pathlength` is reset to zero, and the crystal model is selected. The `pathlength` is accumulated again. The model used for the next collision is again determined by the same rules. This process is repeated until the particle exits the polycrystalline region.

**NOTE** This feature is available to both Sentaurus MC and Crystal-TRIM.

---

## MC Implantation into Compound Materials with Molar Fractions

A compound material with a spatially dependent molar fraction can be defined in the PDB. For example, for single-crystalline silicon, the following PDB entry:

```
array set $Base {BinaryCompounds {String {
  { SiliconGermanium GeTotal "GeTotal/[pdbGetDouble Si LatticeDensity]" }
}}}
```

specifies a binary compound  $\text{Si}_{1-x}\text{Ge}_x$  with the mole fraction of Ge calculated from the germanium concentration (`GeTotal`) divided by the silicon lattice density. This is the default setting for `SiliconGermanium` in the PDB. MC models support implants into these compound materials (binary, ternary, and quaternary).

Compound materials are detected automatically by using `CompoundNumber`, `BinaryCompound`, `TernaryCompound`, `QuaternaryCompound` in the PDB. Due to more computational demands, a minimum concentration is required to trigger MC implantation

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models to treat this material in a more sophisticated way. To specify this minimum concentration, for example, use:

```
pdbSet Silicon SiliconGermanium.MCmin 1e20
```

If the concentration of  $Ge_{Total}$  in any mesh node of silicon regions is greater than or equal to  $1 \times 10^{20} \text{ cm}^{-3}$ , MC implantation model treats this material as a binary compound `SiliconGermanium`. In this case, the average charge and mass of the material are calculated individually for each mesh element. Lattice constant, nonlocal electron stopping power, and Debye temperatures are interpolated linearly based on the mole fractions. The lattice is constructed with the primary material, and each lattice site is assigned to a type of atom with probability proportional to their mole fractions.

Sentaurus MC considers the fact that each specific lattice site will be occupied with certain types of atoms only. Therefore, the substitution of the lattice atoms occurs only for those with the same `Group` number. The default group number for each type of atom is the same as that in the periodic table. To change the group number, for example, use:

```
pdbSet ImplantData Carbon Group 4
```

For example, in compound material  $Si_{1-x-y}Ge_xC_y$ , Ge and C have the same group number (IV) as Si, so both of them can substitute silicon atoms in its lattice sites.

Another example is  $In_xGa_{1-x}As_{1-y}P_y$ ; In and Ga belong to the same group (III), and As and P belong to the same group (V). Suppose Ga occupies site 0, and As site 1 in zinc-blende structures, then In can only occupy site 0, and P site can only occupy 1 with the occupation probabilities proportional to their mole fractions.

**NOTE** Although this feature is available to both Sentaurus MC and Crystal-TRIM, you are strongly encouraged to use Sentaurus MC implant for better results.

---

## MC Implantation into Silicon Carbide

Sentaurus MC supports ion implantation into crystalline silicon carbide (`SiliconCarbide`) with hexagonal lattice. The hexagonal system has four crystallographic axes: three *a*-axes ( $a_1$ ,  $a_2$ ,  $a_3$ ) forming a plane, and a *c*-axis that is normal to the plane. The crystallographic planes and directions normally are described with four Miller indices (*hkil*). For the hexagonal system, since the sum of the first three indices is zero, the third index sometimes can be omitted.

Silicon carbide exists in many different crystal structures, called polytypes. All polytypes have a hexagonal frame with a carbon atom situated above the center of a triangle of Si atoms and underneath a Si atom belonging to the next layer. The difference among the polytypes is the

stacking sequence between the succeeding double layers of carbon and silicon atoms. For example, 2H-SiC, 4H-SiC, and 6H-SiC have the AB, ABCB, and ABCACB stacking sequences, respectively. 3C-SiC has an ABC stacking sequence and is the only form of SiC with a zinc-blende crystal lattice structure. The default polytype for SiC is 4H. To change to a different polytype, use the following command:

```
pdbSet SiliconCarbide Polytype {2H 3C 4H 6H}
```

**NOTE** The lattice constants may be different for different polytypes. For convenience, Tcl procedures (`set2H-SiC`, `set3C-SiC`, `set4H-SiC`, and `set6H-SiC`) are provided to set to different SiC polytypes.

Two silicon carbide wafer orientations (<0001> and <11-20>) are supported. To specify these wafer orientations, use the `pdb` command:

```
pdbSet SiliconCarbide CrystalOrient {0001 1120}
```

The default wafer orientation is <0001>. For (0001) SiC wafer; the primary flat orientation is <10-10>. For (11-20) SiC wafer, the primary flat orientation is <0001>.

For details of the model and comparison with experimental data for various implant conditions, see [\[24\]](#).

A miscut of  $3.5^{\circ}$ – $8.5^{\circ}$  typically exists in SiC (1000) wafers. Sentaurus MC implantation takes into account this wafer miscut by specifying `caxis.tilt` and `caxis.rotation` in the `init` command. `caxis.tilt` is the angle by which the wafer normal is tilted with respect to the a-axis in the crystal coordinate system. `caxis.rotation` is the angle that specifies the direction into which the wafer normal is tilted. The default value of `caxis.rotation` is 0, that is, the projection of the wafer normal to the crystal plane, formed by the b-axis and c-axis, is coincidental to the <110> direction in silicon. If `caxis.rotation=90`, the wafer normal is tilted by `caxis.tilt` towards the right with respect to the crystal coordinate system. (Or, in terms of the simulation coordinate system, if `caxis.rotation=90`, the crystal coordinate system is tilted towards the left with respect to the wafer normal.) By default, there is no wafer miscut, that is, `caxis.tilt=0`.

Here is a simple example illustrating how to perform an MC implantation in SiC:

```
# Set up the structure
line x loc=0.0 tag=oxtop spac=0.001
line x loc=0.0015 tag=top spac=0.001
line x loc=0.5 spac=0.0025
line x loc=2.0 tag=bot spac=0.01

region Oxide xlo=oxtop xhi=top
region SiliconCarbide xlo=top xhi=bot

# Specify wafer miscut
init caxis.tilt=4 caxis.rotation=0
```

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```
# Choose different polytype (default is 4H-SiC)
set6H-SiC

# Do the implantation
implant Aluminum energy=60 dose=1e13 tilt=0 rot=0 sentaurus.mc \
  particles=10000 info=2

# Save the result
struct tdr=sic
```

**NOTE** This feature is available to Sentaurus MC only.

---

## Recoil Implantation

Sentaurus MC implantation provides a general model for recoil implant, such as an oxygen knock-on effect. Generally, recoil species are handled the same way as cascade atoms, except that no vacancies are created at the displaced sites and the recoil species are not recorded as interstitials when they stop. Instead, a separate dataset is created for each recoil species.

The recoil species is specified in the material composition. For example, to simulate the oxygen knock-on effect, the following is defined in the parameter database:

```
Oxide -> Composition -> Component0 -> Name = Silicon
Oxide -> Composition -> Component0 -> StWeight = 1

Oxide -> Composition -> Component1 -> Name = Oxygen
Oxide -> Composition -> Component1 -> StWeight = 2
Oxide -> Composition -> Component1 -> Recoil = 1
```

To initiate oxygen recoil implant simulation, you must specify the keyword `recoils` in the `implant` command:

```
implant <dopant> energy=<n> dose=<n> recoils
```

The datasets `Oxygen_Implant` and `Oxygen` are created, which contain displaced oxygen distributions that can be used to analyze the oxygen knock-on effect.

**NOTE** This feature is available to Sentaurus MC implantation only.

---

## Plasma Implantation

Three-dimensional tri-gate devices (FinFETs) have been employed at the 22 nm node and are expected to continue at and beyond the 16 nm node. Doping of FinFETs must be 3D, and conformal doping with plasma implantation (PLAD) is a promising approach. Likewise,

doping of planar devices is challenging, and PLAD offers capabilities not available in beamline implantations.

To offer this simulation capability, Sentaurus Process provides a PLAD doping module that accurately reflects both the hardware and process signatures as well as the physical properties of the associated deposition, etching, sputtering, implantation, knock-on, defect creation, and annihilation processes. This MC implantation module includes the following features:

- Perform alternating steps of deposition and MC implantation. The number of steps can be specified by users.
- Deposition of material on the surface is performed isotropically (that is, constant growth rate over the surface). The thickness is specified by users. A minimum thickness is imposed by the program, which reduces the number of steps if necessary to prevent the deposition of a layer that is too thin. The deposit material should be defined as usual, and material composition of the layer must be specified by users.
- The MC implantation module allows the specification of multiple ions incidents on the wafer. The ion species should be defined before implantation as usual, and some typical ion species used in plasma implantation will be predefined. You can specify the dose, energy distribution, and angular distribution of each ion species. The dose for each ion is applied evenly for each step.
- An empirical model for conformal doping, in which the level of conformity can be specified by users.
- In addition to computing the concentration of ions that penetrate through the deposited overlayer, the MC implantation module allow for atoms to be knocked out of the overlayer and into the wafer and tracks damage and amorphization as usual.

You must define the plasma source before implantation can be performed. To avoid overly complex syntax in the `implant` command, Sentaurus Process provides two ways to specify the plasma source: simple source and complex source.

## Simple Source

Assuming that the multiple ion species in plasma have the same energy and angle distributions, simply specify the multiple species as a list in the `implant` command (other parameters such as `dose`, `energy`, `tilt`, and so on can be specified like a regular implantation):

```
plasma.source = {<species1>=<n> <species2>=<n> <species3>=<n> ...}
```

where:

- `plasma.source` specifies a list of ion species to be implanted. These species must be predefined in `ImplantData` as usual.
- The number after each species is the fraction of the total dose (as specified by the `dose` parameter) for the given species.

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- All these species will have the same energy, tilt, en.stdev, and tilt.stdev as specified.

## Complex Source

In more complex cases, different species may have different energy and angle distributions. In this case, each species can be specified with their own implantation parameters (energy, tilt, en.stdev, and tilt.stdev). So for each species, define it with an `implant` command:

```
implant species=<species1> energy=<n> tilt=<n> en.stdev=<n> tilt.stdev=<n>
implant species=<species2> energy=<n> tilt=<n> en.stdev=<n> tilt.stdev=<n>
implant species=<species3> energy=<n> tilt=<n> en.stdev=<n> tilt.stdev=<n>
...
```

where `<species1>`, `<species2>`, `<species3>` must be predefined in `ImplantData` as usual. Only parameters that are different from the default values must be specified.

Then, you can perform the real implantation in the same way as in the simple source case:

```
implant plasma.source= {<species1>=<n> <species2>=<n> ...} dose=<n> energy=<n>
tilt=<n> en.stdev=<n> tilt.stdev=<n> ...
```

where:

- `plasma.source` specifies a list of ion species to be implanted. These species must be the same as those in previous `implant` commands.
- The regular implantation parameters (dose, energy, and so on) will be the default for those species that are not specified. Essentially, this syntax is consistent with that for the simple source and reduces to the simple source if no implantation parameters are specified for each individual species.

## Deposition of Material

To specify the deposition of the material during implantation, use the `plasma.deposit` parameter in the `implant` command:

```
implant plasma.source= {<species1>=<n> <species2>=<n> ...}
plasma.deposit= {material=<c> thickness=<n> steps=<n>}
dose=<n> energy=<n> tilt=<n> ...
```

where:

- `material` is the name of the material to be deposited, which must be specified before the implantation.
- `thickness` is the total thickness of the deposit material.



- `steps` is the number of steps of deposition.

The deposition and implantation are performed alternatively. If `plasma.deposit` is not specified, or `material` is not specified, or `thickness` is not specified (or is equal to zero), no deposition is performed.

## Knock-on and Knock-off Effect

The MC implantation module simulates the dopant knock-on and knock-off effect by specifying the `recoils` parameters in the `implant` command. In addition, you must specify the recoil species to be simulated in material composition.

For example, assuming the deposit material is `BHx`, and `Atom0` is Boron, the following commands specify Boron as a recoil species:

```
pdbSetString BHx Composition Atom0 Name Boron
pdbSetDouble BHx Composition Atom0 StWeight 1
pdbSetBoolean BHx Composition Atom0 Recoil 1
pdbSetString BHx Composition Atom1 Name Hydrogen
pdbSetDouble BHx Composition Atom1 StWeight <x>
```

## Conformal Doping

Conformal doping is an important characteristic in plasma implantation. However, due to the complexity of plasma dynamics that involves manybody long-range interactions, the exact mechanism for conformal doping in plasma implantation is still not well understood. Physically, this may be possible if one of the following mechanisms or their combination occurs, for example, in a trench:

- The ions become ionized anywhere in the ambient (including inside the trenches) and start their acceleration towards the silicon surface.
- The ions scatter off other particles in the plasma/ambient (including inside the trenches) and change their direction.

To account for such effects, an empirical model has been developed that is compatible with the current plasma implantation. In this model, instead of launching all ions from above the device, as in standard implantation, some ions are launched along the device surface (that is, the solid–ambient interface). A fraction of ions launched along the surface can be specified by the parameter `conformity` in the `implant` command:

```
implant <dopant> energy=<n> dose=<n> conformity=<n> sentaurus.mc
```

where `conformity` is a number between 0 and 1.0. For example, if `conformity=0`, you will obtain standard plasma implantation results, and if `conformity=1`, you will obtain fully conformal doping.

## Other Plasma Implantation–related Parameters and Procedures

Sentaurus Process provides a simple model for taking into account the energy and tilt angle distributions of the plasma source. Given the mean and standard deviation of the implantation energy and tilt angles, Sentaurus MC implantation samples the given energy and tilt distributions for each implantation particle. When the implantation energy and tilt angle are determined, the particle tracing proceeds in a typical fashion.

In addition to the normal implantation parameters, such as energy and tilt, you can specify the standard deviation of implantation energy (`en.stdev`) or the standard deviation of the tilt angle (`tilt.stdev`) or both. For example:

```
implant <dopant> plasma dose=<n> energy=<n> en.stdev=<n> tilt=<n>  
      tilt.stdev=<n> sentaurus.mc
```

where the implantation parameters `energy` and `tilt` are the mean energy and mean tilt, respectively.

You also can specify the minimum energy that is allowed for implantation using the command:

```
pdbSet MCImplant MinEnergyCutoff <n>
```

Energy below the minimum energy will be truncated. The default minimum energy is zero. In addition, you can specify the maximum energy that is allowed by using the command:

```
pdbSet MCImplant MaxNumStdevCutoff <n>
```

`MaxNumStdevCutoff` must be an integer (default is 5). The highest energy for a given implant should not exceed the mean energy by the amount of `en.stdev` x `MaxNumStdevCutoff`. Energy higher than this number will be truncated.

The energetic distribution of different molecular and atomic ions, after extraction from the plasma, is known to cover the range from zero to the maximum energy  $E_{\max}$ , which is equal to the product of the ion charge multiplied by the extraction voltage. Sentaurus Process allows easy selection and addition of various energy distribution models. In addition to the default Gaussian distribution, Sentaurus Process implements an alternative Burenkov model [25]. In this model, the energy distribution, as presented by Tian *et al.* [26] as an integral number of particles having their energy in a given interval, can be written in a differential form as follows [25]:

$$f(E) = \frac{5}{6 \cdot E_{\max}} \cdot \left(\frac{E}{E_{\max}}\right)^{-1/6} \quad (107)$$

The energy distribution  $f(E)$  presented in Eq. 107 is normalized, that is, the integral over all possible energies of the extracted ions, ranging from 0 to  $E_{\max}$ , is equal to one. Burenkov *et*

*al.* have shown that by using the energy distribution given by Eq. 107, excellent agreement can be obtained between simulations and experiments for BF<sub>3</sub> plasma implantation [25].

To select a different energy distribution model, use the command:

```
pdbSet MCImplant PlasmaEnergyDistributionModel {Gaussian | Burenkov}
```

To provide maximum flexibility for energy and tilt angle distributions, you also can provide your own distributions by modifying the following Tcl procedures in `Plasma.tcl`:

```
Plasma::Energy_Distribution { energy stdev }
```

```
Plasma::Tilt_Distribution { mean stdev }
```

**NOTE** Sentaurus Process does not check the validity of these user-defined distributions. If you change these distributions, you must provide the correct distributions to ensure the correct implantation results.

**NOTE** This feature is available to Sentaurus MC implantation only.

---

## MC Implantation Damage and Point-Defect Calculation

### Sentaurus MC Damage Calculation

The damage in a Sentaurus MC implantation is computed either using the Kinchin–Pease formula [22] (default) or with full cascades if the `cascades` parameter is specified in the `implant` command. See [Damage Accumulation and Dynamic Annealing on page 147](#) for details on damage calculations. The calculation of the damage datasets for Sentaurus MC is consistent with the analytic implantation model. At the end of an implantation step, the damage for this step is added to the Damage profile using `MCDFactor`:

$$\text{Damage} += \text{MCDFactor} \cdot \text{Damage\_LastImp} \quad (108)$$

The default value for `MCDFactor` is 1 and can be changed in the parameter database or at the `implant` command line:

```
pdbSetDouble <material> <dopant> MCDFactor <n>  
implant <dopant> [tmc] [mc.dfactor=<n>]
```

The accumulated damage is taken into account automatically for subsequent MC implantations, unless the Damage dataset is reset by the `diffuse` command.

## Crystal-TRIM: Damage Probability

Defect accumulation in single-crystalline material and de-channeling due to the implantation damage are treated dynamically using a phenomenological model [22]. The model is based on the assumption of the formation of complex defects, such as amorphous pockets (APs) during ion implantation.

The damage information calculated during Crystal-TRIM simulations is stored in the damage probability dataset `PD`. This information is used in the model of APs to treat the nuclear collisions in the partially damaged crystalline region. Within a certain volume element, `PD` gives the probability that the collision can be treated as if the material were amorphous. The material is locally considered to be completely amorphized if  $PD = 1$ .

The `PD` dataset is not deleted after an implant step and, consequently, can be reused in subsequent Crystal-TRIM runs (damage history).

If the `PD` dataset has been deleted or has not yet been created, the `Damage` dataset is used to initialize the damage history in all crystalline materials:

$$PD = \text{Damage} / \text{Threshold}, \max(PD) = 1 \quad (109)$$

where `Threshold` is the amorphous threshold, which is the minimum of the lattice density and amorphous density. Both parameters can be set in the parameter database:

```
pdbSet <material> LatticeDensity <n>
pdbSet <material> AmorpDensity <n>
```

At the end of the simulation, the `Damage` dataset is increased according to:

$$\text{Damage} = \text{Damage} + PD\_LastImp \cdot \text{Threshold} \quad (110)$$

## Point Defects

### Elemental Material

Point-defect profiles after a MC run can be generated from the ballistic dopant profile using the `plus.one` or `effective.plus.n` model, or from the ballistic vacancy (Frenkel pair) and recoil profiles using the `frenkel.pair` model. The `effective.plus.n` model is the default for all MC simulations. In this case, the ballistic dopant profile `<dopant>_LastImp` is used according to [Eq. 49, p. 116](#).

Interstitial and vacancy profiles can also be calculated using the ballistic vacancy dataset `Vac_LastImp` generated during a MC run. The switch `defect.model` must be set to `frenkel.pair`:

```
implant <dopant> [crystaltrim | sentaurus.mc] [defect.model=frenkel.pair]
```

Using the MC-specific factors `MCIFactor` and `MCVFactor`, the profiles are calculated according to:

$$\begin{aligned} \text{Int\_Implant} &+= \text{MCIFactor} \cdot \text{Vac\_LastImp} + \text{IFactor} \cdot \langle \text{dopant} \rangle \_ \text{LastImp} \\ \text{Vac\_Implant} &+= \text{MCVFactor} \cdot \text{Vac\_LastImp} \end{aligned} \quad (111)$$

The default values for `MCIFactor`, `MCVFactor`, and `IFactor` are 1. These factors can be changed in the parameter database:

```
pdbSet <material> <dopant> IFactor <n>
pdbSet <material> <dopant> MCIFactor <n>
pdbSet <material> <dopant> MCVFactor <n>
```

or on the command line:

```
implant <dopant> [crystaltrim | sentaurus.mc] [ifactor=<n>] [mc.ifactor=<n>]
[mc.vfactor=<n>]
```

Setting `ifactor`, `mc.ifactor`, and `mc.vfactor` in the `implant` command overwrites the parameter database entries.

If `cascades` is enabled in MC implantation and the point-defect model is set to `frenkel.pair`, the interstitial and vacancy profile is calculated using the concentration of the recoil and vacancy as calculated based on the physics model:

```
implant <dopant> [crystaltrim | sentaurus.mc] [cascades] \
[defect.model=frenkel.pair]
```

In this case, the interstitial and vacancy densities increase according to the following:

$$\begin{aligned} \text{Int\_Implant} &+= \langle \text{recoil} \rangle \_ \text{LastImp} + \langle \text{dopant} \rangle \_ \text{LastImp} \\ \text{Vac\_Implant} &+= \langle \text{vacancy} \rangle \_ \text{LastImp} \end{aligned} \quad (112)$$

## Multicomponent Materials

In multicomponent materials, such as silicon carbide (SiC), the material is composed of different types of atom. When an impurity is implanted into SiC, both silicon and carbon lattice atoms can be displaced, thereby forming silicon interstitials or carbon interstitials, and leaving behind silicon-site or carbon-site vacancies. Instead of classifying them together as interstitials or vacancies, as in silicon, Sentaurus Process provides a mechanism to distinguish different types of interstitial or vacancy.

To generate distinct types of point defect in multiple-component materials, you must switch on the `DistinctDefects` flag, for example:

```
pdbSetBoolean SiliconCarbide DistinctDefects 1
```

### 3: Ion Implantation

#### Monte Carlo Implantation

By default, this flag is true for SiC but false for other materials. As a result, instead of `Int_Implant` and `Vac_Implant`, the generated point-defect datasets in SiC are `IntSilicon_Implant`, `IntCarbon_Implant`, `VacSilicon_Implant`, and `VacCarbon_Implant`.

In this model, the total point-defect concentration is computed the same way as the elemental material. The implantation parameters `defect.model`, `ifactor`, `vfactor`, `mc.ifactor`, and `mc.vfactor` in the `implant` command still work. `ifactor` and `vfactor` are scaling factors for interstitial profiles and vacancy profiles, respectively, in the `plus.one` defect model; while `mc.ifactor` and `mc.vfactor` are scaling factors for interstitial profiles and vacancy profiles, respectively, in the `frenkel.pair` defect model. The same Tcl procedure `CalcPlusNFactor` calculates automatically the plus factors for the `effective.plus.n` defect model.

Then, the individual point-defect concentration is computed by multiplying the total point-defect concentration by the fraction of each component. The fraction of each component is, by default, their stoichiometric weight, but it can be changed in the parameter database with the parameters `IFractor.Fraction` and `VFactor.Fraction`.

For example, in SiC:

```
pdbSet SiC Composition Component0 IFractor.Fraction <n>
pdbSet SiC Composition Component1 IFractor.Fraction <n>
pdbSet SiC Composition Component0 VFactor.Fraction <n>
pdbSet SiC Composition Component1 VFactor.Fraction <n>
```

If `cascades` is enabled in MC implantation and the point-defect model is set to `frenkel.pair`, the interstitial and vacancy profile is calculated using the concentration of the recoils and vacancies as calculated based on the physical model.

In this case, the interstitial and vacancy densities increase according to the following:

$$\begin{aligned} \text{Int}<\text{component}>_{\text{Implant}} &+= <\text{component}>_{\text{LastImp}} + \text{IFractor.Fraction} \cdot <\text{dopant}>_{\text{LastImp}} \\ \text{Vac}<\text{component}>_{\text{Implant}} &+= <\text{vacancy-component}>_{\text{LastImp}} \end{aligned} \quad (113)$$

---

## Statistical Enhancement

The energetic pseudoparticles in a MC simulation are statistical objects representing several actual particles or only a fraction of an actual particle. Pseudoparticles start their motion at a plane above the target parallel to the wafer surface. The starting surface is subdivided into segments of equal size. The size of these segments can be controlled by setting `dy` and `dz` in the `MCImplant -> Intervals` entry in the parameter database.

The number of pseudoparticles can be set by using:

```
pdbSet MCImplant Particles <n>
```

or:

```
implant <dopant> [crystaltrim | sentaurus.mc] [particles=<n>]
```

The default value for `particles` is 1000. The random number generator can be started with a specified random seed. The integer value used can be set with the parameter `RandomSeed`:

```
pdbSet MCImplant RandomSeed <n>
```

The default is 1. Random seeds also can be chosen randomly by using the internal clock, thereby giving different results for different runs. This feature is useful for statistical analysis for MC implantations. To use this feature, use the following command:

```
pdbSet MCImplant Randomize 1
```

## Trajectory Splitting

Trajectory splitting artificially increases the number of trajectories calculated in regions with low trajectory density. It can be switched on or off by using:

```
pdbSet MCImplant TrajectorySplitting 1
```

If a projectile reaches an element with a small trajectory density, a split point is set, that is, the particle is replaced by two daughter particles having half the statistical weight of the mother projectile. Then, the trajectories of both daughter particles are simulated in the same manner as for the original particle. Further splitting may occur that leads to a splitting tree related to the mother projectile. At a split point, the two daughter projectiles start under identical conditions.

However, the consideration of thermal vibrations of target atoms leads to a deviation of the trajectories of the daughter projectiles after a few collisions. In this manner, a high number of different particle trajectories with low statistical weight is obtained, which leads to an important decrease of the statistical noise in the tail parts of the dopant distribution.

In Setaurus MC, the maximum depth of the splitting tree is defined by a global parameter `MaxSplitLevels`:

```
pdbSet MCImplant MaxSplitLevels <n>
```

In Crystal-TRIM, a similar parameter is defined for each species. For a given ion species, the maximum depth of the splitting tree is defined by the parameter `MaxSplits`:

```
pdbSet <material> <dopant> MaxSplits <n>  
pdbSet <material> <dopant> MaxSplitsPerElement <n>
```

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#### Monte Carlo Implantation

The parameter `MaxSplitsPerElement` defines the maximum number of split events within one element.

**NOTE** The trajectory splitting model is available to both Sentaurus MC and Crystal-TRIM.

## Dose Split

In the conventional pseudoparticle Monte Carlo approach, all particles have the same weighting. In contrast, dose split algorithm uses *smart* particle weighting with first-coming ions weighing less than later ions. This prevents crystalline from amorphizing too quickly, thereby allowing more ions to enter the channeling regions. This model can drastically reduce the noises of the channeling tails. By default, dose split is switched off. To activate the model, use the command:

```
pdbSet MCImplant DoseSplit 1
```

The dose split model is especially effective for high-dose amorphizing implants, such as arsenic implant with a dose of  $8 \times 10^{15} \text{ cm}^{-2}$ . For a typical run, the CPU time is about 2 to 3 times slower than that without dose split for the same number of particles. However, dose split improves the statistics in the channeling tails by at least two orders of magnitude.

To achieve the same statistical significance, the conventional approach requires at least 100 times more particles; this means that the effective speedup is about 30 to 50 times.

**NOTE** The dose split model is available to Sentaurus MC only.

## Trajectory Replication

The trajectory replication algorithm uses the fact that in almost all 2D or 3D target structures, several regions with 1D topology can be found. A particle trajectory going through such a part can be copied many times by shifting its origin. Within the 1D region, each shifted trajectory is a valid particle trajectory. Its reproduction by copying is much faster than its physical calculation.

The subdivision into 1D parts or *equivalence classes* is performed automatically during the implantation. A subdivision is performed using the segments of the start surface. At the beginning, all the start segments are in the same equivalence class.

First, the whole trajectory tree is calculated including splits and recoils. The increments of all concentration-type values between entering and leaving a grid element are stored for each trajectory point (at least one per grid element). A start segment is chosen from the same equivalence class. The starting point of the copy trajectory is set randomly within this start segment. The point where the copied trajectory enters the material is found in the same way as



for the original trajectory. The vector between the first material point of the master and the copied trajectory serves as a shift vector. All the increments of the master trajectory are transferred point by point into grid elements that correspond to the shifted points.

If the materials are not identical within geometry tolerance ( $1.5 \times 10^{-4} \mu\text{m}$ ), or the initial damage is different by more than 1% at the master and the replica points, replication fails and the start segment is taken out of the present equivalence class and placed into a new equivalence class. The generation of new equivalence classes stops after a certain number of particles has been implanted. These initial particles are called *probing ions*.

Due to the random nature of ion trajectories, for the same structure, the equivalent classes as discovered by the probing ions could be slightly different depending on the random seeds, implanted species, or the number of probing ions.

The number of probing ions is empirically set to the total number of start segments. However, depending on the situation, this number may be too small for 2D simulations; whereas, it may be too large for 3D simulations. You can control this number by using the command:

```
pdbSet MCImplant ReplicationLearningFactor <n>
```

After this command, the new number of probing ions will be equal to the original number of probing ions multiplied by `ReplicationLearningFactor`. Generally, the more probing ions, the more equivalent classes will be created for a given structure. More equivalent classes will reduce the ratio of the replicated trajectories to the calculated trajectories, thereby providing more accurate results at the expense of more CPU time.

The total number of implanted particles is given as the number of start segments multiplied by the number of particles per segment, which can be set by using the parameter `particles`. Due to the replication, the number of physically calculated trajectories is usually much smaller and is given rather by the number of equivalence classes multiplied by `particles`.

The trajectory replication algorithm is based on the heuristic argument that the 1D part of the structure should be equivalent. However, some parts of the 1D region may be close to the sidewalls. Therefore, the dopant concentration is contributed to not only from the direct exposure to the ion beam, but also from the particles scattered from the sidewalls and re-entering the 1D region. In such situations (such as high-energy implant into a photoresist mask or pocket implants), trajectory replication may not give accurate results near the sidewalls. In addition, for high tilt pocket implants, saving CPU time by trajectory replication is limited. Therefore, under such circumstances, you should switch off the trajectory replication.

**NOTE** Trajectory replication is switched on by default. To switch off trajectory replication, use the global switch:

```
pdbSet MCImplant TrajectoryReplication 0
```

**NOTE** This feature is available in both Sentaurus MC and Crystal-TRIM.

---

## Boundary Conditions and Domain Extension

Boundary conditions determine how particles leaving the simulation domain at its outer boundaries will be processed. It is assumed that the simulation domain is rectangular if viewed from the top and is contained between:

LeftBoundary and RightBoundary (y-direction)

and:

BackBoundary and FrontBoundary (z-direction)

### Transparent Boundary

```
pdbSet MCImplant LeftBoundary Transparent
pdbSet MCImplant RightBoundary Transparent
pdbSet MCImplant BackBoundary Transparent
pdbSet MCImplant FrontBoundary Transparent
```

All particles crossing the boundary leave the simulation domain and are lost.

### Periodic Structure

```
pdbSet MCImplant BoundaryPeriodicY 1
```

This switches periodicity in the left-right direction. Correspondingly, for the back-front direction:

```
pdbSet MCImplant BoundaryPeriodicZ 1
```

All particles leaving the material will re-enter the material at the opposite side.

### Reflective Boundary

```
pdbSet MCImplant LeftBoundary Reflect
pdbSet MCImplant RightBoundary Reflect
pdbSet MCImplant BackBoundary Reflect
pdbSet MCImplant FrontBoundary Reflect
```

A particle hitting the boundary will have its position and direction of motion reflected with respect to the boundary plane.

## TrueReflect Boundary Condition

Instead of reflecting the direction of the moving particles at the boundary, Sentaurus Process provides a new boundary condition `TrueReflect`, which automatically reflects the structure, performs the implantation, and then cuts the structure to its original domain. To specify the `TrueReflect` boundary condition, use the following commands:

```
pdbSet MCImplant LeftBoundary TrueReflect
pdbSet MCImplant RightBoundary TrueReflect
pdbSet MCImplant FrontBoundary TrueReflect
pdbSet MCImplant BackBoundary TrueReflect
```

**NOTE** Generally, reflective boundary conditions (including both `Reflect` and `TrueReflect`) can be used only if there are the same reflect-symmetric ion beams, such as `tilt=0` (or projected `tilt2D=0` in 2D), or approximately, multiple rotation implantations. To improve performance, the averaging of the simulation results (including dopant and damage fields) over the original and reflected domains can be performed. If `tilt` (or `tilt2D`)  $< 2^\circ$ , Sentaurus Process automatically averages the simulation results. In the case of `mult.rot` implantations (or a sequence of multiple `implant` commands consisting of `mult.rot` implantation), no automatically averaging is performed. However, you can specify `average` in the `implant` command to do the averaging. To overwrite such default behaviors, specify `average` or `!average` in the `implant` command.

**NOTE** In cases where `average` is applied successfully, `TrueReflect` generally achieves more accurate results than `Reflect` without the significant performance penalty.

## Extending the Simulation Domain

```
pdbSet MCImplant LeftBoundary Extend
pdbSet MCImplant RightBoundary Extend
pdbSet MCImplant BackBoundary Extend
pdbSet MCImplant FrontBoundary Extend
```

The simulation domain is artificially extended in the corresponding direction. This compensates for the decay of the profile at the sides of the domain. Sentaurus Process determines these extension lengths automatically by using `tilt`, `rotation`, and `slice.angle`, and the user-defined parameters `MinExtension` and `ExtensionLength`:

$$\text{Ext Length} = \text{MinExtension} + \text{ExtensionLength} \cdot f(\text{tilt}, \text{rotation}, \text{slice.angle}) \quad (114)$$

where the function  $f$  is between 0 and 1. If `tilt` equals 0,  $f$  equals 0. Therefore, for `tilt` equals 0, extension length equals `MinExtension`. The default value for `MinExtension` is

### 3: Ion Implantation

#### Monte Carlo Implantation

0.1  $\mu\text{m}$ , which is usually sufficient for low-energy implants. For high-energy implants, you may need to increase `MinExtension` to avoid decaying concentration at the boundaries.

You can control the size of the extension by using:

```
pdbSet MCImplant ExtensionLength <n>
pdbSet MCImplant MinExtension <n>
```

**NOTE** For given boundary conditions other than `Transparent`, it is important that the boundaries, which are lines in 2D and planes in 3D, are continuous, that is, they should show no holes. The crossing of a particle can only be registered if it happens within the material region. The particle will finally leave the structure if it crosses the side while in a gas region.

---

## Datasets

The datasets used in a MC run follow the same naming conventions as those used in analytic implantation. Datasets unique to the MC implantation method are:

- The ballistic vacancy density `Vac_LastImp`.
- The damage probability `PD`, which is used to store and initialize damage history in Crystal-TRIM.
- The nuclear energy deposition `EnergyDeposition`, which is created in Sentaurus MC implantation.

Table 10 Datasets used in MC implantations

Dataset	Description
<code>EnergyDeposition</code>	Accumulated energy deposition (in units of $\text{eV}/\text{cm}^3$ ) from nuclear collisions. This dataset is created in Sentaurus MC implant only.
<code>Damage</code>	Accumulative damage (damage history). This dataset is deleted by the <code>diffuse</code> command. For Sentaurus MC, at the end of an <code>implant</code> step, the <code>Damage_LastImp</code> concentration is added to <code>Damage</code> , similar to analytic implantation. For Crystal-TRIM, damage is generated using the <code>PD</code> dataset after an <code>implant</code> step.
<code>Damage_LastImp</code>	Damage created during the last <code>implant</code> step. This dataset is used by Sentaurus MC only.
<code>&lt;dopant&gt;</code>	Accumulative density of the dopant concentration. At the end of an <code>implant</code> step, the <code>&lt;dopant&gt;_LastImp</code> concentration is added to <code>&lt;dopant&gt;</code> .
<code>&lt;dopant&gt;_Implant</code>	Accumulative density of the dopant concentration. At the end of an <code>implant</code> step, the <code>&lt;dopant&gt;_LastImp</code> concentration is added to <code>&lt;dopant&gt;_Implant</code> . This dataset is deleted by the <code>diffuse</code> command.

Table 10 Datasets used in MC implantations

Dataset	Description
<dopant>_LastImp	Ballistic dopant concentration generated during the last implant step. It is reset at the beginning of each implant step.
Int_Implant	Accumulative interstitial profile updated at the end of an implant step.
Int<component>_Implant	Accumulative interstitial profiles in multicomponent material with <code>DistinctDefects</code> set to true, where <component> is the component of the composition of the material. For example, in SiC, interstitial profiles include <code>IntSilicon_Implant</code> and <code>IntCarbon_Implant</code> .
PD	Damage probability. This dataset is used by Crystal-TRIM only.
Vac_Implant	Accumulative vacancy profile updated at the end of an implant step.
Vac_LastImp	Ballistic vacancy density generated during the last implant step.
Vac<component>_Implant	Accumulative vacancy profiles in multicomponent material with <code>DistinctDefects</code> set to true, where <component> is the component of the composition of the material. For example, in SiC, interstitial profiles include <code>VacSilicon_Implant</code> and <code>VacCarbon_Implant</code> .

---

## Smoothing Implantation Profiles

The implantation profiles as produced by MC simulations are typically noisy, especially in low concentration regions. This may sometimes cause converging problems or may require a very small time step in diffusion. To overcome this problem, Sentaurus Process provides a facility for smoothing the implant profiles.

The smoothing is enabled by using the following simple diffusion equation:

$$\frac{\partial C}{\partial t} - (D \cdot \nabla C) = 0 \quad (115)$$

where:

- $C$  is the concentration.
- $D$  is the diffusion coefficient.
- $\sqrt{D \cdot t}$  is the characteristic diffusing distance.

### 3: Ion Implantation

#### Smoothing Implantation Profiles

#### Smoothing All As-Implanted Profiles

To smooth all as-implanted profiles, specify the Boolean parameter `smooth` in the `implant` command or, alternatively, use the global switch `Smoothing`, which can be specified as follows:

```
pdbSet MCImplant Smoothing 1
```

In this case, all as-implanted fields are smoothed including dopant, damage, and point-defect profiles.

#### Smoothing Dopant and Damage Fields

For flexibility, Sentaurus Process also provides facilities for smoothing selected fields by using parameter `smooth.field=<list of fields>`. If this parameter is specified, only the specified fields are smoothed. The valid fields are `<dopant>` or `Damage`. For example, for BF2 implantation, the valid fields are `Boron`, `Fluorine`, or `Damage`. Note that point defects (interstitial and vacancy) are generally not independent and cannot be specified in `smooth.field`. In addition, depending on the point-defect model used, the smoothing of dopant or damage fields also may cause the point defects being smoothed.

You can control smoothing behavior by specifying the parameter `smooth.distance=<double array>`. This list specifies the smoothing distances (diffusing distance) for each of the fields as specified in `smooth.field`. If this list is missing, the smoothing distances are retrieved from the PDB:

```
pdbSetDouble MCImplant Smooth <dopant> Smooth.Distance <n>
```

If no `pdb` parameter is available for a given species, the global default (2 nm) is used.

#### Smoothing Point Defects

If only point defects are smoothed, you must use the `smooth` command after the `implant` command (instead of specifying `smooth` or `smooth.field` in the `implant` command). The syntax is as follows:

```
smooth smooth.field=<list of fields> smooth.distance=<double array>
```

This is a general command that can be used to smooth any field. For example, to smooth point defects after implantation, use the command:

```
smooth smooth.field= {Int_Implant Vac_Implant} smooth.distance= {1<nm> 5<nm>}
```

**NOTE** If using the `smooth` command to smooth a field, the `pdb` parameter for `smooth distance` will not be read. Therefore, `smooth.distance` must be specified in the `smooth` command if it is different from the default 2 nm.

---

## Automatic Extraction of Implant Moments

Implant moments are one of the most critical elements in analytic implantation. By default, Sentaurus Process provides a large set of implant tables that cover many species and materials, and a wide range of implantation conditions. However, occasionally, users want to explore new species, new materials, or the implantation parameter space, which is outside of the supplied implant tables. In this case, you need to do the experiments or to run the MC implantation simulations to obtain accurate implantation profiles. Automatically extracting implant moments bridges the gap of converting these raw profiles into the moments that can be used in analytic implantation.

The critical part of automatic extraction of implant moments is the optimization (or least square fit) algorithm, that is, given a profile or a set of  $m$  pairs of data points  $(x_i, y_i)$ , optimize the parameter set  $\beta$  of the model function  $f(x, \beta)$ , so that the sum of the squares of the errors at each point becomes minimal:

$$S(\beta) = \sum_{i=1}^m [y_i - f(x_i, \beta)]^2 \quad (116)$$

Sentaurus Process uses the same optimizer as TSUPREM-4, which implements the popular Levenberg–Marquardt algorithm, also known as the damped least-squares method. Since this algorithm only finds the local minimum, the initial parameter values may affect the extracted results.

---

## Required Parameters

To extract the moments, you must specify the parameters `extract.moments` and `data.file` in the `implant` command. The parameter `extract.moments` simply indicates that instead of performing an implantation or setting implantation parameters, the `implant` command is used to extract implant moments. The parameter `data.file` specifies the ASCII data file from where implant moments will be extracted.

---

## Optional Parameters

To better control the extraction process, the following optional parameters are available in the `implant` command:

- `dualpearson` (default), `gaussian`, and `pearson` specify the type of moments to be extracted.

### 3: Ion Implantation

#### Automatic Extraction of Implant Moments

- `rp`, `stdev`, `gamma`, `beta`, `rp2`, `stdev2`, `gamma2`, `beta2`, and `ratio` specify the initial values for optimization. If not specified, initial values will be guessed from the profile data.
- `data.units`, `data.xco`, `data.col`, `data.xlo`, `data.xhi`, `data.min`, and `data.max` specify how the data in `data.file` will be interpreted and retrieved.
- `max.iter` specifies the maximum number of iterations allowed in the optimization loop. Default is 500.
- `tolerance` specifies the tolerance of target errors. Default is 0.1.

---

## Output Format

Extracting implant moments provides two types of output, at the same time, to facilitate further manipulation of the moments:

- **Command line.** This is useful for copying and inserting the output into the `implant` command. The extracted moments are printed on the screen and in the log file in the format:

```
rp=<n> stdev=<n> gamma=<n> beta=<n> ...
```

- **Tcl list.** The output list of moments has the format:

```
{model dualpearson rp <n> stdev <n> gamma <n> beta <n> ...}
```

The output Tcl list can be converted into a Tcl array by using `array set`, which then can be used to access the moments conveniently. For example:

```
set moms [implant extract.moments data.file=myfile]
array set m $moms
LogFile ''model = $m(model)''
LogFile ''rp = $m(rp)''
LogFile ''stdev = $m(stdev)''
```

---

## Utilities

The Tcl script `ImplantTableMaker` can be used to guide users through selecting implantation conditions to automatically create a Taurus format implant table from MC implantations. This script must be run in interactive mode, and you must input various implant parameters that are necessary to create an implant table. The resulting table is named `<species>_in_<material>_mystandard`.



**NOTE** Since each implant profile is extracted independently, and the Levenberg–Marquardt optimization algorithm can only find the local minima, slightly different profiles may result in totally different implant moments. Interpolation between these moments may not give optimal results. Therefore, when using the Tcl script `ImplantTableMaker`, the quality of implant tables cannot be guaranteed.

---

## Loading External Profiles

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### Loading Files Using `load.mc`

---

Precomputed profiles can be loaded to a given structure using the `load.mc` facility in Sentaurus Process, that is:

```
implant <dopant> load.mc file=<name>
```

If the `load.mc` switch is set in the `implant` command, Sentaurus Process takes the TDR file specified with the `file` selector and loads the datasets into the present structure. Interpolation of the datasets is performed if the structure in the TDR file is different from the present structure.

Sentaurus Process attempts to find the doping profiles required from the implant species and the damage probability (for Crystal-TRIM) or damage dataset (for Sentaurus MC). For example, in the following statement:

```
implant Boron load.mc file=my_data energy=10 dose=1e14
```

Sentaurus Process opens the files `my_data{fps}.tdr`, and checks for the datasets `Boron_LastImp` and `PD_LastImp` (for Crystal-TRIM) or `Damage_LastImp` (for Sentaurus MC). If successful, these datasets are restored. If one or more of the required datasets is missing, the respective fields remain empty. Then, during implantation postprocessing, `Boron_LastImp` and `Damage_LastImp` are added to the `Boron_Implant` and `Damage` datasets.

The following options are available in 2D structures:

- `shift=<n>`: Shifts the dataset along the y-axis.
- `flip`: Flips the dataset; the default is a flip to the left.
- `left`, `right`: Specifies the flipping direction.
- `multiply=<n>`: Multiplies the dopant data in the dataset by a factor; the damage remains untouched.

**NOTE** The switch `load.mc` restores the datasets from the files without checking the implant conditions specified in the `implant` command. Therefore, `load.mc` by itself does not require the implant parameters such as `energy` and `dose` be specified. However, Advanced Calibration and CoImplant models may use these parameters (`energy` and `dose`) for their calculations. Therefore, it is recommended that `energy` and `dose` always be specified along with `load.mc`.

---

## Automated Monte Carlo Run

If no TDR file with the specified name is found or the `file` selector is empty, a separate run of Crystal-TRIM or Sentaurus MC is started to generate these files and the required datasets, depending on the setting of the MC implantation model in the PDB (default is `sentaurus.mc`):

```
pdbSet MCImplant model {crystaltrim | sentaurus.mc}
```

Sentaurus Process internally switches from the `load.mc` to `crystaltrim` or `sentaurus.mc` mode. All implant parameters related to MC implantation (`particles`, `cascades`, `full.molecular`) are used in this run.

**NOTE** The `load.mc` feature is designed to reuse precomputed MC results. However, the profiles to load do not necessarily need to be generated using the MC method.

### Example

```
implant BF2 dose=1e14 energy=40 tilt=20 rotation=-90 load.mc \  
file=bf2_1e14_40 particles=500 cascades
```

In the first run of this command, Sentaurus Process checks for the TDR file with the name `bf2_1e14_40`. Since there is no file with this name, a full-cascade Crystal-TRIM or Sentaurus MC run is started using the process parameters specified. At the end, the TDR file `bf2_1e14_40_fps.tdr` is saved. The following are stored as well:

- All datasets related to the BF2 impurity profile (`Boron_LastImp`, `Fluorine_LastImp`).
- The damage probability (`PD_LastImp`) or damage (`Damage_LastImp`).
- The recoil profile (`Silicon_LastImp`) and vacancy profile (`Vac_LastImp`) because the command is run in the full-cascade mode.

In a subsequent run of the same command, Sentaurus Process loads and restores these datasets in a preprocessing step. The postprocessing is the same as after a MC run.

---

## Multithreaded Parallelization of 3D Analytic Implantation

Parallel processing has become ubiquitous with the advent of multicore processors. The performance of 3D analytic implantation can be improved dramatically by exploiting the parallel processing power of multicore processors. In multithreaded mode, each thread works on separate nodes, sharing the workload, thereby reducing the computation time.

To engage the multithreaded parallelization of 3D analytic implantation, use the `math` command:

```
math [ numThreads = <n> | numThreadsImp3d = <n> ]
```

where `numThreads` is a general keyword for MC implantation, 3D analytic implantation, KMC, matrix assembly, and linear solver. However, `numThreadsImp3d` has a higher priority over `numThreads` for 3D analytic implants and can be used to create the number of threads specifically for 3D analytic implantation, which is different from that for other multithreaded operations. The value of `numThreads` or `numThreadsImp3d` must be equal to the number of cores in multicore processors.

You also can modify the stack size for each thread using the command:

```
math [ threadStackSize = <n> ]
```

The default stack size ( $2^{18} = 262144$  bytes) is usually sufficient for 3D analytic implantation.

---

## Multithreaded Parallelization of Sentaurus MC Implantation

**NOTE** This feature is available to Sentaurus MC only.

The performance of MC implantation (Sentaurus MC) also can be significantly improved by using multithreaded parallelization. In this approach, a large job with many particles ( $N$ ) is divided into multiple ( $m$ ) separate jobs with a smaller number of particles ( $N/m$ ). Sentaurus Process then creates multiple threads and launches  $m$  instances of Sentaurus MC implant. Each instance of Sentaurus MC implant runs independently on its own thread. After these threads are finished, the results are averaged, thereby improving the effective execution speed for a large job.

To engage the multithreaded parallelization of Sentaurus MC implantation, use the `math` command:

```
math [ numThreads = <n> | numThreadsMC = <n> ]
```

### 3: Ion Implantation

#### References

where `numThreads` is a general keyword for MC implantation, 3D analytic implantation, KMC, matrix assembly, and linear solver. However, `numThreadsMC` has higher priority over `numThreads` for MC implants and can be used to create the number of threads specifically for Sentaurus MC implant, which is different from that for other multithreaded operations. The value of `numThreads` or `numThreadsMC` should be equal to the number of cores in multicore processors.

You also can modify the stack size for each thread using the command:

```
math [ threadStackSize = <n> ]
```

The default stack size ( $2^{18} = 262144$  bytes) is usually sufficient for MC implantation.

---

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*This chapter provides information on the continuum models for dopant and defect diffusion models and parameters. (For an atomistic approach, see [Chapter 5](#).)*

---

### Overview

During the fabrication process, dopants are introduced into the substrate with different concentration profiles. As processing proceeds through various thermal annealing cycles, the dopants diffuse and redistribute through the structure. The following effects contribute to dopant redistribution and can be modeled by Sentaurus Process:

- Dopant (de)activation
- Dopant–defect interaction
- Chemical reactions at interfaces and in bulk materials
- Material flow
- Moving material interfaces
- Internal electric fields

Sentaurus Process is designed to address the challenges of integrated-circuit process modeling. As technology development continues, the need for new process models increases. The Alagator language is a versatile way to add and modify diffusion models quickly. This chapter describes the diffusion models in Sentaurus Process. To modify or add new diffusion models, see [Modifying Diffusion Models on page 596](#).

The `diffuse` command represents the main simulation capabilities of Sentaurus Process. It simulates:

- Thermal annealing of impurities.
- Material growth processes during annealing, for example, oxidation, silicidation, and epitaxy (see [Epitaxy on page 270](#) and [Oxidation on page 603](#)).
- Process-induced stress (see [Chapter 9 on page 629](#)).

---

## Basic Diffusion

The `diffuse` command is used to model the diffusion of impurities under oxidizing and non-oxidizing conditions. The options of the `diffuse` command set diffusion conditions as well as time-stepping options. (See [diffuse on page 875](#) for all options.) For example, a command for a simple non-oxidizing annealing at a temperature of 900°C for 10 s is:

```
diffuse temperature=900<C> time=10<s>
```

If you want to perform the same anneal with a wet (H<sub>2</sub>O) oxidizing ambient, execute the following command:

```
diffuse temperature=900<C> time=10<s> H2O
```

A simple temperature ramp can be specified directly in the `diffuse` command by the keyword `ramprate`. This keyword sets the change in the temperature over time:

```
diffuse temperature=900<C> time=10<min> O2 ramprate=10<C/min>
```

This example describes a dry oxidation of 10 minutes, starting at 900°C and ending at 1000°C. The same example can be repeated using the `temp_ramp` command as follows:

```
temp_ramp name=MyTempRamp temperature=900 time=10 O2 ramprate=10<C/min>
diffuse temp.ramp=MyTempRamp
```

The first line creates a temperature ramp with given conditions, and the second line specifies a diffusion referring to this temperature ramp.

To describe more complex temperature cycles within one `diffuse` command, multiple instances of the `temp_ramp` command can be used. A temperature ramp can consist of several segments and, for each segment, one `temp_ramp` command is required. In addition, segments can be grouped by using the same name for each segment. For example, a ramp-up, plateau, and ramp-down can be specified as:

```
temp_ramp name=MyCycle temperature=500<C> time=5<min> H2O ramprate=100<C/min>
temp_ramp name=MyCycle temperature=1000<C> time=10<min> O2
temp_ramp name=MyCycle temperature=1000<C> time=10<min> ramprate=-50<C/min> \
last
diffuse temp.ramp=MyCycle
```

The keyword `last` in the third `temp_ramp` command declares the last segment of the temperature ramp.

Sentaurus Process allows for thermal oxidation from O<sub>2</sub> and H<sub>2</sub>O. The `gas_flow` command is used to specify a mixed gas flow by specifying directly either the partial pressures of the gas components or the flow [volume/time]. If the flows are defined, they are converted to partial



pressures by taking ratios. The use of the `gas_flow` command is similar to the `temp_ramp` command; however, multiple gas flows using the same name must not be specified. When a `gas_flow` is specified, it can be referred to from both the `temp_ramp` and `diffuse` commands:

```
gas_flow name=MyGasFlow pH2O=0.5 pO2=0.5 pH2=0.1
```

To invoke the gas flow specification as given above, use:

```
temp_ramp name=MyTempRamp temperature=1000<C> time=10<min> gas.flow=MyGasFlow  
diffuse temp.ramp=MyTempRamp
```

or:

```
diffuse temperature=1000<C> time=10<min> gas.flow=MyGasFlow
```

Sentaurus Process also allows you to select various diffusion models for point defects and dopants (see [Transport Models on page 197](#)). Diffusion model setting and parameter setting are performed with the `pdbSet` command. The basic settings are:

```
pdbSet <material> Dopant DiffModel <model>
```

where `<model>` can be any of `Constant`, `Fermi`, `Pair`, `React`, `ChargedFermi`, `ChargedPair`, or `ChargedReact`.

Epitaxy can be simulated if either the `Epi` (also known as `epi`) or `LTE` ambient is specified in either the `temp_ramp` or `diffuse` command. If `Epi` is specified, `Silicon` will grow on `Silicon` and `PolySilicon` will grow on `PolySilicon`. If the `LTE` ambient is specified, `Silicon` will again grow on `Silicon`, but `PolySilicon` will grow on `Oxide`, `Nitride`, and `PolySilicon`.

```
pdbSet Silicon Dopant DiffModel Pair  
diffuse temperature=800<C> time=60<min> Epi thick=0.01 \  
epi.doping = {Germanium = 8e21}
```

This example sets the dopant diffusion model for all dopants in silicon to the `Pair` model and grows a 0.01  $\mu\text{m}$  thick `epi` layer with a Germanium concentration of  $8 \times 10^{21}$ .

It is also possible to set the initial diffusion time-step and the minimum annealing temperature with the `diffuse` command.

```
diffuse temp.ramp=MyCycle minT=600<C> init=0.01<s>
```

This example uses the `temp_ramp` created in the earlier example. The initial time step is set to 0.01 s and the minimum annealing temperature is set to 600°C. The diffusion and reaction equations will be switched off below 600°C but the mechanics will be solved.

## 4: Diffusion

### Basic Diffusion

If you want to set the minimum annealing temperature and initial time-step globally for all diffusion commands, the following commands can be used:

```
pdbSet Diffuse minT {<n>}
pdbSet Diffuse InitTimeStep {<n>}
```

It is also possible to set minimum and maximum temperature limits for the annealing process using the following commands:

```
pdbSet Diffuse minAnnealT <n>
pdbSet Diffuse maxAnnealT <n>
```

If the annealing temperature goes above or below these limits, Sentaurus Process will quit with an error message.

See [Viewing the Defaults: Parameter Database Browser on page 58](#) for other parameters related to Diffuse.

---

## Obtaining Active and Total Dopant Concentrations

By default, active and total dopant concentrations are only updated during diffusion steps. For example, after an implant, the active concentrations (`BoronActiveConcentration`, `ArsenicActiveConcentration`, and so on) and the total concentrations (`BoronConcentration`, `ArsenicConcentration`, and so on) are not modified, which makes them out of date.

Similarly for other commands that can change the dopant concentrations, the active and total concentrations are not updated. These commands include, but are not limited to, `select`, `load`, `init`, and `profile`.

After one of these commands is issued, the active and total dopant concentrations may not be current. To update the active and total dopant concentrations use the `diffuse time=0 ...` command.

**NOTE** To update the active and total concentrations of the dopants without dopant redistribution, the `diffuse` command with zero time can be used. For example, to calculate the active dopant concentration at 850°C for the chosen diffusion model, use:

```
diffuse time=0.0 temperature=850
```

**NOTE** Since the `diffuse` command performs the recrystallization and the initialization of clusters even with zero time, it must not be added between consecutive implantation steps.

See [diffuse on page 875](#) for all options of the `diffuse` command.

---

## Transport Models

Sentaurus Process has several basic transport models with varying levels of complexity for computing flux,  $J$ . This diversity of models is needed to balance accuracy with simulation times, which vary widely depending on the model selection:

- The `React` (see [React Diffusion Model on page 204](#)) and `ChargedReact` (see [ChargedReact Diffusion Model on page 198](#)) diffusion models, also known as five-stream diffusion models, are the most advanced dopant diffusion models in Sentaurus Process. They solve up to three separate equations per dopant – a substitutional dopant – and up to two dopant–defect pairs and two defect equations. The `ChargedReact` model is the most accurate model available in Sentaurus Process. but because of the large number of equations required, it also is the most computationally expensive. The `React` model, which is an uncharged version of the `ChargedReact` model, is provided for backward compatibility.
- The `Pair` (see [Pair Diffusion Model on page 208](#)) and `ChargedPair` (see [ChargedPair Diffusion Model on page 206](#)) diffusion models, also known as three-stream diffusion models, assume that dopant–defect pairs are in local equilibrium but still solve for separate point-defect equations. These models solve one equation per dopant and two defect equations. The `ChargedPair` diffusion model allows the pairing coefficients to vary with charge state. These models are the most commonly used for advanced CMOS processes as they represent a balance between accuracy and computational expense. For extremely fast ramp rates or for customized initial conditions, the `ChargedReact` model or `React` model is a better choice. The `Pair` model, which is an uncharged version of the `ChargedPair` model, is provided for backward compatibility.
- The `Fermi` (see [Fermi Diffusion Model on page 211](#)) and `ChargedFermi` (see [ChargedFermi Diffusion Model on page 209](#)) diffusion models both assume that point defects as well as dopant–defect pairs are in equilibrium. The `ChargedFermi` diffusion model allows the diffusivity of each charge state to be set separately. An uncharged version of the model is provided for backward compatibility. These models can be used for long-term high-temperature anneals where the transient effect of annealing implant damage is minimal.
- The `Constant` diffusion model (see [Constant Diffusion Model on page 212](#)), unlike all other transport models, assumes a constant diffusivity and no electric-field effect, and is used mainly for dopant diffusion in oxide.

The selection of transport model is specified as follows:

```
pdbSet <material> Dopant DiffModel <model>
```

## 4: Diffusion

### Basic Diffusion

where <model> must have one of the valid diffusion model names – Constant, Fermi, Pair, React, ChargedFermi, ChargedPair, or ChargedReact.

It is also possible to select a different diffusion model for each dopant in the same material. In this case, use the command:

```
pdbSet <material> <dopant> DiffModel <model>
```

where <dopant> is a valid dopant name (for example, Boron).

The ChargedFermi, ChargedPair, and ChargedReact diffusion models take into account each charged point defect individually. Otherwise, they are very similar to the Fermi and Pair diffusion models.

**NOTE** Even though you can select any diffusion model individually for each dopant, it is not recommended to mix the ChargedFermi, ChargedPair, or ChargedReact models with the uncharged versions.

Table 11 Summary of dopant diffusion models and parameters

pdb command	Diffusion model							
	Type	ChargedReact	React	ChargedPair	Pair	ChargedFermi	Fermi	Constant
pdbSet <material> <dopant> <defect> D	Diffusivity	X	X	X	X			
pdbSet <material> <dopant> <defect> Dstar	Diffusivity					X	X	
pdbSet <material> <dopant> Dstar	Diffusivity							X
pdbSet <material> <defect> D	Diffusivity	X	X	X	X	X		
pdbSet <material> <dopant> <defect> ChargePair	Pairing Coeff.	X		X				
pdbSet <material> <dopant> <defect> Binding	Pairing Coeff.		X		X			
pdbSet <material> <dopant> <defect> kfFTM	Rate	X						
pdbSet <material> <dopant> <defect> kfKickOut	Rate	X						
pdbSet <material> <defect> ChargeStates	Charging Coeff.	X	X	X	X	X		
pdbSet <material> <defect> ChargeStatesScale	Charging Coeff.	X	X	X	X	X		
pdbSet <material> <defect> Cstar	Concentration	X	X	X	X	X	X	X
pdbSet <material> <defect> KbulkChargeStates	Charging Coeff.	X	X	X	X	X		

In [Table 11](#), <material> is a valid material name, <dopant> is a valid dopant name, and <defect> is either `Int` or `Vac`.

---

## Recombination and Reaction Models

Many reactions and recombination models are available in Sentaurus Process. Different diffusing species such as dopants, defects, and impurities will all have different recombination and reaction terms. These terms come from the following models:

- Dopant clusters—solid solubility, transient, and dopant–defect cluster models (see [Dopant Activation and Clustering on page 279](#)).
- Defect clusters—Equilibrium, {311}, Loop, LoopEvolution, 1Moment, 2Moment, Full, and FRENDECH models (see [Defect Clusters on page 306](#)).
- Impurity species:
  - Carbon model, Nitrogen model (see [NeutralReact Diffusion Model on page 212](#)).
  - Fluorine model (see [Dopant Active Model: FVCluster on page 291](#)).

---

## Boundary Conditions

Sentaurus Process can simulate various boundary conditions for dopants and defects. You can select eight different boundary conditions:

- HomNeumann can be applied to any boundary (see [HomNeumann on page 344](#)).
- Natural is for point defects (see [Natural on page 345](#)).
- Segregation is for dopants (see [Segregation on page 348](#)).
- Dirichlet is for dopants and defects (see [Dirichlet on page 351](#)).
- ThreePhaseSegregation is for dopants (see [ThreePhaseSegregation on page 352](#)).
- GrainBoundarySegregation is for dopants in polycrystalline materials (see [Boundary Conditions on page 248](#)).
- GrainGrainBoundarySegregation is for dopants in polycrystalline materials (see [Boundary Conditions on page 248](#)).
- Trap is for dopants such as fluorine and nitrogen in trap-dependent oxidation.
- TrapGen is for dopants such as nitrogen in N<sub>2</sub>O oxidation.
- Continuous is for dopants used only during epi growth (see [Continuous on page 356](#)).

The `Natural` and `Dirichlet` boundary conditions consider interstitial injection during oxidation for oxidation-enhanced diffusion (OED) of dopants.

---

## Other Materials and Effects

In addition to generic transport and recombination and reaction models, other effects can be simulated:

- Polysilicon model (see [Diffusion in Polysilicon on page 233](#)).
- SiGe diffusion model (see [Dopant Diffusion in SiGe on page 250](#)).
- Epitaxy (see [Epitaxy on page 270](#)).

---

## General Formulation

The general expression for the particle current of a diffusing species  $A$  of charge  $c$  is given by:

$$\mathbf{J}_{A^c} = -d_{A^c} \left(\frac{n}{n_i}\right)^{-c} \nabla \left( A^c \left(\frac{n}{n_i}\right)^c \right) \quad (117)$$

where  $A^c$  is the concentration,  $d_{A^c}$  is the diffusivity,  $n$  is the electron concentration, and  $n_i$  is the intrinsic electron concentration.

The continuity equation for species  $A$  of charge  $c$  is given by:

$$\frac{\partial A^c}{\partial t} = -\nabla \cdot \mathbf{J}_{A^c} + R_{A^c}^{trans} - R_{A^c}^{clus} \quad (118)$$

where the recombination/reaction term is split into two parts:  $R_{A^c}^{trans}$  is a possible contribution coming from the transport model selection (see [Transport Models on page 197](#)) and  $R_{A^c}^{clus}$  can contain terms from other reactions, which are most often clustering reactions but could include any type of reaction. Reactions that transform species  $A^c$  into another species will introduce positive terms into the expression for  $R_{A^c}^{clus}$ . Total dopant concentration of dopant  $A$  will be equal to the sum of all dopants, dopant-defect pairs, and any related clusters (for example,  $A_{Total}^c = A^c + A_{pair}^c + A_{clus}^c$ ).

For the models that do not consider different charge states, computation of the electron concentration by default is given by the charge neutrality condition  $-n + p + \Delta N = 0$ , where  $\Delta N$  is given by the active dopant concentrations (for example,  $\Delta N = N_d - N_a$  where  $N_d$  is the active donor concentration and  $N_a$  is the active acceptor concentration). For the charged models, the charge states of the defects or defect pairs are considered individually.

It is expected that the charge reactions are in equilibrium, so that the ratio in the various charged states is set by the Fermi level:

$$A^{c+r} = k_{A^c} C_{A^r} \left(\frac{n}{n_i}\right)^{-c} \quad (119)$$

where  $r$  is a reference charge state, which is chosen as 0 for interstitials and vacancies, and is chosen as the dopant charge for dopant–defect pairs. The  $k_{A^c}$  are parameters that are set by default to an Arrhenius expression. In addition, for the charged models, it is necessary to solve a coupled equation for the electron concentration. The default equation is the same as for the uncharged case, that is, the charge neutrality equation  $-n + p + \Delta N = 0$  but, in this case,  $\Delta N$  is a function of  $n$  because it contains contributions from charged defects or charged defect pairs as well as dopants. It is also possible for both the charged and uncharged models to solve the Poisson equation (see [Electron Concentration on page 267](#)).

## Transport Models

Transport models compute the particle flux of dopants and are the core diffusion models solved by Sentaurus Process. In addition to particle flux, pairing reactions can be computed depending on the transport model selection. Transport models are usually used with one or more clustering or activation models available. The reaction or clustering models will not modify the dopant flux, but will compute terms to be added to  $R_{clus}^c$  from Eq. 118. The models are described in detail here.

The selection of the transport model is made with the command:

```
pdbSet <material> <dopant> DiffModel <model>
```

where <material> is the material name; <dopant> can be either "Dopant" to apply to all dopants or a named dopant such as boron, arsenic, phosphorus, antimony, and indium; and <model> is one of the models ChargedReact, React, ChargedPair, Pair, ChargedFermi, Fermi, or Constant.

Table 12 Solution names

Symbol	Boron	Arsenic	Phosphorus	Antimony	Indium
$C_A$	Boron	Arsenic	Phosphorus	Antimony	Indium
$C_{AI}$	BoronInt	ArsenicInt	PhosphorusInt	AntimonyInt	IndiumInt
$C_{AV}$	BoronVac	ArsenicVac	PhosphorusVac	AntimonyVac	IndiumVac
$C_A^+$	BActive	AsActive	PActive	SbActive	InActive

Table 13 Point-defect names

Symbol	Interstitial	Vacancy
$C_X$	Int	Vac
$C_X^*$	EqInt	EqVac
$C_{X^0}^*$	IntNeutralStar	VacNeutralStar
$C_{X^0}$	IntNeutral	VacNeutral

The transport for point defects is computed when `Compute.Point.Defect` is set to 1:

```
pdbSet <material> Compute.Point.Defect <0 | 1>
```

---

## ChargedReact Diffusion Model

The `ChargedReact` diffusion model is the most general transport model in Sentaurus Process. The model has an immobile substitutional dopant and up to two mobile charged dopant–defect pair species. Mobile charged point defects are also included in the model.

The following reactions are considered:



The differential equations that are solved in this model are:

$$\frac{\partial C_A}{\partial t} = -R_{AI} - R_{AV} + R_{AI,V} + R_{AV,I} - R_A^{clus} \quad (125)$$

$$\frac{\partial C_{AI}}{\partial t} = -\nabla \cdot \mathbf{J}_{AI} + R_{AI} - R_{AI,V} - R_{AI}^{clus} \quad (126)$$



$$\frac{\partial C_{AV}}{\partial t} = -\nabla \cdot \mathbf{J}_{AV} + R_{AV} - R_{AV,I} - R_{AV}^{clus} \quad (127)$$

$$\frac{\partial C_I}{\partial t} = -\nabla \cdot \mathbf{J}_I - R_{IV} - R_{AI} - R_{AV,I} - R_I^{clus} \quad (128)$$

$$\frac{\partial C_V}{\partial t} = -\nabla \cdot \mathbf{J}_V - R_{IV} - R_{AV} - R_{AI,V} - R_V^{clus} \quad (129)$$

where  $C_A$  is the concentration of substitutional (and assumed to be immobile) dopants,  $C_X$  is the concentration of ‘free’ defects of type  $X$  (either interstitials or vacancies), in other words, those defects not in clusters or pairs. The reaction rates of the different species ( $R$ ) are defined later in this section.

Next, the flux of the mobile defect pair is considered. Working with [Eq. 117, p. 196](#) for the charged pairs, the equation will be written in terms of the total concentration of pairs.

It is expected that the dopant-defect pairing reaction is in equilibrium, therefore, a set of constants for this pairing is defined:

$$C_{AX^{z+c}} = k_{AX^c} C_A^z C_{X^c} \quad (130)$$

where  $X$  is either I or V,  $z$  is the charge of the dopant  $A$ , and  $k_{AX^c}$  is the pairing coefficient for the pair  $AX$ , and is given by:

$$k_{AX^c} = k_{AX^c}^0 \exp\left(\frac{-k_{AX^c}^E}{k_B T}\right) \quad (131)$$

To set  $k_{AX^c}$ , use:

```
pdbSet <material> <dopant> <defect> ChargePair <c> {<n>}
```

where <material> is a material name (see), <dopant> is one of the existing Sentaurus Process dopants, <defect> is either Interstitial or Vacancy, <c> is the charge state, and <n> is a Tcl expression that returns a number – it can be simply a number.

One commonly used Tcl procedure for setting parameters is `Arrhenius`. This procedure takes a prefactor and an energy as arguments and returns `prefactor · exp( $\frac{-energy}{k_B T}$ )`.

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The flux of the pairs is computed from Eq. 117, p. 196:

$$\begin{aligned}
 J_{AX} &= -\sum_c J_{AX^c} \\
 &= -\sum_c D_{AX^c} \left(\frac{n}{n_i}\right)^{-c-z} \nabla \left( \frac{C_{AX}}{C_{X^0}^* \sum_q k_{AX^q} k_{X^q} \left(\frac{n}{n_i}\right)^{-q}} \left(\frac{n}{n_i}\right)^z \right)
 \end{aligned} \tag{132}$$

where  $C_{AX}$  is the total concentration of pairs that is the sum of the concentrations of pairs at every charge state and  $D_{AX^c}$  is an effective diffusivity of dopant point-defect pairs at charge state  $c$  and is related to the self diffusivity  $d_{AX^c}$  by:

$$\begin{aligned}
 D_{AX^c} &= C_{X^0}^* k_{AX^c} k_{X^c} d_{AX^c} \\
 &= D_{AX^c}^0 \exp\left(\frac{-D_{AX^c}^E}{k_B T}\right)
 \end{aligned} \tag{133}$$

where  $C_{X^0}^*$  is the equilibrium concentration of the neutral defects and is related to the total equilibrium intrinsic concentration of defect  $X$  by:

$$C_{X^0}^* = \frac{C_{X(intrinsic)}^*}{\sum_c k_{X^c}} \tag{134}$$

The quantities  $C_{I(intrinsic)}^*$  and  $C_{V(intrinsic)}^*$ , which by default follow an Arrhenius law, can be changed by using the command:

```
pdbSet <material> <defect> Cstar {<n>}
```

To set  $D_{AX^c}$ , use:

```
pdbSet <material> <dopant> <defect> D <c> {<n>}
```

A set of equilibrium-charging constants,  $k_{X^c}$ , for defect  $X$  is defined:

$$C_{X^c} = k_{X^c} C_{X^0}^* \left(\frac{n}{n_i}\right)^{-c} \tag{135}$$

where  $X$  is either I or V, and  $k_{X^c}$  is the charging coefficient for the defect  $X$  and is given by:

$$k_{X^c} = k_{X^c}^0 \exp\left(\frac{-k_{X^c}^E}{k_B T}\right) \tag{136}$$

To set  $k_{X^c}$ , use:

```
pdbSet <material> <defect> ChargeStates <c> {<n>}
```

**NOTE** The neutral charge state must always be 1.0.

Similar to the pairs, the defect fluxes are computed from [Eq. 117, p. 196](#):

$$\begin{aligned} J_X &= -\sum_c J_{X^c} \\ &= -\frac{\sum_c k_{X^c} D_{X^c} \left(\frac{n}{n_i}\right)^{-c} C_X^*}{\sum_q k_{X^q} \left(\frac{n}{n_i}\right)^{-q}} \nabla \left(\frac{C_X}{C_X^*}\right) \end{aligned} \quad (137)$$

where  $C_X$  is the total concentration of defects that is the sum of the concentrations of defect  $X$  at every charge state and  $D_{X^c}$  is the diffusivity of the defect  $X$  of charge state  $c$  and is given by:

$$\begin{aligned} D_{X^c} &= d_{X^c} \\ &= D_{X^c}^0 \exp\left(\frac{-D_{X^c}^E}{k_B T}\right) \end{aligned} \quad (138)$$

To set  $D_{X^c}$ , use:

```
pdbSet <material> <defect> D <c> {[Arrhenius <prefactor> <energy>]}
```

Now, the reaction rates can be written by considering [Eq. 120, p. 198](#) to [Eq. 124, p. 198](#) and the general formula for the rate of all combinations of charge states:

$$\begin{aligned} A^a + B^b &\leftrightarrow AB^c + (c - a - b)e \\ R_{A^a, B^b, c} &= k_{A^a, B^b, c}^f \left( C_{A^a} C_{B^b} - k_{A^a, B^b, c}^r C_{AB^c} \left(\frac{n}{n_i}\right)^{(c-a-b)} \right) \end{aligned} \quad (139)$$

Therefore, summing all possible charge states gives:

$$R_{AX} \equiv -\bar{K}_{AX}^f \left( C_A C_X - \frac{C_{AX}}{\bar{K}_{AX}^r} \right) \quad (140)$$

$$R_{AI, V} \equiv \bar{K}_{AI, V}^f (C_{AI} C_V - \bar{K}_{AX}^r C_I^* C_V^* C_A) \quad (141)$$

$$R_{AV, I} \equiv \bar{K}_{AV, I}^f (C_{AV} C_I - \bar{K}_{AX}^r C_I^* C_V^* C_A) \quad (142)$$

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where:

$$\bar{K}_{AX}^f \equiv \frac{\sum_i K_{fXKOi} k_{X^i} \left(\frac{n}{n_i}\right)^{-i}}{\sum_c k_{X^c} \left(\frac{n}{n_i}\right)^{-c}} \quad (143)$$

$$\bar{K}_{AX}^r \equiv \frac{\sum_i k_{AX^i} k_{X^i} \left(\frac{n}{n_i}\right)^{-i}}{\sum_c k_{X^c} \left(\frac{n}{n_i}\right)^{-c}} \quad (144)$$

$$\bar{K}_{AI,V}^f \equiv \frac{\sum_i \sum_j K_{f_{AI^i,V^j}FT} k_{AI^i} k_{V^j} \left(\frac{n}{n_i}\right)^{-(i+j)}}{\sum_c k_{AI^c} \left(\frac{n}{n_i}\right)^{-c} \sum_z k_{V^z} \left(\frac{n}{n_i}\right)^{-z}} \quad (145)$$

$$\bar{K}_{AV,I}^f \equiv \frac{\sum_i \sum_j K_{f_{AV^i,I^j}FT} k_{AV^i} k_{I^j} \left(\frac{n}{n_i}\right)^{-(i+j)}}{\sum_c k_{AV^c} \left(\frac{n}{n_i}\right)^{-c} \sum_z k_{I^z} \left(\frac{n}{n_i}\right)^{-z}} \quad (146)$$

where  $\bar{K}_{AX}^f$  is the forward reaction rate for the kick-out mechanism, and X is either interstitial or vacancy,  $\bar{K}_{AI,V}^f$  and  $\bar{K}_{AV,I}^f$  are forward reaction rates for the Frank–Turnbull mechanism and  $\bar{K}_{AX}^r$  is the equilibrium constant.

The forward ( $K_{fXKOi,j}$ ) kick-out reaction rates can be set by using the following commands:

```
pdbSet <material> <dopant> <defect> kfKickOut <c> {<n>}
```

where c is the charge state. By default, kfKickOut values for each charge state are given as:

$$K_{fXKOi} \equiv \frac{D_{AX} C_X^* \sum_i k_{X^i}}{k_{X^0} \lambda^2} \quad (147)$$

where  $\lambda$  is the hopping length, which can be set using the command:

```
pdbSet <material> <dopant> <defect> lambdaK
```

Similarly, the forward ( $\bar{K}_{AI,V}^f$ ,  $\bar{K}_{AV,I}^f$ ) Frank–Turnbull reaction rates can be defined using the commands:

```
pdbSet <material> <dopant> <defect> kfFTM <i,j> {<n>}
```

**NOTE** The indices of the forward recombination rates have the form of  $i, j$ . Both  $i$  and  $j$  are integers and are separated by a comma; no space is allowed between the indices.

The  $I$ - $V$  recombination reaction is given as:

$$R_{IV} = \bar{K}_{IV}(C_I C_V - C_I^* C_V^*) \quad (148)$$

where:

$$\bar{K}_{IV} = \frac{C_{I(intrinsic)}^* C_{V(intrinsic)}^*}{C_I^* C_V^* \sum_z k_{I^z} \sum_z k_{V^z}} \sum_i \sum_j K_{IVij} k_{I^i} k_{V^j} \left(\frac{n}{n_i}\right)^{-(i+j)} \quad (149)$$

The superscript ‘\*’ refers to the equilibrium concentration, and the subscripts  $I$  and  $V$  are for the interstitials and vacancies, respectively. The subscripts  $z, i, j$  are the charge states of the defects.  $K_{I^i V^j}$  is the bulk recombination rate for interstitials and vacancies at the charge stated  $i$  and  $j$ , respectively. The bulk recombination rate  $K_{I^i V^j}$  for each charged point defect can be set using the command:

```
pdbSet <mater> <defect> KbulkChargeStates <i, j> {<n>}
```

The equilibrium concentration of the unpaired point defect can be calculated by:

$$C_X^* = C_{X(intrinsic)}^* \frac{\sum_c k_{X^c} \left(\frac{n}{n_i}\right)^{-c}}{\sum_c k_{X^c}^s} \quad (150)$$

where  $k_{X^c}^s$  is the scaled charging coefficient for the defect  $X$  and can be set by using:

```
pdbSet <material> <defect> ChargeStatesScale <c> {<n>}
```

$k_{X^c}^s$  is set to  $k_{X^c}$  as a default.

**NOTE** The indices for the parameter `KbulkChargeStates` have the form of  $i, j$ . Both  $i$  and  $j$  are integers and are separated by a comma; no space is allowed between the indices.

## React Diffusion Model

The `React` model is similar to the `ChargedReact` model, except that the reaction rates are not charge state-dependent and the electron concentration is computed directly from the net doping concentration. In addition, the Frank–Turnbull mechanism is not considered.

The reactions considered are:



where  $A$  is the dopant,  $I$  is the interstitial, and  $V$  is the vacancy.

The following set of differential equations represents the model:

$$\frac{\partial C_A}{\partial t} = -R_{AI} - R_{AV} - R_A^{clus} \quad (153)$$

$$\frac{\partial C_{AX}}{\partial t} = -\nabla \cdot \mathbf{J}_{AX} + R_{AX} - R_{AX}^{clus} \quad (154)$$

$$\frac{\partial C_X}{\partial t} = -\nabla \cdot \mathbf{J}_X - R_{IV} - R_{AX} - R_X^{clus} \quad (155)$$

where  $C_A$  is the concentration of substitutional (and assumed to be immobile) dopant and  $C_X$  is the concentration of ‘free’ defects of type  $X$  (either interstitials or vacancies), that is, those defects not in clusters or pairs.

Next, the flux of the mobile-defect pair is considered. In this model, the reaction rates are assumed to be independent of the charge state, so the pair charging constants are only needed for the flux of the pairs and are absorbed into the diffusivity of the pairs in this way:

$$\mathbf{J}_{AX} = \frac{-\sum (D_{AX^c} \left(\frac{n}{n_i}\right)^{-c-z})}{B_{AX}} \nabla \frac{C_{AX} \left(\frac{n}{n_i}\right)^z}{C_X^*} \quad (156)$$

where  $z$  is the charge state of dopant  $A$ ,  $X$  is either interstitial or vacancy, and  $D_{AX^c}$  is the effective diffusivity of dopant point-defect pair at charge state  $c$  and is related to the bare diffusivity,  $d_{AX^c}$  by:

$$\begin{aligned} D_{AX^c} &= C_{X^0}^* B_{AX} k_{X^c} d_{AX^c} \\ &= D_{AX^c}^0 \exp\left(\frac{-D_{AX^c}^E}{k_B T}\right) \end{aligned} \quad (157)$$

where  $k_{X^c}$  is a set of equilibrium charging constants for defect  $X$  defined by [Eq. 135, p. 200](#) and [Eq. 136, p. 200](#), and  $C_{X^0}^*$  is the equilibrium concentration of the neutral defects defined by [Eq. 134, p. 200](#).

To set  $D_{AX^c}$ , use:

```
pdbSet <material> <dopant> <defect> D <c> {<n>}
```

where:

- <material> is a material name (see [Material Specification on page 50](#)).
- <dopant> is one of the existing Sentaurus Process dopants.
- <defect> is either Interstitial or Vacancy.
- <c> is the charge state.
- <n> is a Tcl expression that returns a number; it can be simply a number.

One commonly used Tcl procedure for setting parameters is `Arrhenius`. This procedure takes a prefactor and an energy as arguments and returns  $\text{prefactor} \cdot \exp\left(\frac{-\text{energy}}{k_B T}\right)$ .

You can modify the entire array with the command (for example, arsenic–vacancy pairs):

```
pdbSet Si Arsenic Vac D {
    0 {[Arrhenius 0.0 3.45]}
    -1 {[Arrhenius 12.8 4.05]}
}
```

The defect flux  $J_X$  is the same as the `ChargedReact` model and is given by [Eq. 137, p. 201](#). The reaction can be written as:

$$R_{AX} \equiv K_{AXr} \left( C_A^+ C_X - \frac{C_{AX}}{B_{AX}} \right) \quad (158)$$

where  $X$  is either interstitial or vacancy,  $B_{AX}$  is the binding coefficient of defect  $X$  and dopant  $A$ ,  $K_{AXr}$  is the rate constant for the chemical reaction, and  $C_A^+$  is the active portion of  $C_A$ .

The binding term between the defect and dopant also follows the Arrhenius law:

$$B_{AX} = B_{AX0} \exp\left(\frac{-B_{AXE}}{kT}\right) \quad (159)$$

The term can be changed with the command:

```
pdbSet <material> <dopant> <defect> Binding {<n>}
```

The chemical reaction term is expressed with:

$$K_r = K_{r0} \exp\left(\frac{-K_{rE}}{kT}\right) \quad (160)$$

and can be modified by using the command:

```
pdbSet <material> <dopant> <defect> Krate {<n>}
```

The defect recombination rate  $R_{IV}$  is the same as in the `ChargedReact` model and is given by [Eq. 148, p. 203](#).

## ChargedPair Diffusion Model

The `ChargedPair` diffusion model assumes that the dopant–defect pairs are in local equilibrium with the dopant and defect concentration. Point defects themselves are not assumed to be in equilibrium. The kick-out mechanism that describes the dopant–defect pairing is given by:



and is assumed to be in equilibrium. In these two equations,  $A$  is the dopant,  $I$  is the interstitial,  $V$  is the vacancy, and  $c$  is the charge state.

The differential equations solved with this model are:

$$\frac{\partial C_A}{\partial t} = -\nabla \bullet \mathbf{J}_A - R_A^{clus} \quad (163)$$

$$\frac{\partial}{\partial t}(C_X^{total}) = -\nabla \bullet \mathbf{J}_X - \nabla \bullet \mathbf{J}_A - R_{IV} - R_X^{clus} \quad (164)$$



where  $C_{X^{total}} \equiv C_X + C_{AX}$  is the total interstitial concentration including dopant–defect  $X$  pairs but excluding clusters,  $J_A$  is the sum of AI and AV pair fluxes,  $J_X$  is the defect flux, and  $C_A$  is the total dopant concentration excluding clusters.

To write an expression for the pair fluxes, it is necessary to first define the equilibrium constants,  $k_{AX^c}$ , for the pairing reactions:

$$C_{AX} \equiv C_A^+ C_{X^0} \sum_c k_{AX^c} k_{X^c} \left(\frac{n}{n_t}\right)^{-c} \quad (165)$$

where  $X$  is either interstitial or vacancy,  $c$  is the charge state of the point defect,  $C_A^+$  is the active portion of  $C_A$ , and  $C_{X^0}$  is the concentration of the neutral point defect  $X$ . The ionization equilibrium constant  $k_{X^c}$  is given by [Eq. 135, p. 200](#) and [Eq. 136, p. 200](#).

The pairing coefficients for the dopant–defect pairs with different charge states,  $k_{AX^c}$ , can be modified with the command:

```
pdbSet <material> <dopant> <defect> ChargePair <c> {<n>}
```

where <material> is a material name (see [Material Specification on page 50](#)), <dopant> is one of the existing Sentaurus Process dopants, <defect> is either Interstitial or Vacancy, <c> is the charge state, and <n> is a Tcl expression that returns a number; it can be simply a number.

The flux for the impurity is given by:

$$J_A = -\sum_{c,X} D_{AX^c} \left(\frac{n}{n_t}\right)^{-c-z} \nabla \left( C_A^+ \frac{C_{X^0}}{C_{X^0}^*} \left(\frac{n}{n_t}\right)^z \right) \quad (166)$$

where  $D_{AX^c}$  is the effective diffusivity of dopant point-defect pair at charge state  $c$ ,  $z$  is the charge state of dopant  $A$ ,  $C_A^+$  is the active portion of  $C_A$ ,  $C_{X^0}$  is the concentration of the neutral point defect  $X$ , and  $C_{X^0}^*$  is the equilibrium concentration of the same defect and is given by [Eq. 134, p. 200](#).

The effective diffusivity is related to the bare dopant–defect diffusivity,  $d_{AX^c}$ , by:

$$\begin{aligned} D_{AX^c} &= C_{X^0}^* k_{X^c} k_{AX^c} d_{AX^c} \\ &= D_{AX^c}^0 \exp\left(\frac{-D_{AX^c}^E}{k_B T}\right) \end{aligned} \quad (167)$$

You can set  $D_{AX^c}$  by using:

```
pdbSet <material> <dopant> <defect> D <c> {<n>}
```

**NOTE** Diffusion coefficients  $D$  for the `ChargedPair` model and  $D_{star}$  for the `ChargedFermi` model include the interstitial efficiency factors.

Both the flux for the defects ( $J_X$ ) and the defect recombination rate ( $R_{IV}$ ) are the same as the `ChargedReact` model and are given by [Eq. 137, p. 201](#) and [Eq. 148, p. 203](#), respectively.

---

## Pair Diffusion Model

The `Pair` diffusion model is similar to the `ChargedPair` model except that the reaction rates are not charge state-dependent, and the electron concentration is computed directly from the net doping concentration. In addition, the Frank–Turnbull mechanism is not considered. The kick-out mechanism, which describes the dopant–defect pairing, is given by:



and is assumed to be in equilibrium. In these two equations,  $A$  is the dopant,  $I$  is the interstitial, and  $V$  is the vacancy.

As in the `ChargedPair` model, the following set of differential equations is solved:

$$\frac{\partial C_A}{\partial t} = -\nabla \cdot \mathbf{J}_A - R_A^{clus} \quad (170)$$

$$\frac{\partial}{\partial t}(C_{X^{total}}) = -\nabla \cdot \mathbf{J}_X - \nabla \cdot \mathbf{J}_A - R_{IV} - R_X^{clus} \quad (171)$$

where  $C_{X^{total}} \equiv C_X + C_{AX}$  is the total interstitial concentration including dopant–defect  $X$  pairs but excluding clusters,  $\mathbf{J}_A$  is the sum of AI and AV pair fluxes,  $\mathbf{J}_X$  is the defect flux, and  $C_A$  is the total dopant concentration excluding clusters.

An equilibrium constant for the pairing reactions is defined and given by:

$$C_{AX} \equiv B_{AX} C_A^+ C_X \quad (172)$$

where  $X$  is either interstitial or vacancy,  $B_{AX}$  is the binding coefficient of defect  $X$  and dopant  $A$ , and  $C_A^+$  is the active portion of  $C_A$ .

The binding term between the defect and dopant also follows the Arrhenius law:

$$B_{AX} = B_{AX0} \exp\left(\frac{-B_{AXE}}{kT}\right) \quad (173)$$

The term can be changed with the command:

```
pdbSet <material> <dopant> <defect> Binding {<n>}
```

The flux for the impurity is given by:

$$\mathbf{J}_A = -\sum_{c,X} D_{AX^c} \left(\frac{n}{n_i}\right)^{-c-z} \nabla \left( C_A^+ \frac{C_X}{C_X^*} \left(\frac{n}{n_i}\right)^z \right) \quad (174)$$

where  $D_{AX^c}$  represents the diffusivity of dopant point-defect pairs at charge state  $c$ ,  $z$  is the charge state of dopant  $A$ ,  $C_A^+$  is the active portion of  $C_A$ , and  $X$  is either interstitial or vacancy. The effective diffusivity is related to the bare dopant–defect diffusivity,  $d_{AX^c}$ , by:

$$\begin{aligned} D_{AX^c} &= C_{X^0}^* k_{X^c} B_{AX^c} d_{AX^c} \\ &= D_{AX^c}^0 \exp\left(\frac{-D_{AX^c}^E}{k_B T}\right) \end{aligned} \quad (175)$$

where  $C_{X^0}^*$  is the equilibrium concentration of the neutral point defect  $X$  and the ionization equilibrium constant,  $k_{X^c}$ , is defined by [Eq. 135, p. 200](#) and [Eq. 136, p. 200](#).

To modify diffusivity terms, use the command:

```
pdbSet <material> <dopant> <defect> D <charge> {<n>}
```

Both the flux for the defects ( $\mathbf{J}_X$ ) and the defect recombination rate ( $R_{IV}$ ) are the same as the `ChargedReact` model and are given by [Eq. 137, p. 201](#) and [Eq. 148, p. 203](#), respectively.

---

## ChargedFermi Diffusion Model

The `ChargedFermi` diffusion model is similar to the `ChargedPair` diffusion model, except that charged point defects are considered to be in equilibrium; no point-defect equations are solved for inert diffusion conditions if the point defect clusters are not turned on. If the point defect clusters are turned on or the oxidation is on, the point defect equations will be turned on automatically. The substitutional dopants are immobile and the total dopant flux is due to the dopant–defect pairs. The following set of differential equations is solved along with the potential equation [Eq. 357, p. 267](#):

$$\frac{\partial C_A}{\partial t} = -\nabla \cdot \mathbf{J}_A \quad (176)$$

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As in the `ChargedPair` model, a set of pairing constants ( $k_{AX^c}$ ) that define the pair concentration is defined:

$$C_{AX} \equiv C_A^+ C_{X^0} \sum_c k_{AX^c} k_{X^c} \left(\frac{n}{n_i}\right)^{-c} \quad (177)$$

where:

- $X$  is either interstitial or vacancy.
- $c$  is the charge state of the point defect.
- $z$  is the charge state of dopant  $A$ .
- $C_A^+$  is the active portion of  $C_A$ .

The ionization equilibrium constant  $k_{X^c}$  is given by [Eq. 135, p. 200](#) and [Eq. 136, p. 200](#).

The dopant flux  $J_A$  is given by:

$$J_A = - \sum_{c, X} D_{AX^c} \left(\frac{n}{n_i}\right)^{-c-z} \nabla \left( C_A^+ \frac{C_{X^0}}{C_{X^0}^*} \left(\frac{n}{n_i}\right)^z \right) \quad (178)$$

where:

- $D_{AX^c}$  is the effective diffusivity of dopant point-defect pairs at charge state  $c$ .
- $C_{X^0}$  is the concentration of the neutral point defect  $X$ .
- $C_{X^0}^*$  is the equilibrium concentration of the same defect and is given by [Eq. 134, p. 200](#).
- $C_{X^0}$  will be equal to  $C_{X^0}^*$  if the point-defect equations are switched off.
- $D_{AX^c}$  is related to the bare diffusivity  $d_{AX^c}$  by:

$$\begin{aligned} D_{AX^c} &= C_{X^0}^* k_{AX^c} k_{X^c} d_{AX^c} \\ &= D_{AX^c}^0 \exp\left(\frac{-D_{AX^c}^E}{k_B T}\right) \end{aligned} \quad (179)$$

You can set  $D_{AX^c}$  by using:

```
pdbSet <material> <dopant> <defect> Dstar <c> {<n>}
```

The pairing coefficients for the dopant-defect pairs with different charge states,  $k_{AX^c}$ , can be defined with the command:

```
pdbSet <material> <dopant> <defect> ChargePair <c> {<n>}
```

**NOTE** If the point-defect clusters are switched off and oxidation is switched on, only the interstitial point-defect equation will be switched on.

## Fermi Diffusion Model

The Fermi diffusion model is more complex than the Constant diffusion model. It assumes that point defects are in equilibrium and it includes electric-field effects. Therefore, the point-defect equations are not solved.

As in the ChargedPair model, the following set of differential equations is solved:

$$\frac{\partial C_A}{\partial t} = -\nabla \cdot \mathbf{J}_A \quad (180)$$

where  $\mathbf{J}_A$  is the sum of AI and AV pair fluxes, and  $C_A$  is the total dopant concentration including clusters.

An equilibrium constant for the pairing reactions is defined and given by:

$$C_{AX} \equiv B_{AX} C_A^+ C_X \quad (181)$$

where  $X$  is either interstitial or vacancy,  $B_{AX}$  is the binding coefficient of defect  $X$  and dopant  $A$ , and  $C_A^+$  is the active portion of  $C_A$ . The dopant flux is given by:

$$J_A = -\sum_{X,c} D_{AX^c} \left(\frac{n}{n_i}\right)^{-c-z} \nabla \left( C_A^+ \left(\frac{n}{n_i}\right)^z \right) \quad (182)$$

where:

- $c$  is the charge state of the point defect.
- $z$  is the charge state of dopant  $A$ .
- $C_A^+$  is the active portion of  $C_A$ .
- $X$  is either interstitial or vacancy.
- $D_{AX^c}$  is the effective diffusivity of dopant point-defect pairs at charge state  $c$  and is related to the bare diffusivity  $d_{AX^c}$  by:

$$\begin{aligned} D_{AX^c} &= C_{X^0}^* B_{AX^c} k_{X^c} d_{AX^c} \\ &= D_{AX^c}^0 \exp\left(\frac{-D_{AX^c}^E}{k_B T}\right) \end{aligned} \quad (183)$$

The pairing ratio  $B_{AX}$  only appears in the formula for  $D$  and cannot be modified independently in the Fermi model. You can set  $D_{AX^c}$  by using:

```
pdbSet <material> <dopant> <defect> Dstar <c> {<n>}
```

---

## Constant Diffusion Model

The `Constant` diffusion model is the simplest diffusion model used in Sentaurus Process and is mainly for dopant diffusion in oxide. It assumes that there is no interaction between dopants and point defects, and that there are no electric-field effects on dopant diffusion. The point-defect equations are also switched off. The impurity diffusion is given by:

$$\frac{\partial C_A}{\partial t} = \nabla \cdot (D_{star} \nabla C_A^+) \quad (184)$$

where  $D_{star}$  is the intrinsic diffusivity of the impurity  $A$  and  $C_A^+$  is the active portion of  $C_A$ . The diffusivity follows the Arrhenius law:

$$D_{star} = D_{star0} \exp\left(\frac{-D_{starE}}{kT}\right) \quad (185)$$

For example, the command:

```
pdbSet Silicon Arsenic Dstar {[Arrhenius 6.66e-2 3.44]}
```

sets the  $D_{star0}$  to  $6.66 \times 10^{-2}$  cm<sup>2</sup>/s and  $D_{starE}$  to 3.44 eV. The general format of the command is:

```
pdbSet <material> <dopant> Dstar {<n>}
```

**NOTE** Unlike the `ChargedFermi` model, `Dstar` is not defined as an array for the `Constant` model.

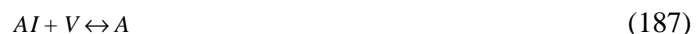
---

## NeutralReact Diffusion Model

`NeutralReact` diffusion in silicon is close to the `React` model (see [React Diffusion Model on page 204](#)) except that there are no charged atoms. The model can be switched on using the command:

```
pdbSet <material> <dopant> DiffModel NeutralReact
```

`NeutralReact` diffusion in silicon is described by a kick-out mechanism [1]. Other mechanisms such as dissociation and clustering can also be taken into account. In the integration in Sentaurus Process, each of these mechanisms is described by one or more terms:



where  $A$  is the substitutional dopant,  $AI$  is the mobile dopant–interstitial pair,  $I$  is interstitial, and  $V$  is vacancy. The first reaction is the kick-out reaction and the second one is the dissociation reaction. These reaction can be written as:

$$R_{KickOut} \equiv K_{fI}(C_A C_I - B_{AI} C_{AI}) \quad (188)$$

$$R_{Dissociation} \equiv K_{fV}(C_{AI} C_V - C_I^* C_V^* B_{AV} C_A) \quad (189)$$

where:

- $C_A$  is the concentration of substitutional dopant atoms.
- $C_{AI}$  is the concentration of mobile dopant atoms.
- $K_{fI}$  and  $K_{fV}$  are the forward reaction rates.
- $B_{AI}$  and  $B_{AV}$  are the binding coefficients.

They can be set using the following commands:

```

pdbSet <material> <dopant> Interstitial Kf {<n>}
pdbSet <material> <dopant> Vacancy Kf {<n>}
pdbSet <material> <dopant> Interstitial Bind {<n>}
pdbSet <material> <dopant> Vacancy Bind {<n>}

```

The differential equations that describe the model are:

$$\frac{\partial C_A}{\partial t} = R_{Dissociation} - R_{KickOut} \quad (190)$$

$$\frac{\partial C_{AI}}{\partial t} = \nabla \cdot (D_{AI} \nabla C_{AI}) + R_{KickOut} - R_{Dissociation} \quad (191)$$

where  $D_{AI}$  is the diffusivity of mobile dopant–interstitial pairs and can be set using the command:

```

pdbSet <material> <dopant> Interstitial D 0 {<n>}

```

## Carbon Diffusion Model

Carbon diffusion is a typical example for the NeutralReact diffusion model. The kick-out reaction rate is defined by:

```

pdbSet Silicon Carbon Interstitial Kf { \
  [expr ([pdbGetElement Si Carbon D 0]/([pdbDelayDouble Si Carbon\
  MigrationLength]* [pdbDelayDouble Si Carbon\
  MigrationLength]*[pdbDelayDouble Si Int Cstar]))]\
}

```

#### 4: Diffusion

##### Transport Models

will set  $K_{fl}$  to  $\frac{D_{C_0}}{\lambda^2 C_I^*(intrinsic)}$ .

$\lambda$  is the migration length (cm) of carbon atoms and  $D_{C_0}$  is the diffusivity of carbon, and these parameters can be set using the commands:

```
pdbSet <material> Carbon MigrationLength {<n>}
pdbSet <material> Carbon D 0 {<n>}
```

For the details of the carbon-clustering model, see [Carbon Cluster on page 290](#).

### Nitrogen Diffusion Model

Nitrogen diffusion is defined according to the `Constant` diffusion model by default. However, instead of the `Constant` model, the `NeutralReact` diffusion model can be used for nitrogen diffusion. If the `NeutralReact` model is specified for nitrogen diffusion, the nitrogen dimer forms and diffuses. The dimer is formed by the following reaction:



In the above reaction,  $NI$  is the monomer, in other words, nitrogen interstitial  $N_i$ , and  $N2$  denotes the dimer  $(N_i)_2$ , which has the solution name `NDimer`. The nitrogen monomer and dimer equations are formulated by:

$$\frac{\partial C_N}{\partial t} = R_{Dissociation} - R_{KickOut} - R_{NV} \quad (193)$$

$$\frac{\partial C_{NI}}{\partial t} = \nabla \cdot (D_{NI} \nabla C_{NI}) + R_{KickOut} - R_{Dissociation} - R_{N2} \quad (194)$$

$$\frac{\partial C_{N2}}{\partial t} = \nabla \cdot (D_{N2} \nabla C_{N2}) + R_{N2} - R_{N2V} \quad (195)$$

$$\frac{\partial C_{N2V}}{\partial t} = R_{N2V} - R_{N2V2} \quad (196)$$

$$\frac{\partial C_{N2V2}}{\partial t} = R_{N2V2} \quad (197)$$

The reaction  $R_{N2}$  for dimer formation is given by:

$$R_{N2} \equiv K_{fN2}(C_{NI}C_{NI} - B_{N2}C_{N2}) \quad (198)$$



where:

- $C_{N1}$  is the concentration of nitrogen monomers.
- $C_{N2}$  is the concentration of nitrogen dimers.
- $K_{fN2}$  is the forward reaction rate.
- $B_{N2}$  is the binding coefficient.

They can be set using the following commands:

```
pdbSet <material> NDimer Kf {<n>}
pdbSet <material> NDimer Bind {<n>}
```

For details on the nitrogen clusters NV, N<sub>2</sub>V, and N<sub>2</sub>V<sub>2</sub>, see [Nitrogen Cluster on page 291](#).

---

## Mobile Impurities and Ion-Pairing

The ion-pairing model includes the pairing of positively and negatively charged dopant ions [2][3][4]. Ion-pairing reduces the diffusivity of dopants where the concentration of dopants of the opposite type is large. The ion-pairing model assumes that positively charged donors can bind with negatively charged acceptors to form neutral pairs. The ion-pairing model is significant because it allows the dependency of the impurity diffusivity to be modeled in both n-type and p-type materials. In particular, it reduces the effective diffusivity of boron in n-type materials without affecting its diffusivity at high p-type concentrations.

The model reduces the mobile concentration of dopant species by the following factors:

$$f_{pd} = \left(1 - \frac{N_p}{N_d}\right) \text{ for donor species} \quad (199)$$

$$f_{pa} = \left(1 - \frac{N_p}{N_a}\right) \text{ for acceptor species} \quad (200)$$

where:

- $N_d$  and  $N_a$  are the total concentrations of electrically active donors and acceptors, respectively.
- $N_p$  is the concentration of ion pairs.
- $f_{pd}$  and  $f_{pa}$  are the ion-pairing factors for donors and acceptors, respectively.

The concentration of ion pairs  $N_p$  is given by:

$$N_p = \frac{1}{2}((N_d + N_a + \Omega) - \sqrt{(N_d + N_a + \Omega)^2 - 4N_dN_a}) \quad (201)$$

## 4: Diffusion

### Solid Phase Epitaxial Regrowth Model

The parameter  $\Omega$  is given by:

$$\Omega = \text{Ion.Pair.Omega} \cdot n_i \quad (202)$$

where `Ion.Pair.Omega` is a parameter for material; the default value for silicon and polysilicon is 6.0 [3].

The ion-pairing model is enabled or disabled for each material by the `Ion.Pair` parameter. By default, it is disabled for all materials.

---

## Solid Phase Epitaxial Regrowth Model

The solid phase epitaxial regrowth (SPER) model simulates the movement of amorphous and crystalline boundaries due to the recrystallization of the amorphous silicon and the dopant dynamics during such process. The SPER model is switched on by:

```
pdbSet Diffuse SPER 1
```

The boundary movement is described with the specific solution fields, either the distance field by the level-set method or the phase field by the phase-field method. You can select one of the models by:

```
pdbSet Diffuse SPER.Model {LevelSet | PhaseField} ;# default=LevelSet
```

---

## Level-Set Method

The level-set method solves the equation for the distance field  $\phi$ , which is named with `AmorpDistance`:

$$\frac{\partial \phi}{\partial t} + v |\vec{\nabla} \phi| = 0 \quad (203)$$

where:

- $v$  is the recrystallization velocity perpendicular to a boundary surface.
- $\phi$  is positive in an amorphous region, negative in a crystalline region, and zero at an amorphous–crystalline boundary.

The velocity  $v$  is defined by:

$$v = f_v \cdot v_{ori}(\text{V100}, \text{V110}, \text{V111}) \cdot \left(1 - (1 - s_v) \exp\left(-\frac{d}{L_{vr}}\right)\right) \quad (204)$$

where:

- $f_v$  is the scaling factor.
- $v_{ori}$  is the orientation-dependent velocity.
- $s_v$  is the scaling factor of velocity near surfaces.
- $d$  is the shortest distance from the surface.
- $L_{vr}$  is the characteristic length for velocity reduction near surfaces.

```

pdbSet Silicon SPER V.Factor {<expression>}      ;# f_v (unitless)
pdbSet Silicon SPER V100 {<n>}                    ;# cm/sec
pdbSet Silicon SPER V110 {<n>}                    ;# cm/sec
pdbSet Silicon SPER V111 {<n>}                    ;# cm/sec
pdbSet Silicon SPER VsurfScale {<n>}              ;# s_v (unitless)
pdbSet Silicon SPER VsurfScaleLength {<n>}        ;# L_vr (um)

```

The tensor mesh structure to solve the level-set equation is defined by:

```

pdbSet Grid SPER TensorMeshSpacing {X <n> Y <n> Z <n>} ;# (um)

```

The level-set algorithm used is the general time-stepping initial-value formulation as described in [MGOALS Interface on page 754](#).

It is assumed that all dopant atoms are mobile in an amorphous region. The diffusion coefficient of the mobile species in the amorphous region is specified by:

```

pdbSet Silicon <dopant> DAmor {<n>} ;# cm2/sec

```

It has been experimentally observed that during regrowth of an amorphous layer, dopants can be swept along by the amorphous–crystalline boundary. The physical mechanism for this sweeping behavior is not well understood. To model this effect, a phenomenological model has been introduced as follows:

$$\frac{\partial X}{\partial t} = \vec{\nabla} \cdot \left( f_D \alpha_v v_D L_d \left( 1 - (1 - P) \exp\left(-\frac{d}{L_{dr}}\right) \right) X \vec{\nabla} \alpha_s \right) \quad (205)$$

where:

- $f_D$  is the user-defined multiplication factor.
- $v_D$  is the local speed of distance variation.
- $L_d$  is the characteristic length of dopant drift.
- $P$  is the drift probability near material interfaces.
- $d$  is the shortest distance from material interfaces.
- $L_{dr}$  is the characteristic length for drift reduction near material interfaces.

#### 4: Diffusion

##### Solid Phase Epitaxial Regrowth Model

- $\alpha$  is the amorphous state calculated by:

$$\alpha = \frac{1}{2} \cdot \operatorname{erfc}\left(-\frac{\varphi}{w_T}\right) \quad (206)$$

where  $w_T$  is the phase transition width.  $\alpha$  is 1.0 and 0.0 in a completely amorphous and crystalline region, respectively.

- $\alpha_S$  is the shifted amorphous state given by:

$$\alpha_S = \frac{1}{2} \cdot \operatorname{erfc}\left(-\frac{\varphi - d_D}{w_D}\right) \quad (207)$$

```

pdbSet Silicon SPER PhaseTransWidth {<n>}           ;# w_T (um)
pdbSet Silicon SPER DriftWidth {<n>}                ;# w_D (um)
pdbSet Silicon SPER DriftFactor {<expression>}      ;# f_D (unitless)
pdbSet Silicon SPER DriftDistance {<n>}            ;# d_D (um)
pdbSet Silicon SPER SurfaceDriftProbability {<n>}   ;# P (unitless)
pdbSet Silicon SPER DriftReductionLength           ;# L_dr (um)
pdbSetDouble Silicon <dopant> SPER.DriftLength {<n>} ;# L_d (um)

```

The parameters `SurfaceDriftProbability` and `DriftReductionLength` can be specified for a specific dopant by:

```

pdbSetDouble Silicon <dopant> SPER.SurfaceDriftProbability {<n>}
pdbSetDouble Silicon <dopant> SPER.DriftReductionLength {<n>}

```

To control the clustering rate in the region between amorphous and crystalline regions, an additional term can be defined by:

```

pdbSetString Si <cluster> SPERBoundaryTerm {<expression>}
pdbSetString Si <dopant> SPERBoundaryTerm {<expression>}

```

**NOTE** The term added by `SPERBoundaryTerm` of `<cluster>` must be correctly subtracted by `SPERBoundaryTerm` of `<dopant>` so that the total dose conservation is kept, for example:

```

pdbSetString Si As3 SPERBoundaryTerm "-1e1*(0.99*AsTotal-3.0*As3)"
pdbSetString Si Arsenic SPERBoundaryTerm "3e1*(0.99*AsTotal-3.0*As3)"

```

The full equation of a dopant is described by:

$$\frac{\partial X}{\partial t} = (1 - \alpha) \frac{\partial X}{\partial t} \Big|_{crystal} + \alpha \vec{\nabla} \cdot \left( D_{amor} \vec{\nabla} X \right) + \vec{\nabla} \cdot \left( f_D \alpha v_D L_d \left( 1 - (1 - P) \exp\left(-\frac{d}{L_{dr}}\right) \right) X \vec{\nabla} \alpha_S \right) - R \cdot \exp\left(-\frac{9\varphi^2}{w_T^2}\right) \quad (208)$$

where  $R$  is defined by `SPERBoundaryTerm`.

The maximum time step during SPER is set by:

$$\Delta t_{max} = \min(\text{SPER.TimeStepScale} \cdot \frac{W_T}{\max(v)}, \text{SPER.MaxTimeStep}) \quad (209)$$

## Phase Field Method

Since the level-set method requires Cartesian grids to calculate the distance field, it may cause instability from the difficult time-step control as well as the interpolation error due to the decoupled method with the different mesh structure. The phase field method uses a consistent mesh structure, so that the phase and the other solutions are coupled seamlessly into the hydrodynamic Scharfetter–Gummel discretization scheme, which improves the convergence if there is high drift due to an abrupt phase change.

The phase field method solves the equation for the phase field  $\varphi$ , which is named with SPERPhase:

$$\tau \frac{\partial \varphi}{\partial t} = w^2 \nabla^2 \varphi - (\varphi^2 - 1)(\varphi - \lambda(\varphi^2 - 1)) \quad (210)$$

where:

- $\tau$ ,  $w$ , and  $\varphi$  are the relaxation time, the phase transition width, and the phase (–1 for completely amorphous, 1 for completely crystalline), respectively.
- $w$  and  $\lambda$  are given by the parameters `PhaseTransWidth` and `Lambda.Fac`, respectively.

The inverse of the relaxation time  $\tau$  is calculated by:

$$\tau^{-1} = f_{iso} f_{aniso} R \exp\left(-\frac{E_{aniso} + E_{Sv} + E_{Ss}}{kT}\right) \quad (211)$$

where:

- $f_{iso}$  and  $f_{aniso}$  are the isotropic and anisotropic multiplication factors, respectively.
- $R$  is the relaxation rate.
- $E_{aniso}$ ,  $E_{Sv}$  and  $E_{Ss}$  are the orientation-dependent, the hydrostatic stress-dependent, and shear stress-dependent activation energies, respectively.

$$E_{aniso} = \sum_{100, 110, 111} E.Aniso \cdot \frac{\nabla \varphi}{\|\nabla \varphi\|} \quad (212)$$

$$E_{Sv} = P \cdot VFreqrys \quad (213)$$

$$E_{Ss} = \text{Shear.Coupling} \cdot (|\varepsilon_{xy}| + |\varepsilon_{yz}| + |\varepsilon_{zx}|) \quad (214)$$

## 4: Diffusion

### Flash or Laser Anneal Model

```
pdbSet Silicon SPER Relax.Rate {<n>} ;# R(1/sec)
pdbSet Silicon SPER R.Fac {<expression>} ;# f_iso (unitless)
pdbSet Silicon SPER R.Fac.Aniso {100 <n> 110 <n> 111 <n>} ;# f_aniso (unitless)
pdbSet Silicon SPER E.Aniso {100 <n> 110 <n> 111 <n>} ;# E_aniso (eV)
pdbSet Silicon SPER VFreocrs {<n>} ;# (cm-3)
pdbSet Silicon SPER Shear.Coupling {<n>} ;# (eV)
```

The phase field method assumes no diffusion in a crystalline region during SPER, so that the diffusion equation of a dopant is formulated by:

$$\frac{\partial X}{\partial t} = \left(\frac{1-\phi}{2}\right) \vec{\nabla} \cdot \left( D_{amor} \vec{\nabla} X + D_{amor} X \frac{E_{seg}}{kT} \vec{\nabla} \phi \right) \quad (215)$$

where  $E_{seg}$  is the chemical potential energy difference to cause the dopant segregation at an amorphous–crystalline boundary.

$E_{seg}$  is given by the parameter SPER.Energy that you can define with a string expression:

```
pdbSet Silicon <dopant> SPER.Energy {<expression>} ;# E_seg (eV)
```

The maximum time step during SPER is set by:

$$\Delta t_{max} = \min(\text{SPER.TimeStepScale} \cdot \frac{\tau_{min}}{4}, \text{SPER.MaxTimeStep}) \quad (216)$$

As soon as regrowth is completed, the dopant activation in the regrowth region is performed with the `pdb` parameter `AmInit` or the term  $\$\{Sol\}AmInit$ .

**NOTE** Since the dopant active concentration is initialized after regrowth is completed, the evaluated values of some terms, such as  $\$\{Sol\}Total$  and  $\$\{Sol\}Active$  can be incorrect during SPER.

---

## Flash or Laser Anneal Model

The flash or laser anneal model becomes necessary for an advanced process that requires diffusionless, but high activation. The model can simulate the inhomogeneous thermal distribution, which results in better accuracy for stress calculation as well as heat transfer delay to the region in which the devices form. The flash or laser model is not available for 3D simulation yet.

The solution name of the local temperature  $T$  (in kelvin) is `Temperature`. The model is switched on by specifying the Boolean parameter `laser` in a diffusion statement. For example:

```
diffuse temperature=500 time=1<ms> laser
```

For a melting laser anneal, the phase field variable  $\phi$  is introduced to describe whether the material is liquid or solid. The solution name of the phase  $\phi$  is `HeatPhase`. The melting laser anneal model is invoked by switching on the Boolean parameter `Use.Melting.Laser`:

```
pdbSet Heat Use.Melting.Laser 1
```

The heat transfer equation is:

$$\rho c_P \frac{\partial T}{\partial t} = \nabla \cdot (\kappa \nabla T) + G + 30\rho L \phi^2 (1 - \phi) \frac{\partial \phi}{\partial t} \quad (217)$$

where:

- $\kappa$ ,  $\rho$ , and  $c_P$  are the conductivity, the mass density, and the specific heat capacity, respectively.  $\kappa$  and  $c_P$  can depend on temperature.
- $L$  is the unit mass latent heat (Eq. 229). The phase-dependent term takes the heat consumption (or generation) due to the solid-to-liquid (or liquid-to-solid) phase change into account.

$\kappa$  and  $c_P$  vary with the liquid or solid phase as follows:

$$c_P = \phi c_{P_S} + (1 - \phi) c_{P_L} \quad (218)$$

$$\kappa = \phi \kappa_S + (1 - \phi) \kappa_L \quad (219)$$

```

pdbSet <material> SpecificHeatCapacity {<expression>}      ;# Cps (J/kg/K)
pdbSet <material> Liquid.SpecificHeatCapacity {<expression>} ;# Cpl (J/kg/K)
pdbSet <material> ThermalConductivity {<expression>}      ;# ks (W/cm/K)
pdbSet <material> Liquid.ThermalConductivity {<expression>} ;# kl (W/cm/K)

```

The heat generation rate  $G$  is calculated by:

$$G = I \cdot \alpha \exp\left(-\int_{l=0}^{l=d} \alpha dl\right) \quad (220)$$

where  $I$ ,  $\alpha$ , and  $d$  represent the intensity, absorptivity, and depth, respectively. The absorptivity is given by the user-defined expression:

```

pdbSet <material> Absorptivity {<expression>}      ;# cm-1

```

See [Intensity Models for Flash Anneal on page 227](#) and [Intensity Model for Scanning Laser on page 229](#) for the intensity models.

The governing equation of the phase field  $\phi$  is given by:

$$\frac{\partial \phi}{\partial t} = \mu \gamma \nabla^2 \phi - \frac{\mu \gamma}{\delta^2} \phi (1 - \phi) (1 - 2\phi) + 5 \frac{v_{\text{int}}}{\delta} \phi^2 (1 - \phi)^2 + s(T, \phi) \quad (221)$$

#### 4: Diffusion

##### Flash or Laser Anneal Model

where:

- $\mu$ ,  $\gamma$ , and  $\delta$  are the melting interface mobility, the surface tension, and the interface thickness, respectively.  $\mu$  and  $\gamma$  depend on material crystallinity.
- $s(T, \varphi)$  is the seed function to start liquidation.
- $v_{\text{int}}$  is the interface response function to describe the front moving velocity of the flat melting interface:

$$\mu = \alpha\mu_a + (1 - \alpha)\mu_c \quad (222)$$

$$\gamma = \alpha\gamma_a + (1 - \alpha)\gamma_c \quad (223)$$

where the subscripts  $a$  and  $c$  of  $\mu$  and  $\gamma$  indicate the amorphous and crystalline materials, respectively. The  $\alpha$  is the degree of the structural disorder in a material that is calculated by:

$$\alpha = \frac{1}{2} \left( 1 + \tanh \left( 10 \ln \left( \frac{D_{\text{FP}}}{D_{\text{max}}} \right) \right) \right) \quad (224)$$

where  $D_{\text{FP}}$  is the Frenkel pair concentration by implantation damage, and  $D_{\text{max}}$  is the amorphous threshold to determine the amorphous and crystal transition.

```

pdbSet <material> Melting.Interface.Mobility {<n>}           ;# uc (cm4/J/sec)
pdbSet <material> Amorphous.Melting.Interface.Mobility {<n>} ;# ua (cm4/J/sec)
pdbSet <material> Surface.Tension {<n>}                     ;# gammac (J/cm2)
pdbSet <material> Amorphous.Surface.Tension {<n>}           ;# gammaa (J/cm2)
pdbSet <material> AmorpDensity {<n>}                       ;# Dmax (cm-3)

```

The seed function is modeled by:

$$s(T, \varphi) = -f_s \frac{\delta^2}{\mu\gamma} \varphi \left( 1 - \frac{1}{2} \operatorname{erfc} \left( \frac{T - T_m}{T_s} \right) \right) \quad (225)$$

where  $T_m$  is the melting point, the multiplier to control initial liquidation.  $f_s$  and  $T_s$  are the multiplier and the temperature to control initial liquidation. The seed term in Eq. 221 is switched off when  $\varphi$  is reduced to less than the `SeedOffPhase` value:

```

pdbSet Heat Seed.Factor {<expression>} ;# fs (unitless)
pdbSet Heat Seed.Temperature {<n>}     ;# Ts (K)
pdbSet Heat SeedOffPhase {<n>}        ;# unitless

```

It is known that the melting point varies with the dopant concentration, such as for germanium, as well as material crystallinity. The melting point is calculated by:

$$T_m = \alpha \left( T_{ma0} + (T_{ma1} - T_{ma0}) \frac{C_x}{C_{\text{max}}} \right) + (1 - \alpha) \left( T_{mc0} + (T_{mc1} - T_{ma0}) \frac{C_x}{C_{\text{max}}} \right) \quad (226)$$



where  $\alpha$ ,  $T_{ma0}$ , and  $T_{mc0}$  are the degree of structural disorder, and the melting point of amorphous material and crystalline material, respectively.  $C_x$  is the concentration of the dopant that affects the melting point. For example:

```

pdbSet Silicon Melting.Point 1690 ;# Tmc0
pdbSet Silicon Amorphous.Melting.Point 1420 ;# Tma0
pdbSet Silicon Dop.Dep.Melting.Point { Ge {960 1211} } ;# Tma1 and Tmc1

```

The interface response function  $V_{\text{int}}$  is modeled by the Frenkel–Wilson law [5]:

$$V_{\text{int}} = v \left( 1 - \exp\left(\frac{\rho L / C_{\text{max}}}{k T T_m} (T - T_m)\right) \right) \quad (227)$$

where  $C_{\text{max}}$  is the lattice density. The liquid-to-solid interface transfer rate  $v$  is given by:

$$v = \begin{cases} v_0 \exp\left(-\frac{H}{kT}\right) & \text{for Arrhenius model} \\ v_{0f} \exp\left(-\frac{B}{k(T - T_g)}\right) & \text{for Vogel–Fulcher model} \end{cases} \quad (228)$$

where the model can be selected by:

```

pdbSet <material> Melting.Velocity.Model {Arrhenius | FulcherVogel}

```

The latent heat and the liquid-to-solid interface transfer rate depend on crystallinity as follows:

$$L = \alpha L_a + (1 - \alpha) L_c \quad (229)$$

$$v_0 = \alpha v_{0a} + (1 - \alpha) v_{0c} \quad (230)$$

$$H = \alpha H_a + (1 - \alpha) H_c \quad (231)$$

$$v_{0f} = \alpha v_{0fa} + (1 - \alpha) v_{0fc} \quad (232)$$

$$B = \alpha B_a + (1 - \alpha) B_c \quad (233)$$

$$T_{g0} = \alpha T_{ga} + (1 - \alpha) T_{gc} \quad (234)$$

where the subscripts  $a$  and  $c$  indicate the parameter for the amorphous and crystalline materials, respectively.

```

pdbSet <material> Latent.Heat {<n>} ;# Lc (J/kg)
pdbSet <material> Amorphous.Latent.Heat {<n>} ;# La (J/kg)
pdbSet <material> Melting.Velocity.0 {<n>} ;# v0c (cm/sec)
pdbSet <material> Melting.Velocity.E {<n>} ;# Hc (eV)
pdbSet <material> Amorphous.Melting.Velocity.0 {<n>} ;# v0a (cm/sec)

```

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```

pdbSet <material> Amorphous.Melting.Velocity.E {<n>}      ;# Ha (eV)
pdbSet <material> FV.Melting.Velocity.0 {<n>}            ;# v0c (cm/sec)
pdbSet <material> FV.Melting.Velocity.E {<n>}            ;# Hc (eV)
pdbSet <material> FV.Melting.Velocity.T {<n>}            ;# Tgc (K)
pdbSet <material> FV.Amorphous.Melting.Velocity.0 {<n>} ;# v0a (cm/sec)
pdbSet <material> FV.Amorphous.Melting.Velocity.E {<n>} ;# Ha (eV)
pdbSet <material> FV.Amorphous.Melting.Velocity.T {<n>} ;# Tga (K)

```

---

## Dopant Diffusion in Melting Laser Anneal

Since the liquidation or solidification process occurs too quickly to observe the dopant diffusion in a solid region, it is assumed that the dopant atoms diffuse only by entropic force and temperature gradient. The different chemical potentials of dopants at liquid, solid, and boundary regions induce the segregation. During melting laser anneal, the temperature varies greatly depending on the location. Therefore, the dopant diffusion equation must be solved by coupling it to the heat equation (Eq. 217) and the phase equation (Eq. 221):

$$\frac{\partial C}{\partial t} = \nabla \cdot \left( D \frac{C_{eq}}{C_{eq0}} \nabla \left( C \frac{C_{eq0}}{C_{eq}} \right) \right) \quad (235)$$

$$D = \begin{cases} D_{\text{liquid}} + (D_{\text{ils}} - D_{\text{liquid}}) \frac{\varphi}{\varphi_L} & \text{for } (\varphi \leq \varphi_L) \\ D_{\text{ils}} & \text{for } (\varphi_L < \varphi \leq \varphi_S) \\ D_{\text{solid}} + (D_{\text{ils}} - D_{\text{solid}}) \frac{1-\varphi}{1-\varphi_S} & \text{for } (\varphi_S \leq \varphi) \\ \varphi D_{\text{solid}} + (1-\varphi) D_{\text{liquid}} & \text{if } (\varphi_L > \varphi_S) \end{cases} \quad (236)$$

$$\frac{C_{eq}}{C_{eq0}} = \exp \left( - \frac{\varphi E_{\text{seg}} + 16\varphi^2(1-\varphi)^2 E_{\text{intf}}}{kT} \right) \quad (237)$$

where:

- $D_{\text{liquid}}$ ,  $D_{\text{ils}}$ , and  $D_{\text{solid}}$  are the dopant diffusivities in a liquid, a liquid–solid interface, and solid regions, respectively.  $D_{\text{solid}}$  is calculated by an Arrhenius formula with global temperature.
- $E_{\text{seg}}$  and  $E_{\text{intf}}$  are the chemical potential energies in a solid state and an interface state relative to that in a liquid state, respectively.

```

pdbSet Heat Max.Liquid.Phase {<n>}                      ;# phi_L (unitless)
pdbSet Heat Min.Solid.Phase {<n>}                       ;# phi_S (unitless)
pdbSet <material> <dopant> Dliquid.0 {<n>}               ;# cm2/sec
pdbSet <material> <dopant> Dliquid.E {<n>}               ;# eV
pdbSet <material> <dopant> Dils.0 {<n>}                  ;# cm2/sec

```

```

pdbSet <material> <dopant> Dils.E {<n>}           ;# eV
pdbSet <material> <dopant> Dstar {<n>}           ;# cm2/sec (Dsolid)
pdbSet <material> <dopant> Melting.Seg.E {<n>}    ;# eV
pdbSet <material> <dopant> Melting.Intf.Seg.E {<n>} ;# eV

```

To solve the dopant diffusion equation by coupling it with the heat and phase equations, use:

```
solution name= <solution> Heat
```

By default, it is applied to boron, phosphorus, arsenic, antimony, and indium impurities.

The instant recrystallization of an amorphous region, that is, the initialization of cluster solutions, is performed before diffusion. The cluster solutions are reset to zero in a melted region during diffusion by multiplying  $\phi$  by the cluster solutions, which implies that all dopants in a liquid region are activated fully. Like the cluster solutions, the point-defect and defect-cluster solutions are reset to zero in liquid regions.

## Saving a Thermal Profile

To save the thermal profile computed during this step to a file, use the `write.temp.file` parameter of the `diffuse` command. In a subsequent simulation, you can use this file to create a temperature ramp using the `read.temp.file` parameter of the `temp_ramp` command. For more information, see [diffuse on page 875](#) and [term on page 1099](#).

## Boundary Conditions

At the top surface, that is, the gas interface, the heat emission flux from the top material is given by:

$$F = -5.6703 \cdot 10^{-12} \cdot \text{Emissivity} \cdot (T^4 - T_0^4) \quad (238)$$

where  $T_0$  is the environment temperature specified by `temperature` in the `diffuse` command.

At the bottom, the boundary condition depends on whether the thermal resistor is attached. If `AttachThermalResistor` is switched on, the emission flux at bottom is calculated by:

$$F = -\left(\frac{\kappa}{t_w - x_{bot}}\right)(T - T_0) \quad (239)$$

## 4: Diffusion

### Flash or Laser Anneal Model

where  $t_w$  and  $x_{bot}$  are the wafer thickness and the bottom coordinate of a simulation structure, respectively. Otherwise:

$$F = -\text{HeatSinkTransfer}(T - T_0) \quad (240)$$

The wafer thickness in micrometers is specified by:

```
pdbSet Heat WaferThickness <n>
```

At the sides, the flux is calculated by:

$$F = -\text{SideHeatTransfer}(T - T_0) \quad (241)$$

By default, `SideHeatTransfer` is set to zero for all materials.

---

## Structure Extension

The heat transfer is much faster in comparison with an impurity or a point-defect diffusion. For example, in silicon, the diffusion length of the heat temperature is 20–30 times longer than that of interstitials at 800°C. Therefore, solving the heat equation requires a much larger structure size than for diffusion equations. The model provides the method to temporarily extend the current structure for solving the heat equation, and then recovers the original structure after finishing the laser or flash anneal. The downward extension is controlled by the Boolean parameter `ExtendBottom`.

The location of the extended bottom is specified by `WaferThickness`, for example:

```
pdbSet Heat ExtendBottom 1
pdbSet Heat WaferThickness 700
```

which are defined by default.

Since the flash light source transfers heat to the whole wafer surface at the same time, no heat flux is assumed at the structure sides so that you do not have to extend the structure along the side directions. However, since the laser anneal scans a wafer by beaming a laser on a localized spot, the structure must be extended to the side directions to correctly take into account the heat transfer from the beamed spot. The extended distance in micrometers to the sides is defined with:

```
pdbSet Heat SideExtension <n>
```

To reduce the computation time for the extension, one side among the left and right sides is extended first, and then the extended structure is reflected on the side that is defined by:

```
pdbSet Heat ReflectSide <Left | Right | None>
```

For example, the following statements specify an extension of 200  $\mu\text{m}$  in the right direction and a reflection of the extended structure on the left side:

```
pdbSet Heat SideExtension 200  
pdbSet Heat ReflectSide Left
```

When `ReflectSide` is set to `None`, each side (that is, both the left and right sides) is extended.

The material of all the extended regions is set to `HeatSubstrate`. The thermal properties of the `HeatSubstrate` material are defined internally to the same as the `BulkMaterial` material (default value: Si). In the region of `HeatSubstrate`, only the heat equation is solved.

---

## Intensity Models for Flash Anneal

Intensity can be specified by a Gaussian model, or a table lookup method, or a user-specified model:

```
pdbSet Heat Intensity.Model { Gaussian | Table | User }
```

### Gaussian Model

The intensity  $I$  can be given by the Gaussian profile as follows:

$$I = \frac{\text{Fluence}}{\sqrt{2\pi}t_s} \exp\left(-\frac{(t-t_0)^2}{2t_s^2}\right) \quad (242)$$

$$t_s = \frac{\text{Pulse}}{2\sqrt{2\ln 2}} \quad (243)$$

where `Pulse` is the full width at half maximum (FWHM) time interval. The parameter `Fluence` is the energy dose in  $\text{J}/\text{cm}^2$ .

**4: Diffusion**  
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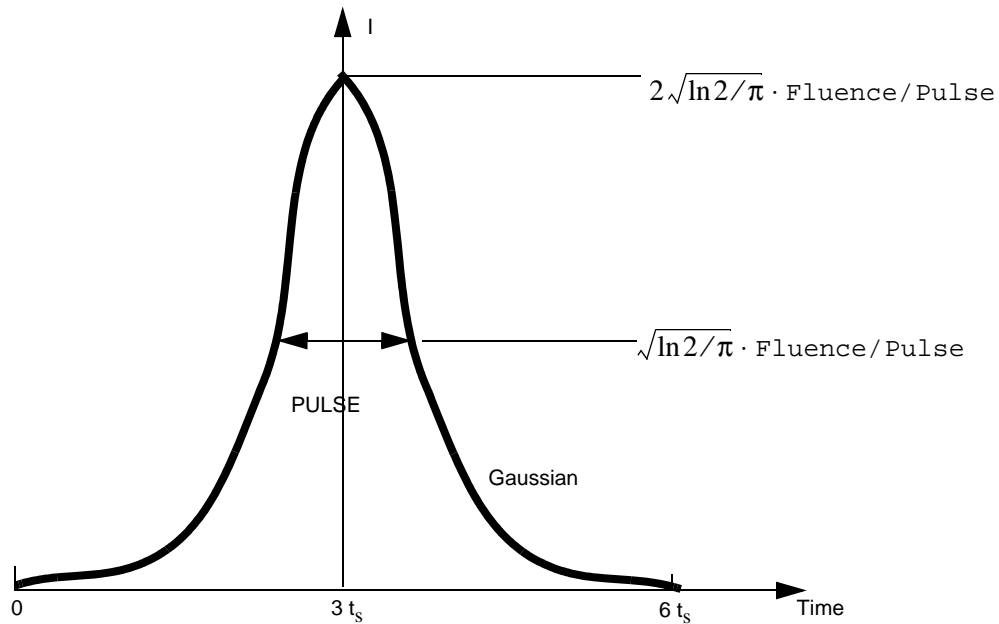


Figure 34 Heat Intensity for flash anneal with respect to time

### Table Lookup Method

The table of time versus intensity can be given by:

```
pdbSet Heat Intensity.Table { <t1> <I1> <t2> <I2> ... <tn> <In> }
```

The intensity values in the table can be scaled by:

```
pdbSet Heat Intensity.Table.Factor {<n>}
```

### User-specified Model

You can define the heat intensity profile by using `IntensityProfile` (unit is  $\text{J}/\text{cm}^2/\text{s}$ ). The heating time, that is, the light-sourcing time for the user-specified intensity is given by the parameter `HeatingTime`. For example, for the sum of two different Gaussian intensities:

```
set ttime "[simGetDouble Heat time]"
set rt2pi [expr sqrt(2*3.141592)]
set tp1 3e-3 #from 3*sigma = 3*1e-3
set tp2 6e-3 #from 3*sigma = 3*2e-3
set ts1 2e-6 #from 2*sigma*sigma = 2*1e-3*1e-3
set ts2 8e-6 #from 2*sigma*sigma = 2*2e-3*2e-3
```

```

pdbSet Heat HeatingTime 12e-3
pdbSet Heat IntensityProfile "1e4/\$rt2pi*exp(-(((\$ttime-\$tp1)^2)/\$ts1)) \
                             +2.5e3/\$rt2pi*exp(-(((\$ttime-\$tp2)^2)/\$ts2))"

```

Here, [simGetDouble Heat time] returns the current time that is used to solve the heat equation.

---

## Intensity Model for Scanning Laser

The scanning laser beam is characterized with the scanning speed (cm/s), the beam width ( $\mu\text{m}$ ), and the beam fading distance ( $\mu\text{m}$ ) by diffraction:

```

pdbSet Heat ScanSpeed <n>
pdbSet Heat BeamWidth <n>
pdbSet Heat BeamFadeDistance <n>

```

The intensity specification for laser beam precedents that of a flash light source. When a positive ScanSpeed is specified, the laser scanning model is assumed and the heat intensity is calculated with the laser beam parameters.

Two complementary error functions are multiplied to generate the laser beam intensity as shown in [Figure 35](#).

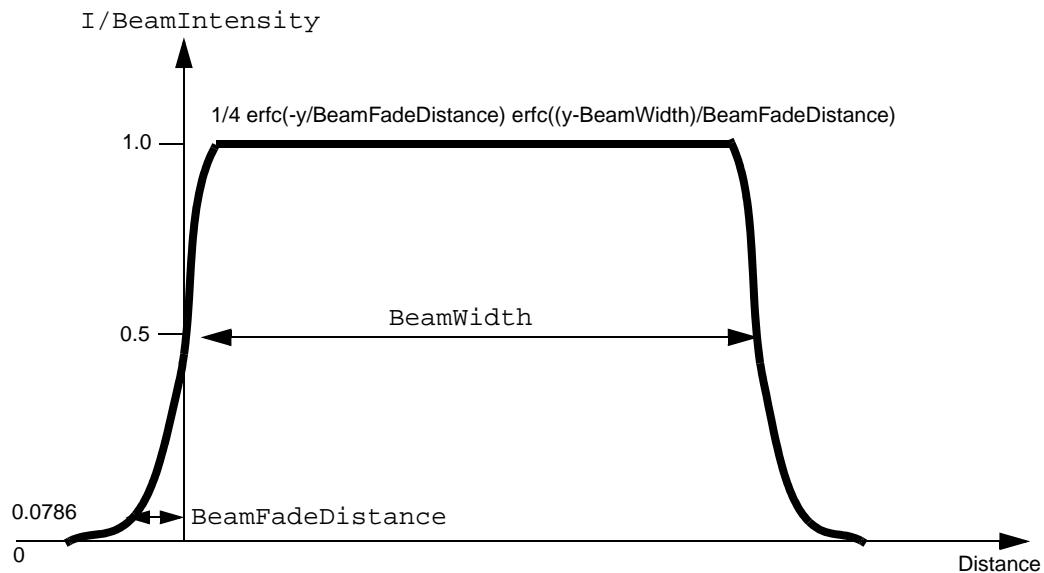


Figure 35 Heat intensity profile for laser beam

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The laser beam moves by the distance  $(\text{BeamWidth} - \text{BeamOverlap})$  after  $(\text{BeamWidth} - \text{BeamOverlap}) / \text{ScanSpeed}$  anneal time step. As  $\text{BeamOverlap}$  approaches  $\text{BeamWidth}$ , the simulation accuracy is improved.

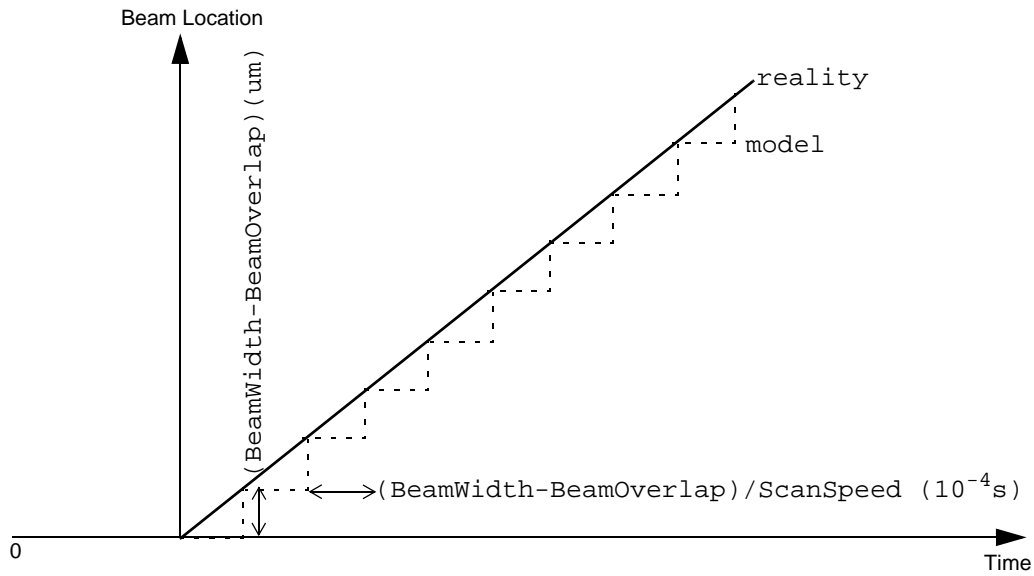


Figure 36 Beam location along time

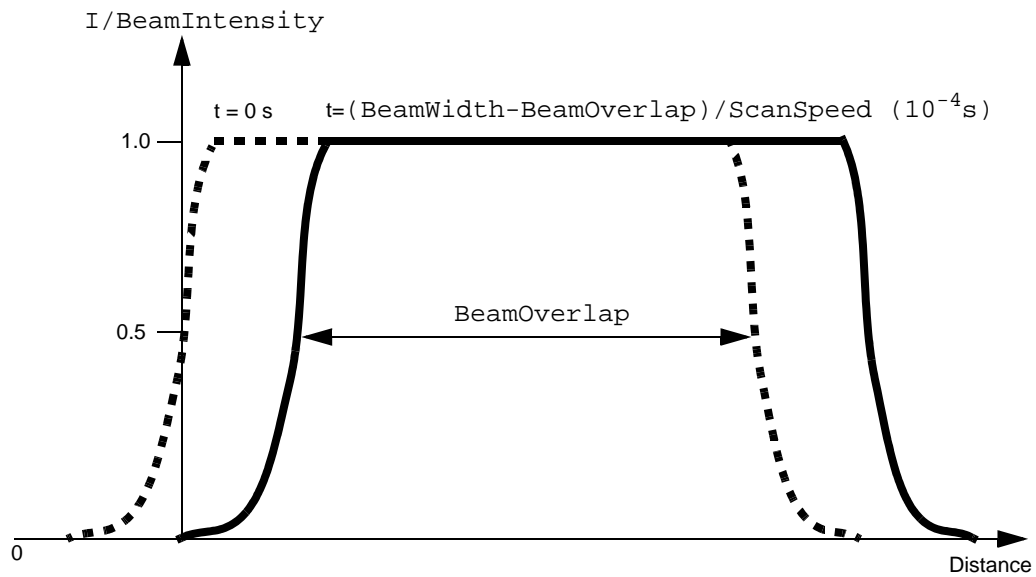


Figure 37 Laser beam displacement at each time step



## Control Parameters

Table 14 lists the control parameters. These parameters must be used with:

```
pdbSet Heat
```

For example:

```
pdbSet Heat HeatingTime 12e-3
```

```
pdbSet Heat MaxTimeStep 500
```

Table 14 Control parameters

Parameter (with available options)	Default value Unit (if applicable)	Description
AttachThermalResistor <0 1>	0	Used to attach the thermal resistor to the bottom. Options are 0   1.
BulkMaterial <material>	Si	Indicates that the global temperature for solving diffusion equations will be calculated by averaging the local temperatures at interfaces of the specified material. In addition, the material HeatSubstrate of the extended region will have the same thermal properties as BulkMaterial ones.
ExtendBottom <0 1>	1	Extends bottom of the simulation structure to the WaferThickness thickness. Options are 0   1.
HeatingTime <n>	0.0 ms	Defines the time the heating source is switched on. Not applicable to the scanning laser model.
HeatSinkTransfer <n>	1e5 W/(cm <sup>2</sup> K)	Defines the heat transfer rate coefficient at the extended structure bottom. Only applicable when AttachThermalResistor is set to 0.
MaxTimeStep <n>	600.0 s	Defines the maximum time step for solving the heat equation.
ReflectSide <Left Right None>	Left	Specifies the side at which the structure will be reflected after extending the structure to the other side by SideExtension. Only applicable for positive SideExtension. Options are Left   Right   None.

## 4: Diffusion

### Flash or Laser Anneal Model

Table 14 Control parameters

Parameter (with available options)	Default value Unit (if applicable)	Description
SideExtension <n>	0.0 μm	Defines the extended distance to side. The extended region is set to the HeatSubstrate material, which has the same thermal properties as the BulkMaterial ones. Note that only the heat equation is solved in the region of HeatSubstrate.
TempAverageBox "<x1,y1,z1,x2,y2,z2>"	–	Defines the box area to average the local temperatures for calculating the global temperature. It must be satisfied that $x1 \leq x2$ and $y1 \leq y2$ and $z1 \leq z2$ .  pdbSet Heat TempAverageBox "-0.1 0.1 0.0 1.0 2.0 0.0"
TimeSampleSize <n>	20.0	Specifies the number of time steps during the sourcing of the heat energy. Not applicable to the scanning laser model. The maximum time step is given by the minimum time step among MaxTimeStep and  $\frac{3 \cdot \text{Pulse}}{\text{TimeSampleSize} \cdot \sqrt{2 \ln 2}} \text{ (ms)}$ for HeatingTime ≤ 0.0, or HeatingTime/TimeSampleSize.
UpdateHeatRate <0 1>	0	Updates heat rate at each time step. Options are 0   1.
WaferThickness <n>	700.0 μm	Defines the wafer thickness to which the simulation structure is to be extended if ExtendBottom is set to 1.

## Notes

- It takes three times the standard deviation time to reach the peak intensity. After six times the standard deviation time, the heat source is switched off.
- The global temperature, which is calculated by averaging the local temperature distribution, is used for solving the diffusion equations.
- When the Boolean parameter UseTemperatureField in mechanics is on, the local temperature is used for solving the mechanics equations.

- The global temperature is calculated by:

$$T_{global} = \frac{\sum_{i=1}^n V_i T_i}{\sum_{i=1}^n V_i} \quad (244)$$

where  $V_i$  and  $T_i$  are the volume and the local temperature at a node in `BulkMaterial` material. By default, the nodes on the nonreflecting surfaces of `BulkMaterial` are taken. When you set `TempAverageBox`, the nodes within the specified box are taken.

---

## Diffusion in Polysilicon

Polysilicon has a microstructure composed of small monocrystalline grains of different crystalline orientation. The grains are separated by 2D surfaces – the grain boundaries.

Sentaurus Process uses a two-stream model to simulate polycrystalline or granular materials. Granular diffusion can be switched on with:

```
pdbSet PolySilicon Arsenic DiffModel Granular
```

---

## Isotropic Diffusion Model

The dopant concentration for species  $A$  is split into a fraction of dopants in the grain and a fraction of dopants in the grain boundary, that is:

$$C_A = f_g \cdot c_A^g + f_{gb} \cdot c_A^{gb} \quad (245)$$

Here,  $c_A^g$  denotes the total concentration inside the grain per grain volume and  $c_A^{gb}$  denotes the concentration inside the grain boundaries per grain boundary volume. Both quantities are defined in the entire polysilicon region representing average concentrations.

The ratio of grain volume to the polysilicon volume is known as the *volume share*. The volume share of the grain regions  $f_g$  depends on the shape and size of the grain. The volume share of the grain boundary is defined as:

$$f_{gb} = 1 - f_g \quad (246)$$

The grain volume share and grain boundary share are defined by the terms `GVolShare` and `GbVolShare`, respectively.

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Diffusion in Polysilicon

The concentration of the grain boundary is assumed to be electrically inactive. The grain density is identified with the active portion of the total concentration  $C_A^+$ . The active concentration is stored in the dataset <dopant>Active. The grain boundary concentration  $C_A^{gb} = f_{gb} \cdot c_A^{gb}$  is stored in the dataset <dopant>Gbc and is initialized with the portion of the total dopant concentration in the grain boundary  $f_{gb} \cdot C_A$ . In the absence of clusters, the total dopant concentration is given as:

$$C_A = f_g \cdot C_A^+ + C_A^{gb} \quad (247)$$

### Grain Shape and the Grain Growth Equation

The microscopic shape and size of the grains is not described in the model. Instead the size, orientation, and type of a prototype grain is used to compute all parameters that depend on the grain size.

The growth model can be switched on by:

```
pdbSet PolySilicon Dopant DiffModel Granular
```

In Sentaurus Process, a columnar grain structure is assumed by default. The grains are assumed to be columns that are oriented along the vertical axis, extending through the entire polycrystalline layer.

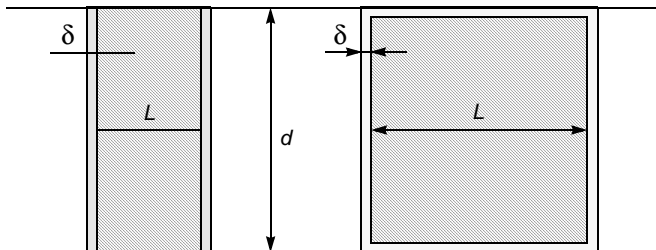


Figure 38 Columnar (left) and cubic (right) grains:  $L$  is the grain size,  $\delta$  is the grain boundary thickness, and  $d$  is the layer thickness

The grain size  $L$  defines the average edge length of the square cross section of the columns. The grain size is stored in the dataset GSize. The volume share of the grain region is given as:

$$f_g = \left( \frac{L}{L + \delta} \right)^2 \quad (248)$$

For cubic grains, the volume share is:

$$f_g = \left( \frac{L}{L + \delta} \right)^3 \quad (249)$$

The grain shape and the initial values for the grain size  $L$  (cm) and grain boundary thickness  $\delta$  (cm) can be set in the parameter database, that is:

```

pdbSet PolySilicon GrainShape <model>
pdbSet PolySilicon GrainSize 5.0e-6
pdbSet PolySilicon GrainBoundaryThickness 5.0e-8

```

where <model> is either Columnar or Cubic. It is assumed that the layer thickness  $d$  is a constant value set as:

```

pdbSet PolySilicon LayerThickness 1.0e-6

```

The grains grow during thermal processes. During the grain growth, the volume share of the grains increases and the volume share of the grain boundary decreases. The grain growth is modeled by:

$$\frac{dL}{dt}L = \frac{\tau^2 a_0 b_0^2 D \lambda}{kT} \cdot \frac{1}{1 + \frac{1}{a_r}} \cdot \left( 1 - \frac{\sum c_{gb}}{C_{Si}} \right) \quad (250)$$

where  $a_r$  denotes the ratio between the grain boundary volume inside the polycrystalline layer and the grain boundary volume at the material interfaces of the polycrystalline layer bounding other materials. The grain size,  $L$ , is represented with the solution name GSize and can be monitored like other solution fields.

The grain growth parameters can be specified in the parameter database in the material entry. The following names are used:  $\tau$  Tau,  $\lambda$  Lambda, and  $a_0$  A0. The parameter  $b_0$  is twice the lattice spacing of silicon. The Arrhenius values for the various contributions to the silicon self-diffusivity  $D$  can be specified with the parameter Dself.

For columnar grains:

$$a_r = \frac{(2L + \delta)d}{2(L + \delta)^2} \quad (251)$$

$$\frac{dL}{dt}L \left( 1 + \frac{2(L + \delta)^2}{(2L + \delta)d} \right) = \frac{\tau^2 a_0 b_0^2 D \lambda}{kT} \cdot \left( 1 - \frac{\sum c_{gb}}{C_{Si}} \right) \quad (252)$$

For cubic grains, this is:

$$a_r = \frac{(3L^2 + 3L\delta + \delta^2)d}{2(L + \delta)^3} - \frac{1}{2} \quad (253)$$

## 4: Diffusion

### Diffusion in Polysilicon

$$\frac{dL}{dt} L \frac{d(3L^2 + 3L\delta + \delta^2) + (L + \delta)^3}{d(3L^2 + 3L\delta + \delta^2) - (L + \delta)^3} = \frac{\tau^2 a_0 b_0^2 D \lambda}{kT} \cdot \left( 1 - \frac{\sum c_{gb}}{C_{Si}} \right) \quad (254)$$

The grain shape switches from `Columnar` to `Cubic` when the grain size  $L$  reaches the layer thickness  $d$  and the grain shape is set to `Columnar`, that is:

```
pdbSet PolySilicon GrainShape Columnar
```

This is the default. No switching is performed if the grain shape is set to `Cubic`. The grain growth equation is solved with the dopant diffusion equations.

Note that the `GSize` and the dopant distribution in the grain boundary `<dopant>Gbc` are not reset automatically at the beginning of a new diffusion step. The `pdb` switch `GbcNew` can be used to reset the grain size dataset `GSize` to the current value of `GrainSize`, that is:

```
pdbSet PolySilicon GrainSize 1e-6
```

```
pdbSet PolySilicon GbcNew 1
```

will reset the grain size in polysilicon to 10 nm. It also resets the `<dopant>Gbc` dataset to the value calculated using the grain size and the grain-boundary volume share.

The `GSize` and the initial `<dopant>Gbc` distribution in a newly deposited layer can be specified in the fields and in the values list in the `deposit` command, that is:

```
deposit PolySilicon type=isotropic rate=1.0 time=0.1 fields= {GSize Arsenic} \  
values= {4e-6 1e19}
```

This will initialize the `GSize` to 40 nm and the arsenic concentration to a constant value of  $10^{19} \text{ cm}^{-3}$ . The `ArsenicGbc` solution will be created and the value of the corresponding dataset will be set automatically.

## Diffusion Equations

The diffusion in polycrystalline materials is modeled with two separate diffusion fluxes for the diffusion of  $C_A^+$  inside the grains and the diffusion of  $c_A^{gb}$  along the grain boundaries. The diffusion inside the grain regions is modeled as for crystalline silicon with the `ChargedFermi` diffusion model. The diffusion fluxes are scaled with the ratio of the grain boundary volume to the polysilicon volume, that is:

$$J_A = -f_g \sum_{X,c} D_{AX} \left( \frac{n}{n_i} \right)^{-c-z} \nabla \left( C_A^+ \left( \frac{n}{n_i} \right)^z \right) \quad (255)$$

$$\frac{\partial C_A}{\partial t} = -\nabla \cdot J_A - R \quad (256)$$

For details on the ChargedFermi model parameters, see [ChargedFermi Diffusion Model on page 209](#). The diffusivity  $D_{AX^c}$  for the grain interior is set as usual for the ChargedFermi model, for example:

```
pdbSet PolySilicon Boron Int Dstar \
    { 0 {[Arr 0.743e2 3.56]} 1 {[Arr 0.617e2 3.56]} }
```

For the fluxes along the grain boundaries, the gradient of the concentration in the grain boundary is multiplied by a constant diffusivity and the grain boundary volume share  $f_{gb}$ :

$$\frac{\partial C_A^{gb}}{\partial t} = -\nabla \bullet J_A^{gb} + R \quad (257)$$

$$J_A^{gb} = -f_{gb} D_A^{gb} \left( 1 - \frac{c_A^{gb}}{C_{Si}} \right) \nabla (c_A^{gb}) \quad (258)$$

The grain boundary diffusivity  $D_A^{gb}$  can be set in the parameter database using:

```
pdbSet PolySilicon Arsenic Dgb {[Arrhenius 1100.0 3.53]}
```

In polycrystalline materials, a segregation reaction is assumed to occur at the surface of the grains. The reaction describes the exchange of dopants between grain and grain boundary regions. The reaction term  $R$  is given as:

$$R = a(L) \cdot K \cdot \left[ C_A^+ \cdot \left( 1 - \frac{c_A^{gb}}{C_{Si}} \right) - \frac{c_A^{gb}}{s_g} \cdot \left( 1 - \frac{C_A^+}{C_{Si}} \right) \right] \quad (259)$$

The segregation term depends on the transport coefficient  $K$ , multiplied by the grain surface area per unit volume of polysilicon  $a(L)$ .

The transport coefficient  $K$  can be specified in the parameter database using:

```
pdbSet PolySilicon Arsenic Ksgb {[Arrhenius 1.630e4 3.586]}
```

The dopant segregation coefficient  $s_g$  for the segregation between the grain and grain boundary can be specified by using:

```
pdbSet PolySilicon Arsenic Sgb {[Arrhenius 2.75 -0.44]}
```

The grain surface area per unit volume  $a(L)$  depends on the grain structure. For columnar grain structures, this is:

$$a(L) = \frac{4 \cdot L}{(L + \delta)^2} \quad (260)$$

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and, for cubic grains, this is:

$$a(L) = \frac{6 \cdot L^2}{(L + \delta)^3} \quad (261)$$

Table 15 Solution names

Symbol	Boron	Arsenic	Phosphorus	Antimony	Indium
$C_A$	Boron	Arsenic	Phosphorus	Antimony	Indium
$C_A^{gb}$	BoronGbc	ArsenicGbc	PhosphorusGbc	AntimonyGbc	IndiumGbc
$C_A^+$	BActive	AsActive	PActive	SbActive	InActive

Table 16 Solution names for granular model

Symbol	Solution name
$L$	GSize

---

## Anisotropic Diffusion Model

The behavior of dopants in polycrystalline materials is strongly influenced by the boundaries between crystalline grains. Dopant atoms tend to segregate from the interior of a grain to the boundaries, which provide paths for rapid diffusion. The rate of segregation depends on the rate of grain growth, while the number of diffusion paths along the boundaries depends on the grain size. In addition, the boundaries of the polycrystalline material act like grain boundaries, providing sites for electrically inactive dopant atoms and paths for diffusion. The diffusion equations for the grain-interior and grain-boundary components of the doping profile are solved separately. The equations are coupled by terms describing the segregation between the grain interiors and grain boundaries. To determine the rate of segregation and the density of grain-boundary diffusion paths, you also solve for the growth in grain size during high-temperature processing. The boundaries of the polycrystalline region are included as explicit grain boundaries in the diffusion and segregation equations. The model has been implemented in Sentaurus Process [6][7][8][9].

The model is invoked by specifying the polycrystalline material, for example:

```
pdbSet PolySilicon PolyCrystalline 1
```

To set the model to the TSUPREM-4 compatible mode, use the command:

```
SetTS4PolyMode
```



## Diffusion in Grain Interiors

Redistribution of dopants in polycrystalline materials occurs by the parallel diffusion of dopants through the interiors of grains and along grain boundaries.

In the grain interiors, diffusion of the active dopant is given by:

$$\frac{\partial c_g}{\partial t} = -\vec{\nabla} \cdot \left[ -D_g \left( \vec{\nabla} c_g - z_s c_g \frac{qE_g}{kT} \right) \right] - G \quad (262)$$

where  $c_g$  is the active concentration in the grain interior. The diffusivity  $D_g$  and electric field  $E_g$  in the grain interior are calculated from the electron concentration  $n_g$ , which is in turn calculated from the doping concentrations  $c_g$ .  $G$  accounts for the segregation of dopant to grain boundaries as described in [Segregation Between Grain Interior and Boundaries on page 241](#).

The parameter `Grain.Crystallinity` specifies the initial crystallinity of the grain interiors. If `Grain.Crystallinity` is set to `Crystalline`, the initial active concentration is determined by the `pdb` parameter `AcInit` or the term `#{Sol}AcInit`. If `Grain.Crystallinity` is set to `Amorphous`, the initial active concentration is determined by the `pdb` parameter `AmInit` or the term `#{Sol}AmInit`. The initialization is performed for the remainder after some implantation atoms go to a grain boundary according to [Eq. 271, p. 241](#).

## Grain Boundary Structure

Diffusion along grain boundaries is described in terms of the dopant concentration *per unit area* of grain boundary  $c_{gb}$ , and the average area of grain boundaries per unit volume:

$$\rho' = \rho + \delta_{if} \quad (263)$$

where  $\rho$  is the average area of grain boundaries per unit volume in the bulk of the poly layer and  $\delta_{if}$  accounts for the dopant at interfaces between poly and other materials (or ambient).  $\rho$  is inversely proportional to the average grain size  $L_g$ :

$$\rho = \frac{\text{GBGeomFactor}}{L_g} \quad (264)$$

where `GBGeomFactor` is a geometric factor specified for the polycrystalline material, for example:

```
pdbSet PolySilicon GBGeomFactor 2.0
```

#### 4: Diffusion

##### Diffusion in Polysilicon

$\delta_{if}$  is a function of position defined by the fact that its integral over any volume is equal to the area  $A_{if}$  of the polysilicon interface passing through that volume:

$$\int \delta_{if} dV = A_{if} \quad (265)$$

The concentration of dopants in the grain boundaries per unit volume of material is then given by:

$$c_A^{gb} = \rho' c_{gb} \quad (266)$$

### Diffusion along Grain Boundaries

The diffusion of dopant in the grain boundaries is given by:

$$\frac{\partial c_A^{gb}}{\partial t} = -\vec{\nabla} \cdot \left[ -FD_{gb} \left( \vec{\nabla} c_{gb} - z_s c_{gb} \frac{\vec{E}_{gb}}{kT} \right) \right] + G \quad (267)$$

The diffusivity  $D_{gb}$  and electric field  $\vec{E}_{gb}$  along the grain boundaries are calculated from the electron concentration  $n_{gb}$ ;  $n_{gb}$  is calculated by assuming that the net donor and acceptor concentrations are calculated from  $c_{gb}/K$ , the equilibrium dopant concentrations in the grain interior near the grain boundary, where  $K$  is the segregation coefficient given by [Eq. 273, p. 241](#).  $G$  accounts for the segregation of dopant to grain boundaries as described in [Segregation Between Grain Interior and Boundaries on page 241](#).

Diffusivity  $D_{gb}$  is given by:

$$D_{gb} = D_{gb} \cdot \sum D_{gb} \cdot \text{Fermi} \cdot \left( \frac{n_{gb}}{n_i} \right)^{-c} \quad (268)$$

$D_{gb}$  and  $D_{gb} \cdot \text{Fermi}$  are defined by:

```

pdbSet <material> <dopant> Dgb <value>
pdbSet <material> <dopant> Dgb.Fermi <array>

```

$F$  is a tensor that describes the diffusion paths available to dopant in the grain boundaries. It is composed of two parts:  $F = F_b + (1 - F_{bu})F_{if}$ .  $F_b$  describes the available paths within the bulk of the poly layer. For a horizontal poly layer, it is given by:

$$F_b = \text{diag} \left( \frac{D_{gb} \cdot F_{22}}{L_g}, \frac{D_{gb} \cdot F_{11}}{L_g}, \frac{D_{gb} \cdot F_{11}}{L_g} \right) \quad (269)$$

Because of the columnar grain structure,  $D_{gb} \cdot F_{22}$  is larger than  $D_{gb} \cdot F_{11}$ , which implies that diffusion through the layer is faster than diffusion parallel to the layer.

Dgb.F11 and Dgb.F22 are defined for the polycrystalline material, for example:

```
pdbSet PolySilicon Dgb.F11 1.0
pdbSet PolySilicon Dgb.F22 2.0
```

$F_{if}$  describes the available paths for diffusion along material interfaces. In the vicinity of a horizontal interface, it has the value:

$$F_{if} = \text{diag}(0, \delta_{if}, \delta_{if}) \quad (270)$$

For the interface between polysilicon and silicon, the phenomenon of interfacial breakup accompanied by epitaxial realignment can occur, as described in [Interface Oxide Breakup and Epitaxial Regrowth on page 245](#).  $F_{bu}$  is the fraction of the polysilicon–silicon interface that has broken up. For layers or interfaces that are not horizontal,  $F_b$  and  $F_{if}$  are rotated by the angle of the layer or interface, respectively, with respect to the horizontal axis.

## Segregation Between Grain Interior and Boundaries

When dopant is initially introduced into a polycrystalline material, some of the dopant occupies sites in the interior of a grain and some occupies sites on a grain boundary. The initial segregation of dopant is given by:

$$c_{gb} = \frac{\text{GBMaxDensity}}{\text{GMaxConc}} \text{GSegInit } c_g \quad (271)$$

GBMaxDensity, GMaxConc, and GSegInit represent the density of available sites on grain boundaries, and in the grain interiors and the initial segregation entropy, respectively. In the case of ion implantation,  $c_g$  and  $c_{gb}$  describe the additional dopant introduced by the implantation; dopant that is present before the implantation is not redistributed.

Dopant atoms are free to move between sites in the interior of a grain and sites on the grain boundary during high-temperature processing. The rate of segregation is given by:

$$G = (\rho q_b + (1 - F_{bu})\delta_{if}q_{if}) \left( f_{gb} c_g - f_g \frac{c_{gb}}{K} \right) \quad (272)$$

The segregation coefficient  $K$  is given by [\[10\]](#):

$$K = \frac{\text{GBMaxDensity}}{\text{GMaxConc}} \text{Sgb} \quad (273)$$

GBMaxDensity, GMaxConc, GSegInit, and Sgb are defined for dopants, for example:

```
pdbSet PolySilicon Dopant GBMaxDensity 2.5e15
pdbSet PolySilicon Dopant GMaxConc 5e22
pdbSet PolySilicon Dopant GSegInit 1.0
pdbSet PolySilicon Boron Sgb {[Arrhenius 0.2 -0.38]}
```

## 4: Diffusion

### Diffusion in Polysilicon

The segregation velocities associated with the bulk of the poly region and the material interfaces are given by:

$$q_b = \frac{1}{\text{GBVFactor}} \frac{\partial L_g}{\partial t} + \text{KsgbFactor} \frac{D_g}{L_g} \quad (274)$$

GBVFactor is the parameter for the material. KsgbFactor and  $q_{if}$ , which is defined by Vsgb, are specified for dopants. For example:

```
pdbSet PolySilicon GBVFactor 1.33
pdbSet PolySilicon Dopant KsgbFactor {[Arr 4.0 0.0]}
pdbSet PolySilicon Dopant Vsgb {[Arr 1e7 3.0]}
```

$f_g$  and  $f_{gb}$  are the fractions of unfilled interior and boundary sites:

$$f_g = 1 - \frac{c_g}{\text{GMaxConc}} \quad (275)$$

$$f_{gb} = 1 - \sum \frac{c_{gb}}{\text{GBMaxDensity}} \quad (276)$$

where the sum is taken over all the dopant species present in the structure.  $F_{bu}$  is the fraction of the polysilicon–silicon interface that has broken up, as described in [Interface Oxide Breakup and Epitaxial Regrowth on page 245](#).

## Grain Size Model

The grains in the polycrystalline material are assumed to be oriented as columns that extend through the wafer. The structure is characterized by  $L_g$ , the average grain size in the lateral direction (in other words, in the plane of the layer), and a vector describing the orientation of the columnar grains.

The initial grain size is determined by the temperature of the poly deposition process:

$$L_g = \begin{cases} \max(\text{Frac.TA} \times t_a, \text{GrainSize}) & T_c \leq \text{GrainSizeTempC} \\ \text{GrainSize} + 2 \cdot \text{GrainSizeFactor} \cdot z & T_c > \text{GrainSizeTempC} \end{cases} \quad (277)$$

where:

- $T_c$  is the deposition temperature (specified on the deposit command) in degree Celsius.
- $t_a$  is the thickness of the amorphous silicon layer produced by low-temperature deposition.
- $z$  is the distance from the bottom of the layer.

For high-temperature depositions, grain size depends on the thickness specified in the `deposit` command. Dividing a deposition into multiple smaller depositions produces different results for the grain size. For low-temperature depositions, the material is assumed to be amorphous (a negative grain size is reported in printing or plotting). The initial grain size is calculated from the thickness  $t_a$  of the amorphous layer at the beginning of the next diffusion step.

`Frac.TA`, `GrainSize`, `GrainSizeFactor`, and `GrainSizeTempC` are the material parameters, for example:

```
pdbSet PolySilicon Frac.TA 0.5
pdbSet PolySilicon GrainSize 5e-6 ;# cm
pdbSet PolySilicon GrainSizeFactor {[Arr 0.1 0.0]}
pdbSet PolySilicon GrainSizeTempC 600.0
```

## Surface Nucleation Model

An alternative model for the standard grain size model (see [Grain Size Model on page 242](#)) is the surface nucleation model. In this model, grains are assumed to grow from small clusters formed at the early stages of deposition. The kinetics of nucleation, under this assumption, determines the average distance between clusters, thereby, the average starting grain size near the surface upon which deposition occurs. The model for atomistic nucleation is derived from rate equations for growth, surface diffusion, and desorption [11]. Several different regimes are considered:

- Large deposition rates (compared to surface diffusion or evaporation) are labeled “complete condensation”.
- Conditions where the deposition rate between surface diffusion and evaporation are labeled “incomplete condensation”.
- Low deposition rates are labeled “extremely incomplete condensation”.

Besides the deposition rates, two types of nuclei are considered: 2D or 3D islands. The following formulas are used to compute the nucleation density:

$$n = n_0 R^p \exp\left(\frac{E}{kT}\right) \quad (278)$$

where  $p$  and  $E$  are given by [Table 17 on page 244](#). The choice of regime is set with:

```
pdbSet SNG.Model <regime>
```

where `<regime>` is one of `Complete`, `Initially.Incomplete`, `Extreme.Incomplete`, or `None` (default) meaning the model is switched off.

**4: Diffusion**  
Diffusion in Polysilicon

Table 17 Formulas for surface nucleation model

Regime	3D islands	2D islands
Extremely incomplete	$p = \frac{2}{3}i$ $E = \frac{2}{3}(E_i + (i + 1)E_a - E_d)$	$p = i$ $E = E_i + (i + 1)E_a - E_d$
Incomplete	$p = \frac{2}{5}i$ $E = \frac{2}{5}(E_i + iE_a)$	$p = \frac{i}{2}$ $E = E_i + iE_a$
Complete	$p = i/(i + 2.5)$ $E = (E_i + iE_d)/(i + 2.5)$	$p = i/(i + 2)$ $E = (E_i + iE_d)/(i + 2)$

**NOTE** Default values for parameters of the surface nucleation model have not been calibrated for any process. They have simply been set to give approximately the same values as the grain size model in polysilicon diffusion. This model is in an experimental state. The default values of the model may change in the future if reasonable values can be found for typical technology conditions.

Table 18 Parameters of surface nucleation model set with  
pdbSet PolySilicon <parameter> <value>

Symbol	Parameter Name
Island dimension	SNG.Island.Dim
$R$	SNG.Growth.Flux
$n_0$	SNG.Prefactor
$i$	SNG.Critical.Island.Size
$E_a$	SNG.Adsorption.Energy
$E_d$	SNG.Diffusion.Energy
$E_i$	SNG.Critical.Island.Energy

## Grain Growth

The growth of the grains during high-temperature processing is given by [12]:

$$\frac{\partial L_g}{\partial t} = \frac{1}{L_g} A_0 \times D_{selfFactor} \times D_{self} \times \frac{E_{gb}}{kT} \times F_{seg} + G_{EA} \quad (279)$$

$A_0$ ,  $D_{selfFactor}$ , and  $D_{self}$  represent the empirical geometric factor, the enhancement factor of silicon self-diffusivity at the grain boundary, and the silicon self-diffusivity in the vicinity of a grain boundary, respectively:

```

pdbSet PolySilicon A0 6.0
pdbSet PolySilicon DselfFactor {[Arrhenius 5.6e-6 -1.73]}
pdbSet PolySilicon Dself { -2 {[Arrhenius 5.6e-6 2.86]}
                           -1 0.0
                           0 {[Arrhenius 4.29e-7 2.18]}
                           1 0.0
                           2 0.0 }

```

$E_{gb}$  is the surface energy per atom associated with the grain boundary [12][13][14];  $F_{seg}$  models the segregation drag effect; and  $G_{EA}$  models epitaxial regrowth of the poly layer (see [Interface Oxide Breakup and Epitaxial Regrowth on page 245](#)).

$$E_{gb} = (2 \cdot \text{LatticeSpacing} \cdot \text{Tu})^2 \cdot \text{Lambda} \cdot \left( \frac{1}{1 + \text{Lambda} \cdot h f_n} + \text{Lambda} \cdot 1 \frac{L_g}{t_{poly}} \right) \quad (280)$$

$$f_n = \begin{cases} \frac{L_g}{2t_{poly} - L_g} & L_g < t_{poly} \\ \frac{L_g}{t_{poly}} & L_g \geq t_{poly} \end{cases} \quad (281)$$

$t_{poly}$  is the thickness of the polycrystalline layer.

The segregation drag effect reduces the grain growth rate [15]:

$$F_{seg} = \left( 1 + \sum \frac{c_{gb}}{\text{GBMaxDensity}} \right)^{-\text{SegDragExponent}} \quad (282)$$

$\text{SegDragExponent}$  is defined for the material, for example:

```

pdbSet PolySilicon SegDragExponent 2.0

```

## Interface Oxide Breakup and Epitaxial Regrowth

A thin interfacial oxide layer is typically present between a deposited polysilicon layer and any underlying single-crystal silicon. This interfacial oxide presents a barrier to epitaxial realignment of the poly layer. With sufficient high-temperature processing, the oxide layer breaks up into a discrete set of small spheres, allowing epitaxial regrowth of the poly to proceed.

#### 4: Diffusion

##### Diffusion in Polysilicon

The oxide breakup is modelled by the formation of voids in the interfacial oxide layer [16]–[19]. The radius of the voids  $R_{void}$  increases as:

$$\frac{dR_{void}}{dt} = \frac{\beta}{t_{ox}^3} \times \exp\left(-\frac{E_{bu}}{kT}\right) \quad (283)$$

where:

- $\beta$  is a constant.
- $t_{ox}$  is the initial oxide thickness.
- $E_{bu}$  is the activation energy of the breakup process.
- $R_{void}$  is initialized to zero whenever poly is deposited on exposed silicon.

The fraction of the interface that is broken up is given by:

$$F_{bu} = 1 - \exp(-\pi N_{EA} R_{void}^2) \quad (284)$$

where  $N_{EA}$  is the areal density of the voids.

The parameters for the model are specified in terms of a characteristic breakup time for the thinnest (5 Å) interfacial oxide layers:

$$t_{bu} \equiv \frac{5\text{Å}^3}{\sqrt{\pi N_{EA} \beta}} \times \exp\frac{E_{bu}}{kT} \quad (285)$$

$t_{bu}$  is defined with the parameter `PolyOxBreakTime`, for example:

```
pdbSet PolySilicon PolyOxBreakTime {[Arrhenius 1.0 -5.0]} ;# seconds
```

$$\frac{dR_{void}}{dt} = \frac{1}{t_{bu}} \left(\frac{5\text{Å}}{t_{ox}}\right)^3 \frac{1}{\sqrt{\pi N_{EA}}} \quad (286)$$

In the present implementation, assume that all polycrystalline or single-crystalline interfaces share a common oxide thickness given by:

$$t_{ox} = \text{PolyOxThickness} \quad (287)$$

`PolyOxThickness` is defined in the material:

```
pdbSet PolySilicon PolyOxThickness 5e-8 ;# cm
```



Epitaxial regrowth is modeled by increasing the poly grain size to a value larger than the thickness of the poly layer. This grain growth is described by  $G_{EA}$  in Eq. 270, p. 241 for the grain size:

$$G_{EA} = F_{bu} v_{EA} \delta_{if} \quad (288)$$

It serves as a driving force for epitaxial regrowth from the interface at the silicon–polysilicon interface. Parameters for this model are given by:

$$v_{EA} = \text{EpiGrowthVelocity} \quad (289)$$

```
pdbSet PolySilicon EpiGrowthVelocity {[Arrhenius 100.0 3.0]} ;# cm2/sec
```

## Dependence of Polysilicon Oxidation Rate on Grain Size

It has been observed experimentally that the oxidation rate for fine-grained polysilicon is faster than for coarser-grained polycrystalline or single-crystalline silicon, presumably because of enhanced oxidation at the grain boundaries.

This enhancement can be modeled by assuming a faster surface reaction rate where grain boundaries intersect the oxide–poly interface:

$$k_s = (1-f)k_g + fk_{gb} \quad (290)$$

where:

$$k_g = \frac{B C_{ox}}{A C^*} \quad (291)$$

is the surface reaction rate in the absence of grain boundaries,  $k_{gb}$  is the reaction rate at a grain boundary, and:

$$f = \min\left(\frac{\delta T}{L_g}, 1\right) \quad (292)$$

is the fraction of the surface within a distance  $\delta T/2$  of a grain boundary. The enhancement factor at grain boundaries is specified as:

$$\frac{k_{gb}}{k_g} = \text{GBFactor} \quad (293)$$

```
pdbSet Oxide_PolySilicon H2O GBFactor {[Arr 10.0 0.0]}
pdbSet Oxide_PolySilicon O2 GBFactor {[Arr 10.0 0.0]}
pdbSet Oxide_PolySilicon N2O GBFactor {[Arr 10.0 0.0]}
```

The effective thickness of the grain boundaries is given by  $\delta T = \text{GBEffThick}$ , where  $\text{GBEffThick}$  is specified for each material.

---

## Boundary Conditions

### Boundary Conditions for Grain Growth Equation

Several boundary conditions to control the grain size ( $\text{GSize}$ ) in the grain growth equation are available. The reflective ( $\text{HomNeumann}$ ) boundary condition assumes that the interface value grows like the bulk value. The minimum value ( $\text{MinimumSize}$ ) boundary condition sets the interface value at the minimum value for  $\text{GSize}$ . The minimum value is set with:

```
pdbSet <material> GSize minConc {<n>}
```

The initial size ( $\text{InitialSize}$ ) boundary condition fixes the interface value at the initial value of  $\text{GSize}$ .

The boundary conditions can be switched on using:

```
pdbSet Oxide_PolySilicon <dopant> BoundaryCondition [{HomNeumann  
MinimumSize InitialSize}]
```

The default setting for the grain growth boundary condition is  $\text{HomNeumann}$ .

### Dopant Diffusion Boundary Conditions

There are three additional segregation-type boundary conditions available with the polycrystalline diffusion model. The first can be selected with:

```
pdbSet Oxide_PolySilicon Arsenic BoundaryCondition GrainBoundarySegregation
```

The total dopant fluxes at the interfaces between the grain boundary and the neighboring layer are balanced. The fluxes are given by:

$$\mathbf{j} \cdot \mathbf{n} = k_{Transfer} \left( C_A^{other} - \frac{C_A^{gb}}{f_{gb} s_g k_{Segregation}^{gb}} \right) \quad (294)$$

where  $C_A^{other}$  is the concentration of dopant on the other side of the interface,  $C_A^{gb}$  is the grain boundary concentration,  $k_{Transfer}$  is the transfer rate, and  $k_{Segregation}^{gb}$  is the segregation rate of dopant  $A$  in the grain boundary. To set these parameters, use:

```
pdbSet <interface material> <dopant> Transfer {<n>}  
pdbSet <interface material> <dopant> SegregationGb {<n>}
```

The coefficient  $s_g$  is the grain–grain boundary segregation coefficient.

To select the second boundary condition, use:

```
pdbSet Oxide_PolySilicon Arsenic BoundaryCondition
      GrainGrainBoundarySegregation
```

The total dopant fluxes at the interfaces between the grain and the neighboring layer and the grain boundary and neighboring layer are balanced. The fluxes are given by:

$$\mathbf{j}_g \cdot \mathbf{n} = k_{Transfer} \left( C_A^{other} - \frac{f_g C_A^+}{k_{Segregation}} \right) \quad (295)$$

$$\mathbf{j}_{gb} \cdot \mathbf{n} = k_{Transfer} \left( C_A^{other} - \frac{C_A^{gb}}{s_g k_{Segregation}^{gb}} \right) \quad (296)$$

and:

$$\mathbf{j} \cdot \mathbf{n} = \mathbf{j}_g \cdot \mathbf{n} + \mathbf{j}_{gb} \cdot \mathbf{n} \quad (297)$$

where  $C_A^+$  is the active concentration of dopant in the grain and  $k_{Segregation}$  is the segregation rate of dopant A in the grain. To set this parameter, use:

```
pdbSet <interface material> <dopant> Segregation {<n>}
```

To select the third boundary condition, use:

```
pdbSet Oxide_PolySilicon Arsenic BoundaryCondition \
      BulkGrainBoundarySegregation
```

The total dopant fluxes at the interfaces between the grain and the neighboring layer and between the grain and the grain boundary are balanced. The fluxes are given by:

$$\mathbf{j} \cdot \mathbf{n} = k_{Transfer} \left( C_A^{other} - \frac{f_g C_A^+}{k_{Segregation}} \right) \quad (298)$$

$$\mathbf{j}_{gb} \cdot \mathbf{n} = k_{Transfer} \left( \frac{f_g C_A^+}{k_{Segregation}} - \frac{C_A^{gb}}{f_{gb} s_g k_{Segregation}^{gb}} \right) \quad (299)$$

## 4: Diffusion

### Dopant Diffusion in SiGe

**NOTE** For the anisotropic polycrystalline model, use the Segregation model for the boundary condition:

```
pdbSet PolySilicon_Silicon Boron BoundaryCondition Segregation
pdbSet Oxide_PolySilicon Boron BoundaryCondition Segregation
pdbSet Gas_PolySilicon Boron BoundaryCondition Segregation
```

---

## Dopant Diffusion in SiGe

The presence of germanium in silicon affects the dopant diffusion in various ways. First, the band gap of silicon is lowered in the presence of germanium. Second, germanium affects the point-defect equilibrium concentration. In addition, germanium can pair with boron forming an immobile but electrically active species.

---

### Bandgap Effect

The effect of the bandgap narrowing on the dopant diffusion arises from the change in the intrinsic carrier concentration  $n_i(Si)$ . This has been implemented in Sentaurus Process as follows:

$$n_i = n_i(Si)e^{\frac{-\Delta E_g}{2kT}} \quad (300)$$

where  $\Delta E_g$  is bandgap narrowing due to germanium content. It can be defined using the command:

```
pdbSet <material> Germanium delEg {<n>}
```

The band gap,  $\text{delEg}$  ( $\Delta E_g$ ), is a function of germanium concentration and is given by:

$$\Delta E_g \equiv \Delta E_{gs} + (\Delta E_{gr} - \Delta E_{gs})(1 - Fpm) \quad (301)$$

$$\Delta E_{gs} = 0.835x^2 - 1.01x \quad (302)$$

$$\Delta E_{gr} = 0.33x^2 - 0.55x \quad (303)$$

$$x = \frac{C_{Ge}}{5.0 \times 10^{22}} \quad (304)$$

where  $\Delta E_{gs}$  [20] is the bandgap narrowing in strained silicon,  $\Delta E_{gr}$  [21] is the bandgap narrowing in the relaxed silicon,  $Fpm$  is a pseudomorphic factor that shows the degree of the

relaxation, and  $x$  is the germanium fraction in silicon.  $Fpm$  is calculated with respect to lattice mismatch in the substrate. For example:

$$Fpm = \frac{(a_{SiGe} - a)}{a_{SiGe} - a_{Si}} \quad (305)$$

where:

- $a_{SiGe}$  is the lattice-spacing of the silicon-germanium region.
- $a_{Si}$  is the lattice-spacing of silicon.
- $a$  is the lattice-spacing calculated in the mechanics.

If the system is fully relaxed,  $Fpm$  is zero. If it is fully strained,  $Fpm$  is one.  $\Delta Eg$  will be used if the germanium percentage is greater than 0.1%, and the bandgap narrowing effects due to other strain sources will be ignored (see [Pressure-dependent Defect Diffusion on page 266](#)).

---

## Potential Equation

The permittivity of “Ge-doped” silicon can be calculated by the following formula, in which  $x_{Ge}$  is the germanium concentration in silicon:

$$\varepsilon = (1 - x_{Ge}) \times \varepsilon_{Si} + x_{Ge} \times \varepsilon_{Ge} \quad (306)$$

where  $\varepsilon_{Si}$  and  $\varepsilon_{Ge}$  are defined as PDB parameters:

```
pdbSet Ge Potential Permittivity 15.8
pdbSet Si Potential Permittivity 11.7
```

This calculation is included when setting:

```
pdbSetString Si CompSpecies "Germanium"
pdbSetBoolean Si Potential PermittivityContentEffect 1
```

The product of the density-of-states in the conduction and valence bands,  $N_c \times N_v$ , is multiplied by the factor defined as:

```
pdbSetFunction Si Ge factorNcNv [GefactorNcNv]
```

when the following PDB value is set:

```
pdbSetBoolean Si Potential BandgapContentEffect 1
```

Such a factor can be defined as:

$$(1 - x_{Ge} \times 0.47/0.81)^{3/4} \quad (307)$$

with the following line:

```
fproc GefactorNcNv { } { return "(1.0-(Germanium/5.0e22)*0.47/0.81)^0.75" }
```

---

## Effects on Point-Defect Equilibrium Concentrations

The introduction of germanium acts thermodynamically on the equilibrium of the silicon matrix. Compressive strain increases the equilibrium concentration of vacancies and decreases the equilibrium concentration of interstitials, and the tensile strain has the opposite effect on the point-defect equilibrium concentrations [22][23].

These effects are modeled in Sentaurus Process by modifying the equilibrium point-defect concentrations:

$$C_X^* = C_X^*(Si, P \equiv 0) e^{\frac{-(\Delta V_X P + \Delta V_{GeX})}{kT}} \quad (308)$$

$$\Delta V_{GeX} = \Delta V_{olGeX} \Delta a_{SiGe} \frac{C_{Ge}}{5 \times 10^{22}} \quad (309)$$

where  $C_X^*$  is the equilibrium concentration of point defects (interstitial or vacancy), and  $\Delta V_X$  is the activation volume change of equilibrium point defects due to the pressure  $P$ .

The following set of commands can be used to modify  $\Delta V_X$ :

```
pdbSet Silicon Interstitial Volume 8.59e-24
pdbSet Silicon Vacancy Volume -5.52e-24
```

To switch on strain effects on point defects, set the following switches:

```
pdbSet Silicon Interstitial CStarMod FermiPressureDependent
pdbSet Silicon Vacancy CStarMod FermiPressureDependent
```

$\Delta V_{GeX}$  is the total activation volume change of equilibrium point defects due to the presence of germanium and is calculated from the activation volume change  $\Delta V_{olGeX}$ , the lattice mismatch coefficient  $\Delta a_{SiGe}$ , and the germanium fraction in the structure (see Eq. 309). These quantities can be modified using the following commands:

```
pdbSet Silicon Germanium Interstitial delVol 11.8
pdbSet Silicon Germanium Vacancy delVol 25.6
pdbSet Silicon Germanium LatticeMismatch 0.0425
```

**NOTE** delVol is given in units of eV and Volume is given in units of  $\text{cm}^3$ .

---

## Effect of Ge on Point-Defect Parameters

In this version of Sentaurus Process, you can define the arbitrary Alagator expressions for the point-defect basic parameter prefactors. The names of terms used for the vacancy and interstitial equilibrium concentration are `VacCStarFactor` and `IntCStarFactor`, respectively. Corresponding terms for the vacancy and interstitial diffusivity are `VacDiffFactor` and `IntDiffFactor`. These expressions can be used to include the effect of germanium on point-defect parameters. For example, the prefactor for the vacancy equilibrium concentration in SiGe can be calculated as follows:

```
MultiplyTerm Si VacCStarFactor "exp((1.088*($x_Ge))*$Vt_i)"
```

where `x_Ge` is the germanium content, and `vt_i` is  $1/(kT)$  in  $eV^{-1}$ .

**NOTE** The `MultiplyTerm` command is not saved to the TDR files. If the input file is split, the command must be included in the new input file.

---

## Impact of Ge on Extended-Defect Parameters

The parameters `IClusterDissIntFactor`, `C311DiffIntFactor`, and `CLoopTransfer` (used in the `Full` model for I-clusters) can be used to include the impact of germanium on extended defects.

---

## Impact of Dopant Diffusivities

The germanium chemical effect is simulated by the activation energy correction using diffusivity prefactors. For example, in the case of boron, it is performed by the term `BoronIntDiffFactor`, which can be defined in silicon:

```
MultiplyTerm Si BoronIntDiffFactor "exp(-0.227*($x_Ge))*$Vt_i)"
```

**NOTE** The `MultiplyTerm` command is not saved to the TDR files. If the input file is split, the command must be included in the new input file.

During assembly of the diffusion equations, Sentaurus Process checks each dopant and material for whether such diffusion factors exist. The diffusivity through dopant–interstitial or dopant–vacancy pairs is then multiplied by the corresponding diffusion enhancement factors. A separation between interstitial and vacancy effects is necessary because with increasing germanium content of SiGe, the fractions of diffusion mediated by dopant–interstitial and dopant–vacancy pairs change.

---

## SiGe Strain and Dopant Activation

The solid solubility of dopants depends on the strain. In general, for compressive strain, the solubility of atoms smaller than silicon increases; whereas, the solubility of larger atoms decreases. In the Transient model, the stress effect is taken into account by introducing the pressure-dependent parameters `Solubility` and `TotalSolubility`:

$$S(P) = S(P = 0)\exp(-P V/kT) \quad (310)$$

An example of the definition of boron pressure-dependent solid solubility is:

```
pdbSet Si B SS.Factor "exp(3.636e-24*Pressure*$kT_i)"  
pdbSet Si B Total.SS.Factor "exp(3.636e-24*Pressure*$kT_i)"
```

Since the emission rate for the silicon side in the three-phase segregation model is proportional to the solid solubility, a corresponding modification also must be included in the boundary condition. For example, this can be achieved by the following line for boron:

```
pdbSetString Si B Side.SS.Factor "exp(3.636e-24*Pressure_Silicon*$kT_i)"
```

**NOTE** You can define the arbitrary Alagator expressions for the dopant solid solubility prefactors in Sentaurus Process. The name of strings used for the solid solubility, the total solid solubility, and the emission rate correction are `SS.Factor`, `Total.SS.Factor`, and `Side.SS.Factor`, respectively.

---

## Germanium–Boron Pairing

Germanium can pair with boron and the pairs are known to be electrically active [24] but not mobile:



In Sentaurus Process, this reaction is modeled with the following differential equation:

$$\frac{\partial C_{GeB}}{\partial t} = Kf(C_{Ge}C_B - KbC_{GeB}) \quad (312)$$

where  $C_{GeB}$  is the concentration of germanium–boron pairs,  $C_{Ge}$  is the concentration of germanium,  $C_B$  is the concentration of boron, and  $Kf$  and  $Kb$  are the forward reaction rate and equilibrium constant, respectively.



You can specify the model parameters with the commands:

```
pdbSet Silicon Germanium Boron Kf {<n>}
pdbSet Silicon Germanium Boron Kb {<n>}
```

Germanium diffusion is modeled by assuming a constant diffusion model:

$$\frac{\partial C_{Ge}}{\partial t} = \nabla \cdot (D \nabla C_{Ge}) \quad (313)$$

where  $D$  is the diffusivity of germanium and can be set using the command:

```
pdbSet Silicon Germanium Dstar {<n>}
```

**NOTE** The germanium–boron cluster model is switched off by default. To switched it on, use:

```
solution add name=GeB ifpresent = "Germanium Boron" !negative
```

Of course, if boron is present in silicon, the reaction in [Eq. 312](#) is automatically added to [Eq. 313](#).

Table 19 Solution names for germanium model

Symbol	Solution name
$C_{Ge}$	Germanium
$C_{GeB}$	GeB

## Initializing Germanium–Boron Clusters

Initially, germanium–boron cluster concentrations are set to zero. If there is an existing cluster concentration field, the field is used. To initialize the cluster concentration field, use the `select` command in the input command file.

# Diffusion in III–V Compounds

This section discusses diffusion in III–V compounds.

## Material Conversion

At the beginning of a diffusion, the adjacent III–V materials or a III–V material doped with other group III or V atoms can be merged into the proper ternary or quaternary compound

## 4: Diffusion

### Diffusion in III–V Compounds

materials. The conversion is performed when the Boolean parameter `Convert.IIIIVMaterials` is switched on:

```
pdbSet Diffuse Convert.IIIIVMaterials <0|1>    ;# default 1
```

When different III–V material regions are adjacent and there is a common material derived from each III–V material, the regions merge into the common derived material region. For example, if the neighbor region of a GaAs material region is InAs, two regions are merged and converted into InGaAs material if InGaAs is the derived material from both GaAs and InAs. The derived material is specified by:

```
pdbSet <material> Derived.Materials { <derivedmaterial list> }
```

For example:

```
pdbSet GaAs Derived.Materials { InGaAs AlGaAs GaPAs }
pdbSet InAs Derived.Materials { InPAs InGaAs }
```

When group III or group V atoms are doped into a III–V material, and the atoms are a different species from the components of the material, the material is converted to the new III–V material with the component list, including the doping species, if the doping concentration exceeds the minimum concentration `Min.Conv.Conc` for conversion. For example, when indium atoms are doped into a GaAs material region, GaAs is converted to InGaAs if InGaAs is one of the derived materials of GaAs, and the maximum concentration of indium atoms in the region exceeds the indium `Min.Conv.Conc` parameter value of InGaAs:

```
pdbSet InGaAs Indium Min.Conv {<n>}
```

The atoms of the material components are filled into the region before the material conversion for the mole fraction calculation and the interdiffusion simulation.

---

## Physical Parameter Interpolation

The parameter for the mole fraction of a ternary (or quaternary) material is specified by:

```
pdbSet <material> MoleFraction.Atoms { x <atom> }           ;# ternary
pdbSet <material> MoleFraction.Atoms { x <atom1> y <atom2> } ;# quaternary
```

For example:

```
pdbSet InGaAs MoleFraction.Atoms { x Gallium }           ;# In(1-x)Ga(x)As
pdbSet AlInGaAs MoleFraction.Atoms {x Aluminum y Indium} ;# Al(x)In(y)Ga(1-x-y)As
```

If a physical parameter is not specified on a ternary (or quaternary) material, the parameter value is extracted by the linear interpolation with the parameter values of their base materials that is, binary materials. For the value  $P_M$  of the parameter of material  $M$ :

$$P_{III_{A(x)}III_{B(1-x)}V_C} = P_{III_A V_C} \cdot x + P_{III_B V_C} \cdot (1 - x) \quad (314)$$

$$P_{III_{A(x)}III_{B(y)}III_{C(1-x-y)}V_D} = P_{III_A V_D} \cdot x + P_{III_B V_D} \cdot y + P_{III_C V_D} \cdot (1 - x - y) \quad (315)$$

$$P_{III_{A(x)}III_{B(1-x)}V_{C(y)}V_{D(1-y)}} = P_{III_A V_C} \cdot xy + P_{III_A V_D} \cdot x(1 - y) + P_{III_B V_C} \cdot (1 - x)y + P_{III_B V_D} \cdot (1 - x)(1 - y) \quad (316)$$

**NOTE** For the energy bandgap and affinity, the second-order mole-fraction dependency can be specified (see details in [Table 22 on page 264](#)).

---

## Dopant Diffusion

To model dopant diffusion in a III–V material, the following assumptions are applied:

- Point defects diffuse by the second nearest neighbor hopping.
- Group II dopants react only with group III point defects.
- Group VI dopants react only with group V point defects.
- There are no antisite defects.
- The charging reaction is in equilibrium.
- There are two types of vacancy (that is, at group III and V sites):  $V_{acIII}$  and  $V_{acV}$ .

Since the substitutional concentrations of group IV dopants on group III sites and group V sites are modeled and calculated separately, the autocompensation effect due to the amphoteric behavior is implicitly taken into account.

## ChargedReact Model

$$\frac{\partial AI}{\partial t} = \sum_m \left( \nabla \cdot \left( \left( \sum_j D_{AI_m j} \eta^{-j} \right) \eta^{-z_{Am}} \nabla \left( \frac{AI_m}{\alpha_{AI_m}} \eta^{z_{Am}} \right) \right) + \sum_{Y_m} R_{AY_m}^{(ko)} - R_{AIV_m}^{(ft)} \right) \quad (317)$$

$$\frac{\partial AV}{\partial t} = \sum_m \left( \nabla \cdot \left( \left( \sum_j D_{AV_m j} \eta^{-j} \right) \eta^{-z_{Am}} \nabla \left( \frac{AV_m}{\alpha_{AV_m}} \eta^{z_{Am}} \right) \right) + R_{AV_m}^{(ko)} - \sum_{Y_m} R_{AVY_m}^{(ft)} \right) \quad (318)$$

$$\frac{\partial A_{m,s}}{\partial t} = - \sum_{Y_m} R_{AY_m}^{(ko)} - R_{AV_m}^{(ko)} + R_{AIV_m}^{(ft)} + \sum_{Y_m} R_{AVY_m}^{(ft)} \quad (319)$$

#### 4: Diffusion

##### Diffusion in III-V Compounds

where:

$$R_{AY_m}^{(ko)} = \left( \sum_j k_{AY_m j}^{(ko)} Y_{m,i} \phi_{Y_m j} \eta^{-j} \right) \left( A_{m,s} \frac{Y_m}{Y_m^*} - \frac{AI_m Y_{m,s}}{\alpha_{AI_m} Y_{m,s}^*} \right) \quad (320)$$

$$R_{AV_m}^{(ko)} = \left( \sum_j k_{AV_m j}^{(ko)} V_{m,i} \phi_{V_m j} \eta^{-j} \right) \left( A_{m,s} \frac{V_m}{V_m^*} - \frac{AV_m}{\alpha_{AV_m}} \right) \quad (321)$$

$$R_{AIV_m}^{(ft)} = \left( \sum_{j,k} k_{AIV_m jk}^{(ft)} \alpha_{AI_m j} V_{m,i} \phi_{V_m k} \eta^{-(j+k)} \right) \left( \frac{AI_m V_m}{\alpha_{AI_m} V_m^*} - A_{m,s} \right) \quad (322)$$

$$R_{AVY_m}^{(ft)} = \left( \sum_{j,k} k_{AVY_m jk}^{(ft)} \alpha_{AV_m j} Y_{m,i} \phi_{Y_m k} \eta^{-(j+k)} \right) \left( \frac{AV_m Y_m}{\alpha_{AV_m} Y_m^*} - A_{m,s} \frac{Y_{m,s}}{Y_{m,s}^*} \right) \quad (323)$$

$$\alpha_{AI_m} = \sum_j \alpha_{AI_m j} \eta^{-j} \text{ and } \alpha_{AI_m j} \equiv D_{AI_m j} / d_{AI_m j} \quad (324)$$

$$\alpha_{AV_m} = \sum_j \alpha_{AV_m j} \eta^{-j} \text{ and } \alpha_{AV_m j} \equiv D_{AV_m j} / d_{AV_m j} \quad (325)$$

$$AI_{III} = \frac{\alpha_{AI_{III}} \eta^{-1}}{\alpha_{AI_{III}} \eta^{-1} + \alpha_{AI_V} \eta^1 / r_{III V}} AI \quad (326)$$

$$AI_V = \frac{\alpha_{AI_V} \eta^1}{r_{III V} \alpha_{AI_{III}} \eta^{-1} + \alpha_{AI_V} \eta^1} AI \quad (327)$$

$$AV_{III} = \frac{\alpha_{AV_{III}} \eta^{-1}}{\alpha_{AV_{III}} \eta^{-1} + \alpha_{AV_V} \eta^1 / r_{III V}} AV \quad (328)$$

$$AV_V = \frac{\alpha_{AV_V} \eta^1}{r_{III V} \alpha_{AV_{III}} \eta^{-1} + \alpha_{AV_V} \eta^1} AV \quad (329)$$

Table 20 Description of symbols for the ChargedReact model

Symbol	Description	Unit
$m$	The Mendeleev group number of a constituent atom of III–V material, $m \in \{III, V\}$ .	Unitless
$A_{m,s}$	Substitutional dopant concentration at group $m$ lattice sites.	$\text{cm}^{-3}$
$AI$	Dopant–interstitial pair concentration. For example, $AI$ is SiInt for Silicon.	$\text{cm}^{-3}$
$AI_m$	Dopant–group $m$ interstitial pair concentration.	$\text{cm}^{-3}$
$AV$	Dopant–vacancy pair concentration. For example, $AV$ is SiVac for Silicon.	$\text{cm}^{-3}$
$AV_m$	Dopant–group $m$ vacancy pair concentration.	$\text{cm}^{-3}$
$Y_m$	Self-interstitial concentration. For example, $Y_{III}$ is GaInt or InInt, and $Y_V$ is AsInt in InGaAs.	$\text{cm}^{-3}$
$Y_{m,s}$	Constituent atom concentration. For example, $Y_{III,s}$ is Gallium or Indium, and $Y_V$ is Arsenic in InGaAs.	$\text{cm}^{-3}$
$Y_m^*$	Self-interstitial concentration in equilibrium (Eq. 343, p. 262).	$\text{cm}^{-3}$
$Y_{m,i}^*$	Self-interstitial concentration in intrinsic equilibrium: pdbSet InGaAs GaInt Cstar {<n>}	$\text{cm}^{-3}$
$Y_{m,s}^*$	Constituent atom concentration in equilibrium: pdbSet InGaAs Gallium CsubStar {<n>}	$\text{cm}^{-3}$
$\phi_{Y_m}$	Charge-state fractions of self-interstitials: $\phi_{Y_{mj}} = \phi_{Y_{mj}'} / \sum_j \phi_{Y_{mj}'}$ . $\phi_{Y_{mj}'}$ is specified, for example, by: pdbSet GaAs GaInt ChargeStates { -2 <n> ... 2 <n> }	Unitless
$V_m$	Vacancy concentration. $V_{III}$ is VacIII and $V_V$ is VacV.	$\text{cm}^{-3}$
$V_m^*$	Vacancy concentration in equilibrium (Eq. 344, p. 262).	$\text{cm}^{-3}$
$V_{m,i}^*$	Vacancy concentration in intrinsic equilibrium: pdbSet GaAs VacIII Cstar {<n>}	$\text{cm}^{-3}$
$\phi_{V_m}$	Charge-state fractions of vacancies: $\phi_{V_{mj}} = \phi_{V_{mj}'} / \sum_j \phi_{V_{mj}'}$ . $\phi_{V_{mj}'}$ is specified, for example, by: pdbSet GaAs VacIII ChargeStates { -2 <n> ... 2 <n> }	Unitless
$D_{AI_m}$	Effective diffusivity of dopant–group $m$ interstitial: pdbSet <mat> <dopant> IntIII D { -2 <n> ... 2 <n> } pdbSet <mat> <dopant> IntV D { -2 <n> ... 2 <n> }	$\text{cm}^2/\text{s}$
$D_{AV_m}$	Effective diffusivity of dopant–group $m$ vacancy: pdbSet <mat> <dopant> VacIII D { -2 <n> ... 2 <n> } pdbSet <mat> <dopant> VacV D { -2 <n> ... 2 <n> }	$\text{cm}^2/\text{s}$
$d_{AI_m}$	Self-diffusivity of dopant–group $m$ interstitial: pdbSet <mat> <dopant> IntIII Dpair { -2 <n> ... 2 <n> } pdbSet <mat> <dopant> IntV Dpair { -2 <n> ... 2 <n> }	$\text{cm}^2/\text{s}$

#### 4: Diffusion

##### Diffusion in III–V Compounds

Table 20 Description of symbols for the ChargedReact model

Symbol	Description	Unit
$d_{AVm}$	Self-diffusivity of dopant–group $m$ vacancy: pdbSet <mat> <dopant> VacIII Dpair { -2 <n> ... 2 <n> } pdbSet <mat> <dopant> VacV Dpair { -2 <n> ... 2 <n> }	$\text{cm}^2/\text{s}$
$\alpha_{AI_m}$	Ratio of dopant–group $m$ interstitial pair concentration to substitutional concentration in equilibrium.	Unitless
$\alpha_{AV_m}$	Ratio of dopant–group $m$ vacancy pair concentration to substitutional concentration in equilibrium.	Unitless
$z_{Am}$	Charge of ionized substitutional atom at group $m$ lattice sites.	Unitless
$\eta$	Ratio of electron concentration to intrinsic carrier concentration ( $n/n_i$ ).	Unitless
$R_{AY_m}^{(ko)}$	Kick-out reaction rate at which $Y_m$ kicks out $A_{m,s}$ , generates $AI_m$ , and increases the mole fraction of $Y$ .	$\text{cm}^{-3}/\text{s}$
$R_{AV_m}^{(ko)}$	Kick-out reaction rate at which $V_m$ reacts with $A_{m,s}$ and generates a dopant–vacancy pair $AV_m$ .	$\text{cm}^{-3}/\text{s}$
$R_{AIV_m}^{(fi)}$	Frank–Turnbull reaction rate at which $AI_m$ reacts with $V_m$ and generates a substitutional dopant $A_{m,s}$ .	$\text{cm}^{-3}/\text{s}$
$R_{AVY_m}^{(fi)}$	Frank–Turnbull reaction rate at which $AV_m$ reacts with $Y_m$ , generates a substitutional dopant $A_{m,s}$ , and increases the mole fraction of $Y$ .	$\text{cm}^{-3}/\text{s}$
$k_{AY_m}^{(ko)}$	Reaction rate constant associated with $R_{AY_m}^{(ko)}$ , for example: pdbSet GaAs Si Gallium kfKickOut { -2 <n> ... 2 <n> }	$\text{cm}^{-3}/\text{s}$
$k_{AV_m}^{(ko)}$	Reaction rate constant associated with $R_{AV_m}^{(ko)}$ , for example: pdbSet GaAs Si VacV kfKickOut { -2 <n> ... 2 <n> }	$\text{cm}^{-3}/\text{s}$
$k_{AIV_m}^{(fi)}$	Reaction rate constant associated with $R_{AIV_m}^{(fi)}$ , for example: pdbSet GaAs Si VacIII kfFTM { {-2,-2} <n> ... {2,2} <n> }	$\text{cm}^{-3}/\text{s}$
$k_{AVY_m}^{(fi)}$	Reaction rate constant associated with $R_{AVY_m}^{(fi)}$ , for example: pdbSet GaAs Si Gallium kfFTM { {-2,-2} <n> ... {2,2} <n> }	$\text{cm}^{-3}/\text{s}$
$r_{IIIV}$	Ratio of the substitutional concentration at group III lattice sites to group V sites in intrinsic equilibrium. $r_{IIIV} \equiv (A_{III,s}/A_{V,s})_i^*$ . Applies only to group IV dopants. For example: pdbSet GaAs Si Csub.Ratio {<n>}	Unitless

## Fermi Model

The point-defect concentrations are assumed to be at thermal equilibrium:

$$\frac{\partial A}{\partial t} = \sum_m \nabla \cdot \left( (D_{I_m} + D_{V_m}) \eta^{-z_m} \nabla (A_{m,s} \eta^{z_m}) \right) \quad (330)$$

where:

$$A_{III,s} = \frac{\eta^{-1}}{\eta^{-1} + \eta^1 / r_{IIIV}} A_s \quad (331)$$

$$A_{V,s} = \frac{\eta^1}{r_{IIIV} \eta^{-1} + \eta^1} A_s \quad (332)$$

## Constant Model

The point-defect concentrations are assumed to be at intrinsic equilibrium:

$$\frac{\partial A}{\partial t} = \sum_m \nabla \cdot (D^* \nabla (A_{m,s})) \quad (333)$$

where:

$$A_{III,s} = \frac{1}{1 + 1/r_{IIIV}} A_s \quad (334)$$

$$A_{V,s} = \frac{1}{r_{IIIV} + 1} A_s \quad (335)$$

---

## Activation Model

The solid solubility model can be specified. For more information, see [Dopant Active Model: Solid](#) on page 280.

For group IV dopants, the amount of substitutional concentration on group III and group V sites is reduced by the ratio of a given parameter `Csub.Clust.Ratio` to the clustering concentration, respectively:

$$A_{III,s}^+ = A_{III,s} - \frac{1}{1 + 1/C_{\text{sub.Clust.Ratio}}} (A_s - A_s^+) \quad (336)$$

#### 4: Diffusion

Diffusion in III-V Compounds

$$A_{V,s}^+ = A_{V,s} - \frac{1}{\text{Csub.Clust.Ratio} + 1} (A_s - A_s^+) \quad (337)$$

### Point-Defect Diffusion

$$\frac{\partial Y_m}{\partial t} = \nabla \cdot \left( \left( \sum_j d_{Y_m,j} Y_{m,i}^* \phi_{Y_{mj}} \eta^{-j} \right) \nabla \left( \frac{Y_m}{Y_m^*} \right) \right) - R_{YV_m} - \sum_{Y'_m} R_{YY'_m} - \sum_A (R_{AY_m}^{(ko)} + R_{AV_{Y_m}}^{(ft)}) \quad (338)$$

$$\frac{\partial V_m}{\partial t} = \nabla \cdot \left( \left( \sum_j d_{V_m,j} V_{m,i}^* \phi_{V_{mj}} \eta^{-j} \right) \nabla \left( \frac{V_m}{V_m^*} \right) \right) - \sum_{Y_m} R_{YV_m} - \sum_A (R_{AV_m}^{(ko)} + R_{AV_{V_m}}^{(ft)}) \quad (339)$$

$$\frac{\partial Y_{m,s}}{\partial t} = R_{YV_m} + \sum_{Y'_m} R_{YY'_m} + \sum_A (R_{AY_m}^{(ko)} + R_{AV_{Y_m}}^{(ft)}) \quad (340)$$

where:

$$R_{YV_m} = \left( \sum_{j,k} k_{YV_{mj}} (Y_{m,i}^* \phi_{Y_{mj}}) (V_{m,i}^* \phi_{V_{mk}}) \eta^{-(j+k)} \right) \left( \frac{Y_m}{Y_m^*} \frac{V_m}{V_m^*} - \frac{Y_{m,s}}{Y_{m,s}^*} \right) \quad (341)$$

$$R_{YY'_m} = \left( \sum_j k_{YY'_{mj}} Y'_{m,s} (Y_{m,i}^* \phi_{Y_{mj}}) \eta^{-j} \right) \left( \frac{Y_m}{Y_m^*} \frac{Y'_{m,s}}{Y'_{m,s}^*} - \frac{Y'_m}{Y'_m^*} \frac{Y_{m,s}}{Y_{m,s}^*} \right) \quad (342)$$

$$Y_m^* = \sum_j Y_{m,i}^* \phi_{Y_{mj}} \eta^{-j} \quad (343)$$

$$V_m^* = \sum_j V_{m,i}^* \phi_{V_{mj}} \eta^{-j} \quad (344)$$

Table 21 Description of symbols for the pair diffusion model

Symbol	Description	Unit
$m$	The Mendeleev group number of a constituent atom of III-V material, $m \in \{III, V\}$ .	Unitless
$Y_m$	Self-interstitial concentration. For example, $Y_{III}$ is GaInt or InInt, and $Y_V$ is AsInt in InGaAs.	$\text{cm}^{-3}$
$Y_{m,s}$	Constituent atom concentration. For example, $Y_{III,s}$ is Gallium or Indium, and $Y_V$ is Arsenic in InGaAs.	$\text{cm}^{-3}$



Table 21 Description of symbols for the pair diffusion model

Symbol	Description	Unit
$Y_m^*$	Self-interstitial concentration in equilibrium (Eq. 343, p. 262).	$\text{cm}^{-3}$
$Y_{m,i}^*$	Self-interstitial concentration in intrinsic equilibrium: pdbSet InGaAs GaInt Cstar {<n>}	$\text{cm}^{-3}$
$Y_{m,s}^*$	Constituent atom concentration in equilibrium: pdbSet InGaAs Gallium CsubStar {<n>}	$\text{cm}^{-3}$
$\phi_{Y_m}$	Charge-state fractions of self-interstitials: $\phi_{Y_{mj}} = \phi_{Y_{mj}'} / \sum_j \phi_{Y_{mj}'}$ . $\phi_{Y_{mj}'}$ is specified, for example, by: pdbSet GaAs GaInt ChargeStates { -2 <n> ... 2 <n> }	Unitless
$V_m$	Vacancy concentration. $V_{III}$ is VacIII and $V_V$ is VacV.	$\text{cm}^{-3}$
$V_m^*$	Vacancy concentration in equilibrium (Eq. 344, p. 262).	$\text{cm}^{-3}$
$V_{m,i}^*$	Vacancy concentration in intrinsic equilibrium: pdbSet GaAs VacIII Cstar {<n>}	$\text{cm}^{-3}$
$\phi_{V_m}$	Charge-state fractions of vacancies: $\phi_{V_{mj}} = \phi_{V_{mj}'} / \sum_j \phi_{V_{mj}'}$ . $\phi_{V_{mj}'}$ is specified, for example, by: pdbSet GaAs VacIII ChargeStates { -2 <n> ... 2 <n> }	Unitless
$d_{Y_m}$	Self-interstitial diffusivity: pdbSet InGaAs GaInt D { -2 <n> ... 2 <n> }	$\text{cm}^2/\text{s}$
$d_{V_m}$	Vacancy diffusivity: pdbSet GaAs VacIII D { -2 <n> ... 2 <n> }	$\text{cm}^2/\text{s}$
$\eta$	Ratio of electron concentration to intrinsic carrier concentration ( $n/n_i$ ).	Unitless
$R_{AY_m}^{(ko)}$	Kick-out reaction rate at which $Y_m$ kicks out $A_{m,s}$ , generates $AI_m$ , and increases the mole fraction of $Y$ . See Eq. 320, p. 258 for details.	$\text{cm}^{-3}/\text{s}$
$R_{AV_m}^{(ko)}$	Kick-out reaction rate at which $Y_m$ reacts with $A_{m,s}$ and generates a dopant–vacancy pair $AV_m$ . See Eq. 321, p. 258 for details.	$\text{cm}^{-3}/\text{s}$
$R_{AIV_m}^{(ft)}$	Frank–Turnbull reaction rate at which $AI_m$ reacts with $V_m$ and generates a substitutional dopant $A_{m,s}$ . See Eq. 322, p. 258 for details.	$\text{cm}^{-3}/\text{s}$
$R_{AVY_m}^{(ft)}$	Frank–Turnbull reaction rate at which $AV_m$ reacts with $Y_m$ , generates a substitutional dopant $A_{m,s}$ , and increases the mole fraction of $Y$ . See Eq. 323, p. 258 for details.	$\text{cm}^{-3}/\text{s}$
$R_{YV_m}$	Interstitial–vacancy bulk recombination rate for group $m$ .	$\text{cm}^{-3}/\text{s}$
$R_{YY'_m}$	Kick-out reaction rate at which $Y_m$ kicks out $Y'_{m,s}$ and occupies the lattice site by generating $Y'_m$ . The reaction increases the mole fraction of $Y$ but decreases that of $Y'$ .	$\text{cm}^{-3}/\text{s}$
$k_{YV_m}$	Reaction rate constant associated with $R_{YV_m}$ , for example: pdbSet GaAs GaInt KbulkChargeStates { -2 <n> ... 2 <n> }	$\text{cm}^{-3}/\text{s}$
$k_{YY'_m}$	Reaction rate constant associated with $R_{YY'_m}$ , for example: pdbSet InGaAs GaInt Indium kfKickOut { -2 <n> ... 2 <n> }	$\text{cm}^{-3}/\text{s}$

#### 4: Diffusion

##### Diffusion in III-V Compounds

---

## Poisson Equation

$$\begin{aligned} & \nabla \cdot (\epsilon_r \epsilon_0 \nabla (\psi - \theta)) \\ &= -q \left( p - n + \sum_A \sum_m (z_{Am} A_{m,s}) + \sum_A \sum_m \left( \left( \sum_j ((z_{Am} + j) \alpha_{AI_m, j} \eta^{-j}) \right) \frac{AI_m}{\alpha_{AI_m}} + \left( \sum_j ((z_{Am} + j) \alpha_{AV_m, j} \eta^{-j}) \right) \frac{AV_m}{\alpha_{AV_m}} \right) \right. \\ & \left. + \sum_m \left( \sum_{Y_m} \left( \sum_j j Y_{m,i} \phi_{Y_m, j} \eta^{-j} \right) \frac{Y_m}{Y_m^*} + \left( \sum_j j V_{m,i} \phi_{V_m, j} \eta^{-j} \right) \frac{V_m}{V_m^*} \right) \right) \end{aligned} \quad (345)$$

where:

$$q\theta = \chi + \frac{E_g}{2} + \frac{kT}{2} \ln \left( \frac{N_c}{N_v} \right) \quad (346)$$

$$n = n_i \exp \left( \frac{q\psi}{kT} \right) \quad \text{and} \quad p = n_i \exp \left( -\frac{q\psi}{kT} \right) \quad (347)$$

$$N_c = N_{c300} \left( \frac{T}{300} \right)^{3/2} \quad (348)$$

$$N_v = N_{v300} \left( \frac{T}{300} \right)^{3/2} \quad (349)$$

$$n_i = \sqrt{N_c N_v} \exp \left( -\frac{E_g}{2kT} \right) \quad (350)$$

$$E_g = E_{g300} + E_g \alpha \left( \frac{300^2}{300 + \beta} - \frac{T^2}{T + \beta} \right) \quad (351)$$

Table 22 Description of symbols for Poisson equation

Symbol	Description	Unit
$n$	Electron concentration.	$\text{cm}^{-3}$
$p$	Hole concentration.	$\text{cm}^{-3}$
$n_i$	Intrinsic carrier concentration.	$\text{cm}^{-3}$
$q$	Electronic charge ( $1.609 \times 10^{-19}$ C).	C
$\psi$	Intrinsic Fermi potential.	V

Table 22 Description of symbols for Poisson equation

Symbol	Description	Unit
$\theta$	Band structure parameter.	V
$\epsilon_0$	Vacuum permittivity ( $8.854 \times 10^{-12}$ F/m).	F/m
$\epsilon_r$	Relative permittivity: pdbSet <material> Potential Permittivity {<n>}	Unitless
$\eta$	Ratio of electron concentration to intrinsic carrier concentration ( $n/n_i$ ).	Unitless
$\chi$	Affinity that depends on the mole fraction $x$ . If Affinity is specified on the material, then $\chi = \text{Affinity} + \text{Affinity.X1} \cdot x + \text{Affinity.X2} \cdot x(1-x)$ . Otherwise, $\chi = \chi_{\text{interpolated}} + \text{Affinity.X2} \cdot x(1-x)$ , where $\chi_{\text{interpolated}}$ is calculated by <a href="#">Physical Parameter Interpolation on page 256</a> . pdbSet <material> Potential Affinity {<n>} pdbSet <material> Potential Affinity.X1 {<n>} pdbSet <material> Potential Affinity.X2 {<n>}	eV
$E_g$	Band gap.	eV
$E_{g300}$	Band gap at 300 K, which depends on the mole fraction $x$ . If $E_{g300}$ is specified on the material, then $E_{g300} = E_{g300} + E_{g.X1} \cdot x + E_{g.X2} \cdot x(1-x)$ . Otherwise, $E_{g300} = E_{g300\text{interpolated}} + E_{g.X2} \cdot x(1-x)$ , where $E_{g300\text{interpolated}}$ is calculated by <a href="#">Physical Parameter Interpolation on page 256</a> . pdbSet <material> Potential Eg300 {<n>} pdbSet <material> Potential Eg.X1 {<n>} pdbSet <material> Potential Eg.X2 {<n>}	eV
$E_{g\alpha}$	Bandgap modification for temperature dependency: pdbSet <material> Potential Eg.Alpha {<n>}	eV
$\beta$	Temperature constant for band gap depending on temperature: pdbSet <material> Potential Eg.Beta {<n>}	K
$N_c$	Density-of-states of a conduction band.	$\text{cm}^{-3}$
$N_{c300}$	Density-of-states of a conduction band at 300 K: pdbSet <material> Potential Nc300 {<n>}	$\text{cm}^{-3}$
$N_v$	Density-of-states of a valence band.	$\text{cm}^{-3}$
$N_{v300}$	Density-of-states of a valence band at 300 K: pdbSet <material> Potential Nv300 {<n>}	$\text{cm}^{-3}$
$AI_m$	Dopant–group $m$ interstitial pair concentration.	$\text{cm}^{-3}$
$AV_m$	Dopant–group $m$ vacancy pair concentration.	$\text{cm}^{-3}$
$\alpha_{AI_m}$	Ratio of dopant–group $m$ interstitial pair concentration to substitutional concentration in equilibrium. See <a href="#">Eq. 324, p. 258</a> for details.	Unitless
$\alpha_{AV_m}$	Ratio of dopant–group $m$ vacancy pair concentration to substitutional concentration in equilibrium. See <a href="#">Eq. 325, p. 258</a> for details.	Unitless
$z_{Am}$	Charge of ionized substitutional atom at group $m$ lattice sites.	Unitless

---

## Pressure-dependent Defect Diffusion

Eq. 150, p. 203 shows that  $C_X^*$  depends on the Fermi level. However, you can select one of the available models (Constant, FermiLevelDependent, FermiPressureDependent) using the command:

```
pdbSet <material> <defect> CStarMod <model>
```

where `defect` is interstitial or vacancy, and `model` is one of the available models.

The Constant model simply sets  $C_X^*$  to  $C_{X(intrinsic)}$ , the FermiLevelDependent model is given in Eq. 150, and the FermiPressureDependent model includes both Fermi effects and pressure-field effects.

The pressure effects are modeled in Sentaurus Process by modifying the equilibrium point-defect concentrations:

$$C_X^* = C_X^*(Si, P \equiv 0) e^{-\frac{(\Delta V_X P)}{kT}} \quad (352)$$

where  $C_X^*$  is the total equilibrium concentration of point defect  $X$  (interstitial or vacancy).  $\Delta V_X$  is the activation volume change of equilibrium point defects due to the pressure  $P$  and is given by:

$$\Delta V_I = \varepsilon 4\pi r_o^3 \quad (353)$$

$$\Delta V_V = -2\pi r_s^2 3 \frac{(1-\eta)\Gamma}{1+\eta \mu} \quad (354)$$

where  $\varepsilon$  is the dilatation,  $r_o$  is the measure of the sphericity of the interstitial,  $r_s$  is the radius of the vacancy,  $\eta$  is the Poisson ratio of silicon,  $\Gamma$  is the surface tension of the vacancy, and  $\mu$  is the shear modulus of silicon. The following set of commands can be used to modify  $\Delta V_X$ :

```
pdbSet Silicon Interstitial Volume 8.59e-24
pdbSet Silicon Vacancy Volume -5.52e-24
```

The unit of Volume is  $\text{cm}^3$ .

## Electron Concentration

To calculate the electron concentration or, alternatively, the electron potential, Sentaurus Process solves either the Poisson equation or charge balance equation. By default, the ChargedReact, ChargedPair, and ChargedEquilibrium models all solve the charge balance equation. The uncharged models do not require a separate equation because the electron concentration can be computed directly from the net doping.

The Poisson equation is given by:

$$\nabla \cdot (\epsilon \nabla \psi) = -q(p - n + \Delta N) \quad (355)$$

where  $\epsilon$  is the permittivity,  $\psi$  is the potential,  $n$  and  $p$  are the electron and hole concentrations, and  $\Delta N$  is the net charge.

Electrons and holes are always assumed to be in equilibrium, such that:

$$pn = n_i^2 \quad (356)$$

The charge balance equation is:

$$-n + p + \Delta N = 0 \quad (357)$$

In [Eq. 355](#) and [Eq. 357](#), the  $\Delta N$  must be calculated. The net charge is given by:

$$\Delta N = \sum_j z_j C_{A_j}^+ + \sum_c c C_{X^c} + \sum_{X, c, j} (z_j + c) C_{A_j X}^{(c+z_j)} \quad (358)$$

where:

- $c$  is the charge state of the defect  $X$ , interstitial, or vacancy.
- $C_{X^c}$  is the concentration of the defect  $X$  in the charge state  $c$ .
- $z_j$  is the charge state of dopant  $A_j$ .
- $A_j X$  is the dopant  $A_j$  and defect  $X$  pair.

You can exclude or include the charged dopant–defect pairs or charged defects in [Eq. 358](#), for example:

```
pdbSet Si Dopant ChargeModel DopantOnly
pdbSet Si Dopant ChargeModel DopantDefect
```

The first command, which is the default behavior for dopants, includes only the charged dopants in silicon in [Eq. 358](#). The second command includes the charged dopants as well as the charged dopant–defect pairs in [Eq. 358](#).

## 4: Diffusion

### Electron Concentration

In a similar way:

```
pdbSet Si Defect ChargeModel None
pdbSet Si Defect ChargeModel Defect
```

The first command, which is the default behavior for defects, excludes the charged defects in silicon in [Eq. 358](#) and the second command includes them.

**NOTE** The diffusion models `Constant`, `Fermi`, `Pair`, and `React` always exclude the charged dopant–defect pairs.

The Poisson equation is switched on or off with the command:

```
pdbSet Si Potential Poisson 1 | 0
```

**NOTE** The above switch is used to switch from or to the Poisson equation to or from the charge balance equation.

If it is switched off, the charged defects and charged dopant–defect pairs are not included in [Eq. 358](#), and [Eq. 359](#) is used to calculate the potential:

$$\Psi = \frac{1}{V_{ii}} \log\left(\frac{1}{2n_i}(\Delta N + \sqrt{\Delta N^2 + 4n_i^2})\right) \quad (359)$$

where  $V_{ii}$  is  $1/kT$ , and  $n_i$  is the intrinsic concentration of electrons and can be set using the command:

```
pdbSet <material> Potential ni {<n>}
```

To switch on or off the solution of the Poisson equation or the charge balance equation, regardless of the diffusion model selected, use the commands:

```
pdbSetBoolean Potential ForcedTurnOff 0/1
pdbSetBoolean Potential ForcedTurnOn 1/0
```

**NOTE** If the potential equation is switched off, charge neutrality is assumed. If the selected diffusion or cluster models use complex charges, this may lead to instability in the code.

---

## Bandgap Narrowing

If bandgap narrowing effects need to be considered, Sentaurus Process uses the effective intrinsic electron density,  $n_{ie}$ , instead of  $n_i$ .  $n_{ie}$  is given by:

$$n_{ie} = n_i e^{\frac{\Delta E_g}{2kT}} \quad (360)$$

where  $\Delta E_g$  is the reduction in the bandgap energy of silicon and is defined as:

$$\Delta E_g = \Delta E_{gu} + \Delta E_{gs} \quad (361)$$

where  $\Delta E_{gu}$  is the user-defined bandgap narrowing and can be set using the command:

```
pdbSet <material> Potential delEg {<n>}
```

$\Delta E_{gs}$  is the bandgap narrowing due to strain in the structure. To switch on this effect, the intrinsic electron density model (niMod) must be set to StrainDependent. To select the model, use:

```
pdbSet <material> Potential niMod <model>
```

niMod can have either the value Constant or StrainDependent. The Constant model will ignore  $\Delta E_{gs}$ .

If the StrainDependent model is selected,  $\Delta E_{gs}$  will be calculated [25] using:

$$\Delta E_{ci} = D_{ci}(\epsilon_{xx} + \epsilon_{yy} + \epsilon_{zz}) + D_{cxi}\epsilon_{xx} + D_{cxi}\epsilon_{yy} + D_{czi}\epsilon_{zz} \quad (362)$$

$$\Delta E_{vi} = D_{vi}(\epsilon_{xx} + \epsilon_{yy} + \epsilon_{zz}) \pm \sqrt{(0.5D_{vbi}^2((\epsilon_{xx} - \epsilon_{yy})^2 + (\epsilon_{yy} - \epsilon_{zz})^2 + (\epsilon_{zz} - \epsilon_{xx})^2) + D_{vdi}^2(\epsilon_{xy}^2 + \epsilon_{xz}^2 + \epsilon_{yz}^2))} \quad (363)$$

where  $\epsilon$  is the strain in the respected direction, and  $D_{ci}$ ,  $D_{vi}$  are the dilatational deformation potentials for the conduction and valence band valleys, respectively.

They can be set using the commands:

```
pdbSet Silicon Potential Ec Dilatational {
    1 -8.6
    2 -8.6
    3 -8.6
}
pdbSet Silicon Potential Ev Dilatational {
    1 -2.1
    2 -2.1
}
```

$D_{cxi}$ ,  $D_{cxi}$ ,  $D_{cxi}$  and  $D_{vbi}$ ,  $D_{vdi}$  are the deviatoric deformation potential of conduction and valence band valleys. They can be set using the commands:

```
pdbSet Si Potential Ec Deviatoric(1) {
    1 9.5
    2 0.0
    3 0.0
}
```

## 4: Diffusion

### Epitaxy

```
pdbSet Si Potential Ec Deviatoric(2) {
    1 0.0
    2 9.5
    3 0.0
}
pdbSet Si Potential Ec Deviatoric(3) {
    1 0.0
    2 0.0
    3 9.5
}
pdbSet Si Potential Ev Deviatoric(1) {
    1 0.5
    2 4.0
}
pdbSet Si Potential Ev Deviatoric(2) {
    1 0.5
    2 4.0
}
}
```

Sentaurus Process uses the averaged values of conduction and valence bands energies,  $\Delta E_{ci}, \Delta E_{vi}$ :

$$\Delta E_c = -kT \log \left( \frac{1}{3} \sum_{i=1}^3 e^{-\frac{\Delta E_{ci}}{kT}} \right) \quad (364)$$

$$\Delta E_v = kT \log \left( \frac{1}{2} \sum_{i=1}^2 e^{\frac{\Delta E_{vi}}{kT}} \right) \quad (365)$$

The bandgap narrowing becomes:

$$\Delta E_{gs} = \Delta E_c - \Delta E_v \quad (366)$$

**NOTE**  $\Delta E_{gs}$  is ignored where  $\frac{\text{Germanium}}{5e22} > 0.1\%$  (see [Dopant Diffusion in SiGe on page 250](#)).

---

## Epitaxy

Epitaxial growth is simulated when an Epi type ambient is specified on either the diffuse command or in a temp\_ramp ramp used by the diffuse command.

By default, two Epi type ambients are available: one is called Epi and the other is called LTE. If Epi is specified, Silicon will grow on Silicon and PolySilicon will grow on



PolySilicon. If the LTE ambient is specified, Silicon will again grow on Silicon, but PolySilicon will grow on Oxide, Nitride, and PolySilicon. The layer thickness is specified with the `thick` parameter and doping is specified with the `epi.doping` parameter.

Epitaxy is solved using the Alagator general growth scheme (see [Alagator for Generic Growth on page 584](#)). This allows the creation of new epi growth modes (that is, specifying which materials grow) and material-dependent growth rates.

An unlimited number of species can be incorporated into the epitaxial layer. Doping is specified using the `epi.doping` and `epi.doping.final` parameters in either the `diffuse` command or a `temp_ramp` included in a `diffuse` command. The parameters `<material> <solution> Cepi0` and `<material> <solution> CepiE` set the default value of fields in the growing material. The defaults are overwritten by setting the `epi.doping` and `epi.doping.final` parameters of the `diffuse` or `temp_ramp` commands. The same set of equations as for the single-crystalline silicon is solved for the epitaxial silicon during the diffusion step simulation. If the growth temperature goes below the minimum diffusion temperature, the diffusion equations will be switched off, but the boundary conditions for dopant incorporation will be applied. The Continuous boundary condition is applied to all the mobile species at the interface between the epitaxial layer and single-crystalline silicon to take into account the variable jump.

It is also possible to incorporate the auto-doping of dopants during the epitaxial growth using the `auto.doping` parameter in either the `diffuse` command or a `temp_ramp` included in a `diffuse` command. Auto-doping can be switched on only for dopants that are not listed in the `epi.doping` or `epi.doping.final` parameters (see [Epi Auto-Doping on page 272](#)).

In certain examples, it is easier to specify resistivity to obtain the required doping concentration in the epi layer. The resistivity can be specified using the `epi.resist` parameter in either the `diffuse` command or a `temp_ramp` included in a `diffuse` command.

Two different methods can be selected to simulate the epitaxial growth. The `epi.model` parameter of the `diffuse` command is used to switch between them:

- If `epi.model=0` (default), a moving-boundary algorithm similar to the oxidation one is applied.
- If `epi.model=1`, alternating doped deposition and inert annealing steps are used. Model 1 supports selective epitaxy, graded doping, and material-dependent growth rates, and can be used with both the Sentaurus Structure Editor and MGOALS3D modes. Furthermore, for 3D epitaxy, Model 1 is recommended because of the computational time and reliability issues related to moving boundaries (Model 0) in 3D.

To set the grid spacing, use the `epi.layers` parameter. This sets the number of grid layers that are deposited during the corresponding `diffuse` or `temp_ramp` steps.

**NOTE** Model 1 is recommended for 3D epitaxy and can be used with 2D.

---

## Epi Doping

Two parameters of the `diffuse` and `temp_ramp` commands are used to control doping: `epi.doping` and `epi.doping.final`. Both parameters take a list of parameters, that is, dopant and field names, as their arguments.

If a dopant or field name appears in only one of the lists or in both of the lists with the same value, the value of the doping is constant throughout the step. If the dopant or field appears in both lists with different values, a linear gradient of the doping is applied. For example:

```
temp_ramp name=t1 temperature=550 t.final=700 time=1<min>
temp_ramp name=t1 t.final=700 time=5<min> Epi thick=0.1<um> \
  epi.doping = { Boron=1e18 Germanium=1e21 } \
  epi.doping.final = { Germanium=5e21 }
diffuse temp.ramp=t1
```

In this example, epitaxy is simulated after an inert temperature ramp. During epitaxy, the boron concentration is a constant  $10^{18} \text{ cm}^{-3}$ , and germanium is ramped from  $10^{21} \text{ cm}^{-3}$  to  $5 \times 10^{21} \text{ cm}^{-3}$ . In addition, all these parameters can be set in the `diffuse` command, for example:

```
diffuse temperature=700 time=5<min> LTE \
  epi.doping.final = { Arsenic=1e18 } thick = 0.1<um>
```

In this case, a constant arsenic doping of  $10^{18} \text{ cm}^{-3}$  is applied to an LTE epitaxial growth.

---

## Epi Auto-Doping

The `auto.doping` parameter of the `diffuse` and `temp_ramp` commands controls doping. The parameter takes a list of parameters, that is, dopant and field names, as its arguments. If a dopant or field name appears in `auto.doping` and in either `epi.doping` or `epi.doping.final`, auto-doping of this dopant is ignored. For example:

```
temp_ramp name=t1 temperature=550 t.final=700 time=1<min>
temp_ramp name=t1 t.final=700 time=5<min> Epi thick=0.1<um> \
  auto.doping = { Boron Germanium } epi.doping = { Germanium=1e21 } \
diffuse temp.ramp=t1
```

In this example, only auto-doping of boron is simulated. The parameter `auto.doping` switches on the following model automatically at Gas and epitaxially grown material interface:

$$\mathbf{j} \cdot \mathbf{n} = k_{Transfer} \left( \left( C_A^* e^{-\frac{k_{Decay} \Delta t}{t}} + C_A^{min} \right) - \frac{C_A}{k_{Segregation}} \right) \quad (367)$$

where  $k_{Transfer}$  is the transfer rate,  $k_{Segregation}$  is the segregation rate,  $C_A^*$  is the peak value of the dopant concentration in the auto-doped region,  $C_A^{min}$  is the minimum value of the dopant concentration,  $k_{Decay}$  is the decay rate of the auto-doping, and  $C_A$  is the dopant concentration. These parameters can be modified using the commands:

```

pdbSet <interface material> <dopant> TransferAutoDoping <n>
pdbSet <interface material> <dopant> SegregationAutoDoping <n>
pdbSet <interface material> <dopant> Cstar <n>
pdbSet <interface material> <dopant> minConc <n>
pdbSet <interface material> <dopant> DecayRate <n>

```

where <interface material> is the Gas and epitaxially grown material interface. In Eq. 367,  $\Delta t$  is the percentage of the simulation time since the diffusion started, and  $t$  is the total simulation time from the beginning to the end of diffusion. Eq. 367 is created automatically and stored in a term called <dopant>AutoDoping. You can overwrite this by defining your own reactions.

For example:

```

term name=BoronAutoDoping EpiOnSilicon /Gas add eqn = \
"1e-3*(1e16-Boron_EpiOnSilicon/0.1)"

```

**NOTE** Since the model does not solve equations in gas, the dose loss or gain of the dopant is expected.

---

## Epi Doping Using Resistivity

The `epi.resist` parameter of the `diffuse` and `temp_ramp` commands controls doping. The parameter takes a list of parameters, that is, dopant name and resistivity, as its argument.

If more than one dopant name appears in the list, the doping concentration is calculated individually for each dopant by ignoring the other ones. For example:

```

temp_ramp name=t1 temperature=550 t.final=700 time=1<min>
temp_ramp name=t1 t.final=700 time=5<min> Epi thick=0.1<um> \
epi.resist= { Arsenic=1e-2 Phosphorus=2e-3 }
diffuse temp.ramp=t1

```

In this example, epitaxy is simulated after an inert temperature ramp. During epitaxy, the arsenic concentration is a constant  $4.3 \times 10^{19} \text{ cm}^{-3}$  and the phosphorus concentration is  $9.7 \times 10^{19} \text{ cm}^{-3}$ . In addition, all of these parameters can be set in the `diffuse` command, for example:

```

diffuse temperature=700 time=5<min> LTE \
epi.resist= { Arsenic=1e-2 Phosphorus=2e-3 } thick= 0.1<um>

```

The doping concentration calculations use the silicon-based mobility models (see [Resistivity on page 832](#)).

---

## Epi Growth Settings: Low-Temperature Epitaxy

Several parameters are available to allow for the simulation of effects seen in low-temperature epitaxy (LTE). LTE growth can result in the growth of polysilicon on insulators such as oxide and nitride after a seed layer has nucleated. In addition, the growth rate may depend on the starting material where the growth is occurring. To allow different growth rates and nucleation times, Sentaurus Process uses temporary materials with distinct names that are converted back to standard names at the end of the diffusion command. For example, during LTE, `LTEOnOxide` is grown on oxide, and `LTEOnSilicon` is grown on silicon (there are also the materials `LTEOnPolySilicon` and `LTEOnNitride`). After the diffusion step is complete, `LTEOnOxide` is converted to `PolySilicon`, and `LTEOnSilicon` is converted to `Silicon`. In addition, be aware that after material conversion, regions will merge if there are interfaces with the same material on both sides.

To set the nucleation delay for LTE growth on oxide, use:

```
pdbSet Gas_<starting material> <ambient> NucleationDelay <n>
```

where `<n>` is in seconds. For the case of `LTEOnOxide`, `<starting material>` is `Oxide` and `<ambient>` is `LTE`.

**NOTE** The *exposure time* is not saved, so nucleation must happen within one diffuse command (use the `temp_ramp` command to create long diffusion steps with optional ramp-up or ramp-down).

The growth rate for all materials is determined by default from the native layer thickness as well as the `thick` and `time` parameters of the `diffuse` or `temp_ramp` commands. However, the growth rate can be set manually using a callback procedure like this:

```
pdbSet <growing material>_Gas <ambient> GrowthRateProc <proc name>
```

Inside `<proc name>`, you should set the `pdb` parameter `GrowthReaction`. For example:

```
pdbSet Gas_LTEOnOxide LTE GrowthRateProc MyGRProc
proc MyGrProc { Mat Sol } {
    set myGrowthRate 1.0e-7           ;# in cm/s
    pdbSetString $Mat $Sol GrowthReaction "$myGrowthRate"
}
```

It is possible to set `GrowthReaction` to any Alagator expression not involving derivative expressions or element values.

---

## Simulating Facet Growth during Selective Epitaxy

There are two ways to switch on faceting:

- Using the `angles.factors` parameter of the `temp_ramp` (or `diffuse`) command.
- Using the PDB parameter `<epimat gas interface> angles.factors` along with setting the parameter `pdbSet Grid AnisotropicGrowth 1`.

The syntax for both `angles.factors` parameters is similar:

```
temp_ramp angles.factors= {
  <interface material1>= { angle1(degrees) factor1(unitless) \
                          angle2 factor2 ...} \
  <interface material2> = ... \
}
```

or:

```
pdbSet <interface material> angles.factors {
  angle1(degrees) factor1(unitless) angle2 factor2 ...
}
```

where the interface material would be, for example, `EpiOnSilicon_Gas` for epi growth on silicon and `Gas_LTEOnSilicon` for LTE on silicon. There are aliases for all materials, so the order of the interface materials is not important.

**NOTE** Facet growth is only available with `epi.model=0`.

To form facets, a large range of degrees near 0 that have a factor of 1.0 is needed. For larger angles, the factor should monotonously decrease to 0 at the required facet angle. For example, to form 35° facets during epi on silicon, the following setting could be used:

```
temp_ramp thick=<thick> epi time=<time> temperature=<temp> epi.layers=<nlay> \
  angles.factors = {
    EpiOnSilicon_Gas = { 0.0 1.0 20.0 1.0 35.0 0.0 }
  }
```

## Controlling Where Facets Form

By default, facets form at all triple points. To switch off these facets, use:

```
pdbSet AnisoGrowthTriplePoints 0
```

By default, facets will not form on the outer boundaries. To switch on faceting on the outer boundary, use:

```
pdbSet AnisoGrowOuterBoundaries 1
```

## 4: Diffusion

### Other Effects on Dopant Diffusion

## Time-stepping

This algorithm and anisotropic growth in general can be inherently unstable. If a ‘bump’ develops during growth, it may persist or perhaps even grow larger. To prevent bumps from forming, it is necessary to take small time steps. The parameter `dThicknessAnisoGrowth` can be used to control time-stepping during anisotropic growth. It sets a maximum thickness per time step:

```
pdbSet Diffuse dThicknessAnisoGrowth <thickness in um> #; default 0.001um
```

---

## Other Effects on Dopant Diffusion

---

### Pressure-dependent Dopant Diffusion

Dopant diffusivities can be enhanced or retarded due to stress or pressure. In addition to this, shrinking device dimensions can cause significant stress or pressure gradients affecting dopant diffusion further [25]. With this model, Sentaurus Process allows diffusivities and gradients to be multiplied by user-defined factors as follows:

$$j = -DD_{SS}\nabla\frac{C}{D_{SP}} \quad (368)$$

where  $C$  is the concentration,  $D$  is the diffusivity, and  $D_{SS}$  and  $D_{SP}$  are user-definable terms. You can define both factors. To switch the model on or off, use the command:

```
pdbSet <material> <dopant> StressModel <model>
```

where `model` is `None` (off, default value) or `PDependent` (on).

For the definition of terms, see [Chapter 6 on page 559](#).

For example, in the case of specified boron in silicon, this is given by:

```
term name=BoronIntSSFactor add Silicon eqn = {User defined equation}
term name=BoronIntSPFactor add Silicon eqn = {User defined equation}
```

To allow Sentaurus Process to use these terms, specify a term with the name `<dopant><defect>SSFactor` or `<dopant><defect>SPFactor`.

If the model is switched on and you do not provide the terms,  $D_{SS}$  and  $D_{SP}$  are calculated as:

$$D_{SS} = e^{-\frac{(\Delta V_V P)}{kT}} \quad (369)$$

$$D_{SP} = e^{-\frac{(\Delta V_S P)}{kT}} \quad (370)$$

where  $\Delta V_V$  and  $\Delta V_S$  are activation volumes and can be set using the commands:

```
pdbSet <material> <dopant> <defect> delVolV {<n>}
pdbSet <material> <dopant> <defect> delVolS {<n>}
```

---

## Diffusion Prefactors

Dopant diffusivities can be enhanced or retarded due to various new process conditions. If a new model does not exist to simulate the observed behavior, you may want to multiply the existing diffusivity with a prefactor. Sentaurus Process allows diffusivities to be multiplied by user-defined factors as follows:

$$j = -DD_F \nabla C \quad (371)$$

where  $C$  is the concentration,  $D$  is the diffusivity, and  $D_F$  is the diffusion prefactor. For example, in the case of specified boron in silicon, this is given by:

```
term name=BoronDiffFactor add Silicon eqn = "exp(0.042 * $Vti * 125 * \
Germanium / 5e22)"
```

The effective diffusivity of boron ( $D_B = D_{BI} + D_{BV}$ ) will be multiplied by `BoronDiffFactor`. (For the definition of terms, see [Using Terms on page 568](#).) Sentaurus Process also allows each dopant–defect diffusivity to be multiplied by a different user-defined factor:

$$j = -(D_{CI}D_{IF} + D_{CV}D_{VF})\nabla C \quad (372)$$

where  $D_{CI}$  is the diffusivity of the dopant–interstitial pair,  $D_{CV}$  is the diffusivity of the dopant–vacancy pair, and  $D_{IF}$  and  $D_{VF}$  are the diffusion prefactors for each dopant–defect pair. For example:

```
term name=BoronIntDiffFactor add Silicon eqn = "exp(0.042 * $Vti * 125 * \
Germanium / 5e22)"
term name=BoronVacDiffFactor add Silicon eqn = "exp(0.042 * $Vti * 25 * \
Germanium / 5e22)"
```

In this example, diffusivity of boron–interstitial pairs ( $D_{BI}$ ) and the diffusivity of boron–vacancy pairs ( $D_{BV}$ ) will be multiplied by `BoronIntDiffFactor` and `BoronVacDiffFactor`, respectively.

To allow Sentaurus Process to use these terms, specify a term with the name `<dopant>DiffFactor` or `<dopant><defect>DiffFactor`.

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### Other Effects on Dopant Diffusion

Anisotropic (optionally stress-dependent) diffusivities can be specified using the diffusion prefactors as well. To do this, the `diag` operator must be used when specifying the diffusion prefactor. For more information, see [Special Functions on page 561](#).

---

## High-Concentration Effects on Dopant Diffusion

To model experimentally observed sharp increases in arsenic diffusion in silicon at high dopant concentrations, diffusivity coefficients must be modified. Dunham and Wu [26] proposed that interactions of vacancies with more than one dopant result in the enhancement of dopant–vacancy pair diffusivity by a factor:

$$j = -DD_F \nabla C \quad (373)$$

$$D_F = 1 + \left( \frac{C_A}{C_{ref}} \right)^{C_{pow}} \quad (374)$$

where  $C_{As}$  is the active concentration of arsenic, and  $C_{ref} \sim 2 \times 10^{20} \text{ cm}^{-3}$  and  $C_{pow} \sim 4$  for arsenic. The correction factor can be applied to all dopant–defect pairs as long as the parameters are supplied. The model can be switched on with the command:

```
pdbSet <material> <dopant> <defect> HighConcDiffEffect 1
```

The default of the model is off (0). The model parameters are set using the command:

```
pdbSet <material> <dopant> <defect> Cref {<n>}  
pdbSet <material> <dopant> <defect> Cpow {<n>}
```

For example:

```
pdbSet Silicon Arsenic Vacancy Cref 1.6e20  
pdbSet Silicon Arsenic Vacancy Cpow 4.0
```

---

## Hydrogen Effects on Dopant Diffusion

To model experimentally observed sharp increases in boron diffusion in oxide at the presence of hydrogen, diffusivity coefficients of boron must be modified. Chakravarthi *et al.* [27] proposed that the presence of hydrogen results in the enhancement of boron diffusivity by the following factor:

$$j = -DD_F \nabla C \quad (375)$$

$$D_F = 1 + \left( \frac{C_H}{C_{ref}} \right)^{C_{pow}} \quad (376)$$



where  $C_H$  is the active concentration of hydrogen, and  $C_{ref} \sim 1 \times 10^{15} \text{ cm}^{-3}$  and  $C_{pow} \sim 1$  for boron. If hydrogen is present in the structure, the enhancement factor for boron will be applied automatically.

The model parameters are set using the command:

```
pdbSet <material> Hydrogen <dopant> Cref {<n>}  
pdbSet <material> Hydrogen <dopant> Cpow {<n>}
```

For example:

```
pdbSet Oxide Hydrogen Boron Cref 1.6e20  
pdbSet OxideHydrogen Boron Cpow 4.0
```

The correction factor can be applied to other dopants if the dopant is given in the dopant list using the command:

```
pdbSet <material> Hydrogen Dopants <list>
```

where <list> is the list of dopants. For example:

```
pdbSet Oxide Hydrogen Dopants "Boron Arsenic"
```

The diffusion of hydrogen itself is modeled using the constant diffusion model (see [Constant Diffusion Model on page 212](#)).

---

## Dopant Activation and Clustering

It is possible to select a different clustering or activation model for each dopant in different materials with the command:

```
pdbSet <material> <dopant> ActiveModel <model>
```

where <dopant> is a valid dopant name and <model> is one of the valid active models (None, Solid, Transient, Cluster, ChargedCluster, BIC, FVCluster, or Equilibrium).

**NOTE** BIC is valid only for boron and is not recommended because the ChargedCluster model is better suited for modeling boron-interstitial clusters. FVCluster is valid only for fluorine.

---

### Dopant Active Model: None

If ActiveModel is set to None, all dopants are assumed to be active. No solid solubility or dopant clustering effects will be taken into account for dopant activation.

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### Dopant Activation and Clustering

---

## Dopant Active Model: Solid

If `ActiveModel` is set to `Solid`, a simple solid solubility for the dopant activation is considered:

$$C_A^+ = \frac{C_A^{SS} C_A}{(C_A^{SS} + C_A)} \quad (377)$$

$C_A^{SS}$  is calculated by:

$$C_A^{SS} = f \cdot C_A^{SS0} \quad (378)$$

where  $f$  is the multiplication factor that is defined by:

```
pdbSet <material> <dopant> SS.Factor <expression>
```

and the solid solubility  $C_A^{SS0}$  of the dopant  $A$  that can be set with:

```
pdbSet <material> <dopant> Solubility {<n>}
```

when `SS.Model` is set to `Analytic`. However, when `SS.Model` is set to `Table`, the solid solubility is taken from the temperature-versus-solid solubility table.

The `SS.Model` is defined by:

```
pdbSet <material> <dopant> SS.Model <Analytic or Table>
```

The temperature-versus-solid solubility table is defined by:

```
pdbSet <material> <dopant> SS.Table <temp1 ss1 temp2 ss2 ... temp# ss#>
```

With the table, the solid solubility for the given temperature is logarithmically interpolated or extrapolated when the given temperature is out of range.

---

## Dopant Active Model: Precipitation

Setting `ActiveModel` to `Precipitation` or setting `ActiveModel` to the other activation model the list of `More.Active.Model.List` including `Precipitation` solves the transient equation:

$$\frac{\partial C_{AppI}}{\partial t} = -\frac{C_{AppI} - C_{AppI}^*}{\tau_{AppI}} \quad (379)$$

with the constraint:

$$0.0 \leq C_{Apprt} \leq \max(C_A - \sum nC_{ACl} - C_{Amin}^+, 0.0) \quad (380)$$

$C_{Apprt}$  is the precipitates concentration of the dopant and  $C_{Apprt}^*$  is the equilibrium precipitates concentration given by:

$$C_{Apprt}^* = C_A - \sum nC_{ACl} - C_{AEq} \quad (381)$$

where:

- $C_A$  is the total chemical concentration.
- $\sum nC_{ACl}$  represents the total dopant concentration in other clusters than precipitates.
- $C_{AEq}$  is the equilibrium active concentration calculated by [Dopant Active Model: Equilibrium on page 293](#).

$\sum nC_{ACl}$  in Eq. 380 and Eq. 381 are included only when the other clustering model is invoked with the list of `More.Active.Model.List`, for example:

```
pdbSet Si Boron More.Active.Model.List { Precipitation }
pdbSet Si Boron ActiveModel Transient
```

The time constant  $\tau_{Apprt}$  is given by:

$$\tau_{Apprt} = \text{ClusteringTime for } C_{Apprt} \leq C_{Apprt}^* \quad (382)$$

$$\tau_{Apprt} = \text{DeclusteringTime for } C_{Apprt} > C_{Apprt}^* \quad (383)$$

The solution for  $C_{Apprt}$  is named with `<species name>Ppts`; for example, `BPpts` for boron precipitates. The parameters `ClusteringTime` and `DeclusteringTime` are defined for the precipitates in the material, for example:

```
pdbSet Silicon BPpts ClusteringTime {[Arr 8e-16 -4.2]}
pdbSet Silicon BPpts DeclusteringTime {[Arr 8e-16 -4.2]}
```

$C_{Amin}^+$  is the minimum active concentration defined by the parameter `MinimumActive`, for example:

```
pdbSetString Silicon Boron MinimumActive "0.0"
```

## Initializing Precipitation Model

The initialization of the precipitation concentration depends on the value of the parameters `AmInit` and `AcInit`. The initial level of active concentration in amorphized and crystalline

## 4: Diffusion

### Dopant Activation and Clustering

regions can be specified per dopant as `AmInit` and `AcInit`, respectively. You can specify the `AmInit` and `AcInit` parameters using:

```
pdbSet <material> <dopant> AcInit {<n>}
pdbSet <material> <dopant> AmInit {<n>}
```

If the `AcInit` parameter is not defined, the solid solubility of the dopant is used to calculate the `AcInit` parameter. If you want `AcInit` and `AmInit` to be a function of other fields for a specific dopant, define the terms `<dopant>AcInit` and `<dopant>AmInit` in your input files.

The precipitation model can be used with other activation models, for example:

```
pdbSet Si B ActiveModel BIC
pdbSet Si B More.Active.Model.List { Precipitation }
```

**NOTE** The items allowed in `More.Active.Model.List` are `Precipitation` or `ComplexCluster`. The equilibrium activation model cannot be used with the precipitation model.

When the precipitation model is invoked with other activation models, the initial concentrations of the clusters and the precipitates are set as follows.

In the amorphous region:

$$C_{Appt} = f_{Appt} \cdot \max(C_A - \text{AmInit}, 0.0) \quad (384)$$

$$C_{Aclust,i} = f_{Aclust,i} \cdot \max(C_A - \text{AmInit}, 0.0) \quad (385)$$

where the fraction ratio  $f_{Appt}$  for precipitation and  $f_{Aclust,i}$  for the cluster of other activation model  $i$  are written as:

$$f_{Appt} = \frac{\text{FractionAmor}_{ppt}}{\text{FractionAmor}_{ppt} + \text{FractionAmor}_{dopant} + \sum_i \text{FractionAmor}_i} \quad (386)$$

$$f_{Aclust,i} = \frac{\text{FractionAmor}_i}{\text{FractionAmor}_{ppt} + \text{FractionAmor}_{dopant} + \sum_i \text{FractionAmor}_i} \quad (387)$$

In the crystalline region:

$$\Delta C_{Appt} = f_{Appt} \cdot \max(C_{Aimplant} - \text{AcInit}, 0.0) \quad (388)$$

$$\Delta C_{Aclust,i} = f_{Aclust,i} \cdot \max(C_{Aimplant} - \text{AcInit}, 0.0) \quad (389)$$

where:

$$f_{Appt} = \frac{\text{FractionCryst}_{ppt}}{\text{FractionCryst}_{ppt} + \text{FractionCryst}_{dopant} + \sum_i \text{FractionCryst}_i} \quad (390)$$

$$f_{Aclust,i} = \frac{\text{FractionCryst}_i}{\text{FractionCryst}_{ppt} + \text{FractionCryst}_{dopant} + \sum_i \text{FractionCryst}_i} \quad (391)$$

The parameters `FractionAmor` and `FractionCryst` for the precipitation are written as:

```
pdbSet <material> <precipitates> FractionAmor <number>
pdbSet <material> <precipitates> FractionCryst <number>
```

---

## Dopant Active Model: Transient

If `ActiveModel` is set to `Transient`, a transient dopant-cluster model is used. The transient dopant cluster is more complicated than the simple, solid solubility model. The following set of equations is solved along with the appropriate diffusion model equations:

$$\frac{\partial C_{AC}}{\partial t} = k_f \left(\frac{n}{n_i}\right)^{k_c} \left(\frac{1}{1 \times 10^{18}}\right)^{k_c - 1 + l_c} n_i^{k_c} \left(K_{Ffwd} (C_A^+)^{l_c} - K_{Fbwd} k_b (n_{ss})^{z l_c} n_i^{-z l_c} C_{AC} \left(\frac{n}{n_i}\right)^{-z l_c}\right) \quad (392)$$

where:

- $k_f$  is the forward-clustering reaction rate.
- $k_b$  is the de-clustering rate.
- $C_A^+$  is the active dopant concentration.
- $C_{AC}$  is the concentration of clusters.
- $l_c$  is the number of substitutional dopants.
- $k_c$  is the number of electrons participating in the reaction.
- $n$  is the electron concentration.
- $n_i$  is the intrinsic electron concentration.
- $n_{ss}$  is the electron concentration assuming that the dopant  $A$  reached the limits of solid solubility.

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##### Dopant Activation and Clustering

These quantities can be set using the commands:

```
pdbSet <material> <dopant> Kc      {<n>}
pdbSet <material> <dopant> Lc      {<n>}
pdbSet <material> <dopant> KcEqu   {<n>}
pdbSet <material> <dopant> CluRate {<n>}
```

where  $K_{cEqu}$  and  $CluRate$  correspond to  $k_b$  and  $k_f$ . Initialization of transient dopant clusters is explained in [Ion Implantation to Diffusion on page 340](#). The default value of  $K_{cEqu}$  is calculated by using:

$$K_{cEqu} = l_c \left( \frac{C_{ss}^l}{C_{ssTot} - C_{ss}} \right) \quad (393)$$

where  $C_{ss}$  is the solid solubility of the unpaired dopant and  $C_{ssTot}$  is the solid solubility of total concentration of the dopant.  $K_{cEqu}$  can be set directly using the command:

```
pdbSet Silicon Arsenic KcEqu 1e66
```

or can be set indirectly using the commands:

```
pdbSet Silicon Arsenic Solubility 1e20
pdbSet Silicon Arsenic TotSolubility 1e21
```

and its modifying factors:

```
pdbSet Silicon Arsenic SS.Factor 1
pdbSet Silicon Arsenic Total.SS.Factor 1
```

In addition,  $K_{Ffwd}$  and  $K_{Fbwd}$  are forward and backward reaction factors, respectively. They can be defined as:

```
term name = <dopant>TClusterForwardFac <mater>
  eqn = { User defined equation }
term name = <dopant>TClusterBackwardFac <mayer>
  eqn = { User defined equation }
```

If they are not defined, their default value is 1.

Table 23 Solution names for transient model

Symbol	Boron	Arsenic	Phosphorus	Antimony	Indium
$C_{AC}$	B4	As3	P3	Sb3	In3

## Initializing Transient Model

If you switch on the transient dopant cluster model or cluster model, initialization of the dopant clusters is performed in the `diffPreProcess` procedure (see [Ion Implantation to Diffusion on page 340](#)). The initialization of the dopant-cluster concentration depends on the value of the parameters `AmInit` and `AcInit`. The initial level of active concentration in amorphized and crystalline regions can be specified per dopant as `AmInit` and `AcInit`, respectively.

You can specify the `AmInit` and `AcInit` parameters using:

```
pdbSet <material> <dopant> AcInit {<n>}
pdbSet <material> <dopant> AmInit {<n>}
```

If the `AcInit` parameter is not defined, the solid solubility of the dopant is used to calculate the `AcInit` parameter. If you want `AcInit` and `AmInit` to be a function of other fields for a specific dopant, define the terms `<dopant>AcInit` and `<dopant>AmInit` in your input files.

For example:

```
term name=ArsenicAcInit silicon add eqn = "Germanium/5e22 * [pdbDelayDouble
                                         Silicon Arsenic Solubility]"
term name=ArsenicAmInit silicon add eqn = "Germanium/5e22*1e19"
```

In this case `AcInit` and `AmInit` for arsenic are replaced with `ArsenicAcInit` and `ArsenicAmInit`.

If the dopant concentration is lower than `AcInit` in crystalline regions, dopants are considered to be active. If the dopant concentration is higher than `AcInit`, the number of active dopants is initially `AcInit`, and the concentration of clustered dopants is given by `Dopant - AcInit`. The following outlines the initialization of dopant clusters.

In crystalline regions:

$$\begin{aligned} \text{Dopant} &= \text{Dopant} + \min(\text{AcInit}, \text{Dopant\_Implant}) \\ \text{DopantCluster} &= \text{DopantCluster} + \text{Dopant\_Implant} - \min(\text{AcInit}, \text{Dopant\_Implant}) \end{aligned} \quad (394)$$

In amorphous regions:

$$\begin{aligned} \text{Dopant} &= \min(\text{AmInit}, \text{Dopant} + \text{DopantCluster} + \text{Dopant\_Implant}) \\ \text{DopantCluster} &= \text{Dopant} + \text{DopantCluster} + \text{Dopant\_Implant} \\ &\quad - \min(\text{AmInit}, \text{Dopant} + \text{DopantCluster} + \text{Dopant\_Implant}) \end{aligned} \quad (395)$$

where `Dopant` is the dopant name (for example, `Boron`, `B4`, and `Boron_Implant`). Smoothing also can be applied to dopant profiles using the parameter `AmorpGamma` (see [Ion Implantation to Diffusion on page 340](#)).

## Dopant Active Model: Cluster

If `ActiveModel` is set to `Cluster`, a dopant–defect cluster model is used. The model is primarily implemented to simulate arsenic–vacancy clusters, but if the model parameters are provided, it is possible to simulate other dopant–defect clusters.

The model assumes that arsenic–vacancy clusters are formed in silicon during arsenic deactivation [28][29]. It is also assumed that neutral clusters ( $As_mV_k$ ) are formed. Different charge states are taken into account by:



$$f = (m - kj)e, \text{ if } (kj - m) < 0 \quad (397)$$

$$f = (m - kj)h, \text{ if } (kj - m) \geq 0 \quad (398)$$

where  $j$  denotes interstitial charge,  $e$  and  $h$  are the electron and hole densities, and  $m$  and  $k$  are the dopant and defect sizes, respectively.

The following commands can be used to set the reacting defect species,  $m$  and  $k$ , respectively:

```
pdbSet <material> <dopant> ClusterDefects <c>
pdbSet <material> <dopant> <defect> ClusterSizes {{<n> <n>}}
```

for example:

```
pdbSet Silicon Arsenic ClusterDefects Vac
pdbSet Silicon Arsenic Vacancy ClusterSizes {{4 1}}
```

where 4 is the number of arsenic atoms in the cluster and 1 is the number of vacancies in the cluster. They form the  $As_4$ Vacancy clusters.

**NOTE** Cluster sizes are defined as  $\{i\ j\}$  where  $i$  and  $j$  are integers and are separated by a space.

The reaction rate for the cluster formation can be written as:

$$R_j \equiv K_{fj} C_{As}^m \left(\frac{n}{n_i}\right)^{m-kj} - K_{rj} C_{As_mV_k} C_{I^0} \left(\frac{n}{n_i}\right)^{kj} \quad (399)$$

where  $C_{As}$  is the active arsenic concentration,  $C_{As_mV_k}$  is the arsenic–vacancy cluster concentration,  $C_{I^0}$  is the neutral interstitial concentration,  $n$  is the electron concentration,  $n_i$



is the intrinsic electron concentration,  $K_{ff}$  is the forward reaction rate, and  $K_{rj}$  is the backward reaction rate. An additional assumption was made for all  $j$ :

$$\frac{K_{rj}}{K_{ff}} = K_{equ} \quad (400)$$

Then, the total rate  $R$  is the sum of  $R_j$  over all  $j$ :

$$R = \sum_j K_{ff} \left(\frac{n}{n_i}\right)^{kj} \left(C_{As}^m \left(\frac{n}{n_i}\right) - K_{equ} C_{As_m V_k} C_I^0\right) \quad (401)$$

The forward reaction rate  $K_{ff}$  can be set using the command:

```
pdbSet <material> <dopant> <defect> CluRateChargeStates {<n>}
```

for example:

```
pdbSet Silicon Arsenic Vacancy CluRateChargeStates
{-2 {[Arrhenius 5.0e-42 7.8]}
-1 {[Arrhenius 5.0e-42 7.8]}
0 {[Arrhenius 5.0e-42 7.8]}
1 {[Arrhenius 5.0e-42 7.8]}
2 {[Arrhenius 5.0e-42 7.8]}}
```

The equilibrium reaction rate is calculated by:

$$K_{equ} = \frac{K_{cEqu} \left(\frac{n_{ss}}{n_i}\right)^m}{(C_I^*)^k} \quad (402)$$

where  $n_{ss}$  is the electron concentration assuming that arsenic reached the limits of solid solubility and  $C_I^*$  is the equilibrium concentration of interstitials.  $K_{cEqu}$  is given as:

$$K_{cEqu} = m \left( \frac{C_{ss}^m}{C_{ss_{tot}} - C_{ss}} \right) \quad (403)$$

where  $C_{ss}$  is the solid solubility of the unpaired arsenic dopants and  $C_{ss_{tot}}$  is the solid solubility of total arsenic concentration.

You can either set the solid solubility values or  $K_{cEqu}$  using the commands:

```
pdbSet Silicon Arsenic Solubility 1e20
pdbSet Silicon Arsenic TotSolubility 1e21
pdbSet Silicon Arsenic Vac KcEqu 1e66
```

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### Dopant Activation and Clustering

In addition, `Solubility` and `TotSolubility` can be changed through their modifying factors:

```
pdbSet Silicon Arsenic SS.Factor 1
pdbSet Silicon Arsenic Total.SS.Factor 1
```

**NOTE** For high-concentration effects, see [High-Concentration Effects on Dopant Diffusion on page 278](#). For smoothing dopant profiles around amorphous to crystalline regions, see [Ion Implantation to Diffusion on page 340](#).

Table 24 Solution for cluster model

Symbol	Arsenic
$C_{As_m V_k}$	As4Vac

## Initializing Cluster Model

Initially, dopant–interstitial cluster concentrations (for example, `As4Vac`) are set to zero. If there is an existing cluster concentration field, the field is used. If there are amorphized regions, dopant–defect pairs and clusters are redistributed in these regions (see [Dopant and Dopant-Defect Cluster Initialization on page 302](#)). In addition, you can initialize any of the cluster concentration fields using the `select` command in the command file.

---

## Dopant Active Model: NeutralCluster

The `NeutralCluster` model assumes that all reactants as well as clusters are neutral. If the `NeutralCluster` model is selected, the following reactions are taken into account:



where  $i, j$  are the number of dopant and defect atoms in the cluster, respectively. The clusters can be specified using the command:

```
pdbSet <material> <dopant> <defect> ClusterSizes <list>
```

For example, the carbon clusters are defined by:

```
pdbSet Silicon Carbon Interstitial ClusterSizes {{1 0} {1 1} {2 0} {2 1} {3 1}}
```

**NOTE** This sets up the diffusion equations for  $C$ ,  $CI$ ,  $C_2$ ,  $C_2I$ , and  $C_3I$ . Cluster sizes given in the `ClusterSizes` list increase in size. For example, the following is incorrect:

```
pdbSet Si Boron Int ClusterSizes { {1 0} {3 1} {1 1} }
```

**NOTE** If you add new cluster sizes, you must define the aliases for the new clusters, for example:

```
alias C2I2 Carbon2Int2
```

The reactions are written as:

$$R_{IAI} \equiv K_{fIA_iI_j} (C_{A_iI_j} C_I - B_{IA_iI_j} C_{A_{i+1}I_{j+1}}) \quad (410)$$

$$R_{VAI} \equiv K_{fVA_iI_j} (C_{A_iI_j} C_V - B_{VA_iI_j} C_{A_iI_{j-1}}) \quad (411)$$

$$R_{AI} \equiv K_{fAIA_iI_j} (C_{A_iI_j} C_{AI} - B_{AIA_iI_j} C_{A_{i+1}I_{j+1}}) \quad (412)$$

$$R_{VAV} \equiv K_{fVA_iV_j} (C_{A_iV_j} C_V - B_{VA_iV_j} C_{A_iV_{j+1}}) \quad (413)$$

$$R_{IAV} \equiv K_{fIA_iV_j} (C_{A_iV_j} C_I - B_{IA_iV_j} C_{A_iV_{j-1}}) \quad (414)$$

$$R_{AV} \equiv K_{fAVA_iV_j} (C_{A_iV_j} C_{AV} - B_{AVA_iV_j} C_{A_{i+1}V_{j+1}}) \quad (415)$$

where:

- $K_{fIA_iI_j}$ ,  $K_{fVA_iI_j}$ ,  $K_{fAIA_iI_j}$ ,  $K_{fVA_iV_j}$ ,  $K_{fIA_iV_j}$ , and  $K_{fAVA_iV_j}$  are the forward reaction rates.
- $B_{IA_iI_j}$ ,  $B_{VA_iI_j}$ ,  $B_{AIA_iI_j}$ ,  $B_{VA_iV_j}$ ,  $B_{IA_iV_j}$ , and  $B_{AVA_iV_j}$  are the binding coefficients.

To set these parameters, use the following commands:

```
pdbSet <material> <dopant> Interstitial KfCluster <cluster> {<n>}
pdbSet <material> <dopant> Vacancy KfCluster <cluster> {<n>}
pdbSet <material> <dopant> <pair> KfCluster <cluster> {<n>}
pdbSet <material> <dopant> Interstitial BindCluster <cluster> {<n>}
```

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```
pdbSet <material> <dopant> Vacancy      BindCluster <cluster> {<n>}
pdbSet <material> <dopant> <pair>      BindCluster <cluster> {<n>}
```

where <cluster> is a valid cluster name (for example, C2, C2I, C3I, C3I2), and <pair> is a dopant–interstitial pair (for example, CarbonInt) or a dopant–vacancy pair.

For example:

```
pdbSet Silicon Carbon CarbonInt KfCluster C3I2 {[Arrhenius 1e-10 0.3]}
```

sets the forward reaction rate of the CarbonInt and C3I2 reaction to {[Arrhenius 1e-10 0.3]}.

## Initializing NeutralCluster Model

Initially, cluster concentrations are set to zero. If there is an existing cluster concentration field, the field is used. If there are amorphized regions, dopant–defect pairs and clusters are redistributed in these regions (see [Dopant and Dopant-Defect Cluster Initialization on page 302](#)).

In addition, you can initialize any of the cluster concentration fields using the `select` command in the command file.

## Carbon Cluster

The carbon-clustering model uses the NeutralCluster model. The following solutions are solved for the carbon model.

Table 25 Solution names for carbon model

Symbol	Solution name
$C$	Carbon
$CI$	CarbonInt
$C_2$	C2
$C_2I$	C2I
$C_3I$	C3I
$C_3I_2$	C3I2
$C_4I_2$	C4I2
$C_4I_3$	C4I3

Table 25 Solution names for carbon model

Symbol	Solution name
$C_5I_3$	C5I3
$C_5I_4$	C5I4

## Nitrogen Cluster

The nitrogen-clustering model uses the `NeutralCluster` model. The following solutions are solved for the nitrogen model.

Table 26 Solution names for nitrogen model

Symbol	Solution name
$N$	Nitrogen
$NI$	NitrogenInt
$NV$	NV
$N_2$	NDimer
$N_2V$	N2V
$N_2V_2$	N2V2

$NV$  is not a mobile pair but an immobile cluster. For example, the reaction is defined by:

```

pdbSet Si N Vac ClusterSizes { {1 0} {1 1} }
pdbSet Si N Vac KfCluster N {[expr [DiffLimit Silicon Vac 0.0]]}
pdbSet Si N Vac BindCluster N {[Arr 5e22 1.58]}

```

---

## Dopant Active Model: FVCluster

If `ActiveModel` is set to `FVCluster`, the fluorine–vacancy cluster model is used. The model based on fluorine–point defect interaction is implemented [30]. The primary reactions used in the model are:



where  $F$  is mobile fluorine,  $I$  is interstitial,  $V$  is vacancy, and  $F_3V$  is an immobile cluster (three fluorine atoms bound to a vacancy). The model assumes that  $F_3V$  is the dominant cluster.

#### 4: Diffusion

##### Dopant Activation and Clustering

These reactions can be written as:

$$R_1 \equiv K_I D_{I0} \left( C_{F_3V} C_I - \frac{C_F^3}{C_{F_3V}} \right) \quad (418)$$

$$R_2 \equiv K_V D_{I0} \left( C_{F_3V} - \frac{C_F^3 C_V}{C_{F_3V}^* C_I^* C_V^*} \right) \quad (419)$$

where  $K_I$  and  $K_V$  are the forward reaction rates. They can be defined using the commands:

```
pdbSet <material> Fluorine F3V KfI {<n>}
pdbSet <material> Fluorine F3V KfV {<n>}
```

$D_{I0}$  is the diffusivity of neutral interstitials,  $C_{F_3V}$  is the concentration of fluorine–vacancy clusters,  $C_F$  is the concentration of fluorine, and  $C_I$  and  $C_V$  are the concentration of interstitials and vacancies, respectively.

Quantities with a superscript (\*) correspond to their equilibrium values. The equilibrium value of  $C_{F_3V}$  can be set by:

```
pdbSet <material> Fluorine F3V Cstar {<n>}
```

The differential equations that describe the model are:

$$\frac{\partial C_F}{\partial t} = \nabla \cdot (D_0 \nabla C_F) + 3R_1 + 3R_2 \quad (420)$$

$$\frac{\partial C_{F_3V}}{\partial t} = -R_1 - R_2 \quad (421)$$

The fluorine diffusion coefficient,  $D_0$ , can be set using the command:

```
pdbSet <material> Fluorine Dstar {<n>}
```

The quantity  $R_1$  is subtracted from  $R_I^{clus}$  and the quantity  $R_2$  is added to  $R_V^{clus}$ .

**NOTE** The fluorine model is switched off by default. To switch it on, use the following commands:

```
solution add name = Fluorine ifpresent = "Fluorine" !negative
solution add name = F3V ifpresent = "F3V Fluorine" !negative
```

Table 27 Solution names for fluorine model

Symbol	Solution name
$C_F$	Fluorine
$C_{F_3V}$	F3V

## Initializing the FVCluster Model

You can select a different initialization model for fluorine with the command:

```
pdbSet <material> Fluorine FVCluster.Init <model>
```

where <model> is either `FV.Full` or `DAC`.

If the `FV.Full` model is selected, it is assumed that the complete fluorine dose is implanted as fluorine–vacancy clusters ( $C_{F_3V}$ ). Since the ‘+1’ model is used to generate the excess interstitials, this effectively introduces interstitials of a concentration equal to  $C_{F_3V}$ , except in amorphous regions.

If the `DAC` model is selected, initially, the fluorine–vacancy cluster concentration is set to zero. If there is an existing cluster concentration field, this field is used. If there are amorphized regions, clusters are redistributed in these regions (see [Dopant and Dopant-Defect Cluster Initialization on page 302](#)). In addition, you can initialize any of the cluster concentration fields using the `select` command in the input command file.

**NOTE** The `DAC` model does not modify the vacancy field during initialization of  $F_3V$ .

---

## Dopant Active Model: Equilibrium

If `ActiveModel` is set to `Equilibrium`, solid solubility or dopant clustering is considered. In the clustering model, the active concentration of the dopant,  $C_A^+$ , is obtained by solving:

$$C_{AS} = C_A^+ + (K_{CTN} C_A^+)^{K_{CTN.F}} \quad (422)$$

where  $K_{CTN}$  and  $K_{CTN.F}$  are clustering parameters and can be set by:

```
pdbSet <material> <dopant> Kctn {<n>}
pdbSet <material> <dopant> Kctn.F {<n>}
```

#### 4: Diffusion

##### Dopant Activation and Clustering

$C_{AS}$  is also given by:

$$C_{AS} = \begin{cases} C_A & C_A < 0.9C_A^{SS} \\ C_A^{SS} - \frac{(C_A - 1.1C_A^{SS})^2}{0.4C_A^{SS}} & 0.9C_A^{SS} \leq C_A \leq C_A^{SS} \\ C_A^{SS} & C_A > 1.1C_A^{SS} \end{cases} \quad (423)$$

where  $C_A$  is the total unpaired dopant concentration, and  $C_A^{SS}$  is calculated as described in [Dopant Active Model: Solid on page 280](#).

If the clustering parameters  $K_{CTN,F}$  and  $K_{CTN}$  are zero, the active concentration is determined by [Eq. 423](#); otherwise, [Eq. 422](#) is solved numerically.

Table 28 Solution names for equilibrium model

Symbol	Boron	Arsenic	Phosphorus	Antimony	Indium
$C_{AS}$	BoronEqu	ArsenicEqu	PhosphorusEqu	AntimonyEqu	IndiumEqu

When the parameter `Equil.Active.Conc` is specified, the expression of `Equil.Active.Conc` is evaluated for the active concentration in equilibrium, instead of calculating [Eq. 422](#) and [Eq. 423](#). For example:

```
pdbSet Si B Equil.Active.Conc "(Boron>1E19)?(1E19):(Boron)"
```

---

## Dopant Active Model: BIC

`ActiveModel` can be set to `BIC` for boron. The model is implemented to simulate boron–interstitial clusters (BICs).

The model makes no assumptions regarding the diffusion model to generate the diffusion equation for the substitutional and the mobile species. However, it should be used with either the `Pair` or `React` model. The model does not take charge-state–dependent reaction rates into account.

The following types of clustering reaction are taken into account:





where  $i, j$  are the number of boron and interstitial atoms in the cluster  $B_iI_j$ , respectively.

The clusters can be specified using the command:

```
pdbSet Silicon Boron Interstitial ClusterSizes <list>
```

For example:

```
pdbSet Silicon Boron Interstitial ClusterSizes {{1 0} {1 1} {1 2} {2 1} \
{3 1} {3 2}}
```

will set up the diffusion equations for  $BI_2$ ,  $B_2I$ ,  $B_3I$ , and  $B_3I_2$ .

**NOTE** Cluster sizes given in the `ClusterSizes` list are increasing in size. For example, the following command is incorrect:

```
pdbSet Si B Int ClusterSizes { {1 0} {3 1} {1 1} }
```

The reactions are written as:

$$R_I \equiv K_{fIB_iI_j} (C_{B_iI_j} C_I - B_{IB_iI_j} C_{B_{i+1}I_{j+1}}) \quad (427)$$

$$R_V \equiv K_{fVB_iI_j} (C_{B_iI_j} C_V - B_{VB_iI_j} C_{B_{i-1}I_{j-1}}) \quad (428)$$

$$R_{CI} \equiv K_{fBI_{B_iI_j}} (C_{B_iI_j} C_{BI} - B_{BI_{B_iI_j}} C_{B_{i+1}I_{j+1}}) \quad (429)$$

where  $K_{fIB_iI_j}$ ,  $K_{fVB_iI_j}$ , and  $K_{fBI_{B_iI_j}}$  are the forward reaction rates, and  $B_{IB_iI_j}$ ,  $B_{VB_iI_j}$ , and  $B_{BI_{B_iI_j}}$  are the binding coefficients.

To set these parameters, the following commands can be used:

```
pdbSet <material> Boron Interstitial KfCluster <cluster> {<n>}
pdbSet <material> Boron Vacancy KfCluster <cluster> {<n>}
pdbSet <material> Boron BoronInt KfCluster <cluster> {<n>}
pdbSet <material> Boron Interstitial BindCluster <cluster> {<n>}
pdbSet <material> Boron Vacancy BindCluster <cluster> {<n>}
pdbSet <material> Boron BoronInt BindCluster <cluster> {<n>}
```

where `<cluster>` is a valid cluster name, for example, `BI2`, `B2I`, `B3I`, `B3I2`.

For example:

```
pdbSet Silicon Boron BoronInt KfCluster B3I2 {[Arrhenius 1e-10 0.3]}
```

sets the forward reaction rate of the `BoronInt` and `B3I2` reaction to `{[Arrhenius 1e-10 0.3]}`.

## 4: Diffusion

### Dopant Activation and Clustering

The differential equations for the clusters are:

$$\frac{\partial}{\partial t} B_i I_j = -R_I - R_V - R_{BI} \quad (430)$$

The reactions  $R_I$ ,  $R_V$ , and  $R_{BI}$  are added to the appropriate point-defect equations, and substitutional and mobile boron diffusion equations.

Table 29 Solution names for BIC model

Symbol	Solution name
$C_B$	Boron
$C_{BI}$	BoronInt
$C_{BI_2}$	BI2
$C_{B_2I}$	B2I
$C_{B_3I}$	B3I
$C_{B_3I_2}$	B3I2

## Initializing BIC Model

Initially, boron–interstitial cluster concentrations (for example, B3I) are set to zero. If there is an existing cluster concentration field, the field is used. If there are amorphized regions, boron defect pairs, and clusters are redistributed in these regions. For details, see [Dopant and Dopant-Defect Cluster Initialization on page 302](#). In addition, you can initialize any of the cluster concentrations field using the `select` command in the input command file.

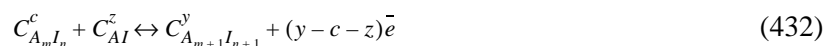
---

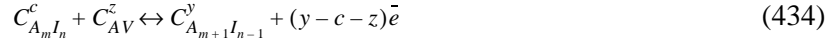
## Dopant Active Model: ChargedCluster

`ActiveModel` can be set to `ChargedCluster` for dopant. The model is implemented to simulate dopant-defect clusters including different charge states.

The model makes no assumptions regarding the diffusion model to generate the diffusion equation for the substitutional and the mobile species. However, it should be used with either the `Pair` or `ChargedPair` or `React` or `ChargedReact` model.

The following types of clustering reaction are taken into account:





where:

- $m, n$  are the number of dopant and interstitial atoms in the cluster  $C_{A_m I_n}$ , respectively, and they are the number of dopant and vacancy atoms in the cluster  $C_{A_m V_n}$ , respectively.
- $C_I, C_V$  are the concentration of interstitials and vacancies.
- $c, y, z$  are different charge states of clusters and point defects.

The clusters can be specified using the command:

```
pdbSet Silicon <dopant> <defect> ClusterSizes <list>
```

For example:

```
pdbSet Silicon Boron Interstitial ClusterSizes {{1 0} {1 1} {1 2} {2 1} \
{3 1} {3 2}}
```

sets up the diffusion equations for  $BI_2, B_2I, B_3I$ , and  $B_3I_2$ .

**NOTE** Cluster sizes given in the `ClusterSizes` list are increasing in size. For example, the following command is incorrect:

```
pdbSet Si Boron Int ClusterSizes { {1 0} {3 1} {1 1} }
```

The reactions are written as:

$$R_{A_m I_{n+1}} \equiv K_{fA_m I_{n+1}} \left( C_{A_m I_n}^c C_I^z - K_{rA_m I_{n+1}} C_{A_m I_{n+1}}^y \left( \frac{n}{n_I} \right)^{(y-c-z)} \right) \quad (435)$$

$$R_{A_{m+1} I_{n+1}} \equiv K_{fA_{m+1} I_{n+1}} \left( C_{A_m I_n}^c C_{AI}^z - K_{rA_{m+1} I_{n+1}} C_{A_{m+1} I_{n+1}}^y \left( \frac{n}{n_I} \right)^{(y-c-z)} \right) \quad (436)$$

$$R_{A_m I_{n-1}} \equiv K_{fA_m I_{n-1}} \left( C_{A_m I_n}^c C_V^z - K_{rA_m I_{n-1}} C_{A_m I_{n-1}}^y \left( \frac{n}{n_I} \right)^{(y-c-z)} \right) \quad (437)$$

$$R_{A_{m+1} I_{n-1}} \equiv K_{fA_{m+1} I_{n-1}} \left( C_{A_m I_n}^c C_{AV}^z - K_{rA_{m+1} I_{n-1}} C_{A_{m+1} I_{n-1}}^y \left( \frac{n}{n_I} \right)^{(y-c-z)} \right) \quad (438)$$

where:

- $K_{fA_m I_{n+1}}, K_{fA_{m+1} I_{n+1}}, K_{fA_m I_{n-1}}$ , and  $K_{fA_{m+1} I_{n-1}}$  are the forward reaction rates.
- $K_{rA_m I_{n+1}}, K_{rA_{m+1} I_{n+1}}, K_{rA_m I_{n-1}}$ , and  $K_{rA_{m+1} I_{n-1}}$  are the equilibrium constants.

#### 4: Diffusion

##### Dopant Activation and Clustering

The forward reaction rates are a function of the lattice spacing ( $L$ ), the capture radius factor ( $r$ ), and the diffusion of point defect ( $D_I^z, D_V^z$ ) or dopant-defect pair ( $D_{AI}^z, D_{AV}^z$ ):

$$K_{fA_m I_{n+1}} \propto 4\pi L r_{A_m I_{n+1}} D_I^z \quad (439)$$

$$K_{fA_{m+1} I_{n+1}} \propto 4\pi L r_{A_{m+1} I_{n+1}} D_{AI}^z \quad (440)$$

$$K_{fA_m I_{n-1}} \propto 4\pi L r_{A_m I_{n-1}} D_V^z \quad (441)$$

$$K_{fA_{m+1} I_{n-1}} \propto 4\pi L r_{A_{m+1} I_{n-1}} D_{AV}^z \quad (442)$$

To set the capture radius factor parameter, use the following command:

```
pdbSet <material> <dopant> <defect|mobile> CaptureRadiusFactor <cluster> \
    {<expression>}
```

where *mobile* is the mobile species (for example, BoronInt, BoronVac). For example:

```
pdbSet Silicon Boron BoronInt CaptureRadiusFactor B2 1.3
```

means that the capture radius for  $B_2 + BoronInt \leftrightarrow B_3I$  is 1.3 times the lattice spacing.

The equilibrium conditions are calculated internally using:

$$C_{A_m I_n}^c = \frac{N C_A^m C_I (n)^{-m-c} e^{\frac{E_{form}}{kT}}}{(5 \times 10^{22})^{m-1} C_I^0 n_I} \quad (443)$$

where  $N$  is the cluster degeneracy,  $c$  is the cluster charge, and  $E_{form}$  is the formation energy of the cluster.

To set these parameters, use the following commands:

```
pdbSet <material> <dopant> <defect> ClusterDegeneracy <cluster> {<n>}
pdbSet <material> <dopant> <defect> ClusterCharge <cluster> {<n>}
pdbSet <material> <dopant> <defect> ClusterFormE <cluster> {<expression>}
```

where *<cluster>* is a valid cluster name, for example, BI2, B2I, B3I, B3I2.

For example:

```
pdbSet Silicon Boron Int ClusterFormE B3I2 {0.3}
```

sets the formation energy of cluster B3I2 to 0.3 eV.

The differential equations for the clusters are:

$$\frac{\partial C_{A_m I_n}}{\partial t} = -R_{A_m I_{n+1}} - R_{A_{m+1} I_{n+1}} - R_{A_m I_{n-1}} - R_{A_{m+1} I_{n-1}} \quad (444)$$

The reactions are added to the appropriate point-defect equations, and substitutional and mobile boron diffusion equations.

Table 30 Solution names for ChargedCluster model assuming the base defect is boron

Symbol	Solution name
$C_B$	Boron
$C_{BI}$	BoronInt
$C_{BI_2}$	BI2
$C_{B_2I}$	B2I
$C_{B_3I}$	B3I
$C_{B_3I_2}$	B3I2

## Initializing ChargedCluster Model

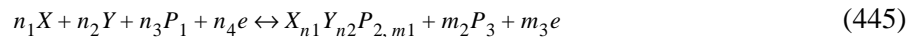
Initially, dopant–interstitial cluster concentrations (for example, B3I) are set to zero. If there is an existing cluster concentration field, the field is used. If there are amorphized regions, dopant-defect pairs and clusters are redistributed in these regions (see [Dopant and Dopant-Defect Cluster Initialization on page 302](#)).

In addition, you can initialize any of the cluster concentration fields using the `select` command in the command file.

---

## Dopant Active Model: ComplexCluster

The reaction of the `ComplexCluster` model is as follows:



where:

- $X$  and  $Y$  denote two different dopant species.
- $X_{n_1} Y_{n_2} P_{2, m_1}$  is a complex cluster.

#### 4: Diffusion

##### Dopant Activation and Clustering

- $P_1$ ,  $P_2$ , and  $P_3$  denote point defects, that is, either a Si self-interstitial or vacancy.
- $e$  indicates an electron.

The reaction is formulated by:

$$R = K_f n_i \left( \frac{C_{A_1}^+}{C_{norm}} \right)^{n_1} \left( \frac{C_{A_2}^+}{C_{norm}} \right)^{n_2} \left( \frac{P_1}{P_1^*} \right)^{n_3} \left( \frac{n}{n_i} \right)^{n_4} - K_r C_{X_{n_1} Y_{n_2} P_{2,m_1}} \left( \frac{P_3}{P_3^*} \right)^{m_2} \left( \frac{n}{n_i} \right)^{m_3} \quad (446)$$

$C_{norm}$  is the normalization factor which is specified by:

```
term name=${Xn1Yn2P2,m1}NormValue <material> add eqn=<equation>
```

By default,  $C_{norm}$  is set to the intrinsic carrier concentration,  $n_i$ .

The chemical elements of the complex cluster  $X_{n_1} Y_{n_2} P_{2,m_1}$  are defined by:

```
pdbSetDoubleArray <material> <Xn1Yn2P2,m1> Component.List \
{<X> <n1> <Y> <n2> <P21>}
```

For example:

```
pdbSetDoubleArray Silicon BCI Component.List { Boron 1 Carbon 1 Int 1 }
```

When the charge state of the complex cluster,  $P_3$ ,  $m_2$ , and  $m_3$  are given, the other unknowns  $P_1$ ,  $n_3$ , and  $n_4$  are determined automatically.

$P_3$ ,  $m_2$ , and  $m_3$  are specified by:

```
pdbSetDoubleArray <material> <Xn1Yn2P2,m1> Product.List \
{<P3> <m2> <Electron or Hole> <|m3|>}
```

For example:

```
pdbSetDoubleArray Silicon BCI Product.List { Electron 1 }
pdbSetDoubleArray Silicon BCI ChargeState { 0 1.0 }
```

With the two examples above, the reaction is defined as follows:

$$R = K_f n_i \left( \frac{C_B^+}{n_i} \right) \left( \frac{C_C^+}{n_i} \right) \left( \frac{I}{I^*} \right) - K_r C_{BCI} \left( \frac{n}{n_i} \right) \quad (447)$$

The forward and reverse reaction rates,  $K_f$  and  $K_r$ , are calculated by:

$$K_f = factor_f \times K_{f0} \quad (448)$$

$$K_r = factor_r \times K_{r0} \quad (449)$$

where  $K_f$ ,  $K_r$ ,  $factor_f$  and  $factor_r$  are specified by:

```

pdbSetDouble <material> <Xn1Yn2P2,m1> KF <number>
pdbSetDouble <material> <Xn1Yn2P2,m1> KR <number>
term name=${Xn1Yn2P2,m1}KFFactor <material> add eqn=<equation>
term name=${Xn1Yn2P2,m1}KRFactor <material> add eqn=<equation>

```

By default,  $factor_f$  and  $factor_r$  are set to 1.0.

## Initializing ComplexCluster Model

The initialization of the clusters in the ComplexCluster model is performed in a similar way to that of the precipitation model (see [Initializing Precipitation Model on page 281](#)).

The ComplexCluster model can be used with other activation models, for example:

```

pdbSet Si B ActiveModel BIC
pdbSet Si B More.Active.Model.List { ComplexCluster }

```

**NOTE** The items allowed in More.Active.Model.List are Precipitation or ComplexCluster.

For the initialization of the clusters with the other activation models, see [Initializing Precipitation Model on page 281](#).

When the multiple dopant species are involved in the reaction of the ComplexCluster model, the initialization is more complicated because the dose conservations of both dopant species must be satisfied. For example, the silicon substrate is doped with  $1 \times 10^{20} \text{ cm}^{-3}$  boron atoms and  $1 \times 10^{20} \text{ cm}^{-3}$  carbon atoms, and the following specifications for their activation models and initializations are given by:

```

pdbSet Si B ActiveModel ComplexCluster
pdbSet Si C ActiveModel ComplexCluster
pdbSet Si B AmInit 4E19
pdbSetDouble Si C AmInit 1E19
pdbSet Si BCI FractionAmor 1.0

```

In the amorphous region, the initial boron active concentration needs to be set to  $4 \times 10^{19} \text{ cm}^{-3}$ . This means that the BCI concentration must be  $6 \times 10^{19} \text{ cm}^{-3}$ , while the initial active concentration of carbon is set to  $1 \times 10^{19} \text{ cm}^{-3}$ . Therefore, the BCI concentration is supposed to be set to  $9 \times 10^{19} \text{ cm}^{-3}$ . In this case, the smaller BCI concentration  $6 \times 10^{19} \text{ cm}^{-3}$  is set for BCI, so that the active concentration of carbon is adjusted to  $4 \times 10^{19} \text{ cm}^{-3}$ ; although, AmInit for carbon is given as  $1 \times 10^{19} \text{ cm}^{-3}$ .

---

## Dopant and Dopant-Defect Cluster Initialization

If you switch on the BIC, ChargedCluster, CarbonCluster, React, ChargedReact, or NeutralReact model, initialization of the dopant and dopant-defect clusters are performed in the `diffPreProcess` procedure (see [Ion Implantation to Diffusion on page 340](#)). It is possible to redistribute dopants and dopant-defect clusters in the amorphous and crystalline regions after implantation.

The initialization of the dopant and dopant-defect clusters depends on the value of the parameters `AmInit`, `AcInit`, `FractionCryst`, and `FractionAmor`. The initial level of active concentration of dopants in amorphized and crystalline regions can be specified per dopant as `AmInit` and `AcInit`, respectively. You can specify the `AmInit` and `AcInit` parameters by using:

```
pdbSet <material> <dopant> AcInit {<n>}
pdbSet <material> <dopant> AmInit {<n>}
```

If the `AcInit` or `AmInit` parameter is not defined, the default value of  $5 \times 10^{22}$  is used. If you want `AcInit` and `AmInit` to be a function of other fields for a specific dopant, define the terms `<dopant>AcInit` and `<dopant>AmInit` in your input files. For example:

```
term name=ArsenicAcInit silicon add eqn = "Germanium/5e22 * [pdbDelayDouble
                                         Silicon Arsenic Solubility]"
term name=ArsenicAmInit silicon add eqn = "Germanium/5e22*1e19"
```

In this case, `AcInit` and `AmInit` for arsenic are replaced with `ArsenicAcInit` and `ArsenicAmInit`.

The `FractionCryst` and `FractionAmor` parameters are used to calculate the fraction of dopants and dopant-defect clusters in crystalline and amorphized regions. To specify the `FractionCryst` and `FractionAmor` parameters, use:

```
pdbSetDouble <material> <dopant | cluster> FractionCryst {<n>}
pdbSetDouble <material> <dopant | cluster> FractionAmor {<n>}
```

The following outlines the initialization of dopant clusters.

In crystalline regions:

$$\text{Crystalline\%} = \frac{\text{FractionCryst}}{\text{DopantSize} \sum_{\text{Dopant/Cluster}} \text{FractionCryst}} \quad (450)$$

$$\begin{aligned} \text{MaxDopant} &= \max(\text{Dopant\_Implant} - \text{AcInit}, 0) \\ \text{DopantCluster} &= \text{DopantCluster} + \text{Crystalline\%} \times \text{MaxDopant} \\ \text{Dopant} &= \text{Dopant} + \text{Dopant\_Implant} - \text{MaxDopant} + \text{Crystalline\%} \times \text{MaxDopant} \end{aligned} \quad (451)$$



In amorphous regions:

$$\text{Amorphous\%} = \frac{\text{FractionAmor}}{\text{DopantSize} \sum_{\text{Dopant|DopantCluster}} \text{FractionAmor}} \quad (452)$$

$$\begin{aligned} \text{MaxDopant} &= \max(\text{DopantTotal} + \text{Dopant\_Implant} - \text{AmInit}, 0) \\ \text{DopantCluster} &= \text{Amorphous\%} \times \text{MaxDopant} \\ \text{Dopant} &= \text{DopantTotal} + \text{Dopant\_Implant} - \text{MaxDopant} + \text{Amorphous\%} \times \text{MaxDopant} \end{aligned} \quad (453)$$

where:

- Dopant is the dopant name (for example, Boron).
- DopantCluster is the cluster name (for example, B4I2).
- DopantTotal is the total dopant (for example, Boron+4\*B4I2).
- Dopant\_Implant is the implanted dopant (for example, Boron\_Implant).
- DopantSize is the size of the dopant (for example, 4 for B4I2).

---

## Dopant Trapping at EOR Defects

To simulate dopant trapping at EOR defects [31], interstitial clusters must be switched on (311 or 2Moment), loops must be switched on, and one of the following dopant diffusion models also must be used:

- React (see [React Diffusion Model on page 204](#))
- ChargedReact (see [ChargedReact Diffusion Model on page 198](#))
- NeutralReact (see [NeutralReact Diffusion Model on page 212](#))

To switch on the model, use:

```
pdbSet <material> <dopant> EORTrap { 1 | 0 }
```

The following type of clustering reactions are taken into account:



where  $C_{AI}$  is the mobile dopant,  $C_{A311}$  is the concentration of mobile dopants trapped at {311} defects, and  $C_{ADL}$  is the concentration of mobile dopants trapped at dislocation loops.

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### Dopant Activation and Clustering

For these reactions:

- The first reaction describes the capture and release of mobile dopants at {311} defects.
- The second one describes the capture and release of mobile dopants at dislocation loops.
- The last reaction explains the transformation of mobile dopants trapped at a {311} defect to mobile dopants trapped at a dislocation loop.

The capture rate for the mobile dopant and {311} defect reaction is written as:

$$R_{A311}^{capture} \equiv k_{f311}(C_{311}C_{max}^{311} - C_{A311}) \quad (457)$$

where  $k_{f311}$  is the forward reaction rate,  $C_{311}$  is the concentration of interstitials in {311} defects and  $C_{max}^{311}$  is the density of traps along the {311} defects for the mobile dopants.

To change  $k_{f311}$ , use:

```
pdbSet <material> <dopant> EORForwardReaction <trapped dopant> <n>
```

where <trapped dopant> is  $C_{A311}$  (for example, B311). For boron, it is currently set to:

$$k_{f311} = 4\pi r_{A311} C_{AI} D_{AI} \quad (458)$$

where  $r_{A311}$  is the capture radius and  $D_{AI}$  is the diffusivity of neutral dopant defect pair,  $C_{AI}$ .

To change the capture radius, use:

```
pdbSet <material> <dopant> EORCaptureRadius <trapped dopant> <n>
```

$C_{max}^{311}$  is proportional to the length of the {311} defect. It is defined as a term and is user definable:

```
term name = EORDopant311_Max <material> add eqn = {c}
```

The release rate for the mobile dopant and {311} defect reaction is written as:

$$R_{A311}^{release} \equiv C_{A311} E_{A311} \quad (459)$$

where  $E_{A311}$  is the emission rate of trapped mobile dopant from {311} defects. To change it, use:

```
pdbSet <material> <dopant> EOREmissionRate <trapped dopant> <n>
```

The capture rate for the mobile dopant and dislocation loop reaction is written as:

$$R_{ADL}^{capture} \equiv k_{fDL}(C_{DL}C_{max}^{DL} - C_{ADL}) \quad (460)$$

where  $k_{fDL}$  is the forward reaction rate and  $C_{max}^{DL}$  is the density of traps along the edge of dislocation loops for the mobile dopants. To change  $k_{fDL}$ , use:

```
pdbSet <material> <dopant> EORForwardReaction <trapped dopant> <n>
```

where <trapped dopant> is  $C_{ADL}$  (for example, BDL). It is set to:

$$k_{fDL} = \pi r_{ADL} C_{AI} D_{AI} \quad (461)$$

where  $r_{ADL}$  is the capture radius. To change the capture radius, use:

```
pdbSet <material> <dopant> EORCaptureRadius <trapped dopant> <n>
```

$C_{max}^{DL}$  is proportional to the density of dislocation loops. It is defined as a term and is user definable:

```
term name = EORDopantDL_Max <material> add eqn = {c}
```

The release rate for the mobile dopant and dislocation loop reaction is written as:

$$R_{ADL}^{release} \equiv C_{ADL} E_{ADL} \quad (462)$$

where  $E_{ADL}$  is the emission rate of trapped mobile dopant from a dislocation loop. To change it, use:

```
pdbSet <material> <dopant> EOREmissionRate <trapped dopant> <n>
```

The unfauling of {311} defects in the presence of trapped mobile dopants is given as:

$$R_{A311 \rightarrow ADL}^{Unfold} \equiv K_{D311 \rightarrow DLoop} s_{311} \frac{C_{A311}}{C_{311}} \quad (463)$$

where  $K_{D311 \rightarrow DLoop}$  is the unfauling rate of {311} defects to dislocation loops and comes from the Loop model (see [Defect Cluster Model: Loop on page 315](#)).  $s_{311}$  is the size of {311} defect.

Table 31 Solution names for EOR trap model

Symbol	Solution name
$C_{AI}$	BoronInt
$C_{A311}$	B311
$C_{ADL}$	BDL

## Initializing Dopant Trapping in EOR Model

Initially, trapped dopants at EOR are set to zero. If there is an existing cluster concentration field, the field is used. If there are amorphized regions, dopant–defect pairs and clusters are redistributed in these regions. For details, see [Dopant and Dopant-Defect Cluster Initialization on page 302](#). In addition, you can initialize any of the cluster concentration fields using the `select` command in the command file.

---

## Defect Clusters

The available cluster models are `None`, `Equilibrium`, `311`, `Loop`, `LoopEvolution`, `FRENDTECH`, `1Moment`, `2Moment`, `Full`, and the model is selected with the command:

```
pdbSet <material> <defect> ClusterModel <model>
```

where `<defect>` is `interstitial` or `vacancy`, and `<model>` is one of the valid model names.

These clusters play an important part in transient-enhanced diffusion (TED) of impurities following ion implantation. The main effect of the models is to delay the onset of TED at low temperatures and to distribute the diffusion enhancement over a longer period of time. This eliminates the excessive diffusion at low temperatures that is predicted without any clustering.

In some cases, multiple cluster equations must be switched on. The following command can be used:

```
pdbSet <material> <defect> MultiClusterModel < < cluster model> <list> >
```

For example:

```
pdbSet Silicon Int MultiClusterModel { Full {1Moment} }  
                                         Loop {311} }
```

switches on the `1Moment` model if the interstitial cluster model `Full` is selected. In the same way, it will switch on the `311` model if the interstitial cluster model `Loop` is selected.

For example:

```
pdbSet Si Int ClusterModel Full  
pdbSet Si Int MultiClusterModel Full {2Moment Loop}
```

switches on the model given in [\[32\]](#).

In this model, seven equations are solved to describe the kinetics of self-interstitial clusters:

- Three data fields (I2, I3, I4) describe small interstitial clusters (SMICs).
- Two data fields (D311, density of {311} defects, and C311, density of interstitials bound in {311} defects) describe the presence of {311} defects.
- Two data fields (DLoop, density of dislocation loops, and CLoop, density of interstitials bound in dislocation loops) describe dislocation loops.

---

## Defect Cluster Model: None

If ClusterModel is set to None, no point-defect clustering effects will be taken into account.

---

## Defect Cluster Model: Equilibrium

If you set the model to Equilibrium, the following nonlinear algebraic equation along with the related diffusion equations are solved:

$$(C_{X^0})^4 - k_b C_{XC} = 0 \quad (464)$$

where  $k_b$  is the equilibrium constant,  $X$  is either interstitial or vacancy, 4 is the size of the cluster, and  $C_{XC}$  is the concentration of point-defect cluster.  $k_b$  can be specified with:

```
pdbSet <material> <defect> KCluster {<n>}
```

**NOTE** The equilibrium cluster model is defined only for interstitials in silicon.

---

## Defect Cluster Model: 311

If you set the defect cluster model to 311, the {311} point-defect model developed by Law and Jones [33] is activated. It solves for the concentration of interstitials in the defects  $C_{311}$  and the concentration of defects  $D_{311}$ , as well as for the concentration of interstitials in small interstitial clusters (SMICs). SMICs come in two types. The small type *SmicS* is assumed to have a cluster size of 2. The larger type *Smic* is assumed to have a cluster size of  $N_{size} = 4$ , by default. This value is, however, user accessible:

```
pdbSet <material> C311 NSize {<n>}
```

Nucleation of defects occurs during the implantation process. Initial distribution of defects comes from the implant code (see [Ion Implantation to Diffusion on page 340](#)), in particular, all interstitials created during the implantation process are assumed to be in immobile *SmicS*. Vacancies and interstitials recombine or may form di-interstitials and di-vacancies. Some

#### 4: Diffusion

##### Defect Clusters

interstitials will also form small interstitial clusters (*SmicS*, *Smic*) or {311} defects. The SMICs dissolve to the surface through the release of interstitials. The capture and release of interstitials on the {311} defects occur only at the end of the defects and, therefore, are proportional to the number of defects  $D_{311}$ .

The reactions involved in the {311} model are given by:



$$R_{I_2form} = k_f(C_I^2 - B_{I_2}C_I) \quad (467)$$

$$R_{V_2form} = k_f(C_V^2 - B_{V_2}C_V) \quad (468)$$

where  $I_2$  and  $V_2$  are di-interstitials and di-vacancies, and  $B_{X_2}$  is the binding coefficient between the di-defect, for example,  $I_2$ , and the base defect,  $I$  (where  $X$  refers to either I or V), and  $k_f$  is the forward reaction rate for the recombination of di-defects.

To change these variables, use the commands:

```
pdbSet <material> <di-defect> Kforward {<n>}
pdbSet <material> <di-defect> Bind {<n>}
```



$$R_{I_2rec} = k_f \left( C_{I_2}C_V - C_{I_2}^*C_V^* \frac{C_I}{C_I^*} \right) \quad (472)$$

$$R_{V_2rec} = k_f \left( C_{V_2}C_I - C_{V_2}^*C_I^* \frac{C_V}{C_V^*} \right) \quad (473)$$

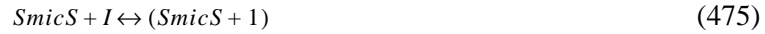
$$R_{I_2V_2rec} = k_f(C_{I_2}C_{V_2} - C_{I_2}^*C_{V_2}^*) \quad (474)$$

where  $C_X^*$  is the equilibrium concentration of the respective defect or di-defect, and  $k_f$  is the forward reaction rate for the respective recombination process.

To change these variables, use the commands:

```
pdbSet <material> <di-defect> KRecomb {<n>}
pdbSet <material> <di-defect> KBiMole {<n>}
pdbSet <material> <di-defect> Cstar {<n>}
```

Aggregation or emission of interstitials from *SmicS* and *Smic* are given by:



$$R_{ISmicSagg} = k_{fI} C_{SmicS} (C_I - B_{ISmicS}) \quad (476)$$

This process increases the concentration of interstitials in *SmicS* by  $1/\text{cm}^3$ .



$$R_{ISmicagg} = k_{fI} C_{Smic} (C_I - B_{ISmic}) \quad (478)$$

This process increases the concentration of interstitials in *Smic* by  $1/\text{cm}^3$ .  $k_{fI}$  is the forward reaction rate for SMIC–interstitial reactions, and  $B_{ISmicS}$  and  $B_{ISmic}$  are the binding coefficients between interstitials and SMICs.

To change these variables, use the commands:

```
pdbSet <material> SmicS KfI {<n>}
pdbSet <material> SmicS Bind {<n>}
pdbSet <material> Smic KfI {<n>}
pdbSet <material> Smic Bind {<n>}
```

The recombination of *SmicS* or *Smic* with a vacancy or bi-vacancies is given by:



$$R_{VSmicSrec} = k_{fV} C_V C_{SmicS} \quad (480)$$

This process decreases the concentration of interstitials in *SmicS* by  $1/\text{cm}^3$ .



$$R_{VSmicrec} = k_{fV} C_V C_{Smic} \quad (482)$$

This process decreases the concentration of interstitials in *Smic* by  $1/\text{cm}^3$ .



$$R_{V_2SmicSrec} = k_{fV_2} C_{V_2} C_{SmicS} \quad (484)$$

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This process decreases the concentration of interstitials in *SmicS* by  $2/\text{cm}^3$ .



$$R_{V_2Smicrec} = k_{fV_2} C_{V_2} C_{Smic} \quad (486)$$

This process decreases the concentration of interstitials in *Smic* by  $2/\text{cm}^3$ .  $k_{fV}$  and  $k_{fV_2}$  are the diffusion-limited SMIC–(di-)vacancy capture rates and are defined as:

$$k_{fV} = 4\pi a D_{V^0} \quad (487)$$

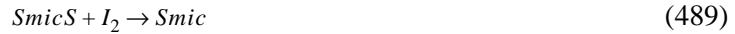
$$k_{fV_2} = 4\pi a D_{V_2^0} \quad (488)$$

where  $D_{V^0}$  and  $D_{V_2^0}$  are the diffusivities of neutral vacancies and di-vacancies, and  $a$  is the lattice spacing of silicon.

To change these variables, use the commands:

```
pdbSet <material> Vacancy D 0 {<n>}
pdbSet <material> V2 D0 {<n>}
pdbSet <material> LatticeSpacing {<n>}
```

A *Smic* is assumed to contain  $N_{size}$  interstitials, with a default value of 4. A *SmicS* contain two interstitials less than a *Smic*. A *SmicS* can be converted to a *Smic* by combining with a di-interstitial. Formation of a *Smic* from a *SmicS* and bi-interstitials is given by:



$$R_{Smicform} = k_{fI_2} C_{SmicS} C_{I_2} \quad (490)$$

This process increases the concentration of interstitials in *Smic* by  $N_{size}/\text{cm}^3$  and decreases the concentration of interstitials in *SmicS* by  $(N_{size} - 2)/\text{cm}^3$ .  $k_{fI_2}$  is the forward reaction rate for SMIC–di-interstitial reactions.

To change these variables, use the commands:

```
pdbSet <material> SmicS KfI2 {<n>}
pdbSet <material> C311 NSize {<n>}
```

When a *Smic* combines with an additional di-interstitial, they form a {311} defect. Formation of a new {311} defect from a *Smic* and bi-interstitials is given by:



$$R_{311nIform} = k_{nI_2} C_{Smic} C_{I_2} \quad (492)$$



This process increases the concentration of {311} defects by  $1/\text{cm}^3$  and the concentration of interstitials in {311} defects by  $(N_{size} + 2)/\text{cm}^3$ , and decreases the number of interstitials in a *Smic* by  $N_{size}/\text{cm}^3$ .  $k_{nI_2}$  is the reaction rate.

To change these variables, use the command:

```
pdbSet <material> C311 KnI2 {<n>}
```

The emission of interstitials from {311} defects is given by:

$$C_{311} \rightarrow (C_{311} - 1) + I \quad (493)$$

$$R_{C_{311}Iem} = C_{311}D_{Rate} \quad (494)$$

This process decreases the concentration of interstitials in {311} defects by  $1/\text{cm}^3$ , but does not change the number of {311} defects. The {311} defect simply became shorter.  $C_{311}$  is the concentration of interstitials in the {311} defects and  $D_{Rate}$  is the decay rate.

To change these variables, use the commands:

```
pdbSet <material> C311 Decay {<n>}
```

The dissolution of a defect is given by:

$$D_{311} \rightarrow D_{311} - 1 \quad (495)$$

$$R_{D_{311}decay} = D_{311}D_{Rate} \quad (496)$$

This process changes the number of {311} defects, but does not affect the number of interstitials in the {311} defects. The interstitials released in this process immediately aggregate on other {311} defects.  $D_{311}$  is the concentration of {311} defects and  $D_{Rate}$  is the defect decay rate.

A set of 14 interstitials can nucleate at the end of a {311} defect. The formation or dissolution of a {311} defect from interstitials is given by:

$$14I \leftrightarrow 311 \quad (497)$$

$$R_{C_{311}Iform} = k_{fI}D_{311}14R_I(C_I - B_{D_{311}I}) \quad (498)$$

This process increases the concentration of interstitials in {311} defects by  $14/\text{cm}^3$ ; the number of defects remains unchanged.  $k_{fI}$  is the forward reaction rate,  $R_I$  is the capture (reaction) range, and  $B_{D_{311}I}$  is the binding coefficient between the {311} defect and the interstitial.

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To change these variables, use the commands:

```

pdbSet <material> C311 KfI      {<n>}
pdbSet <material> C311 BindI    {<n>}
pdbSet <material> C311 RangeI   {<n>}

```

A set of 14 di-interstitials can nucleate at the end of a {311} defect. The formation of two {311} defects from seven bi-interstitials is given by:



$$R_{C_{311}I_2form} = D_{311}k_{fI_2}14R_{I_2}(C_{I_2} - B_{D_{311}I_2}) \quad (500)$$

This process increases the concentration of interstitials in {311} defects by  $28/\text{cm}^3$ ; the number of defects remains unchanged.  $k_{fI_2}$  is the forward reaction rate,  $R_{I_2}$  is the capture (reaction) range, and  $B_{D_{311}I_2}$  is the binding coefficient between the {311} defect and the interstitial.

To change these variables, use the commands:

```

pdbSet <material> C311 BindI2   {<n>}
pdbSet <material> C311 KfI2     {<n>}
pdbSet <material> C311 RangeI2  {<n>}

```

A {311} defect can dissolve into interstitials or di-interstitials. The probability of this process is proportional to the inverse length of the defect, which can be expressed as the ratio of the concentration of defects and the concentration of interstitials in defects ( $D_{311}/C_{311}$ ). Then, the dissolution of {311} defects is given by:

$$R_{D_{311}Iem} = D_{311}14C_{Rate}\frac{D_{311}}{C_{311}}k_{fI}R_{I}B_{D_{311}I} \quad (501)$$

$$R_{D_{311}I_2em} = D_{311}14C_{Rate}\frac{D_{311}}{C_{311}}k_{fI_2}R_{I_2}B_{D_{311}I_2} \quad (502)$$

This process does not change the number of free interstitials or the number of interstitials in {311} defects. It is assumed that all interstitials were released from the defect aggregate in other {311} defects.  $C_{Rate}$  is the spontaneous combustion rate and gives the percentage of interstitials dissolved from {311} defects by dissolution of all defects.

To change these variables, use the command:

```

pdbSet <material> C311 CombRate {<n>}

```

The following set of differential equations is solved with the {311} model. The point-defect equations are:

$$\begin{aligned} \frac{\partial C_I}{\partial t} = & -\nabla \bullet J_I - R_{IV} - 2R_{I_2form} + R_{I_2rec} - R_{V_2rec} - R_{C_{311}Iform} \\ & + R_{C_{311}Iem} - R_{ISmicSagg} - R_{ISmicagg} \end{aligned} \quad (503)$$

$$\frac{\partial C_V}{\partial t} = -\nabla \bullet J_V - R_{IV} - 2R_{V_2form} + R_{V_2rec} - R_{I_2rec} - R_{VSmicSrec} - R_{VSmicrec} \quad (504)$$

The di-defect equations are:

$$\frac{\partial C_{I_2}}{\partial t} = \nabla \bullet (D_{I_2} \nabla C_{I_2}) + R_{I_2form} - R_{I_2rec} - R_{I_2V_2rec} - R_{Smicform} - R_{311nIform} - R_{C_{311}I_2form} \quad (505)$$

$$\frac{\partial C_{V_2}}{\partial t} = \nabla \bullet (D_{V_2} \nabla C_{V_2}) + R_{V_2form} - R_{V_2rec} - R_{I_2V_2rec} - R_{V_2SmicSrec} - R_{V_2Smicrec} \quad (506)$$

where  $D_{X_2}$  is the diffusivities of di-defects (where  $X$  refers to either I or V).

To change these variables, use the command:

```
pdbSet <material> <di-defect> D0 {<n>}
```

The equation for  $SmicS$  is given by:

$$\frac{\partial C_{SmicS}}{\partial t} = -R_{VSmicSrec} - 2R_{V_2SmicSrec} + R_{ISmicSagg} - R_{Smicform} \quad (507)$$

The equation for  $Smic$  is given by:

$$\frac{\partial C_{Smic}}{\partial t} = -R_{VSmicrec} - 2R_{V_2Smicrec} + R_{ISmicagg} + R_{Smicform} N_{Size} + R_{311nIform} N_{Size} \quad (508)$$

The equation for the density of {311} defects is given by:

$$\frac{\partial C_{D_{311}}}{\partial t} = -R_{D_{311}decay} - R_{D_{311}Iem} - 2R_{D_{311}I_2em} + R_{311nIform} \quad (509)$$

The equation for the concentration of interstitials in {311} defects is given by:

$$\frac{\partial C_{C_{311}}}{\partial t} = -R_{C_{311}Iem} + R_{C_{311}Iform} + 2R_{C_{311}I_2form} + (N_{size} + 2)R_{311nIform} \quad (510)$$

The initialization of {311} defect fields is given in [Ion Implantation to Diffusion on page 340](#).

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Defect Clusters

**NOTE** Even though the {311} model and the model parameters are given in general format, they are defined only for silicon. If these models need to be used in other materials, their parameters must be copied.

Table 32 Solution names for 311 model

Symbol	Solution name
$C_{311}$	C311
$D_{311}$	D311
$C_{Smic}$	Smic
$C_{SmicS}$	SmicS
$C_{I_2}$	I2
$C_{V_2}$	V2

## Initializing 311 Model

The defect-cluster concentrations I2, V2, C311, SmicS, Smic, and D311 are initialized in the `diffPreProcess` procedure. The model assumes that all the free implant interstitials (`Int_Implant`) are transferred to `SmicS`. Initially, other transient defect-cluster concentrations are set to zero. If there is an existing cluster concentration field, the field is used. By default, clusters are assumed to break apart in the amorphous regions. You can specify the percentage of clusters retained in the amorphous region per cluster solution variable using the parameter `AmPercent`:

```
pdbSet <mater> <cluster> AmPercent {<n>}
```

For example:

$$SmicS = \begin{cases} SmicS * AmPercent & \text{Amorphous regions} \\ SmicS + Int\_Implant & \text{Crystalline regions} \end{cases} \quad (511)$$

$$C_{311} = \begin{cases} C_{311} * AmPercent & \text{Amorphous regions} \\ C_{311} & \text{Crystalline regions} \end{cases} \quad (512)$$

The value of the `AmPercent` parameter must be between 0 and 1.

## Defect Cluster Model: Loop

If you set the defect cluster model to `Loop`, the modified version of the dislocation loop nucleation model [34] is used to solve for the concentration of interstitials in the defects  $C_{Loop}$  and the concentration of defects  $D_{Loop}$ . The model assumes that the dislocation loops come from unfaulted {311} defects. The unfaulting rate can be defect size-dependent or not.

The following switch can be used to change the unfaulting rate:

```
pdbSet <material> CLoop Unfault.Model <model>
```

where `<model>` is either `Direct` or `SizeDependent`.

### Direct Model

If the `Unfault.Model` is set to `Direct`, the following reaction equations as well as the {311} defect equations (see [Defect Cluster Model: 311 on page 307](#)) are solved:

$$\frac{\partial C_{Loop}}{\partial t} = K_{311}C_{311} + 2\pi^2 R_{Loop} D_{Loop} D_{I\rho} K_{CLoop} (C_I - C_{ILoop}^*) \quad (513)$$

$$C_{ILoop}^* \equiv C_I^* e^{\left(\frac{\gamma\Omega}{bkT}\right) \left(\frac{\mu b\Omega}{4\pi R_{Loop} kT(1-\nu)} \ln\left(\frac{8R_{Loop}}{b}\right)\right)} \quad (514)$$

$$\frac{\partial D_{Loop}}{\partial t} = K_{311}D_{311} - K_{DLoop} \frac{2D_{Loop}}{R_{Loop}^2} \quad (515)$$

where:

- $K_{311}$  is the unfaulting rate of {311} defects to dislocation loops.
- $R_{Loop}$  is the average radius of loops.
- $D_{I\rho}$  is the diffusivity of neutral interstitials.
- $\mu$  is the shear modulus (dyn/cm<sup>2</sup>).
- $\gamma$  is the stacking fault energy (dyn/cm).
- $\Omega$  is the atomic value of silicon ( $2 \times 10^{-23}$ ).
- $\nu$  is the Poisson ratio.
- $b$  is the magnitude of Burger's vector.
- $K_{CLoop}$  and  $K_{DLoop}$  are fitting parameters for the model.

#### 4: Diffusion

##### Defect Clusters

These parameters can be set using the following commands:

```

pdbSet <material> CLoop      K311                {<n>}
pdbSet <material> Mechanics  ShearModulus          {<n>}
pdbSet <material> CLoop      StackingFaultEng      {<n>}
pdbSet <material> CLoop      BurgersVec            {<n>}
pdbSet <material> CLoop      KCLoop                {<n>}
pdbSet <material> DLoop      KDLoop                {<n>}

```

### Size-dependent Model

If the `Unfault.Model` is set to `SizeDependent`, the following reaction equations and the {311} defect equations (see [Defect Cluster Model: 311 on page 307](#)) are solved:

$$\frac{\partial C_{Loop}}{\partial t} = K_{311} C_{311}^2 C_T + 2\pi^2 R_{Loop} D_{Loop} D_I \rho K_{CLoop} (C_I - C_{ILoop}^*) \quad (516)$$

$$\frac{\partial D_{Loop}}{\partial t} = K_{311} D_{311} C_{311} C_T K_{D311} - \frac{2\pi^2 R_{Loop} D_{Loop}^2 D_I \rho K_{CLoop} C_{ILoop}^*}{C_{Loop}} \quad (517)$$

where  $K_{D311}$  is the scaling factor for the unfaulting rate and can be defined using the command:

```

pdbSet <material> CLoop KD311 {<n>}

```

$C_T$  is the user-defined term to further modify the unfaulting rate and can be defined using the command:

```

term name=CLoopTransfer <material> eqn = {User defined Equation}

```

The model is used to simulate all three phases of dislocation nucleation and evolution: nucleation, Ostwald ripening, and dissolution.

To modify the equilibrium concentration of interstitials at the loop boundaries ( $C_{ILoop}^*$ ) by complex prefactors, you can define the following terms in the command file:

```

term name=CLoopDissIntFactor silicon add eqn = { equation }

```

$C_{ILoop}^*$  increases dramatically as the loop radius becomes smaller. To avoid convergence problems,  $C_{ILoop}^*$  is limited by a minimum loop radius ( $R_{LoopMin}$ ) and  $C_{Loop}^{dFactor}$  as follows:

$$C_{ILoop}^* = \frac{C_{ILoop}^*(R_{LoopMin}) C_{ILoop}^*(R_{Loop})}{C_{ILoop}^*(R_{LoopMin}) + C_{ILoop}^*(R_{Loop})} \left( 1 - \frac{C_{Loop}^{dFactor}}{C_{Loop} + C_{Loop}^{dFactor}} \right) \quad (518)$$

The minimum radius and the damping factor are set with the commands:

```
pdbSet <material> CLoop RLoopMin {<n>}
pdbSet <material> CLoop DampFactor {<n>}
```

If the Loop model is used with the 2Moment model, to avoid convergence problems, the interstitial evaporation terms in Eq. 556, Eq. 557, Eq. 558, and Eq. 559 are scaled by:

$$R_{limit} = \left( 1 - \frac{C_{311}^{dFactor}}{C_{311}^{dFactor} + C_{311}} \right) \quad (519)$$

The damping factor for the {311} defects can be set:

```
pdbSet <material> C311 DampFactor {<n>}
```

Table 33 Solution names for loop model

Symbol	Solution name
$C_{Loop}$	CLoop
$D_{Loop}$	DLoop

## Initializing Loop Model

Since the loop model relies on the {311} defect model, first, the {311} defect model is initialized (see [Initializing 311 Model on page 314](#)). Then, the loop model fields CLoop and DLoop are initialized. If there is no preexisting data field, the fields are set to  $1 \times 10^{10}$  and  $5 \times 10^7$ , respectively. If there is an existing data field, the existing fields are used. By default, the loops are assumed to break apart in the amorphous regions.

You can specify the percentage of loops retained in the amorphous region per solution variable using the parameter AmPercent:

```
pdbSet <mater> DLoop AmPercent {<n>}
pdbSet <mater> CLoop AmPercent {<n>}
```

For example:

$$D_{Loop} = \begin{cases} D_{Loop} * \text{AmPercent} & \text{Amorphous regions} \\ D_{Loop} & \text{Crystalline regions} \end{cases} \quad (520)$$

$$C_{Loop} = \begin{cases} C_{Loop} * \text{AmPercent} & \text{Amorphous regions} \\ C_{Loop} & \text{Crystalline regions} \end{cases} \quad (521)$$

The value of the AmPercent parameter must be between 0 and 1.

---

## Defect Cluster Model: LoopEvolution

If you set the defect cluster model to `LoopEvolution`, the TS4 style loop evolution model [35] is used. The rate of absorption of interstitials by dislocation loops is given by:

$$R_I \equiv 2\pi^2 R_{Loop} K_{CLoop} D_{Loop} D_I (C_I - C_{ILoop}^*) \quad (522)$$

$$C_{ILoop}^* \equiv C_I^* e^{\left(\frac{\gamma\Omega}{bkT}\right)} e^{-\left(\frac{\mu b\Omega}{4\pi R_{Loop} kT(1-\nu)} \ln\left(\frac{8R_{Loop}}{b}\right)\right)} \quad (523)$$

where:

- $R_{Loop}$  is the average loop radius.
- $D_{Loop}$  is the loop density.
- $D_I$  is the diffusivity of interstitials.
- $K_{CLoop}$  is the fitting parameter.
- $\mu$  is the shear modulus (dyn/cm<sup>2</sup>).
- $\gamma$  is the stacking fault energy (dyn/cm).
- $\Omega$  is the atomic value of silicon ( $2 \times 10^{-23}$ ).
- $\nu$  is the Poisson ratio.
- $b$  is the magnitude of Burger's vector.

These parameters can be set using the following commands:

```

pdbSet <material> CLoop ShearModulus    {<n>}
pdbSet <material> CLoop StackingFaultEng {<n>}
pdbSet <material> CLoop BurgersVec      {<n>}
pdbSet <material> CLoop KCLoop          {<n>}

```

The evolution of the loop radius is given by:

$$\frac{\partial R_{Loop}}{\partial t} = \frac{\pi}{N_0} K_{CLoop} D_I (C_I - C_{ILoop}^*) \quad (524)$$

where  $N_0$  is the {111} planar density of silicon ( $1.57 \times 10^{15}$  cm<sup>-2</sup>).



The equilibrium concentration of interstitials at the loop boundaries ( $C_{ILoop}^*$ ) increases dramatically as the loop radius becomes smaller. To avoid convergence problems,  $R_I$  is limited by a minimum loop radius ( $R_{LoopMin}$ ) as follows:

$$Damp_0 \equiv \frac{R_{Loop}}{R_{LoopMin}}; \quad Damp \equiv \frac{Damp_0(4.605)}{Damp_0 + 4.605} \quad (525)$$

$$R_I \equiv R_I(R_{Loop})(1 - e^{-(Damp)})$$

To set the minimum radius, use the command:

```
pdbSet <material> CLoop RLoopMin {<n>}
```

To set the density of loops to a fixed value, use the command:

```
pdbSet <mater> DLoop ConstantDensity {<n>}
```

Table 34 Solution names for LoopEvolution model

Symbol	Solution name
$R_{Loop}$	RLoop

## Initializing LoopEvolution Model

To specify the initial loop radius, use:

```
pdbSet <mater> RLoop InitialRadius {<n>}
```

To set the density of loops to a fixed value, use the command:

```
pdbSet <mater> DLoop ConstantDensity {<n>}
```

or it will be calculated using the following:

$$D_{Loop} = \frac{Fraction(C_I - Threshold)}{\pi N_0 R_{Loop}^2} \quad (526)$$

where *Fraction* and *Threshold* can be set with:

```
pdbSet <material> CLoop Fraction {<n>}
pdbSet <material> CLoop Threshold {<n>}
```

**NOTE** If ConstantDensity is zero, [Eq. 526](#) will be used.

Loops are produced in that portion of the structure where the interstitial concentration (due to implant damage, before recombination) is in the range:

$$Dmax > Damage > Dmin \quad (527)$$

#### 4: Diffusion

##### Defect Clusters

$D_{max}$  and  $D_{min}$  can be set:

```
pdbSet <material> CLoop Dmin {<n>}  
pdbSet <material> CLoop Dmax {<n>}
```

The concentration of interstitials corresponding to the edge of the amorphous region is from the work of Fair and Pappas [2]. The concentration of interstitials is not reduced by the formation of end-of-range loops if `DLoop` is set to a constant value. Pre-existing dislocation loops in the region are presumed to be destroyed by the implant.

**NOTE** In this model, `CLoop` and `DLoop` are terms. Therefore, they should be converted to data fields with the `select` command or added to the `plx/DFISE` list to save in a file.

---

## Defect Cluster Model: FRENDECH

If you set the model to `FRENDECH`, this activates the extended defect model developed by FRENDECH partners [36][37][38]. The model assumes the following reactions:



where  $I_n$  and  $I_{n+1}$  are the interstitial defects consisting of  $n$  and  $n + 1$  silicon atoms. The reactions can be written as:

$$R_1 \equiv k_{f_{n-1}} C_{I_{n-1}} - k_{r_n} C_{I_n} \quad (530)$$

$$R_2 \equiv -(k_{f_n} C_{I_n} - k_{r_{n+1}} C_{I_{n+1}}) \quad (531)$$

and the model is given by:

$$\frac{\partial C_{I_n}}{\partial t} = R_1 + R_2 \quad (532)$$

where  $C_{I_n}$  is the density of defects containing  $n$  atoms.

The emission rate  $k_{r_n}$  is given by:

$$k_{r_n} = D_{I^0} C_I^* \frac{A_{n-1}}{R_{eff}} e^{\left(\frac{-E_{fn}}{kT}\right)} \quad (533)$$

where:

- $D_{I^0}$  is the diffusion coefficient of neutral interstitials.
- $C_I^*$  is the equilibrium concentration of interstitials.
- $\frac{A_{n-1}}{R_{eff}}$  is the capture efficiency of the defect.
- $E_{fn}$  is its formation energy.

The capture rate  $k_{f_n}$  is:

$$k_{f_n} = D_{I^0} C_I \frac{A_n}{R_{eff}} \quad (534)$$

where  $C_I$  is the concentration of interstitials.  $\frac{A_n}{R_{eff}}$  and  $E_{fn}$  can be defined using the command:

```
pdbSet <material> Interstitial BindCluster <cluster> {<n>}
```

where <cluster> is a valid cluster name (for example, I2, I3, I21) and <n> must be an Arrhenius expression with a prefactor of  $\frac{A_n}{R_{eff}}$  and an activation energy of  $E_{fn}$ .

For example:

```
pdbSet Silicon Interstitial BindCluster I6 {[Arrhenius 3.82578e-07 -1.29]}
```

sets the  $\frac{A_n}{R_{eff}}$  to  $3.82578 \times 10^{-7}$  eV and  $E_{fn}$  to  $-1.29$  eV for  $n = 6$ .

Since cluster sizes can change easily from a few atoms to a few thousand atoms, it is not feasible to solve all cluster equations. Therefore, the number of equations to be solved is reduced by using the method proposed by FRENTECH partners [39]. The method allows for the logarithmic discretization of clusters:

$$\begin{aligned} \frac{d}{dt} \rho(u) = & - \left(1 + \frac{e^{-u}}{2}\right) \frac{e^{-u}}{2\alpha} (k_{F_{u+\alpha}} \rho_{u+\alpha} - k_{F_{u-\alpha}} \rho_{u-\alpha}) \\ & + \left(1 - \frac{e^{-u}}{2}\right) \frac{e^{-u}}{2\alpha} (k_{R_{u+\alpha}} \rho_{u+\alpha} - k_{R_{u-\alpha}} \rho_{u-\alpha}) \\ & + \frac{e^{-2u}}{2\alpha^2} (k_{F_{u+\alpha}} \rho_{u+\alpha} - 2k_{F_u} \rho_u + k_{F_{u-\alpha}} \rho_{u-\alpha}) \\ & + \frac{e^{-2u}}{2\alpha^2} (k_{R_{u+\alpha}} \rho_{u+\alpha} - 2k_{R_u} \rho_u + k_{R_{u-\alpha}} \rho_{u-\alpha}) \end{aligned} \quad (535)$$

#### 4: Diffusion

##### Defect Clusters

where  $\rho(u)$  is the density function, and  $\alpha$  is the step of the logarithmic discretization.  $k_{F_u}$  and  $k_{R_u}$  are related to the capture and emission rate  $k_{f_n}$  and  $k_{r_n}$  by the relations:

$$k_{F_u} = k_{f_{n=e^u}} \quad (536)$$

$$k_{R_u} = k_{r_{n=e^u}} \quad (537)$$

The discretization is regular on a regularities scale. For example, the step in the reduced region is calculated by:

$$\alpha = \frac{\log(n_{\max}(-1)) - \log(n_{\text{lastlin}} + 1)}{n_{\text{logsteps}}} \quad (538)$$

where  $n_{\max}$  is the biggest cluster size,  $n_{\text{lastlin}}$  is the number of small interstitial clusters in the linear region, and  $n_{\text{logsteps}}$  is the number of steps in the reduced region.

You can specify  $n_{\max}$ ,  $n_{\text{lastlin}}$ , and  $n_{\text{logsteps}}$  using the following commands:

```

pdbSet <material> Int BiggestClusterSize    {<n>}
pdbSet <material> Int NumberofSmallClusters {<n>}
pdbSet <material> Int logSteps              {<n>}

```

For example:

```

pdbSet Silicon Int BiggestClusterSize    10000
pdbSet Silicon Int NumberofSmallClusters 11
pdbSet Silicon Int logSteps              5

```

allow Sentaurus Process to solve the cluster equations for I2, I3, I4, I5, I6, I7, I8, I9, I10, I11, I12, I46, I177, I679, I2605, I10000.

The capture and emission rate  $k_{f_n}$  and  $k_{r_n}$  are stored in the parameter database for cluster sizes less than 10. If you do not specify the rates for bigger clusters, they will be calculated using the following formulas:

$$\left. \frac{A_n}{R_{\text{eff}} \right|_{\{311\}} = \frac{4\pi aL + 4\pi aW + 8\pi a^2}{\log\left(1 + \sqrt{1 + \left(\frac{2a}{W}\right)^2}\right) - \log\left(\frac{2a}{W}\right) + \log\left(1 + \sqrt{1 + \left(\frac{2(L+a)}{W}\right)^2}\right) - \log\left(\frac{2(L+a)}{W}\right)} \quad (539)$$

$$\frac{\frac{1}{a}\sqrt{1 + \left(\frac{2a}{W}\right)^2} + \frac{1}{L+a}\sqrt{1 + \left(\frac{2(L+a)}{W}\right)^2}}$$

$$E_{\text{strain}}^n = \frac{\mu b^2 L}{2\pi(1-\nu)} \log\left(\frac{2W}{b}\right) + \frac{\mu b^2 W}{2\pi} \left( (\cos\theta)^2 + \left(\frac{\sin\theta}{1-\nu}\right)^2 \right) \log\left(\frac{2L}{b}\right) \quad (540)$$

$$E_{fn} = E_{strain}^{n+1} + \gamma \cdot (n + 1) - E_{strain}^n + \gamma \cdot n \quad (541)$$

where:

- $L$  and  $W$  are the length and width of the {311} defect ( $L = n \cdot 5 \times 10^{-9}$  cm and  $W = 4 \times 10^{-7}$  cm).
- $a$  is the lattice spacing of silicon.
- $\mu$  denotes the shear modulus of silicon ( $\mu = 7.55 \times 10^{11}$  dyn/cm).
- $\nu$  is the Poisson ratio ( $\nu = 0.3$ ).
- $b$  is the length of Burger's vector ( $b = 1.1 \times 10^{-8}$  cm).
- $\theta$  is the angle between Burger's vector and the normal vector perpendicular to the plane of the defect ( $\theta = 77.8^\circ$ ).
- $\gamma$  is the stacking fault energy per atom ( $\gamma = 0.38$  eV).

Burger's vector and the stacking fault energy can be set using the commands:

```
pdbSet <material> C311 BurgersVec {<n>}
pdbSet <material> Int StackingFauldEng {<n>}
```

**NOTE** Since FRENDTECH models solve for a range of cluster sizes, simulations may be slower.

Table 35 Solution names for FRENDTECH model

Symbol	Solution name
$C_{I_2}$	I2
$C_{I_3}$	I3
$C_{I_{10}}$	I10

## Initializing FRENDTECH Model

By default, the interstitial clusters are assumed to break apart in the amorphous regions. You can specify the percentage of clusters retained in the amorphous region per solution variable using the parameter `AmPercent`:

```
pdbSetDouble <mater> I200 AmPercent {<n>}
pdbSetDouble <mater> I100 AmPercent {<n>}
```

For example:

$$I_{200} = \begin{cases} I_{200} * \text{AmPercent} & \text{Amorphous regions} \\ I_{299} & \text{Crystalline regions} \end{cases} \quad (542)$$

Since not all clusters have been incorporated into the parameter database, the `pdbSetDouble` command must be used; the shorthand `pdbSet` command cannot be used to specify these parameters. The value specified for the `AmPercent` parameter must be between 0 and 1.

---

## Defect Cluster Model: 1Moment

### Interstitial

If you set the model to `1Moment`, the model for the formation and dissolution of interstitial clusters ( $\{311\}$  or  $\{113\}$  defects) is included. The `1Moment` model uses a single equation to calculate the total number of interstitials bound in clusters. The following nonlinear algebraic equation along with the related diffusion equations are solved:

$$\frac{\partial C_{I\text{cluster}}}{\partial t} = R_{CI} - R_{CV} \quad (543)$$

where  $C_{I\text{cluster}}$  is the concentration of clustered interstitials, and  $R_{CI}$  and  $R_{CV}$  describe cluster interaction with interstitials and vacancies, respectively.

The interstitial interaction includes two terms describing the clustering of interstitials and one describing the de-clustering:

$$R_{CI} = I_{kfi} \frac{(C_I)^{I_{fi}}}{(C_I^*)^{I_{sfi}}} + I_{kfc} \frac{(C_I)^{I_{fc}}}{(C_I^*)^{I_{sfc}}} (C_{I\text{cluster}} + I_{kfc} C_I) - I_{kr} (C_{I\text{cluster}})^{I_{cr}} \quad (544)$$

where  $C_I$  is the concentration of unclustered interstitials, and  $C_I^*$  is the equilibrium concentration of interstitials. The first term models nucleation of the interstitial clusters at high interstitial supersaturation. The second term models growth of the interstitial clusters by consuming free interstitials. The third term models dissolution of the interstitial clusters by emitting interstitials. If the `1Moment` model is used with the `Full` cluster model, [Eq. 544](#) is modified as follows:

$$R_{CI} = (max + 1) R_{sIcl(max+1)} + I_{kfc} \frac{(C_I)^{I_{fc}}}{(C_I^*)^{I_{sfc}}} (C_{I\text{cluster}} + I_{kfc} C_I) - I_{kr} (C_{I\text{cluster}})^{I_{cr}} \quad (545)$$

where  $R_{sIcl(max+1)}$  is given in [Defect Cluster Model: Full on page 333](#). The smallest large cluster forms when the small cluster captures one free interstitial by the reaction rate  $R_{sIcl(max+1)}$ . The vacancy interaction includes one recombination and one generation term:

$$R_{CV} = V_{krv} \frac{(C_V)^{V_{rv}}}{(C_V^*)^{V_{svv}}} (C_{I\text{cluster}})^{V_{crv}} - V_{kf} (C_V^*)^{V_{svv}} (C_{I\text{cluster}})^{V_{cfv}} \quad (546)$$

where  $C_V$  is the concentration of free vacancies and  $C_V^*$  is the equilibrium concentration of vacancies. The first term models dissolution of the interstitial clusters by consuming vacancies. The second term models the emission of vacancies by the interstitial clusters.

To modify the dissolution rates  $I_{kr}$  and  $V_{kf}$  by complex prefactors, you can define the following terms in the input file:

```
term name=IClusterDissIntFactor silicon add eqn = { equation }
term name=IClusterDissVacFactor silicon add eqn = { equation }
```

For extrinsic silicon, the prefactors can be made a function of  $\left(\frac{n}{n_i}\right)$  to provide consistent TED results.

If the 1Moment model is used with the Full cluster model, Eq. 546 is modified as follows:

$$R_{CV} = (max + 1)R_{sIcV(max + 1)} + V_{krv} \frac{(C_V)^{V_{rv}}}{(C_V^*)^{V_{srv}}} (C_{ICluster})^{V_{crv}} - V_{kf} (C_V^*)^{V_{sfv}} (C_{ICluster})^{V_{cfv}} \quad (547)$$

where  $R_{sIcV(max + 1)}$  is given in [Defect Cluster Model: Full on page 333](#). It is the reaction rate of small interstitial clusters with vacancies. The reaction constants of the model can be modified using the following commands:

```
pdbSet <material> ICluster Ikfi {<n>}
pdbSet <material> ICluster Ikfc {<n>}
pdbSet <material> ICluster Ikr {<n>}
pdbSet <material> ICluster Ifi {<n>}
pdbSet <material> ICluster Isfi {<n>}
pdbSet <material> ICluster Ifc {<n>}
pdbSet <material> ICluster Isfc {<n>}
pdbSet <material> ICluster Icf {<n>}
pdbSet <material> ICluster Icr {<n>}
pdbSet <material> ICluster Ikfci {<n>}
pdbSet <material> ICluster Vkrv {<n>}
pdbSet <material> ICluster Vrv {<n>}
pdbSet <material> ICluster Vsrv {<n>}
pdbSet <material> ICluster Vcrv {<n>}
pdbSet <material> ICluster Vkf {<n>}
pdbSet <material> ICluster Vsfv {<n>}
pdbSet <material> ICluster Vcfv {<n>}
```

#### 4: Diffusion

##### Defect Clusters

The changes are accompanied by corresponding inverse changes in  $C_I$ . Therefore, clustering reduces the number of free interstitials, while the dissolution of clusters releases interstitials.

Table 36 Solution names for 1Moment model of interstitials

Symbol	Solution name
$C_{ICluster}$	ICluster

## Vacancy

If you set the model to 1Moment, the model for the formation and dissolution of vacancy clusters or voids is included. The 1Moment model uses a single equation to calculate the total number of vacancies bound in clusters. The following nonlinear algebraic equation along with the related diffusion equations are solved:

$$\frac{\partial C_{VCluster}}{\partial t} = R_{CV} - R_{CI} \quad (548)$$

where  $C_{VCluster}$  is the concentration of clustered vacancies, and  $R_{CV}$  and  $R_{CI}$  describe cluster interaction with vacancies and interstitials, respectively.

The vacancy interaction includes two terms describing the clustering of vacancies and one describing the declustering:

$$R_{CV} = V_{kfi} \frac{(C_V)^{V_{fi}}}{(C_V^*)^{V_{fi}}} + V_{kfc} \frac{(C_V)^{V_{fc}}}{(C_V^*)^{V_{fc}}} (C_{VCluster} + V_{kfc} C_V) - V_{kr} (C_{VCluster})^{V_{cr}} \quad (549)$$

where  $C_V$  is the concentration of unclustered vacancies, and  $C_V^*$  is the equilibrium concentration of vacancies. The first term models nucleation of the vacancy clusters at high vacancy supersaturation. The second term models growth of the vacancy clusters by consuming free vacancies. The third term models dissolution of the vacancy clusters by emitting vacancies. If the 1Moment model is used with the Full cluster model, Eq. 549 is modified as follows:

$$R_{CV} = (max + 1) R_{sVcl(max+1)} + V_{kfc} \frac{(C_V)^{V_{fc}}}{(C_V^*)^{V_{fc}}} (C_{VCluster} + V_{kfc} C_V) - V_{kr} (C_{VCluster})^{V_{cr}} \quad (550)$$

where  $R_{sVcl(max+1)}$  is given in [Defect Cluster Model: Full on page 333](#). The smallest large-cluster forms when the small cluster captures one free vacancy by the reaction rate  $R_{sVcl(max+1)}$ .



The interstitial interaction includes one recombination and one generation term:

$$R_{CI} = I_{krv} \frac{(C_I)^{I_{rv}}}{(C_I^*)^{I_{srv}}} (C_{VCluster})^{I_{crv}} - I_{kf} (C_I^*)^{I_{sfv}} (C_{VCluster})^{I_{cfv}} \quad (551)$$

where  $C_I$  is the concentration of free interstitials, and  $C_I^*$  is the equilibrium concentration of interstitials. The first term models dissolution of the vacancy clusters by consuming interstitials. The second term models the emission of interstitials by the vacancy clusters.

To modify the dissolution rates  $V_{kr}$  and  $I_{kf}$  by complex prefactors, you can define the following terms in the command file:

```
term name=VClusterDissVacFactor silicon add eqn = { equation }
term name=VClusterDissIntFactor silicon add eqn = { equation }
```

If the 1Moment model is used with the Full cluster model, Eq. 551 is modified as follows:

$$R_{CI} = (max + 1)R_{sVcl(max+1)} + I_{krv} \frac{(C_I)^{I_{rv}}}{(C_I^*)^{I_{srv}}} (C_{VCluster})^{I_{crv}} - I_{kf} (C_I^*)^{I_{sfv}} (C_{VCluster})^{I_{cfv}} \quad (552)$$

where  $R_{sVcl(max+1)}$  is given in [Defect Cluster Model: Full on page 333](#). It is the reaction rate of small vacancy clusters with interstitials. The reaction constants of the model can be modified using the following commands:

```
pdbSet <material> VCluster Vkfi {<n>}
pdbSet <material> VCluster Vkfc {<n>}
pdbSet <material> VCluster Vkr {<n>}
pdbSet <material> VCluster Vfi {<n>}
pdbSet <material> VCluster Vsfi {<n>}
pdbSet <material> VCluster Vfc {<n>}
pdbSet <material> VCluster Vsfc {<n>}
pdbSet <material> VCluster Vcf {<n>}
pdbSet <material> VCluster Vcr {<n>}
pdbSet <material> VCluster Vkfci {<n>}
pdbSet <material> VCluster Ikrv {<n>}
pdbSet <material> VCluster Irv {<n>}
pdbSet <material> VCluster Isrv {<n>}
pdbSet <material> VCluster Icrv {<n>}
pdbSet <material> VCluster Ikfv {<n>}
pdbSet <material> VCluster Isfv {<n>}
pdbSet <material> VCluster Icfv {<n>}
```

#### 4: Diffusion

##### Defect Clusters

The changes are accompanied by corresponding inverse changes in  $C_V$ . Therefore, clustering reduces the number of free vacancies; while the dissolution of clusters releases vacancies.

Table 37 Solution names for 1Moment model for vacancies

Symbol	Solution name
$C_{VCluster}$	VCluster

### Initializing 1Moment Model

The initial concentration of interstitial clusters or vacancy clusters after implantation is set in the `diffPreProcess` procedure (see [Ion Implantation to Diffusion on page 340](#)) and can be changed using the parameter `InitPercent` as follows:

```
pdbSet <material> ICluster InitPercent {<n>}
pdbSet <material> VCluster InitPercent {<n>}
```

`InitPercent` is the percentage of free implant interstitials used to initialize the model, for example:

$$ICluster = \begin{cases} Int\_Implant * InitPercent & \text{Crystalline regions} \\ 0 & \text{Amorphous regions} \end{cases} \quad (553)$$

$$VCluster = \begin{cases} Vac\_Implant * InitPercent & \text{Crystalline regions} \\ 0 & \text{Amorphous regions} \end{cases} \quad (554)$$

The value of `InitPercent` must be between 0 and 1. The model assumes that existing interstitial or vacancy clusters in the amorphized region break apart.

---

## Defect Cluster Model: 2Moment

### Interstitial

If you set the model to `2Moment`, the model for the formation and dissolution of interstitial clusters ( $\{311\}$  or  $\{113\}$  defects) and conversion of  $\{311\}$  clusters into dislocation loops are included [39]. The model calculates the first two moments of the size distribution of interstitial clusters, in other words, the number of clusters and the number of interstitials contained in the clusters. It can be used with the existing model for dislocation loops (`LoopEvolution`), although it is designed to include modeling of at least some dislocation loops.

The 2Moment clustering model is an implementation of the Gencer analytic kinetic precipitation model (AKPM). The density of clusters ( $D_{311}$ ) and concentration of interstitials ( $C_{311}$ ) contained in clusters are calculated as:

$$\frac{\partial D_{311}}{\partial t} = D_I \lambda_0 (C_I^2 - D_{311} C_{II}^* C_s \gamma_0) \quad (555)$$

$$\frac{\partial C_{311}}{\partial t} = 2 \frac{\partial D_{311}}{\partial t} + D_I \lambda_1 D_{311} (C_I - C_s C_{II}^* \gamma_1) \quad (556)$$

where  $C_I$  and  $D_I$  are the concentration and diffusivity of free interstitials. If the 2Moment model is used with the Full cluster model, Eq. 555 and Eq. 556 are modified as follows:

$$\frac{\partial D_{311}}{\partial t} = R_{sIcl(max+1)} - R_{sIcV(max+1)} - D_I \lambda_0 D_{311} C_{II}^* C_s \gamma_0 \quad (557)$$

$$\frac{\partial C_{311}}{\partial t} = (max+1)(R_{sIcl(max+1)} - R_{sIcV(max+1)}) + D_I \lambda_1 D_{311} (C_I - C_s C_{II}^* \gamma_1) \quad (558)$$

$C_s \gamma_0$ , which gives the dependence of the dissolution rate on the average cluster size, is given by:

$$C_s \gamma_0 = \begin{cases} C_{ss} \frac{K_1}{s-1} & s < n_{crit} \\ C_{sl} K_3 \left( \frac{1}{s-1} \right)^\alpha & s > n_{crit} \end{cases} \quad (559)$$

where:

- $K_1$  controls the dissolution of two atom clusters.
- $s = C_{311}/D_{311}$  is the average number of interstitials in a cluster.

$C_s \gamma_1$ , which gives the dependence of the rate of interstitial release on the average cluster size, is given by:

$$C_s \gamma_1 = \begin{cases} C_{ss} \frac{s-2}{s+K_0} \left[ 1 + \frac{(K_0+2)K_2}{s+K_0} \right] & s < n_{crit} \\ C_{sl} \left[ 1 + K_4 \left( \frac{K_0+2}{s+K_0} \right)^\alpha \right] & s > n_{crit} \end{cases} \quad (560)$$

where  $K_3$  and  $K_4$  are chosen to make  $C_s \gamma_0$  and  $C_s \gamma_1$  continuous at  $s = n_{crit}$ .  $C_{ss}, C_{sl}$  are the solid solubility of smaller and larger clusters.

#### 4: Diffusion

##### Defect Clusters

To modify  $C_s\gamma_0$  and  $C_s\gamma_1$  by complex prefactors, you can define the following terms in the command file:

```
term name=C311DissIntFactor silicon add eqn = { equation }
```

To set the model parameters, use the following commands:

```
pdbSet <material> C311 Lambda0 {<n>}
pdbSet <material> C311 Lambda1 {<n>}
pdbSet <material> C311 K0 {<n>}
pdbSet <material> C311 K1 {<n>}
pdbSet <material> C311 K2 {<n>}
pdbSet <material> C311 Alpha {<n>}
pdbSet <material> C311 NCritical {<n>}
pdbSet <material> Int SolubilitySmall {<n>}
pdbSet <material> Int SolubilityLarge {<n>}
```

Eq. 555 models the nucleation and dissolution of two-atom clusters.  $\lambda_0$  is the capture length for these processes.

Eq. 556 models the absorption and release of interstitials by clusters. The three terms on the right side model the absorption of interstitials during nucleation, the absorption of interstitials by nucleated clusters, and the release of interstitials by nucleated clusters.  $\lambda_1$  is the capture length for absorption and release of interstitials by nucleated clusters.  $C_{Ii}^*C_{ss}$  is the concentration of interstitials in equilibrium with a population of large {311} clusters.

For  $s > n_{crit}$ , some of the {311} defects unfault to form dislocation loops. These dislocation loops are included in the 2Moment model by modifying the cluster dissolution rates.  $\alpha$  controls the dissolution rate when loops are present, and  $C_{Ii}^*C_{sl}$  is the concentration of interstitials in equilibrium with a population of large dislocation loops,  $C_{Ii}C_{sl}$ .

Table 38 Solution names for 2Moment model of interstitials

Symbol	Solution name
$C_{311}$	C311
$D_{311}$	D311

## Vacancy

If you set the model to 2Moment – the model for the formation and dissolution of vacancy clusters – the model calculates the first two moments of the size distribution of vacancy clusters, that is, the number of clusters and the number of vacancies contained in the clusters.

The 2Moment clustering model is an implementation of the Gencer analytic kinetic precipitation model (AKPM). The density of clusters ( $D_{void}$ ) and concentration of vacancies ( $C_{void}$ ) contained in clusters are calculated as:

$$\frac{\partial D_{void}}{\partial t} = D_V \lambda_0 (C_V^2 - D_{void} C_{Vi}^* C_s \gamma_0) \quad (561)$$

$$\frac{\partial C_{void}}{\partial t} = 2 \frac{\partial D_{void}}{\partial t} + D_V \lambda_1 D_{void} (C_V - C_s C_{Vi}^* \gamma_1) \quad (562)$$

where  $C_V$  and  $D_V$  are the concentration and diffusivity of free vacancies.

If the 2Moment model is used with the Full cluster model, Eq. 561 and Eq. 562 are modified as follows:

$$\frac{\partial D_{void}}{\partial t} = R_{sVcl(max+1)} - R_{sVcl(max+1)} - D_V \lambda_0 D_{void} C_{Vi}^* C_s \gamma_0 \quad (563)$$

$$\frac{\partial C_{void}}{\partial t} = (max+1)(R_{sVcl(max+1)} - R_{sVcl(max+1)}) + D_V \lambda_1 D_{void} (C_V - C_s C_{Vi}^* \gamma_1) \quad (564)$$

$C_s \gamma_0$ , which gives the dependence of the dissolution rate on the average cluster size, is given by:

$$C_s \gamma_0 = C_{ss} \frac{K_1}{s-1} \quad (565)$$

where:

- $K_1$  controls the dissolution of two atom clusters.
- $s = C_{void}/D_{void}$  is the average number of vacancies in a cluster.

$C_s \gamma_1$ , which gives the dependence of the rate of vacancy release on the average cluster size, is given by:

$$C_s \gamma_1 = C_{ss} \frac{s-2}{s+K_0} \left[ 1 + \frac{(K_0+2)K_2}{s+K_0} \right] \quad (566)$$

$C_{ss}$  are the solid solubility of clusters.

To modify  $C_s \gamma_0$  and  $C_s \gamma_1$  by complex prefactors, you can define the following terms in the command file:

```
term name=CVoidDissVacFactor silicon add eqn = { equation }
```

#### 4: Diffusion

##### Defect Clusters

To set the model parameters, use the following commands:

```

pdbSet <material> CVoid Lambda0 {<n>}
pdbSet <material> CVoid Lambda1 {<n>}
pdbSet <material> CVoid K0           {<n>}
pdbSet <material> CVoid K1           {<n>}
pdbSet <material> CVoid K2           {<n>}
pdbSet <material> Vac SolubilitySmall {<n>}

```

Eq. 561 models the formation and dissolution of di-vacancy clusters.  $\lambda_0$  is the capture length for these processes.

Eq. 562 models the absorption and release of vacancies by clusters. The three terms on the right side model the absorption of vacancies during di-vacancy cluster formation, the absorption of vacancies by clusters, and the release of vacancies by clusters.  $\lambda_1$  is the capture length for absorption and release of vacancies by clusters.  $C_{Vi}^*C_{ss}$  is the concentration of vacancies in equilibrium with a population of large vacancy clusters.

Table 39 Solution names for 2Moment model of vacancies

Symbol	Solution name
$C_{void}$	CVoid
$D_{void}$	DVoid

### Initializing 2Moment Model

The initial concentration of interstitial clusters after implants is set in the `diffPreProcess` procedure (see [Ion Implantation to Diffusion on page 340](#)). By default, clusters are assumed to break apart in the amorphous regions. You can specify the percentage of clusters retained in the amorphous region per cluster solution variable using the parameter `AmPercent`:

```

pdbSet <material> C311 AmPercent {<n>}
pdbSet <material> D311 AmPercent {<n>}

pdbSet <material> CVoid AmPercent {<n>}
pdbSet <material> DVoid AmPercent {<n>}

```

For example:

$$D_{311} = \begin{cases} D_{311} * \text{AmPercent} & \text{Amorphous regions} \\ D_{311} & \text{Crystalline regions} \end{cases} \quad (567)$$

The value of the `AmPercent` parameter must be between 0 and 1.

## Defect Cluster Model: Full

### Interstitial

If you set the defect cluster model to `Full`, the TS4 style transient small interstitial cluster model is used. The reactions associated with the size- $n$  small interstitial cluster is as follows:



$I_n$  denote the  $n$ -size interstitial small cluster;  $I, V$  are the interstitials and vacancies. The transient equation for the  $n$ -size small interstitial cluster is:

$$\frac{\partial C_n}{\partial t} = R_{cI(n)} - R_{cV(n)} \quad 2 \leq n < n_{max} \quad (572)$$

$n_{max}$  can be set using the following command:

```
pdbSet Si Int CL.Size {<n>}
```

and  $R_{cI(n)}$  and  $R_{cV(n)}$  are described as follows:

$$R_{cI(n)} = R_{cI((n-1) \rightarrow (n))} - R_{cI((n) \rightarrow (n+1))} \quad (573)$$

$$R_{cV(n)} = R_{cV((n) \rightarrow (n-1))} - R_{cV((n+1) \rightarrow (n))} \quad (574)$$

$$R_{cI((n-1) \rightarrow (n))} = k_{fi}^{(n)} C_{I(n-1)} \frac{C_I}{C_I^*} - k_{ri}^{(n)} C_{I(n)} \quad (575)$$

$$R_{cI((n) \rightarrow (n+1))} = k_{fi}^{(n+1)} C_{I(n)} \frac{C_I}{C_I^*} - k_{ri}^{(n+1)} C_{I(n+1)} \quad (576)$$

$$R_{cV((n) \rightarrow (n-1))} = k_{rv}^{(n)} C_{I(n)} \frac{C_V}{C_V^*} - k_{fv}^{(n)} C_{I(n-1)} \quad (577)$$

**4: Diffusion**  
Defect Clusters

$$R_{cV((n+1) \rightarrow (n))} = k_{rv}^{(n+1)} C_{I(n+1)} \frac{C_V}{C_V^*} - k_{fv}^{(n+1)} C_{I(n)} \quad (578)$$

here:

$$k_{fi}^{(n)} = C_{li}^* \sum_z f_{nz}^i k_{fz} \left(\frac{n}{n_i}\right)^{-z} \quad n > 2 \quad (579)$$

$$k_{fi}^{(2)} = \frac{C_{li}^{*2}}{C_{I,z,q}^*} \sum_{z,q} f_{2qz}^i k_{fz} k_{fq} \left(\frac{n}{n_i}\right)^{-(z+q)} \quad n = 2 \quad (580)$$

$$k_{ri}^{(n)} = C_{li}^* \sum_z r_{nz}^i k_{fz} \left(\frac{n}{n_i}\right)^{-z} \quad n > 2 \quad (581)$$

$$k_{ri}^{(2)} = C_{li}^* \sum_{z,q} r_{2qz}^i k_{fz} k_{fq} \left(\frac{n}{n_i}\right)^{-(z+q)} \quad n = 2 \quad (582)$$

$$k_{fv}^{(n)} = C_{vi}^* \sum_z f_{nz}^v k_{vz} \left(\frac{n}{n_i}\right)^{-z} \quad n > 2 \quad (583)$$

$$k_{fv}^{(2)} = \frac{C_{li}^* C_{vi}^*}{C_{I,z}^*} \sum_z f_{2z}^v k_{vz} \left(\frac{n}{n_i}\right)^{-z} \quad n = 2 \quad (584)$$

$$k_{rv}^{(n)} = C_{vi}^* \sum_z r_{nz}^v k_{vz} \left(\frac{n}{n_i}\right)^{-z} \quad (585)$$

The reaction rate constants,  $f^i = k_{fi}, f^v = k_{fv}, r^i = k_{ri}, r^v = k_{rv}$ , can be set using the commands:

```

pdbSet Si I2 kfI {<i, j>} {<n>}
pdbSet Si I2 krI {<i, j>} {<n>}
pdbSet Si I2 kfV {<i>} {<n>}
pdbSet Si I2 krV {<i>} {<n>}
pdbSet Si I3 kfI {<i>} {<n>}
pdbSet Si I3 krI {<i>} {<n>}
pdbSet Si I3 kfV {<i>} {<n>}
pdbSet Si I3 krV {<i>} {<n>}
pdbSet Si I4 kfI {<i>} {<n>}
pdbSet Si I4 krI {<i>} {<n>}
pdbSet Si I4 kfV {<i>} {<n>}
pdbSet Si I4 krV {<i>} {<n>}
pdbSet Si I5 kfI {<i>} {<n>}

```



The indices  $i$  and  $j$  are integers representing the charge state of interstitials and reacting interstitials. The shorthand `pdbSet` command can be used for clusters up to size 5. For all other clusters, the longhand `pdbSetDoubleArray` command must be used.

**NOTE** The indices for the parameters `kfI` and `krI` for  $I_2$  clusters have the form  $i, j$ . The indices are separated by a comma; no space is allowed between the indices.

If you want to use same reaction rate constants for all charges, use the command:

```
pdbSet Si Int CL.All {1|0}
```

If `CL.ALL` is set to 1, the model uses the 0th indexed reaction rate constants (for example, `kfI(0,0)` or `kfI(0)`, `krV(0)` and so on) in the reaction calculation for all charged states.

To modify  $k_{ri}$  and  $k_{fv}$  by complex prefactors, you can define the following terms in the command file, for example, for  $I_2$ :

```
term name=I2DissIntFactor silicon add eqn = { equation }
term name=I2DissVacFactor silicon add eqn = { equation }
```

The net capture rate of free interstitials by the small interstitial clusters is given by:

$$R_{sIcl} = R_{cl(1 \rightarrow 2)} + \sum_{n=1}^{max} R_{cl(n \rightarrow n+1)} \quad (586)$$

The net capture rate of free vacancies by the small interstitial clusters is given by:

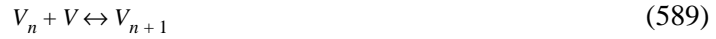
$$R_{sIcV} = \sum_{n=1}^{max} R_{cV(n \rightarrow n+1)} \quad (587)$$

Table 40 Solution names for full model of interstitials

Symbol	Solution name
$C_{I_2}$	I2
$C_{I_3}$	I3
$C_{I_4}$	I4
$C_{I_5}$	I5

## Vacancy

If you set the defect cluster model to `Full`, the TSUPREM-4-style transient small-vacancy cluster model is used. The reactions associated with the  $n$ -size small interstitial cluster are:



where  $V_n$  denotes the  $n$ -size small vacancy cluster, and  $I, V$  are the interstitials and vacancies.

The transient equation for the  $n$ -size small vacancy cluster is:

$$\frac{\partial C_n}{\partial t} = R_{cV(n)} - R_{cI(n)} \quad 2 \leq n < n_{max} \quad (592)$$

$n_{max}$  can be set using the following command:

```
pdbSet Si Vac CL.Size {<n>}
```

$R_{cV(n)}$  and  $R_{cI(n)}$  are described as follows:

$$R_{cV(n)} = R_{cV((n-1) \rightarrow (n))} - R_{cV((n) \rightarrow (n+1))} \quad (593)$$

$$R_{cI(n)} = R_{cI((n) \rightarrow (n-1))} - R_{cI((n+1) \rightarrow (n))} \quad (594)$$

$$R_{cV((n-1) \rightarrow (n))} = k_{fv}^{(n)} C_{V(n-1)} \frac{C_V}{C_V^*} - k_{rv}^{(n)} C_{V(n)} \quad (595)$$

$$R_{cV((n) \rightarrow (n+1))} = k_{fv}^{(n+1)} C_{V(n)} \frac{C_V}{C_V^*} - k_{rv}^{(n+1)} C_{V(n+1)} \quad (596)$$

$$R_{cI((n) \rightarrow (n-1))} = k_{ri}^{(n)} C_{V(n)} \frac{C_I}{C_I^*} - k_{fi}^{(n)} C_{V(n-1)} \quad (597)$$

$$R_{cI((n+1) \rightarrow (n))} = k_{ri}^{(n+1)} C_{V(n+1)} \frac{C_I}{C_I^*} - k_{fi}^{(n+1)} C_{V(n)} \quad (598)$$

here:

$$k_{fv}^{(n)} = C_{Vi}^* \sum_z f_{nz}^i k_{Vz} \left(\frac{n}{n_i}\right)^{-z} \quad n > 2 \quad (599)$$

$$k_{fv}^{(2)} = \frac{C_{Vi}^{*2}}{C_{Vz,q}^*} \sum_{z,q} f_{2qz}^i k_{Vz} k_{Vq} \left(\frac{n}{n_i}\right)^{-(z+q)} \quad n = 2 \quad (600)$$

$$k_{rv}^{(n)} = C_{Vi}^* \sum_z r_{nz}^i k_{Vz} \left(\frac{n}{n_i}\right)^{-z} \quad n > 2 \quad (601)$$

$$k_{rv}^{(2)} = C_{Vi}^* \sum_{z,q} r_{2qz}^i k_{Vz} k_{Vq} \left(\frac{n}{n_i}\right)^{-(z+q)} \quad n = 2 \quad (602)$$

$$k_{fi}^{(n)} = C_{Ii}^* \sum_z f_{nz}^i k_{Iz} \left(\frac{n}{n_i}\right)^{-z} \quad n > 2 \quad (603)$$

$$k_{fi}^{(2)} = \frac{C_{Ii}^* C_{Vi}^*}{C_V^*} \sum_z f_{2z}^i k_{Iz} \left(\frac{n}{n_i}\right)^{-z} \quad n = 2 \quad (604)$$

$$k_{ri}^{(n)} = C_{Ii}^* \sum_z r_{nz}^i k_{Iz} \left(\frac{n}{n_i}\right)^{-z} \quad (605)$$

The reaction rate constants,  $f^v = k_{fv}$ ,  $f^i = k_{fi}$ ,  $r^v = k_{rv}$ ,  $r^i = k_{ri}$ , can be set using the commands:

```

pdbSet Si V2 kfV {<i>, j>} {<n>}
pdbSet Si V2 krV {<i>, j>} {<n>}
pdbSet Si V2 kfI {<i>} {<n>}
pdbSet Si V2 krI {<i>} {<n>}
pdbSet Si V3 kfV {<i>} {<n>}
pdbSet Si V3 krV {<i>} {<n>}
pdbSet Si V3 kfI {<i>} {<n>}
pdbSet Si V3 krI {<i>} {<n>}
pdbSet Si V4 kfV {<i>} {<n>}
pdbSet Si V4 krV {<i>} {<n>}
pdbSet Si V4 kfI {<i>} {<n>}
pdbSet Si V4 krI {<i>} {<n>}
pdbSet Si V5 kfV {<i>} {<n>}
pdbSet Si V5 krV {<i>} {<n>}
pdbSet Si V5 kfI {<i>} {<n>}
pdbSet Si V5 krI {<i>} {<n>}
pdbSet Si V6 kfV {<i>} {<n>}

```

#### 4: Diffusion

##### Defect Clusters

```

pdbSet Si V6 krV {<i>} {<n>}
pdbSet Si V6 kfI {<i>} {<n>}
pdbSet Si V6 krI {<i>} {<n>}
pdbSet Si V7 kfV {<i>} {<n>}
pdbSet Si V7 krV {<i>} {<n>}
pdbSet Si V7 kfI {<i>} {<n>}
pdbSet Si V7 krI {<i>} {<n>}
pdbSet Si V8 kfV {<i>} {<n>}

```

The indices  $i$  and  $j$  are integers representing the charge state of vacancies and reacting vacancies. The shorthand `pdbSet` command can be used for clusters up to size 8. For all other clusters, the longhand `pdbSetDoubleArray` command must be used.

**NOTE** The indices for the parameters `kfV` and `krV` for  $V_2$  clusters have the form of  $i, j$ . The indices are separated by a comma; no space is allowed between the indices.

If you want to use same reaction rate constants for all charges, use the command:

```

pdbSet Si Vac CL.All {1|0}

```

If `CL.ALL` is set to 1, the model uses the 0th indexed reaction rate constants (for example, `kfV(0,0)` or `kfV(0)`, `krI(0)` and so on) in the reaction calculation for all charged states.

To modify  $k_{rv}$  and  $k_{fi}$  by complex prefactors, you can define the following terms in the command file, for example, for  $V_2$ :

```

term name=V2DissVacFactor silicon add eqn = { equation }
term name=V2DissIntFactor silicon add eqn = { equation }

```

The net capture rate of free vacancies by the small vacancy clusters is given by:

$$R_{sVcl} = R_{cV(1 \rightarrow 2)} + \sum_{n=1}^{max} R_{cV(n \rightarrow n+1)} \quad (606)$$

The net capture rate of free interstitials by the small vacancy clusters is given by:

$$R_{sVcl} = \sum_{n=1}^{max} R_{cI(n \rightarrow n+1)} \quad (607)$$

Table 41 Solution names for full model of vacancies

Symbol	Solution name
$C_{V_2}$	V2
$C_{V_3}$	V3
$C_{V_4}$	V4
$C_{V_5}$	V5
$C_{V_6}$	V6
$C_{V_7}$	V7
$C_{V_8}$	V8

## Initializing Full Model

The initial concentration of interstitial or vacancy clusters after implantation is set in the `diffPreProcess` procedure (see [Ion Implantation to Diffusion on page 340](#)). By default, clusters are assumed to break apart in the amorphous regions. You can specify the percentage of clusters retained in the amorphous region per cluster solution variable using the parameter `AmPercent`:

```
pdbSet <material> <cluster> AmPercent {<n>}
```

For example:

$$I_4 = \begin{cases} I_4 * \text{AmPercent} & \text{Amorphous regions} \\ I_4 & \text{Crystalline regions} \end{cases} \quad (608)$$

The value of the `AmPercent` parameter must be between 0 and 1.

In addition, you can specify the initial concentration of interstitial or vacancy clusters after implantations by using the parameter `InitPercent` as follows:

```
pdbSet <material> <cluster> InitPercent {<n>}
```

The parameter `InitPercent` is the percentage of free implant interstitials or vacancies used to initialize the model, for example:

$$I_{\text{cluster}} = \begin{cases} \text{Int\_Implant} * \text{InitPercent} & \text{Crystalline regions} \\ 0 & \text{Amorphous regions} \end{cases} \quad (609)$$

The value of `InitPercent` must be between 0 and 1.

---

## Ion Implantation to Diffusion

During the implantation, important data fields (see [Chapter 3 on page 79](#)) such as `Int_Implant`, `Vac_Implant`, and `Damage` are created

`Int_Implant` and `Vac_Implant` represent the total number of interstitial and vacancy point-defects coming from the ion implantation. Since it is possible that the point defects already exist in the structure or amorphization occurred due to ion implantation, the point-defect fields must be updated before any diffusion step.

Sentaurus Process calls a default procedure, `diffPreProcess`, to process these fields. The main goal of the procedure is to process the point-defect fields and to store the processed fields in the `Interstitial` and `Vacancy` data fields. These data fields represent the total number of interstitials and vacancies that will be used to initialize the total number of unpaired interstitials (`Int`) and vacancies (`Vac`) (see [Initializing Solution Variables on page 342](#)):

$$\text{Interstitial} = \begin{cases} \text{Interstitial} + \text{Int\_Implant} & \text{Crystalline regions} \\ C_I^* & \text{Amorphous regions} \end{cases} \quad (610)$$

$$\text{Vacancy} = \begin{cases} \text{Vacancy} + \text{Vacancy\_Implant} & \text{Crystalline regions} \\ C_V^* & \text{Amorphous regions} \end{cases} \quad (611)$$

First, interstitials and vacancies from implants (`Int_Implant`, `Vac_Implant`) are added to existing `Interstitial` and `Vacancy` fields in the crystalline regions. If the fields do not exist, they are created and set to their equilibrium values.

The `Damage` field is used to determine whether the material is amorphized. The threshold value for the amorphization can be set by:

```
pdbSet <material> AmorpDensity {<n>}
```

It is assumed that if a material amorphizes due to ion implantation, the amorphized portion of the material will grow to a perfect crystalline material and point-defect densities in this region will be equal to their thermal equilibrium values (see [Eq. 611](#)). If a material is an amorphized material (that is, polysilicon), the point-defect densities in this material are set automatically to their equilibrium values.

The abovementioned amorphization algorithm leads to very steep interstitial profiles at the amorphous–crystalline boundary. This boundary can be softened using an error function. The degree of smoothing can be controlled using the parameter `AmorpGamma`, that is:

```
pdbSet <material> AmorpGamma {<n>}
```

The value of this parameter must be between 0 and 1, where 1 means a very steep transition. Smoothing also will be applied to dopant profiles if the transient or cluster model is selected. To find out whether a material is amorphous, use the commands:

```
pdbGet <material> Amorphous
pdbSet <material> Amorphous 1 or 0
```

When the point-defect concentrations are set to their equilibrium values in the amorphous regions, their densities in non-amorphous regions are compared to the solid solubility values of these defects in each material. If the solid solubility values are defined, the defect profiles are cut off at the solid solubility values. To specify the solid solubility numbers for the Interstitial and Vacancy fields, use:

```
pdbSet <material> Int TotSolubility {<n>}
pdbSet <material> Vac TotSolubility {<n>}

Interstitial = min(Interstitial, IntTotSolubility)
Vacancy = min(Vacancy, VacTotSolubility) (612)
```

In addition to the processing of implant data fields, the `diffPreProcess` procedure determines whether point-defect equations need to be solved. As a default behavior, Sentaurus Process does not solve the defect equations if the dopant diffusion models are set to `Fermi` (see [Fermi Diffusion Model on page 211](#)), `Constant` (see [Constant Diffusion Model on page 212](#)), or `ChargedFermi` (see [ChargedFermi Diffusion Model on page 209](#)) in all materials.

However, the interstitial point-defect equation will be solved for the same dopant diffusion models if the oxidation is switched on and dopants are present in the structure. Both point-defect equations are solved if the dopant diffusion models are set to `Pair`, `React`, `ChargedPair`, or `ChargedReact` in any material.

Although it is not recommended, you may want to switch on or off the point-defect equations for any chosen dopant diffusion model. In this case, use the commands:

```
pdbSetBoolean Defect Int ForcedTurnOff 1
pdbSetBoolean Defect Vac ForcedTurnOff 1
pdbSetBoolean Defect Int ForcedTurnOn 1
pdbSetBoolean Defect Vac ForcedTurnOn 1
```

**NOTE** These parameters are not in the parameter database and are provided for advanced users.

To change the initialization of point defects in the amorphous regions, use:

```
pdbSet <material> Int Truncation.Model <model>
pdbSet <material> Vac Truncation.Model <model>
```

## 4: Diffusion

### Initializing Solution Variables

where `<model>` is either `None` or `Equilibrium`. The default is `None` and follows the initialization procedure previously explained in [Initializing Solution Variables on page 342](#).

The `Equilibrium` model sets the unpaired total interstitial (`Int`) and vacancy (`Vac`) concentrations to the user-defined equilibrium values,  $C_x^*$  (see [Eq. 150, p. 203](#)).

The `diffPreProcess` procedure also initializes the fluorine model (see [Initializing the FVCluster Model on page 293](#)), the active dopant models `Cluster` and `Transient` (see [Initializing Transient Model on page 285](#)), the `{311}` defect-clustering model (see [Initializing 311 Model on page 314](#)), and the `1Moment` defect-clustering model (see [Initializing 1Moment Model on page 328](#)).

When the preprocessing of the data fields is completed, most implant fields are deleted. Sentaurus Process also calls the `diffPostProcess` procedure as soon as diffusion has finished. In this procedure, remaining implant fields are cleared and total defect concentrations are stored for use with the next diffusion command during initialization.

---

## Initializing Solution Variables

Initialization of solution variables is typically a minor task in Sentaurus Process. You can manipulate data and easily modify any data field using the `select` command (see [select on page 1053](#)). Data fields can be added, subtracted, truncated, or manipulated in many ways.

You also can define special callback procedures to initialize solution variables in different ways. This section covers the callback procedures and the keywords used by Sentaurus Process to initialize solution variables.

No nonlinear or partial differential equations are solved to initialize dopant solutions. Dopant data fields generated during implantation are simply added to existing ones. For example, if you select the dopant diffusion model `React` (see [React Diffusion Model on page 204](#)), there is no contribution to the dopant–defect pair fields from the implant. However, you can use the `select` command to distribute dopants among the other fields as required.

Conversely, Sentaurus Process uses callback procedures (see [Using Callback Procedures on page 574](#)) to initialize the total number of unpaired interstitials (`Int`) and vacancies (`Vac`), which are used as solution names. Since extra dopant–defect equations are not solved for the `Pair`, `ChargedPair`, or `ChargedFermi` dopant diffusion models, transferring all point defects from implantation to their respective solution names may cause an artificial increase of dopant–defect pairs in the structure. To prevent this artificial dopant–defect pair increase, defects from implantation must be added to the total interstitials and vacancies.

There are two main callback procedures to initialize solution variables: `InitSolve` and `EquationInitProc`. To initialize a solution variable, the keyword `InitStep` must be



defined with the solution variable. This is different from the typical use of callback procedures (see [Using Callback Procedures on page 574](#)):

```
pdbSetString <material> <solution> InitSolve <callback procedure>
pdbSetString <material> <solution> EquationInitProc <callback procedure>
```

The procedures take three arguments: a material, a solution, and the name of the callback procedure. For example, the command:

```
pdbSetString Si Int InitSolve ResetInt
```

‘informs’ the code to invoke the `ResetInt` procedure every time that solutions are checked. This is usually performed at the very beginning of a diffusion step.

The `ResetInt` procedure could be defined as:

```
proc ResetInt { Mat Sol } {
  pdbUnSetString $Mat $Sol Equation
}
```

When a solution variable requires initialization, Sentaurus Process searches for whether the `EquationInitProc` callback procedure is used for the solution name. If it is used, Sentaurus Process executes the procedure given with the command. Otherwise, you must provide the initialization equation. The command:

```
pdbSetString Si Int EquationInitProc InitializeInt
```

‘informs’ Sentaurus Process to call the procedure `InitializeInt` before parsing the initialization equation for the solution `Int`.

The `InitializeInt` procedure could be defined as:

```
proc InitializeInt { Mat Sol } {
  pdbSetString $Mat $Sol Equation "$Sol - 1e17"
}
```

In this case, the initialization equation for the solution name `Int` will be set to `Int-1e17=0`.

When the initialization is completed, `Int` will have the value of  $1 \times 10^{17}$  in the specified material. This is a trivial example, but you can define any valid equation in this procedure.

For example, the default initialization equation for `Int` in Sentaurus Process, which can change depending on the dopants and diffusion models, can be:

```
Interstitial - (Int + (I0 * BActive * (( [expr [Arrhenius 5.68 0.48]] * \
  [pdbGetDouble Si Boron Int Binding] ] + [expr 0.0 * \
  [pdbGetDouble Si Boron Int Binding] ] * Noni) * Noni + ( \
```

#### 4: Diffusion Boundary Conditions

```
[expr [Arrhenius 5.68 0.42] * [pdbGetDouble Si Boron Int Binding] ] + \  
[expr 0.0 * [pdbGetDouble Si Boron Int Binding] ] * Poni) * Poni + \  
([expr 1.0 * [pdbGetDouble Si Boron Int Binding] ])) = 0
```

where `I0`, `BActive`, `Noni`, and `Poni` are a function of the solution `Int`.

**NOTE** `InitPostProcess` (see [Figure 86 on page 589](#)) can be used to save and plot solution variables after the initialization is completed.

---

## Boundary Conditions

Different boundary conditions can be selected in Sentaurus Process:

- `HomNeumann`
- `Natural`
- `Segregation`
- `Dirichlet`
- `ThreePhaseSegregation`
- `Trap`
- `Trapgen`
- `Continuous`

Even though you can select any boundary conditions, they should be used with appropriate species. It is possible to set a general boundary condition for all dopants or a specific boundary condition for a single species, for example:

```
pdbSet Oxide_Silicon Boundary BoundaryCondition HomNeumann  
pdbSet Oxide_Silicon Int BoundaryCondition Dirichlet
```

The first line switches the boundary condition for dopants at an oxide–silicon interface from its default `Segregation` boundary condition to the `HomNeumann` boundary condition. The second line sets the boundary condition at the oxide–silicon interface for interstitials to the `Dirichlet` boundary condition.

---

### HomNeumann

It is assumed that there are no fluxes and transfers across the interface. This is chosen by default at the left, right, and bottom boundaries, and can be applied to any boundary.

## Natural

This is the default boundary condition for point defects at gas–silicon and oxide–silicon interfaces. The normal flux across an outer surface is given by:

$$\mathbf{j} \cdot \mathbf{n} = h(C - C^*) \quad (613)$$

where  $h$  is the surface recombination rate, and  $C$  and  $C^*$  are the concentration of interstitials or vacancies and equilibrium concentration of interstitials and vacancies, respectively. The equilibrium concentration of point defects at the surface can be modified using user-defined parameters (see [Modifying Point-Defect Equilibrium Values at Surface on page 348](#)). There are four surface recombination velocity models:

- PDependent
- InitGrowth
- Simple
- Normalized

To set the models, use the command:

```
pdbSet <interface material> <defect> Surf.Recomb.Vel <model>
```

where:

- <interface material> is an interface material name (see [Material Specification on page 50](#)).
- <defect> is either `Interstitial` or `Vacancy`.
- <model> is one of the model names.

In each case, the surface recombination rate depends on the motion of the interface due to oxidation.

## Surface Recombination Model: PDependent

The PDependent model is the pressure-dependent surface recombination model. The flux that takes into account the interstitial injection during oxidation is given by:

$$\mathbf{j} \cdot \mathbf{n} = k_s \left( 1 + k_{Rat} \left( \frac{\|V_{ox}\|}{V_{Scale}} \right)^{k_{pow}} P_o^{k_{ppow}} \right) (C_{X^0} - C_{X^0}^*) - G_{ox} \quad (614)$$

#### 4: Diffusion

##### Boundary Conditions

where:

- $k_s$  is the surface recombination rate.
- $G_{ox}$  is the generation rate.
- $P_o$  is the oxygen partial pressure.
- $\|V_{ox}\|$  is the local oxidation rate (ReactionSpeed).
- $V_{Scale}$  is the reference oxidation rate for bare, undoped silicon.
- $k_{Rat}$ ,  $k_{pow}$ , and  $k_{ppow}$  are model parameters.

To modify these parameters, use the commands:

```

pdbSet <interface material> <defect> Ksurf {<n>}
pdbSet <interface material> <defect> Scale {<n>}
pdbSet <interface material> <defect> Krat {<n>}
pdbSet <interface material> <defect> Kpow {<n>}
pdbSet <interface material> <defect> Kppow {<n>}

```

The generation term,  $G_{ox}$ , is given by:

$$G_{ox} = \theta \|V_{ox}\| L_{den} \left( \frac{\|V_{ox}\|}{V_{Scale}} \right)^{G_{pow}} P_o^{G_{gpow}} G_{Scale} \quad (615)$$

$G_{pow}$ ,  $G_{gpow}$ , and  $\theta$  are model parameters to adjust the interstitial injection during oxidation.

To modify these parameters, use:

```

pdbSet <interface material> <defect> Gpow {<n>}
pdbSet <interface material> <defect> Ggpow {<n>}
pdbSet <interface material> <defect> theta {<n>}

```

$L_{den}$  is the lattice density of silicon and can be set by:

```

pdbSet <material> LatticeDensity {<n>}

```

$G_{Scale}$  is the scaling factor for the generation rate and given by:

$$G_{Scale} = \begin{cases} G_0 & G_{low} = 0 \text{ and Charged Model} \\ G_1 G_{low} & G_{low} \neq 0 \end{cases} \quad (616)$$

$$G_0 = \frac{C_{Xi}^*}{C_X} \quad (617)$$

$$G_1 = \frac{mm + m + 1 + p + pp}{mm \left( \frac{n}{n_i} \right)^{2PotOx} + m \left( \frac{n}{n_i} \right)^{PotOx} + 1 + p \left( \frac{p}{n_i} \right)^{PotOx} + pp \left( \frac{p}{n_i} \right)^{2PotOx}} \quad (618)$$

If the dopant diffusion model is set to `ChargedFermi` or `ChargedPair` or `ChargedReact` and  $G_{low}$  is zero,  $G_{Scale}$  will be set to  $G_0$ ; otherwise, it will be set to  $G_1$ .

$G_{low}$ ,  $PotOx$ ,  $mm$ ,  $m$ ,  $p$ , and  $pp$  are model parameters that can be modified with the commands:

```

pdbSet <interface material> <defect> PotOx {<n>}
pdbSet <interface material> <defect> mm {<n>}
pdbSet <interface material> <defect> m {<n>}
pdbSet <interface material> <defect> p {<n>}
pdbSet <interface material> <defect> pp {<n>}
pdbSet <interface material> <defect> Glow {<n>}

```

## Surface Recombination Model: InitGrowth

The `InitGrowth` model is almost identical to `PDependent` (see [Surface Recombination Model: PDependent on page 345](#)) surface recombination model except that  $\|V_{ox}\|/V_{Scale}$  is set to 1 for nonoxidizing cases in [Eq. 614](#).

## Surface Recombination Model: Simple

The `Simple` model takes into account the interstitial injection through total free and equilibrium point-defect concentrations during oxidation. The recombination flux is given by:

$$\mathbf{j} \cdot \mathbf{n} = k_s \left( 1 + k_{Rat} \left( \frac{\|V_{ox}\|}{V_{Scale}} \right) \right) (C_X - C_X^*) - G_{ox} \quad (619)$$

$$G_{ox} = \theta \|V_{ox}\| L_{den} G_{Scale} \quad (620)$$

$G_{Scale}$  is given by [Eq. 616](#).

## Surface Recombination Model: Normalized

The `Normalized` model is a TSUPREM-4-type surface recombination model. This model provides both the time dependence and the dependence on the oxidation conditions by using a constant normalizing factor:

$$\mathbf{j} \cdot \mathbf{n} = \left( k_s + k_{svel} \left( \frac{\|V_{ox}\|}{V_{Scale}} \right)^{kpow} \right) (C_X - C_X^*) - G_{ox} \quad (621)$$

$$G_{ox} = \theta L_{den} \|V_{ox}\| \left( \frac{\|V_{ox}\|}{V_{Scale}} \right)^{Gpow} G_{Scale} \quad (622)$$

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Boundary Conditions

To set the normalizing factor, use the command:

```
pdbSet <interface material> <defect> Ksvel {<n>}
```

$G_{Scale}$  is given by [Eq. 616](#).

### Modifying Point-Defect Equilibrium Values at Surface

The equilibrium value of point defects at the interface can be enhanced as follows:

$$C_{X Enhanced}^* = C_X^* \left( 1 + F_{ox} G_1 \left( \frac{\|V_{ox}\|}{V_{ref}} \right)^{P_{ox}} \right) \quad (623)$$

$G_1$  is given by [Eq. 618](#).

$V_{ref}$ ,  $F_{ox}$ , and  $P_{ox}$  are model parameters that can be modified with the commands:

```
pdbSet <interface material> <defect> VrefRate {<n>}
pdbSet <interface material> <defect> Fox      {<n>}
pdbSet <interface material> <defect> Pox     {<n>}
```

To switch on the enhancement, use the command:

```
pdbSet <interface material> <defect> HybridBC {1 | 0}
```

---

## Segregation

This is the default boundary condition for dopants. The total dopant fluxes at the interfaces are balanced. The fluxes are assumed to be proportional to the deviation from the segregation equilibrium. The fluxes are given by:

$$\mathbf{j} \cdot \mathbf{n} = h \left( C_A^a - \frac{C_A^b}{s} \right) \quad (624)$$

where:

- $C_A^a$  is the concentration of dopant on one side of the interface.
- $C_A^b$  is the concentration of dopant on the other side of the interface.
- $h$  is the transfer rate.
- $s$  is the segregation rate of dopant  $A$ .

If the charge states of the dopants must be included or the boundary condition for dopant defect pairs must be set, use the command:

```
pdbSet <interface material> <dopant> Surf.Recomb.Model <diffmodel> <model>
```

where:

- <interface material> is an interface material name (see [Material Specification on page 50](#)).
- <dopant> is a valid dopant name.
- <diffmodel> is the Constant or Fermi or ChargedFermi or Pair or ChargedPair or React or ChargedReact dopant diffusion model.
- <model> is either Default or PairSegregation.

## Surface Recombination Model: Default

If the surface recombination model is set to Default for any dopant diffusion model, the segregation fluxes are given by:

$$\mathbf{j} \cdot \mathbf{n} = k_{Transfer} \left( C_A^a - \frac{C_A^b}{k_{Segregation}} \right) \quad (625)$$

To set these parameters, use the commands:

```
pdbSet <interface material> <dopant> Transfer {<n>}
pdbSet <interface material> <dopant> Segregation {<n>}
```

**NOTE** If the dopant diffusion model is set to React or ChargedReact,  $C_A$  will be the substitutional dopant.

## Surface Recombination Model: PairSegregation

If the surface recombination model is set to PairSegregation for the Constant, Fermi, ChargedFermi, Pair, or ChargedPair diffusion models, the segregation fluxes are given by:

$$\mathbf{j} \cdot \mathbf{n} = k_{Transfer} k_{rate}^a k_{rate}^b \left( C_A^a \left( \frac{n}{n_i} \right)^z - \frac{C_A^a \left( \frac{n}{n_i} \right)^z}{k_{Segregation}} \right) \quad (626)$$

$$k_{rate}^{a/b} = \left( f_I \left[ \frac{C_I^*}{C_I^0} \right]_{a/b} + (1 - f_I) \left[ \frac{C_V^*}{C_V^0} \right]_{a/b} \right) \quad (627)$$

#### 4: Diffusion

Boundary Conditions

where  $f_I$  is the interstitial fraction of dopant trapping in equilibrium and can be set using the following command:

```
pdbSet <interface material> <dopant> Trap.Fi {<n>}
```

To use the total unpaired interstitial concentration, instead of the neutral one, use the command:

```
pdbSet <interface material> <dopant> UseUnpairedTotalInt { 1|0 }
```

In this case, [Eq. 627](#) will be:

$$k_{rate}^{a/b} = \left( f_I \left[ \frac{C_I^*}{C_I^*} \right]_{a/b} + (1-f_I) \left[ \frac{C_V^*}{C_V^*} \right]_{a/b} \right) \quad (628)$$

If the dopant diffusion model is not `Pair` or `ChargedPair` model on interface side  $a$ ,  $k_{rate}^a$  is set to 1. If the same is true for interface side  $b$ ,  $k_{rate}^b$  is set to 1.

If the surface recombination model is set to `PairSegregation` for `React` or `ChargedReact` diffusion models, the segregation fluxes are given by:

$$\mathbf{j} \cdot \mathbf{n} = k_{Transfer} k_{AIrate}^a \left( [C_{I^0}^*]^b C_A^a \left( \frac{n}{n_i} \right)^z - \frac{C_{AI}^b \left( \frac{n}{n_i} \right)^z}{k_{Segregation} \sum_z k_{AI^z}^b k_{I^z}^b \left( \frac{n}{n_i} \right)^{-z}} \right) \quad (629)$$

$$\mathbf{j} \cdot \mathbf{n} = k_{Transfer} k_{AVrate}^a \left( [C_{V^0}^*]^b C_A^a \left( \frac{n}{n_i} \right)^z - \frac{C_{AV}^b \left( \frac{n}{n_i} \right)^z}{k_{Segregation} \sum_z k_{AV^z}^b k_{V^z}^b \left( \frac{n}{n_i} \right)^{-z}} \right) \quad (630)$$

$$k_{AIrate}^a = \frac{f_I}{[C_{I^0}^*]^b} k_{rate}^a \quad (631)$$

$$k_{AVrate}^a = \frac{1-f_I}{[C_{V^0}^*]^b} k_{rate}^a \quad (632)$$

where  $C_{AI}$  and  $C_{AV}$  are the concentration of dopant-defect pairs.  $C_A$  is the concentration of the total unpaired dopant.



To use the total unpaired interstitial and vacancy concentrations, Eq. 631 and Eq. 632 will be:

$$k_{AIrate}^a = \frac{f_I}{[C_{I^0}^*]^b} \frac{\sum_c k_{I^c} \left(\frac{n}{n_I}\right)^{-c}}{\sum_c k_{I^c}^s} k_{rate}^a \quad (633)$$

$$k_{AVrate}^a = \frac{1-f_I}{[C_{V^0}^*]^b} \frac{\sum_c k_{V^c} \left(\frac{n}{n_V}\right)^{-c}}{\sum_c k_{V^c}^s} k_{rate}^a \quad (634)$$

---

## Dirichlet

The Dirichlet boundary condition can be used with both point defects and dopants. However, it can be set only at gas and any other material interfaces for dopants. In this way, ‘in-diffusion’ for a dopant can be simulated using the Dirichlet boundary condition. If the Dirichlet boundary condition is selected, the defect or dopant concentration at the boundary is set to its equilibrium value. The equilibrium value can be specified with:

```
pdbSet <material> <dopant|defect> Cstar <n>
```

where:

- <material> is a material name (see).
- <dopant> is a valid dopant name.
- <defect> is Interstitial or Vacancy.
- Cstar is the equilibrium value of the solution variable.

If the Dirichlet boundary condition is selected and the oxidation is switched on, the modified Dirichlet boundary condition is used for interstitials. The equilibrium value of interstitial point-defects at the interface is enhanced (see [Modifying Point-Defect Equilibrium Values at Surface on page 348](#)) and the new equilibrium at the interface becomes:

$$C_{I^{ox}}^* = C_{I^0}^* \left( 1 + F_{ox} G_1 \left( \frac{\|V_{ox}\|}{V_{ref}} \right)^{P_{ox}} \right) \quad (635)$$

---

## ThreePhaseSegregation

Dose loss during diffusion can be modeled with three-phase segregation in Sentaurus Process. Dopants can segregate from both silicon and oxide to the silicon–oxide interface where they are considered inactive. The model in Sentaurus Process is based on the original model by Lau *et al.* [40], and Oh and Ward [41]. The diffusion equation at the interface is given by:

$$\frac{\partial C_A}{\partial t} = \nabla D_0 \nabla C_A + F_a + F_b \quad (636)$$

where  $D_0$  is the diffusivity of the dopant at the interface, and  $F_a$  and  $F_b$  are the flux towards the interface from material  $a$  and material  $b$ , respectively.

The diffusivity at the interface can be defined by:

```
pdbSet <interface material> <dopant> D <c> {<n>}
```

where:

- <interface material> is an interface material name (see [Material Specification on page 50](#)).
- <dopant> is one of the existing Sentaurus Process dopants.
- <c> is the charge state.
- <n> is a Tcl expression that returns a number; it can be simply a number.

**NOTE** Only a neutral charge state is considered at the interface.

The fluxes  $F_a$  and  $F_b$  depend on the surface recombination model used. The surface recombination models are `Default` or `PairSegregation`, and can be set for different diffusion models using the command:

```
pdbSet <interface material> <dopant> Surf.Recomb.Model <diffmodel> <model>
```

where:

- <diffmodel> is the `Constant`, `Fermi`, `ChargedFermi`, `Pair`, `ChargedPair`, `React`, or `ChargedReact` dopant diffusion model.
- <model> is either `Default` or `PairSegregation`.

## Surface Recombination Model: Default

If the surface recombination model is set to `Default` for any dopant diffusion model, the segregation fluxes are given by:

$$F_{a/b} = T_{Rate}^{a/b} \left( [C_A^{Tmax}]^{a/b} - \sum_i C_{A_i} \right) [C_A^+]^{a/b} \left( \frac{n}{n_i} \right)^z - E_{Rate}^{a/b} C_A ([C_A^{SS}]^{a/b} - [C_A^+]^{a/b}) \quad (637)$$

where:

- $T_{Rate}$  is the trapping rate.
- $C_A^{Tmax}$  is the maximum number of sites in the adjacent bulk regions.
- $C_{A_i}$  is the concentration of trapped dopant  $A_i$ .
- $C_A^{SS}$  is the solid solubility of the dopant.
- $C_A^+$  is the active concentration of dopant  $A$ .
- $z$  is the charge state of the dopant.
- $E_{Rate}$  is the emission rate.

To set the model parameters, use the commands:

```
pdbSet <interface material> <dopant> TrappingRate_<side> {<n>}
pdbSet <interface material> <dopant> EmissionRate_<side> {<n>}
pdbSet <interface material> CMax {<n>}
```

where `<side>` is one side of the interface and `<interface material>` is the interface material. For example, the side would be either `Oxide` or `Silicon` for an oxide-silicon interface.

Sentaurus Process allows the  $C_A^{Tmax}$  parameter to be multiplied by user-defined factors as follows:

$$C_{AFactor}^{Tmax} \times C_A^{Tmax} \quad (638)$$

For example, in the case of oxide silicon interface, this is given by:

```
term name=CMaxFactor add Oxide /Silicon eqn = "exp(0.02)"
```

To allow Sentaurus Process to use this term, specify a term with the name `CMaxFactor` for the interface material.

Similarly, you can modify  $T_{Rate}$  and  $E_{Rate}$  (the trapping and emission rates, respectively) using user-defined factors such as:

$$T_{Rate-Factor} \times T_{Rate} \quad \text{and} \quad E_{Rate-Factor} \times E_{Rate} \quad (639)$$

#### 4: Diffusion

##### Boundary Conditions

The rate factors are specified as follows:

```
term name=<dopant>EmissionRateFactor_<side> add <InterfaceMaterial1> /
<InterfaceMaterial2> eqn="<expr>"
term name=<dopant>TrappingRateFactor_<side> add <InterfaceMaterial1> /
<InterfaceMaterial2> eqn="<expr>"
```

The factors are specified for an interface, for a particular dopant and specific to the side from which the interface is being approached. For example, given an oxide–silicon interface and an arsenic dopant, the `EmissionRateFactor` from the oxide side can be specified as:

```
term name=ArsenicEmissionRateFactor_Oxide add Oxide /Silicon eqn="exp(2.0)"
```

You also can use the individual trap density by switching off the `UseTotalInterfaceTrap` flag by:

```
pdbSet <interface material> <dopant> UseTotalInterfaceTrap 0
```

By default, the flag is switched on (1). If the flag is switched off, [Eq. 637](#) becomes:

$$F_{a/b} = T_{Rate}^{a/b} ([C_A^{max}]^{a/b} - C_A) [C_A^+]^{a/b} \left(\frac{n}{n_i}\right)^z - E_{Rate}^{a/b} C_A ([C_A^{ss}]^{a/b} - [C_A^+]^{a/b}) \quad (640)$$

where  $C_A^{max}$  is the maximum number of sites in the adjacent bulk region for this solution variable.

To change this parameter, use the command:

```
pdbSet <interface material> <dopant> CMax {<n>}
```

**NOTE** If the dopant diffusion model is set to `React` or `ChargedReact`,  $C_A^+$  will be the substitutional dopant.

Sentaurus Process allows the  $C_A^{max}$  parameter to be multiplied by user-defined factors as follows:

$$C_{AFactor}^{max} \times C_A^{max} \quad (641)$$

For example, in the case of specified boron at the oxide–silicon interface, this is given by:

```
term name=BoronCMaxFactor add Oxide /Silicon eqn = "exp(0.02)"
```

To allow Sentaurus Process to use this term, specify a term with the name `<dopant>CMaxFactor` for the interface material.

Sentaurus Process also allows the parameter  $C_A^{SS}$  to be multiplied by a user-defined factor defined as `Side.SS.Factor`, for example:

```
pdbSetString Si B Side.SS.Factor "exp(3.636e-24*Pressure_Silicon/$kBT) "
```

## Surface Recombination Model: PairSegregation

If the Surface Recombination model is set to `PairSegregation` for the `Pair` or `ChargedPair` dopant diffusion model, the segregation fluxes are given by:

$$F_{a/b} = \left( \left[ \frac{C_{I^0}}{C_{I^*}} \right]^{a/b} f_I T_{Rate}^{a/b} + \left[ \frac{C_{V^0}}{C_{V^*}} \right]^{a/b} (1-f_I) T_{Rate}^{a/b} \right) \times \left( \left[ C_A^{Tmax} \right]^{a/b} - \sum_i C_{A_i} \right) \left[ C_A^+ \right]^{a/b} \left( \frac{n}{n_i} \right)^z - C_A [C_A^{SS}]^{a/b} \frac{E_{Rate}^{a/b}}{T_{Rate}^{a/b}} \quad (642)$$

To use the total unpaired interstitial concentration, instead of the neutral one, use the command:

```
pdbSet <interface material> <dopant> UseUnpairedTotalInt { 1|0 }
```

In this case,  $\left[ \frac{C_{X^0}}{C_{X^*}} \right]^{a/b}$  in Eq. 642 will be replaced with  $\left[ \frac{C_X}{C_{X^*}} \right]^{a/b}$ .

If the surface recombination model is set to `PairSegregation` for the `React` or `ChargedReact` diffusion model, the segregation fluxes are given by:

$$F_{a/b} = \frac{f_I T_{Rate}^{a/b}}{\left[ C_{I^0} \right]^{a/b}} \left( \left[ C_A^{Tmax} \right]^{a/b} - \sum_i C_{A_i} \right) \frac{\left[ C_{AI} \right]^{a/b} \left( \frac{n}{n_i} \right)^z}{\sum_z k_{AI^z}^{a/b} k_{I^z}^{a/b} \left( \frac{n}{n_i} \right)^{-z}} - C_A [C_A^{SS}]^{a/b} \frac{E_{Rate}^{a/b}}{T_{Rate}^{a/b}} \left[ C_{I^0} \right]^{a/b} \times \left( \frac{(1-f_I) T_{Rate}^{a/b}}{\left[ C_{V^0} \right]^{a/b}} \left( \left[ C_A^{Tmax} \right]^{a/b} - \sum_i C_{A_i} \right) \frac{\left[ C_{AV} \right]^{a/b} \left( \frac{n}{n_i} \right)^z}{\sum_z k_{AV^z}^{a/b} k_{V^z}^{a/b} \left( \frac{n}{n_i} \right)^{-z}} - C_A [C_A^{SS}]^{a/b} \frac{E_{Rate}^{a/b}}{T_{Rate}^{a/b}} \left[ C_{V^0} \right]^{a/b} \right) \quad (643)$$

where  $f_I$  is the interstitial fraction of dopant trapping in equilibrium and can be set using the command:

```
pdbSet <interface material> <dopant> Trap.Fi {<n>}
```

## 4: Diffusion

### Boundary Conditions

To use the total unpaired interstitial and vacancy concentration,  $f_I$  in Eq. 643 will be scaled with:

$$\frac{\sum_c k_{X^c} \left(\frac{n}{n_I}\right)^{-c}}{\sum_c k_{X^c}^s} \quad (644)$$

All other parameters have the usual meaning as explained above.

If the individual trap density is switched off,  $\left([C_A^{Tmax}]^{a/b} - \sum_i C_{A_i}\right)$  will be replaced with  $\left([C_A^{max}]^{a/b} - C_A\right)$ .

$C_{AI}$  and  $C_{AV}$  are the concentrations of dopant-defect pairs.  $C_A$  is the concentration of the total unpaired dopant. If the surface recombination model is set to `PairSegregation` for the `Constant`, `Fermi`, or `ChargedFermi` diffusion model, the `Default` model will be used.

---

## Trap

The `Trap` boundary condition is used to trap species at the interface. This boundary condition is a combination of the `Segregation` model (see [Segregation on page 348](#)) and the `ThreePhaseSegregation` model (see [ThreePhaseSegregation on page 352](#)).

The model is used mainly to trap nitrogen and fluorine during oxidation to reduce the oxidation rate (see [Trap-dependent Oxidation on page 614](#)).

---

## TrapGen

The `TrapGen` boundary condition defines not only dopant trapping, but also dopant generation depending on the reaction velocity at a boundary.

---

## Continuous

For all of the same material interfaces (for example, `Silicon_Silicon`), by default, continuous flux and solution boundary conditions apply:

$$C_1(x \rightarrow i) = C_2(i \leftarrow x) \quad (645)$$

$$D_1 \cdot \nabla C_1|_{n1} = \kappa_2 \nabla C_2|_{n2} \quad (646)$$

where:

- Indices 1 and 2 indicate the two sides of the interface  $i$ .
- $n$  indicates the component of the dopant gradient normal to the interface.
- $D$  is the diffusivity, and  $C$  is the concentration of the solution variable.

If the boundary condition is not specified using the callback procedures for the solution variable at the interface, the continuous boundary condition can be set using the command:

```
pdbSetBoolean <mater> <dopant> Continuous 1
```

where <mater> is the interface material, and <dopant> is the solution variable name. For example:

```
pdbSetBoolean PolySilicon_Silicon Potential Continuous 1
```

will set the potential solution and its fluxes continuous at the polysilicon–silicon interface if Potential is solved on both sides of the interface.

---

## Periodic Boundary Condition

The periodic boundary condition can be applied when a device structure has a repetitive pattern:

```
pdbSet Diffuse <Left | Right | Front | Back> Periodic <0 | 1>
```

The Front and Back definitions apply to 3D structures only.

---

## Boundary Conditions at Moving Interfaces

---

### Enhanced and Retarded Diffusion

During the growth of materials (for example, oxide and silicide), the reaction speed is calculated at the moving interfaces. The data field is called ReactionSpeed. The reaction speed can be used to simulate the enhanced dopant diffusion (for example, oxidation-enhanced diffusion (OED)) or the retarded dopant diffusion (for example, oxidation-retarded diffusion (ORD)) by allowing for the injection of interstitials and vacancies.

In [Eq. 614, p. 345](#), the injection rate is given as a function of the reaction speed ( $\|V_{ox}\| = \text{ReactionSpeed}$ ) and is used to simulate OED effects.

## 4: Diffusion

### Common Dopant and Defect Dataset Names

---

## Conserving Dose

The mesh of the simulated structure is modified during the growth of materials with each diffusion step. Some elements of the mesh will become bigger and some will shrink during this process. The change in the element size from one diffusion step to another will artificially change the dopant doses in the structure.

This artificial effect has two components. One is due to the change of element sizes and the other is due to the material consumption at the moving boundaries. The first effect is accounted for internally by applying an up-wind term to the solution equations. The second effect is accounted for using the Alagator scripting language. If the total dopant concentration on one side of the interface is different from the other side, the total concentration of the consumed material is used.

For example, if you assume that there are no dopant clusters and the `React` diffusion model for boron is selected on the silicon side and the `Constant` diffusion model is selected on the oxide side of an oxide-silicon interface, the total boron concentration would be `Boron+BoronInt+BoronVac` on the silicon side and `Boron` on the oxide side. Since the consumed material is silicon during the oxidation, the dopant consumption due to growth is passed using the command:

```
pdbSetString Oxide_Silicon Boron Consumed_Silicon \  
  "Boron_Silicon+BoronInt_Silicon+BoronVac_Silicon"
```

This is performed automatically. If the `React` diffusion model for boron was also selected on the oxide side, the total dopant concentration on the oxide side would be `Boron+BoronInt+BoronVac`, and the following command would be used:

```
pdbSetString Oxide_Silicon Boron Consumed_Silicon "Boron_Silicon"
```

---

## Common Dopant and Defect Dataset Names

Sentaurus Process does not solve the diffusion equations for the total dopant or defect concentrations, but solves the equations for the total unpaired dopant and defect concentrations. Sentaurus Process monitors the total dopant and defect concentration through various terms. Depending on the diffusion models selected, Sentaurus Process will update these terms. For example, the commands:

```
pdbSet Silicon Dopant DiffModel React  
pdbSet Silicon B ActiveModel None
```

will set the dopant diffusion model in silicon to `React` and the active model to `None` for boron in silicon. Assuming that there is only boron in the structure, various terms and data fields will



be created after the diffusion. The most important ones are Boron, BActive, BTotal, BoronInt, BoronVac, Int, ITotal, Interstitial, Vac, VacTotal, and Vacancy. Boron, BoronInt, BoronVac, Int, and Vac are the solution names:

BActive	Active boron concentration. (Since the active model is none, it will be equal to Boron).
Boron	Total unpaired boron concentration (for example, no clusters, no boron–defect pairs).
BoronInt	Concentration of boron–interstitial pairs.
BoronVac	Concentration of boron–vacancy pairs.
BTotal	$Boron + BoronInt + BoronVac = \text{Total boron concentration.}$
Int	Total unpaired interstitial concentration.
Interstitial	Total interstitial concentration used to initialize Int. (In this example, it will be Int.)
ITotal	$Int + BoronInt = \text{Total interstitial concentration.}$
Vac	Total unpaired vacancy concentration.
Vacancy	Total vacancy concentration used to initialize Vac. (In this example, it will be Vac.)
VTotal	$Vac + BoronVac = \text{Total vacancy concentration.}$

If the cluster models for both interstitial and boron are switched on, as follows:

```

pdbSet Si Dopant DiffModel React
pdbSet Si B ActiveModel Transient
pdbSet Si I ClusterModel lMoment

```

some of the previous fields will be updated. Two additional solution variables, ICluster and B4, will be solved. ICluster is the clustered interstitials used with the lMoment model (see [Defect Cluster Model: lMoment on page 324](#)), and B4 is the clustered boron used with the Transient model (see [Dopant Active Model: Transient on page 283](#)).

The changed fields will be:

BTotal	$Boron + 4*B4 + BoronInt + BoronVac = \text{Total boron concentration.}$
ITotal	$Int + BoronInt + ICluster = \text{Total interstitial concentration.}$

## 4: Diffusion

### Common Dopant and Defect Dataset Names

If the diffusion and cluster models are changed as follows:

```
pdbSet Si Dopant DiffModel ChargedPair
pdbSet Si B ActiveModel Transient
pdbSet Si I ClusterModel Equilibrium
```

Sentaurus Process uses the `ChargedPair` diffusion model (see [ChargedPair Diffusion Model on page 206](#)) and the `Transient` active model (see [Dopant Active Model: Transient on page 283](#)) for boron, and the `Equilibrium` cluster model (see [Defect Cluster Model: Equilibrium on page 307](#)) for interstitials.

In this case, `Boron`, `B4`, `Int`, and `Vac` will be the solution names. `BoronInt` and `BoronVac` will not be solved, but there will be `BoronInt` and `BoronVac` terms to calculate boron–interstitial and boron–vacancy concentrations. In this case, total unpaired Boron also will include `BoronInt` and `BoronVac` since they are not solved. The important fields are:

<code>BActive</code>	<code>Boron - BoronInt - BoronVac = Active boron concentration.</code>
<code>Boron</code>	Total unpaired boron concentration.
<code>BoronInt</code>	Concentration of boron–interstitial pairs calculated using <a href="#">Eq. 165, p. 207</a> .
<code>BoronVac</code>	Concentration of boron–vacancy pairs calculated using <a href="#">Eq. 165</a> .
<code>BTotal</code>	<code>Boron + 4*B4 = Total boron concentration.</code>
<code>Icluster</code>	Equilibrium interstitial concentration calculated using <a href="#">Eq. 464, p. 307</a> .
<code>Int</code>	Total unpaired interstitial concentration.
<code>Interstitial</code>	<code>Int + 4*Icluster + BoronInt = Total interstitial concentration used to initialize Int.</code>
<code>ITotal</code>	<code>Int + 4*Icluster + BoronInt = Total interstitial concentration.</code>
<code>Vac</code>	Total unpaired vacancy concentration.
<code>Vacancy</code>	<code>Vac + BoronVac = Total vacancy concentration used to initialize Vac.</code>
<code>VTotat</code>	<code>Vac + BoronVac = Total vacancy concentration.</code>

**NOTE** If the dopant, defect, or cluster fields are modified by other process steps (for example, implant, deposition, and so on), terms that define active dopant concentration and total dopant concentration may not be current. They be updated with the next diffusion step.

Table 42 Variable names used in diffusion and reaction solvers

<b>Name</b>	<b>Comment</b>	<b>Solution (S), Term (T), Data field (F)</b>
Antimony	Total unpaired antimony concentration	S, F
AntimonyGbc	Antimony grain boundary concentration	S, F
AntimonyInit	Antimony–interstitial pair concentration	T or (S, F) (depends on the model)
AntimonyVac	Antimony–vacancy pair concentration	T or (S, F) (depends on the model)
Arsenic	Total unpaired arsenic concentration	S, F
ArsenicGbc	Arsenic grain boundary concentration	S, F
ArsenicInt	Arsenic–interstitial pair concentration	T or (S, F) (depends on the model)
ArsenicVac	Arsenic–vacancy pair concentration	T or (S, F) (depends on the model)
As3	Three-arsenic cluster concentration (default size is three, user-configurable)	S, F
As4Vac	Four-arsenic and a vacancy cluster concentration	S, F
AsActive	Arsenic active concentration	T
AsTotal	Total arsenic concentration	T (for example, Arsenic+4*As4Vac)
B2	Two-boron cluster concentration	S, F
B2I	Two-boron and interstitial cluster concentration	S, F
B2I2	Two-boron and two-interstitial cluster concentration	S, F
B2I3	Two-boron and three-interstitial cluster concentration	S, F
B3	Three-boron cluster concentration	S, F
B3I	Three-boron and interstitial cluster concentration	S, F
B3I2	Three-boron and two-interstitial cluster concentration	S, F
B3I3	Three-boron and three–interstitial cluster concentration	S, F
B3I4	Three-boron and four-interstitial cluster concentration	S, F
B4	Four-boron cluster concentration (default size is four, user-configurable)	S, F
BActive	Boron active concentration	T
BI2	Boron and two-interstitial cluster concentration	S, F

#### 4: Diffusion

##### Common Dopant and Defect Dataset Names

Table 42 Variable names used in diffusion and reaction solvers

Name	Comment	Solution (S), Term (T), Data field (F)
Boron	Total unpaired boron concentration	S, F
BoronGbc	Boron grain boundary concentration	S, F
BoronInt	Boron–interstitial pair concentration	T or (S, F) (depends on the model)
BoronVac	Boron–vacancy pair concentration	T or (S, F) (depends on the model)
BTotal	Total boron concentration	T (for example, Boron+2*B2I)
C2	Two-carbon cluster concentration	S, F
C2I	Two-carbon and interstitial cluster concentration	S, F
C311	Concentration of interstitials trapped in {311} defects	S, F
C3I	Three-carbon and interstitial cluster concentration	S, F
C3I2	Three-carbon and two-interstitial cluster concentration	S, F
C4I2	Four-carbon and two-interstitial cluster concentration	S, F
C4I3	Four-carbon and three-interstitial cluster concentration	S, F
C5I3	Five-carbon and three-interstitial cluster concentration	S, F
C5I4	Five-carbon and four-interstitial cluster concentration	S, F
C6I5	Six-carbon and five-interstitial cluster concentration	S, F
C6I6	Six-carbon and six-interstitial cluster concentration	S, F
Carbon	Total unpaired carbon concentration	S, F
CarbonInt	Carbon–interstitial pair concentration	S, F
CLoop	Concentration of interstitials trapped in dislocation loops	T or (S, F) (depends on the model)
CTotal	Total carbon concentration	T
D311	Density of {311} defects	S, F
DLoop	Density of dislocation loops	T or (S, F) (depends on the model)
EqInt	Equilibrium interstitial concentration	T

Table 42 Variable names used in diffusion and reaction solvers

<b>Name</b>	<b>Comment</b>	<b>Solution (S), Term (T), Data field (F)</b>
EqVac	Equilibrium vacancy concentration	T
F3V	Three-fluorine and vacancy cluster concentration	S, F
Fluorine	Total unpaired fluorine concentration	S, F
FluorineTotal	Total fluorine concentration	T
GeB	Germanium–boron pair concentration	S, F
Germanium	Total unpaired germanium concentration	S,F
GermaniumTotal	Total germanium concentration	T
H2O	Wet oxidant concentration	S, F
I2	Two-interstitial cluster concentration	S,F
ICluster	Interstitial cluster concentration	T or (S, F) (depends on the model)
In3	Three-indium cluster concentration (default size is three, user-configurable)	S, F
InActive	Indium active concentration	T
Indium	Total unpaired indium concentration	S, F
IndiumGbc	Indium grain boundary concentration	S, F
IndiumInt	Indium–interstitial pair concentration	T or (S, F) (depends on the model)
IndiumVac	Indium–vacancy pair concentration	T or (S, F) (depends on the model)
Int	Total unpaired interstitial concentration	S, F
Interstitial	Total interstitial concentration excluding cluster solutions, used to initialize Int	F
IntNeutral	Neutral interstitial concentration ( $I_0$ )	T
InTotal	Total indium concentration	T
IntTotal	Total interstitial concentration	T
O2	Dry oxidant concentration	S, F
P3	Three-phosphorus cluster concentration (default size is three, user-configurable)	S, F
PActive	Phosphorus active concentration	T
Phosphorus	Total unpaired phosphorus concentration	S, F
PhosphorusGbc	Phosphorus grain boundary concentration	S, F
PhosphorusInt	Phosphorus–interstitial pair concentration	T or (S, F) (depends on the model)

#### 4: Diffusion References

Table 42 Variable names used in diffusion and reaction solvers

Name	Comment	Solution (S), Term (T), Data field (F)
PhosphorusVac	Phosphorus–vacancy pair concentration	T or (S, F) (depends on the model)
Potential	Electrostatic potential	T or (S, F) (depends on the model)
PTotal	Total phosphorus concentration	T
Sb3	Three-antimony cluster concentration (default size is three, user-configurable)	S, F
SbActive	Antimony active concentration	T
SbTotal	Total antimony concentration	T (for example, Antimony+AntimonyVac)
Smic	Concentration of submicroscopic interstitial clusters (default size 4)	S, F
SmicS	Concentration of smaller submicroscopic interstitial clusters (default size 2)	S, F
V2	Two-vacancy cluster concentration	S, F
Vac	Total unpaired vacancy concentration	S, F
Vacancy	Total vacancy concentration excluding cluster solutions, used to initialize Vac	F
VacNeutral	Neutral vacancy concentration ( $V_0$ )	T
VacTotal	Total vacancy concentration	T

---

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References

## CHAPTER 5 Atomistic Kinetic Monte Carlo Diffusion

---

*This chapter describes an alternative, atomistic simulation approach to the diffusion and activation processes in Sentaurus Process. It also provides alternatives for faceted solid phase epitaxial regrowth and epitaxial deposition. For a continuum approach, see [Chapter 4](#).*

All diffusion models previously described are based on the conventional (continuum) simulation approach. The atomistic approach described in this chapter is based partially on the kinetic Monte Carlo (KMC) diffusion simulator DADOS [1][2][3], and is available with the optional Sentaurus Process Kinetic Monte Carlo license.

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### Overview

The continuum approach to modeling dopant diffusion in process simulation tools is used to solve a system of partial differential equations (PDEs) that describe transport of the dopants and conservation of the dose. This approach has proven to be useful in designing semiconductor devices in the past, but several trends in the manufacturing process of sub-100-nm devices may make it difficult to maintain a high predictability in future devices.

The shrinking thermal budget significantly reduces diffusion and, therefore, reduces the need to accurately model diffusion. On the other hand, dopant activation phenomena, including the formation of a variety of dopant-defect pairs and extended defects of different configurations, often do not reach thermodynamic equilibrium and necessitate transient rather than equilibrium simulation. In the continuum diffusion model, this requires the use of one equation per each dopant-defect configuration, which leads to a large number of equations to be solved.

The trend of reducing device sizes results in a small number of impurity atoms (as small as tens or hundreds) that determine the threshold voltage of a transistor. It is likely that a limit soon will be reached where small discretized distribution can no longer be accurately modeled with a continuum description.

A Monte Carlo (MC)-based diffusion simulation provides a valuable alternative to the continuum approach. Computational resources required for the MC diffusion simulation are decreasing with device dimension because they are proportional to the number of dopants and defects in the device. On the other hand, resources for continuum simulations increase as modeling of ever more complex nonequilibrium phenomena are required. This trend has

already gone a long way towards making the KMC diffusion method competitive with the most detailed continuum diffusion methods today in terms of the required computational resources.

Unlike the continuum approach, the large number of different dopant-defect configurations does not present a problem for the MC approach, which simply needs to introduce the probabilities for the additional reactions. These probabilities are calculated based on the binding energies that can be plugged in directly from experiments, molecular dynamics, or *ab initio* calculations.

Besides, atomistic implantation and diffusion models provide a natural way of determining statistical variations for a specific process flow/device geometry combination.

---

## KMC Method

Sentaurus Process Kinetic Monte Carlo (Sentaurus Process KMC) considers only defects and impurities, and ignores the lattice, (except for some SPER and epitaxial deposition models). This drastically reduces memory requirements compared to molecular dynamics or lattice KMC techniques and allows you to investigate simulation domains that are large enough to contain deep-submicron devices. As Sentaurus Process KMC tracks the diffusion and interaction of defects, the fastest process is the jumping of a point defect with a period of approximately  $10^{-9}$  s. When there are no mobile point defects in the structure, the time step is increased automatically to an emission of mobile particles from the surface or from an extended defect, which has a period of approximately  $10^{-3}$  s.

Therefore, typically, Sentaurus Process KMC would begin with time steps of approximately  $10^{-9}$  s. As the point defects are trapped by the clusters and extended defects, Sentaurus Process KMC switches automatically to the larger time steps of the order of  $10^{-3}$  s that are large enough to model typical process steps.

---

## Operating Modes

Sentaurus Process KMC can operate in two different modes:

- The *atomistic* mode handles data atomistically throughout the simulation and is expected to be the most accurate method.
- The *nonatomistic* mode allows Sentaurus Process KMC to be used for only part of a simulation. Sentaurus Process KMC transfers data back and forth to the continuum solver to allow you to take advantage of the efficiency of the continuum solver for steps closer to equilibrium and to allow Sentaurus Process KMC to handle one or more steps that are far from equilibrium (such as fast RTA/flash annealing) to take advantage of its accuracy.

## Atomistic Mode

When Sentaurus Process KMC is in atomistic mode, the data fields are handled completely atomistically. To select the atomistic mode at the very beginning of the simulation, use:

```
SetAtomistic
```

The `SetAtomistic` command sets the parameter `AtomisticData` to `true`, allowing the Sentaurus Process commands `diffuse`, `deposit`, `etch`, `implant`, `init`, `line`, `photo`, `profile`, `region`, `select`, `strip`, and `struct` to work in the atomistic mode when possible, and to properly synchronize Sentaurus Process KMC when the structure changes. `SetAtomistic` also sets the `diffuse` method as Sentaurus Process KMC, and the `implant` mode as MC implantation. Finally, it calls `PDE2KMC` to atomize the available continuum fields into atomistic ones. The atomistic mode can be finished using:

```
UnsetAtomistic
```

The `UnsetAtomistic` command calls the procedure `KMC2PDE` to translate the atomistic quantities to fields and finishes the atomistic mode.

When `AtomisticData` is `true`, Sentaurus Process KMC does not populate continuum data fields with its own results, unless instructed to do so (using `kmc deatomize`).

## Restrictions

The following restrictions apply when using the atomistic mode:

- Do not use the command `transform stretch`.
- The `load` command only accepts the options `tdr` and `replace`.

The other commands work as expected, although the ones listed in [Table 43](#) have been especially adapted to operate in this mode.

Table 43 Commands adapted to work in atomistic mode

Command	Extension
<code>deposit</code>	Synchronizes the Sentaurus Process KMC structure after deposition.
<code>diffuse</code>	If the parameter <code>kmc</code> is specified or <code>Diffuse KMC</code> is set to 1 in the parameter database, <code>diffuse</code> calls Sentaurus Process KMC. If <code>AtomisticData</code> is not set to 1, a new KMC object is created, and it will be removed at the end of the diffusion step. Oxidation, nitridation, epitaxial deposition, and so on are accepted.
<code>etch</code>	Synchronizes the Sentaurus Process KMC structure removing the etched material, its contained particles, and setting the material to gas.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Operating Modes

Table 43 Commands adapted to work in atomistic mode

Command	Extension
<code>implant</code>	Works in MC mode and sends the cascades directly to Sentaurus Process KMC. Dynamic annealing also is simulated during the implant using Sentaurus Process KMC.
<code>init</code>	If a background concentration is specified, it is atomized and passed as particles to Sentaurus Process KMC.
<code>line</code>	Adds a new line to the Sentaurus Process KMC internal mesh, when possible.
<code>load</code>	Loads a Sentaurus Process KMC distribution from a TDR file and replaces the current one.
<code>math</code>	Accepts <code>numThreadsKMC</code> .
<code>photo</code>	Creates photoresist mask and synchronizes the new Sentaurus Process KMC structure.
<code>profile</code>	Loads and atomizes a profile.
<code>region</code>	When <code>region</code> changes the material, Sentaurus Process KMC is synchronized.
<code>select</code>	(Only when <code>select</code> creates a new field or modifies an existing one). If this field is known by Sentaurus Process KMC, the Sentaurus Process KMC concentration of particles is synchronized with the value of the field, removing or creating extra particles.
<code>strip</code>	Sentaurus Process KMC is synchronized with the new material. If there are particles in the stripped materials, they are removed.
<code>struct</code>	Automatically deatomizes some Sentaurus Process KMC data fields to make them accessible when saving to a file. It also saves Sentaurus Process KMC restart information.
<code>transform</code>	The Sentaurus Process KMC structure is updated after the transformation. Particles are removed or modified depending on the particular materials being created or removed. The option <code>stretch</code> is not allowed.

## Implant

Sentaurus Process KMC requires the damage morphology (coordinates of each point defect) for its damage accumulation model; this information is not available in analytic implantations. In atomistic mode, `implant` automatically uses the Sentaurus MC model as well as the `cascades` option for storing full cascades. The implantation time also is needed because while implanting, Sentaurus Process KMC automatically performs diffusion at the specified temperature (default is ambient). Typically, the temperature and time during the implantation affect only slightly the distribution of dopants, but they may affect damage accumulation, amorphization, and subsequent recrystallization and impurity cluster formation. The implantation time is returned by the function `DoseRate` defined in the file `Implant.tcl`. This time is computed by default using a fixed dose rate equal to  $1 \times 10^{12} / \text{cm}^2 \text{s}$ . If a dose rate is specified in an `implant` command by the `dose.rate` argument, it is used to compute the implantation time for this particular implantation instead.

For each implant dose and surface size, the number of implanted ions is computed. For example,  $1 \times 10^{14} \text{ cm}^{-2}$  boron dose in a simulation cell with a surface of  $40 \times 40 \text{ nm}^2$  and 250-nm depth implants  $40 \times 10^{-7} \times 40 \times 10^{-7} \times 10^{14} = 1600$  boron cascades (being a cascade one ion and all its generated damage). The information is passed to Sentaurus Process KMC for annealing. These diffusion steps occur internally and are not user-specified, but the total “diffused” time can be controlled by the function `DoseRate` explained above. Afterwards, the implant report issued by Sentaurus Process KMC names the backscattered particles as *outside* particles.

Molecular implants are allowed. To perform a molecular implant, specify the name of the molecule as the implant species (see [Implant on page 372](#)). The components of implanted molecules are introduced as isolated species in Sentaurus Process KMC; in other words, an implanted  $\text{BF}_2$  molecule will split into 2F and 1B inside Sentaurus Process KMC.

## Diffuse

For the first diffuse after the implant, the use of a small temperature ramp-up is recommended. The time for this ramp-up should be chosen as realistically as possible. At the end of an implant, the simulation cell contains the implanted ions plus a large amount of damage (point defects). During the ramp-up, this damage recombines and forms different types of clusters. The use of a realistic ramp-up produces more accurate results.

You can set the `pdb` parameters `automaticRampUp` and `automaticRampDown` to `true` to automatically perform ramps whenever the requested diffuse temperature is different from the current one. These ramps are performed with a ramp rate specified by `rampUpRate` and `rampDownRate` in C/s:

```
sprocess> pdbGet KMC rampUpRate
100
sprocess> pdbGet KMC automaticRampUp
0
```

Sentaurus Process KMC performs different annealings at different temperatures during the ramp-up. The objective is to perform few large annealings at low temperature and short ones at high temperatures. This maintains a high accuracy without spending too much time at low temperatures (changes in the temperature have a performance penalty).

The way these ramp-ups are performed can be configured using the following parameters of the parameter database:

```
sprocess> pdbGet KMC dtBase
2.0
sprocess> pdbGet KMC nInit
1
sprocess> pdbGet KMC dtLimit
20.0
```

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Operating Modes

The temperature steps for the highest temperature (the end of the ramp-up or the beginning of the ramp-down) are computed as:

$$(\Delta T_{base})^{n_{init} + n} \quad (647)$$

where  $\Delta T_{base}$  is `dTBase` and  $n_{init}$  is `nInit`.

For example, using the above parameters, in a ramp-down from 600°C to 500°C, the first annealing is performed at  $600^\circ\text{C} - 2^{1+0} = 598^\circ\text{C}$ , the second one is performed at  $598^\circ\text{C} - 2^{1+1} = 594^\circ\text{C}$ , and so on. When  $(\Delta T_{base})^{n_{init} + n}$  is greater than `dTLimit`, the value `dTLimit` is taken.

**NOTE** The above parameters are used only for temperature ramps induced by `automaticRampUp` or `automaticRampDown`. For temperature ramps specified with the command `temp_ramp`, the parameters to control the ramp are specified in the commands `temp_ramp` or `diffuse`.

Oxidation options are allowed in Sentaurus Process KMC. For more information, see [Oxidation-enhanced Diffusion \(OED\) Model on page 500](#) and [Oxidation on page 506](#).

---

## Nonatomistic Mode

Sentaurus Process KMC also can be used only for one diffusion step, synchronizing the status of the simulation before and after the diffuse step. This is performed with the `kmc` parameter in the `diffuse` command as follows:

```
diffuse kmc temperature=<n> time=<n>
```

When Sentaurus Process KMC runs with `AtomisticData` set to `false`, a new Sentaurus Process KMC simulation is launched at the beginning of the `diffuse` command:

- First, it receives the information (atomized from the data fields).
- Second, the diffusion is completed and, at the end of this command, Sentaurus Process KMC transfers the information to Sentaurus Process as data fields.
- Third, the Sentaurus Process KMC information is removed from memory.

This is similar to the following commands:

```
SetAtomistic
diffuse temperature=<n> time=<n>
UnsetAtomistic
```



---

## Atomistic/Nonatomistic Translation

These transformations of information back and forth from concentrations to particles are performed by the Tcl procedures `PDE2KMC` and `KMC2PDE`. These transformations may degrade the accuracy of the obtained results. By default, the transformation to continuum data is mapped to the `ChargedReact` (five-stream) model.

If you need to add a customize transformation, you can rewrite the procedures `PDE2KMCUser` and `KMC2PDEUser` with your own map. `PDE2KMCUser` (`KMC2PDEUser`) returns a string mapping the array of transformation from continuum to atomistic (atomistic to continuum). `KMC2PDEUser` cannot modify already existing fields, but it adds new ones. These maps contain three columns: the name of the original field, the name of the translated field, and the factor to be applied during the translation. For example, the following will transfer a new helium field into Sentaurus Process KMC:

```
fproc PDE2KMCUser {} {  
    return "Helium He 1 \  
           HeInt Hei 1 \  
           HeVac HeV 1"  
}
```

`PDE2KMC` uses the PDB parameter `KMC Si Damage TrimField` to trim the PDE fields exceeding this maximum value. This is useful to trim the concentration of Is and Vs in amorphized regions to more realistic values, avoiding the wasteful creation of excessive point defects. A value being at least 20% higher than the Sentaurus Process KMC amorphization threshold is suggested to properly amorphize the material.

For further customization, you can overload the Tcl procedures with your own. For more information on how to create and manipulate continuum and atomistic data, see [select on page 1053](#) and [kmc on page 954](#).

**NOTE** `KMC2PDE` and `PDE2KMC` may consume CPU time in large simulations. To improve efficiency, `KMC2PDE` keeps track of a previous translation and does not perform a new one if the previous one is still valid.

## Sano Method

The Sano method for converting particles to continuum profiles can be performed inside Sentaurus Process. The conversion is performed using the same module as the one available in Sentaurus Mesh.

For more details about this method, see [Mesh Generation Tools User Guide, Defining Particle Profiles on page 35](#) and [Mesh Generation Tools User Guide, Appendix B on page 179](#).

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Operating Modes

To apply the Sano method to all dopants and the computed quantity `NetActive`, select the `sano` option of the `UnsetAtomistic` command. However, to take full advantage of having the Sano method inside Sentaurus Process, do the following:

1. Generate a mesh tailored for device simulation, including the use of adaptive refinement based on `NetActive`.
2. Add contacts using the `contact` command.
3. Use the `smesh` option of the `struct` command that will, by default, create a mesh with contacts present and will store only those fields appropriate for device simulation.

As an example:

```
# Place mesh settings before UnsetAtomistic command in 3D, because
# a new mesh will be created during UnsetAtomistic using the
# current refinement settings

pdbSet Grid Adaptive 1
refinebox adaptive refine.fields= { BActive AsActive NetActive } \
  rel.error= { BActive = 1.1 AsActive = 1.1 NetActive = 1e30 } \
  max.asinhdiff= { NetActive = 5 } \
  target.length = 1e5 refine.min.edge = 0.5<nm> UnsetAtomistic sano

contact name = c1 box xlo = 0.0 ylo = 0.0025 xhi = 0.04 yhi = 0.0125 \
  silicon adjacent.material=oxide
contact name = c2 box xlo = 0.025 ylo = -0.01 xhi = 0.075 yhi = 0.01 \
  silicon
struct smesh= n10
```

The following parameter is available to control the accuracy of the Sano smoothing computation:

```
pdbSet KMC SanoMethod <species> ScreeningFactor <n>
```

The screening factor sets the inverse of the screening length of the Sano method. The smaller the screening factor, the smoother the profile and the longer the computation time.

For more options of the `UnsetAtomistic` command, see [UnsetAtomistic on page 1110](#). In addition, smoothing and remeshing based on Sano fields can be called directly using the `grid` command (see [grid on page 906](#)).

---

## Simulation Domain

All Sentaurus Process KMC simulations are performed internally in a 3D domain. If the Sentaurus Process structure is 1D or 2D, the missing lateral dimensions are created automatically to form a 3D simulation domain for Sentaurus Process KMC. For a 2D structure, the extension in the z-direction is taken from `MinZum` and `MaxZum`. For a 1D structure, the default extension is `MinYum` to `MaxYum` and `MinZum` to `MaxZum`.

To change the default values, use:

```
pdbSet KMC MinYum <n>  
pdbSet KMC MaxYum <n>
```

The Sentaurus Process KMC simulation domain is the same as the Sentaurus Process simulation domain, including the top of the simulation, and it cannot be changed. For `Y` and `Z`, the values `MinYum`, `MinZum` and `MaxYum`, `MaxZum` are used only when they are not set up in the input file (because the dimensionality of the simulation is smaller).

Consequently, the Sentaurus Process KMC dimensions fit Sentaurus Process dimensions. The size of the Sentaurus Process KMC simulation domain is reported in the output, for example:

```
KMC domain (-0.1, 0, 0) to (0.02, 0.02, 0.025) um Sentaurus domain (-0.1, 0, 0)  
to (0.02, 0.02, 0) um.
```

---

## Recommended Domain Size

For 3D simulations of deep-submicron transistors with twofold symmetry, you should make the simulation domain size one-quarter of the transistor. The Sentaurus Process KMC domain is automatically the same.

For a 1D simulation (that can be compared to SIMS data), Sentaurus Process KMC uses as small as possible lateral domain sizes to save CPU time. However, simulation domains with lateral sizes smaller than 20 nm may be too small to represent extended defects. If you are interested in a 1D profile with less statistical noise, you should increase the lateral size.

**NOTE** The minimum recommended size for accurate implant cascades and damage accumulation is 40 nm x 40 nm.

The lateral domain area is multiplied by the implant dose to obtain the number of ions implanted. For high impurity concentration levels, you may obtain enough particles in a relatively small simulation domain. For example, the implant dose of  $10^{15} \text{ cm}^{-2}$  creates 16000 ions for the 40-nm x 40-nm lateral domain side. This might be sufficient to obtain low

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Internal Grid

statistical noise, while any further increase in the 40-nm x 40-nm lateral domain size only slows the simulation.

To obtain good statistics for lower concentrations or lower doses, you must increase the lateral size of the simulation domain. For example, an implant dose of  $10^{12} \text{ cm}^{-2}$  creates only 16 ions for the 40-nm x 40-nm lateral domain.

One way to reduce the statistical noise without increasing the waiting time is to use the KMC parallel features available for 1D and 2D simulations. For more information, see [Parallelism on page 381](#).

**NOTE** When using Sentaurus Process KMC, try to use the smallest (but realistic) domain possible. If the simulation is too noisy or not representative, increase the lateral size. CPU time typically is proportional to the surface area. If a simulation with a  $20 \times 20 \text{ nm}^2$  surface takes 5 minutes to finish, you can expect a  $40 \times 40 \text{ nm}^2$  simulation to take four times longer.

---

## Internal Grid

Sentaurus Process KMC uses an internal grid to:

- Store the geometry and material assignments of the structure being simulated.
- Accelerate the search for possible interaction partners for each defect in the simulation.
- Compute the electronic properties.
- Be the minimum volume of amorphized silicon.
- Be the base to compute the concentrations written in the TDR file (using the `kmc extract tdrWrite` command).

The Sentaurus Process KMC grid is a tensor-product grid. This grid is different and isolated from the regular Sentaurus Process grid. The minimum size for each rectangular grid box is set to  $0.8 \times 0.8 \times 0.8 \text{ nm}^3$  and a minimum value than 0.8 nm in any axes will not be accepted. There is no maximum size. The grid is built using Sentaurus Mesh and can be adjusted using the following `pdb` parameters (default values in parenthesis):

<code>XGrading</code>	Grading in the x-direction. (1.05)
<code>YMinCell</code>	Minimum cell size in y-direction [ $\mu\text{m}$ ]. (1.5 nm)
<code>YMaxCell</code>	Maximum cell size in y-direction [ $\mu\text{m}$ ]. (2.5 nm)
<code>ZMinCell</code>	Minimum cell size in z-direction [ $\mu\text{m}$ ]. (1.5 nm)

<code>ZMaxCell</code>	Maximum cell size in z-direction [ $\mu\text{m}$ ]. (2.5 nm)
<code>Always3DMeshing</code>	Use Sentaurus Mesh to extrude 2D into 3D. By default, it uses an internal algorithm. (false)
<code>NonUniformTensor</code>	Use a nonuniform tensor grid (true) or use the old uniform tensor method (false) and the obsolete parameters <code>BitsBoxes</code> and <code>MinXum</code> . Setting it to false is strongly discouraged.

There are no `XMinCell` and `XMaxCell` for `x`. The maximum size for `X` is fixed to 100 nm, but is further controlled with refinements, as explained below. The final mesh is similar to the one obtained by Sentaurus Mesh using the following script:

```
tensor {
  mesh {
    mincellsize = 8e-4
    maxcellsize direction "x" 1e-1
    maxcellsize direction "y" $YMaxCell
    mincellsize direction "y" $YMinCell
    maxcellsize direction "z" $ZMaxCell
    mincellsize direction "z" $ZMinCell
    minbndcellsize = 8e-4
    maxbndcellsize = 1e-3
    grading = {$XGrading $XGrading}
  }
}
```

where `$Name` means the value of the parameter. The default parameters are set to try to minimize the Manhattan geometry at the interfaces, while maximizing the performance of the simulation. All of these parameters can be set using `pdbSet KMC`, for example:

```
pdbSet KMC ZMaxCell 3e-3
```

Further customization can be added in the form of refinements. To refine the KMC internal grid, the command `refineBox`, with the parameter `kmc`, is used. By default, Sentaurus Process KMC applies one refinement when using `SetAtomistic`. This refinement is defined as:

```
refinebox kmc min = { 0 0 } max = { 0.1 2 } xrefine = { 0.0012 0.0015 0.0015 }
```

This default refinement can be changed overwriting the procedure `kmcDefaultRefinement` with a user-defined refinement. For example, to remove the default refinement only:

```
fproc kmcDefaultRefinement { } {
  LogFile "Removing the default refinement (by not defining it)..."
}
```

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Randomization

Finally, the lines and spacing specified with the `line` command also will be included in the simulation if possible.

For more information on the internal grid and how it affects the simulation, see [Materials and Space on page 386](#).

---

## Randomization

You can investigate statistical variations of a process flow by selecting a different seed for the random number generator used by Sentaurus Process KMC in each run. You can specify the value of the seed changing the parameter `randomSeed` in the parameter database:

```
pdbSet KMC randomSeed <n>
```

The seed can be set to any value from 0 to 31328.

---

## Boundary Conditions

By default Sentaurus Process KMC uses periodic boundary conditions at the left, right, front, and back sides of the simulation domain. To change these conditions, use the parameters `KMC PeriodicBC_Y` and `KMC PeriodicBC_Z`.

There also is an option to use only periodic boundary conditions for extended defects like {311}s and dislocation loops. To define this option, set `DebugFlag` to 4 in the PDB. This option applies periodic boundary conditions only to the extended defects and still uses reflective boundary conditions for everything else. You can use this option to reduce the lateral simulation domain for investigating 1D simulations. Even when the lateral simulation domain is comparable or smaller than the typical length of the extended defect, the periodic boundary conditions allow you to obtain meaningful results.

**NOTE** This option should not be used for 3D simulations if there are lateral variations in geometry or profiles.

When Sentaurus Process KMC detects an improper choice of the periodic boundary conditions, it changes the periodic conditions:

```
** Warning **  
KMC. The material structure is not the same in the plane y=0 and y=ymax.  
Periodic boundary conditions for defects have been disabled!
```

The boundary conditions for the x-axis are mirror. You can transform them into a sink using the parameter `sinkProbBottom`. This parameter is defined for any material. For example, to

specify that 20% of the incoming positive interstitials should be sunk when reaching the maximum coordinate in silicon, use:

```
pdbSet KMC Silicon I sinkProbBottom IP 0.2
```

It is also possible to define sink boundary conditions for the y- and z-axis, independently of the general *mirror* or *periodic* conditions described below. Similarly to the sinks defined in the x-axis, a probability for particles crossing the boundary to be annihilated will be defined. This probability is applied before the general boundary conditions. For example, if a 50% sink is defined for interstitials at the left boundary, 50% of them surviving the sink will be either mirrored or moved to the opposite side to simulate periodicity.

The parameter names for the y-axis are `sinkProbLeft` and `sinkProbRight` and, for the z-axis, they are `sinkProbFront` and `sinkProbBack`.

---

## Parallelism

You can use several CPUs during a Sentaurus Process KMC simulation. This feature is configured with the `math` command:

```
math numThreadsKMC=<n>
```

where `<n>` is the number of threads to launch. When also using MC implantation, the number of threads used by Sentaurus Process KMC overwrites the number of threads used by MC implantation.

The KMC to PDE "smooth" algorithm (see [Smoothing Out Deatomized Concentrations on page 525](#)) also can work in parallel:

```
math numThreadsDeatomize=<n>
```

Sentaurus Process KMC uses the `sparallel` licenses in the same way as Sentaurus Process does. In particular, if no licenses are available, the code will continue in serial or abort depending on the `go.serial` or `go.abort` options specified by the user.

---

## How Parallelism Works

Sentaurus Process KMC works in parallel by assuming that there is no space anisotropy in the z-direction. This assumption is trivially true for 1D and 2D simulations, and generally false for 3D simulations. Consequently, parallelism is only allowed in simulations that have a 1D or 2D domain in Sentaurus Process (even when internally all atomistic simulations are 3D).

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Estimating CPU Time

The main simulation domain is divided into  $\langle n \rangle$  subdomains;  $n$  is the number of threads to be used. Each subdomain is then run as an independent simulation. Then, the boundary conditions selected for the  $Z$  boundary are applied to the new  $Z_i$  boundaries. At the end of the simulation (implantation or diffusion), the main domain is recreated as the simple addition of all the subdomains. All these “splits” and “forks” of the simulation domains are performed automatically and are transparent to users.

When using parallelization, one big parallel simulation domain is run as several smaller domains. At the end of the simulation, the third dimension will be collapsed and averaged to produce a 2D result (third and second dimensions for 1D results). In any case, the subdomains must be large enough to allow an accurate representation of the physics involved in the simulation. In particular, since a minimum surface of 40 nm by 40 nm is recommended, the minimum suggested size for parallel simulations is 40 nm in the  $y$ -axis and  $n \times 40$  nm in the  $z$ -axis, where  $n$  is the number of threads.

When instructing Sentaurus Process KMC to work in parallel with  $\langle n \rangle$  threads, the domain is divided into  $\langle n \rangle$  subdomains in the  $z$ -direction, and each one is processed by a different CPU. Later, the subdomains are appended together. These manipulations are transparent to users.

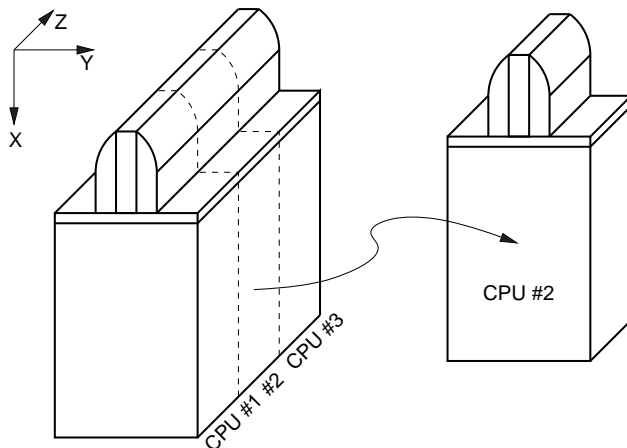


Figure 39 When Sentaurus Process KMC works in parallel with  $\langle n \rangle$  threads, the domain is divided into  $\langle n \rangle$  subdomains in the  $z$ -direction, and each one is processed by a different CPU. Later, the subdomains are appended together. Here,  $\langle n \rangle = 3$ .

---

## Estimating CPU Time

CPU time and memory required for KMC diffusion simulation are directly proportional to the number of particles in the structure. For a typical 2-GHz machine, Sentaurus Process KMC performs up to 1 million events (jumps) per second. In some 64-bit platforms, the number can reach 2 million events per second.



In equilibrium conditions without implant damage, concentrations of mobile species are low and events are rare. Therefore, the simulation requires few events to reach the required diffusion time and proceeds quickly.

For transient-enhanced diffusion after an implant step, it takes some time to anneal the implant damage. Depending on the implant conditions, each implanted ion generates up to  $10^3$  interstitials and vacancies. Each interstitial and vacancy makes up to  $10^5$  jumps before recombining at the surface. This means that it takes approximately 1 second of CPU time to anneal one implanted ion.

**NOTE** The above numbers are only estimations. The CPU speed differs depending on the machine, operative system, and other factors.

Clustering and emission processes take longer internally than diffusion (hops) processes in Sentaurus Process KMC, and similar numbers of simulated clustering or declustering processes may lead to a larger wall clock time.

**NOTE** The use of parallelization also changes the time estimation (see [Parallelism on page 381](#)).

**NOTE** The use of different *hopping modes* (KMC HoppingMode) also changes the time needed to run the simulation, with `doublelong` being the fastest mode (see [Hopping Mode on page 411](#)).

---

## Atomistic Diffusion Simulation with Sentaurus Process KMC

The nonlattice KMC method tracks only atoms in defects, while lattice silicon atoms are not included as shown in [Figure 40](#).

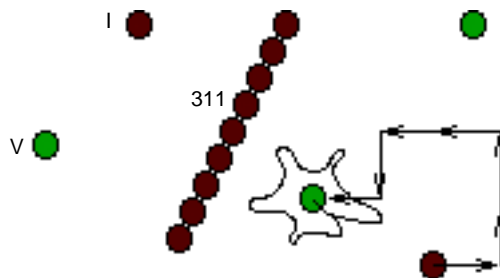


Figure 40 The nonlattice KMC method tracks only atoms in defects; lattice silicon atoms are not included

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Atomistic Diffusion Simulation with Sentaurus Process KMC

In molecular dynamics, all lattice atoms and all defect atoms must be simulated, but in the nonlattice KMC method, only defect atoms are considered. Lattice atoms vibrate with a high frequency because of thermal energy and, occasionally, one of the point defects diffuses and moves to a neighboring position. Since Sentaurus Process KMC uses the nonlattice KMC method, it discards the lattice information and only follows the defect atoms. This greatly affects CPU time, from approximately  $10^{-13}$  s for lattice vibrations to approximately  $10^{-9}$  s for fast diffusing particles. During diffusion, moving particles can be captured by extended defects that emit isolated particles with frequencies orders of magnitude smaller than frequency of point defects jumps.

Sentaurus Process KMC takes the input parameters of migration, binding, emission energies, and so on and simulates the frequencies at which these different events occur. Sentaurus Process KMC starts with short time steps, but when the simulation evolves and the fast moving point defects disappear, the average time step automatically changes to adapt to the new situation.

Single particles can move alone or belong to an extended defect, like a {311}.

- For self-silicon point defects, in other words, interstitial and vacancy models, see [Point Defects, Impurities, Dopants, and Impurity-paired Point Defects on page 403](#).
- For diffusing dopants, see [Impurities on page 405](#).
- For self-silicon extended defects, see [Damage Accumulation Model: Amorphous Pockets on page 420](#) and [Extended Defects on page 430](#).
- For clusters involving dopants, see [Impurity Clusters on page 460](#).

---

## Units

The units used by Sentaurus Process KMC are:

- Micrometer ( $\mu\text{m}$ ) for length
- Second (s) for time
- Electron volt (eV) for binding energies
- Atoms per  $\text{cm}^3$  for concentrations
- $\text{cm}^2\text{s}^{-1}$  for diffusivities
- $\text{nm}^3$  for stress activation volumes

**NOTE** These units are standard in atomistic and continuum simulators. Nevertheless, Sentaurus Process KMC internally uses a nonconventional unit to measure frequencies. For consistency with migration prefactors, frequencies are measured in diffusivity units in the input parameter files. However, even for migration prefactors, which are in diffusivity units to easily compare them with experimental numbers, Sentaurus Process KMC must transform them to frequency units in  $s^{-1}$ . This is performed using the expression  $\nu = \frac{6D}{\lambda^2}$ , where  $\lambda$  is the average jump distance.

---

## Space Management

Sentaurus Process KMC assumes an orthogonal simulation cell to manage space. The minimum and maximum x-, y-, and z-dimensions (that is, the bounding box) are passed to Sentaurus Process KMC as simulation parameters. Sentaurus Process KMC assumes that the x-axis is the depth of the silicon wafer; whereas, yz is the wafer area.

When Sentaurus Process KMC has the simulation cell size, it splits the space (see [Figure 41](#)) using Sentaurus Mesh. This creates an internal grid inside the rectangular simulation boundary box. This grid is used only by Sentaurus Process KMC and is fully isolated from the Sentaurus Process finite-element mesh. These rectangular elements cannot be smaller than twice the jump distance (0.8 nm). To customize the internal grid, see [Internal Grid on page 378](#).

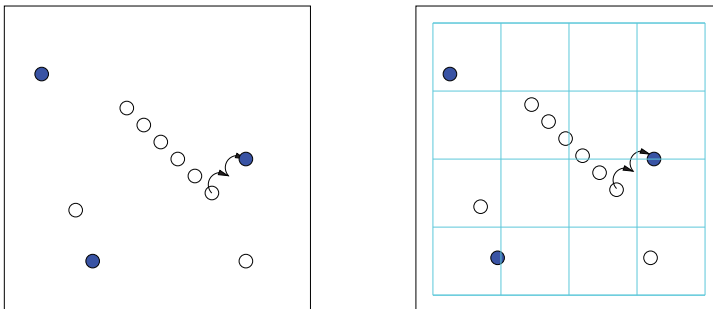


Figure 41 Sentaurus Process KMC divides the space (*left*) into small rectangular elements (*right*); these elements are used for neighbor search, amorphization, and charge models

Sentaurus Process KMC shows the number of elements in its output:

```
KMC domain (-0.1, 0, 0) to (0.3, 0.16, 0.05) um
```

```
KMC NonUniformTensor. Boxes: 430125
```

```
X=155 (1 - 100)nm
```

```
Y=111 (0.903641 - 1.7048)nm
```

```
Z=25 (2 - 2)nm
```

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Atomistic Diffusion Simulation with Sentaurus Process KMC

In the above example, the x-axis minimum cell is 1 nm and the maximum one is 100 nm. For y, these values are 0.9 and 1.7 nm, respectively. Finally, all of the cells have the same size in the z-axis: 2 nm. There are 155 cells in the x-direction, and 11 and 25 for y and z, respectively. The total number of elements is 430125.

**NOTE** Memory allocation depends on the number of internal elements and on the number of particles. To modify the number of internal elements using the parameter, see [Internal Grid on page 378](#).

To add user lines to the simulation, use the `line` command. You also can specify the option `spacing` in this command. In this case, and in contrast with the nonatomistic mode, there is a minimum size of 0.8 nm between lines. If you specify a very thin spacing, and Sentaurus Mesh tries to add some lines later to better refine a surface, these last lines could be discarded in the KMC mesh only to keep the 0.8 nm limitation. Because of this, the use of `spacing` is not suggested, and it is usually better to rely on the results of Sentaurus Mesh.

---

## Materials and Space

The transfer of materials from Sentaurus Process to Sentaurus Process KMC is straightforward: Each Sentaurus Process KMC element is assigned to a material type. Sentaurus Process KMC creates interfaces whenever two elements are set to different materials, except when instructed not to do so. Consequently, the shape and interfaces assigned by Sentaurus Process KMC depend on how smooth the shapes are and how fine the internal elements are (see [Figure 42](#)).

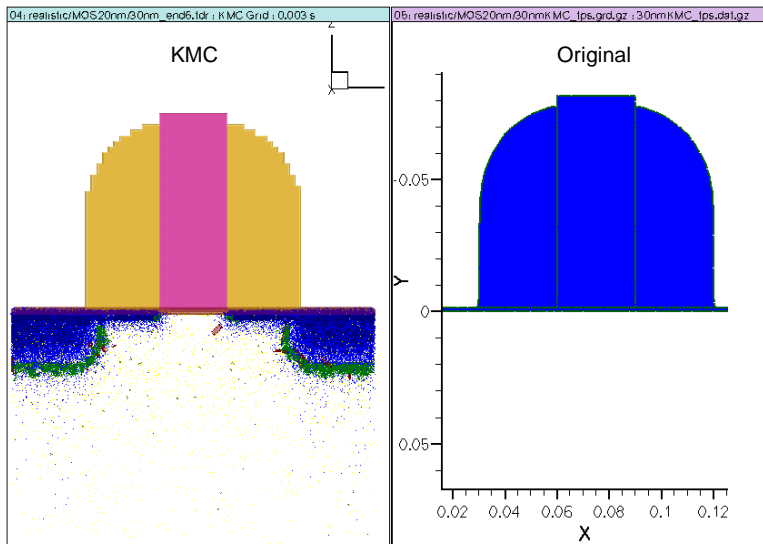


Figure 42 Interfaces between materials have a Manhattan structure in Sentaurus Process KMC; each element is assigned to a material, and elements are always rectangular

The meshing algorithm included in Sentaurus Mesh tries to fit the interfaces using a nonuniform tensor. This fit is perfect when the interfaces are flat, axis-aligned and there are no limitations with the element size due to spacing or very thin features. Since the minimum dimension for an element is 0.8 nm, interfaces thinner than that will not be accurately represented.

After the material assignment, Sentaurus Process KMC checks that there are no mistakes in the translation by reviewing the original interface elements and checking that there is a corresponding KMC interface associated with them. Whenever this correspondence is not satisfied, Sentaurus Process KMC issues a warning:

```
** Warning **  
KMC. 1.79 percent of the Oxide/PolySilicon interface is lost when translating  
to KMC. Please, review the results carefully.  
... continuing execution
```

**NOTE** In some cases, these warnings may be produced by thin, but negligible, structure shapes. In these cases, the percentage of interface lost is small. When the percentage is significant, they point to important problems that must be resolved before continuing the simulation.

---

## Supported Materials

The materials already defined in Sentaurus Process KMC include:

- Silicon (crystalline silicon)
- Amorphous silicon
- Silicon oxide
- Polysilicon
- Nitride
- Gas
- Germanium
- Germanium oxide
- Amorphous germanium

Amorphous can be assigned by users, but it also is created automatically by changing the crystalline regions during simulation when the damage reaches an amorphization level (see [Amorphization and Recrystallization on page 442](#)).

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Atomistic Diffusion Simulation with Sentaurus Process KMC

The materials supported by Sentaurus Process KMC are defined in the PDB:

```
sprocess> pdbGet KMC Materials
Silicon           true
AmorphousSilicon true
Oxide             true
PolySilicon       true
Nitride           true
Gas               true
Unknown          true
```

It is possible to define or remove materials, already known by Sentaurus Process, into Sentaurus Process KMC. They only need to be added as `true` or `false` to this list. For materials not defined in Sentaurus Process, they must be introduced to Sentaurus Process first with `mater add`. For example, to add a new material called `AnotherSilicon` and to remove Nitride:

```
pdbSet KMC Materials AnotherSilicon true
pdbSet KMC Materials Nitride false
```

Every new material in Sentaurus Process KMC requires the following `pdb` parameters:

Model	<p>The options are:</p> <p>The <code>discard</code> model creates a material empty of particles (for example, gas). All particles introduced in this material are discarded.</p> <p>The <code>simple</code> model allows simple diffusion of dopants and impurity clusters. It does not model Fermi-level dependencies, amorphization, solid phase epitaxial regrowth (SPER), and extended defects. Oxide and nitride are examples of ‘simple’ materials.</p> <p>The <code>full</code> model allows all models: point defects (interstitials and vacancies), extended defects, impurity clusters, damage accumulation, amorphization, recrystallization, and the Fermi level–dependent diffusivity models (for example, silicon).</p>
ShortName	<p>This is the short name of the material when reading parameters defined for the interfaces. For example, the interface <code>Oxide_Silicon</code> contains the parameters <code>Eb_SurfOx</code> and <code>Eb_SurfSi</code>, where <code>Ox</code> and <code>Si</code> are the short names of silicon and oxide.</p>
Crystalline	<p>A Boolean value. True if the material is crystalline (silicon) and false if it is amorphous (amorphous silicon).</p>
Equivalent	<p>Name of the amorphous/crystalline equivalent. For example, silicon will have amorphous silicon as its equivalent, and the amorphous silicon equivalent is silicon.</p>

Oxide	Specify with <code>true</code> or <code>false</code> whether the material is an oxide or is not an oxide, respectively. This is used for oxidation models. For example, <code>SiOxide</code> and <code>GeOxide</code> have this field as <code>true</code> .
Alloy	Specify if this material can alloy with another material to form binary alloys with corrections to activation energies. Write the alloy material here. For example, for silicon alloying with germanium, write <code>Germanium</code> in the <code>Alloy</code> field of the silicon material.

After the material is properly defined, the parameters for all the particles in this new material must be defined as well. These parameters depend on the model defined for the new material (for an overview of these parameters, see [Including New Impurities on page 510](#)). Finally, parameters for all interfaces between the existing materials and the new material must also be defined.

**NOTE** To minimize the work of defining parameters for a new material, it is advisable to disable the materials that will not be used, thereby avoiding to define parameters for the interfaces between those materials and the new one. For the dopant parameters in the new material, you can “copy” the parameters from another material and redefine only some of them.

Any other material existing in Sentaurus Process, but not defined by Sentaurus Process KMC, is mapped as ‘Unknown’. The model for this material is `discard`, and all particles inside these materials are discarded and removed. They do not need parameters because they contain no particles to simulate.

---

## Material Alloying

Sentaurus Process KMC allows materials containing an alloying element to be treated in a quasi-atomistic framework. Such an alloying element is specified using the `Alloy` parameter of the material specification. In the following, as an example, it is assumed that the material is silicon and the alloy is germanium (although, this can be reversed, or any pair of materials can be used with “full” modeling).

The quasi-atomistic framework means that alloy particles (Ge) are not created as particles, but they will be taken into account as a field, so as to produce a local concentration. This saves memory and speeds up the concentration. Diffusion of the alloying element is possible using the model specified in [Alloy Diffusion on page 419](#).

The inclusion of an alloy changes the bandgap narrowing as specified in [Narrowing due to Presence of an Alloy on page 492](#). Such a model uses a quadratic interpolation to smooth from the band gap of the pure material to the band gap of the pure alloy. Since the positions in the

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Atomistic Diffusion Simulation with Sentaurus Process KMC

band gap of all particles are scaled with the total band gap, the positions for charged defects are scaled accordingly.

All activation energies for diffusion-, emission-, and activation-related processes are corrected by a term linear on the alloy concentration. If a given mechanism is simulated by following an Arrhenius expression similar to:

$$v = P \exp(-E/k_B T) \quad (648)$$

the mechanisms under an alloy concentration are corrected by a linear term in the activation energy with the concentration of the alloy (Ge):

$$v = P \exp(-(E + \alpha[\text{Ge}])/k_B T) \quad (649)$$

The same applies to the formation energies of point defects and the potential energies of impurity clusters. Examples of these corrections are available in [Alloy Effects on page 420](#).

## Point Defects

Sentaurus Process KMC can distinguish between different interstitials, depending on the material, using different syntax. The syntax "I" refers to an interstitial in the particular material where it is positioned; otherwise, a more concrete notation must be used. For example, in a structure where the first half is Ge and the second half I, "I" refers to Ge<sub>i</sub> in the first half and Si<sub>i</sub> in the second half. While Si<sub>i</sub>, for example, would have the same meaning as in the second half, but it would produce Si in the first half.

## Ambiguous Alloying

Sentaurus Process KMC allows the use of a material (for example, Si) with an alloy (for example, Ge) without having to define the material alloyed (Ge). Nevertheless, it is also possible to define the alloyed material as the main material (Ge) with the other one as the alloyed material (Si). However, having all alloys defined twice is ambiguous. For example, Si<sub>0.2</sub>Ge<sub>0.8</sub> can be defined as main Si with 80% Ge, or as main Ge with 20% Si.

The *main* material is the one specified in the input file as `material`. In this case, it can be silicon, and then you can use the `select` command or similar to include 80% Ge (or germanium) and 20% silicon. Unfortunately, the complexity of the models and their calibration produce different results when these two ways to have the same alloy are used. To solve this issue, using Si as the main material up to 80% Ge concentration and Ge up to 20% silicon is suggested.



## Time Management

The main component in Sentaurus Process KMC is an algorithm that sequentially selects the possible random events (migration of point defects, emission of extended defects, and so on) according to their corresponding frequencies, similar to the Bortz–Kalos–Liebowitz (BKL) algorithm so widely used in KMC methods. Figure 43 illustrates the selection procedure for the atomistic configuration shown in Figure 40 on page 383, consisting of three vacancies ( $V$ ), two interstitials ( $I$ ), and one  $\{311\}$  defect.

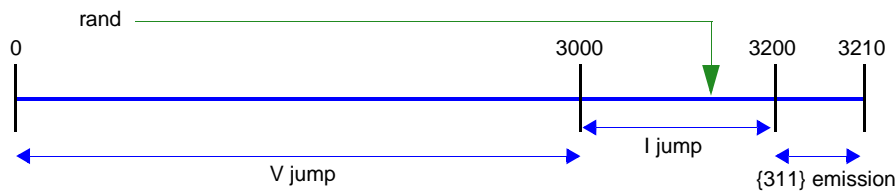


Figure 43 Events are selected according to their rates, which in turn, depend on the current atomistic configuration

Assuming the vacancy and interstitial migration frequencies are  $1000 \text{ s}^{-1}$  and  $100 \text{ s}^{-1}$ , respectively, and the  $\{311\}$  emission rate is  $10 \text{ s}^{-1}$ , to simulate 1 s, you have to simulate a total of 3210 events. Consequently, simulating one event corresponds to simulating  $1/3210 \text{ s}$ . This implies that the simulated time step is not fixed, but depends on the particular simulation configuration. In addition, you must choose a  $V$  with a probability of  $3000/3210$ , and  $I$ s and  $\{311\}$  defects with probabilities of  $200/3210$  and  $10/3210$ . A random number between 1 and 3210 (or 0 and 3209) is generated. For example, in Figure 43, the number 3147 selects an  $I$  migration event.

After several migration events, when one interstitial reaches and interacts with a vacancy, the simulator generates an  $IV$  pair called an *amorphous pocket* (AP) (see [Damage Accumulation Model: Amorphous Pockets on page 420](#)).

The simulation contains two  $V$ s, one  $I$ s, one  $IV$ , and one  $\{311\}$ . You can assume the  $IV$  pair will recombine with a frequency of  $500 \text{ s}^{-1}$ . The new random number will be between 1 and  $2000 + 100 + 500 + 10 = 2610$ . Consequently, the time step will be  $1/2610 \text{ s}$ . If the  $IV$  recombination event is chosen and this  $IV$  pair is annihilated, the new simulation contains only two  $V$ s, one  $I$ , and one  $\{311\}$ , and the following time step is  $1/2110 \text{ s}$ .

**NOTE** The time step is not a fixed quantity in Sentaurus Process KMC, but it depends on the state of the simulation.

The current time step depends on two factors:

- Number of particles in the simulator
- Frequency of the events associated to the particles or defects or both

## 5: Atomistic Kinetic Monte Carlo Diffusion

Atomistic Diffusion Simulation with Sentaurus Process KMC

And these frequencies depend on three factors:

- Type of event
- Arrhenius plot associated with the event
- Temperature

---

## Simulation and CPU Times

The time needed to complete a simulation depends on several factors:

- How fast the computer simulates one event
- How many events need to be simulated
- The hopping mode chosen
- The presence of lattice KMC models (for SPER and epitaxial deposition)
- Whether you use parallel capabilities

The number of events to be simulated is inverse to the average time step (which changes during the simulation, as explained above). The speed at which the simulator processes events depends on the type of simulated events. Migration events usually are simulated rapidly. Simulations involving changes in the electronic concentration or temperature or both are much slower because updating the dependencies with the temperature and the Fermi level takes extra time. Generally, the smaller the simulation, the shorter the time.

In simulations with implants, the implant MC module also adds time to the simulation while computing the cascades. In amorphizing conditions, the Sentaurus Process KMC amorphous model requires extra time to smooth out the damage and create amorphous layers. Finally, simulations with strong gradients in the electronic concentration need more charge updates, which take extra time.

During oxidation, several remeshings must be performed to update the Sentaurus Process KMC structure to the new Sentaurus Process oxide thickness, consuming extra time.

Finally, the hopping mode allows you to choose whether long hops or double hops are allowed, thereby speeding up the simulation. Both are switched on by default (see [Hopping Mode on page 411](#)).

**NOTE** You can estimate the time needed for simulation by running a small simulation and assuming the CPU time is proportional to the number of particles (proportional to the surface area) and to the number of the internal reported time.

**5: Atomistic Kinetic Monte Carlo Diffusion**  
Atomistic Diffusion Simulation with Sentaurus Process KMC

Sentaurus Process KMC shows the status of the current simulation, printing log messages each time the temperature changes during a temperature ramp, or whenever there is a new *snapshot* (see [Snapshots on page 394](#)). These log messages are as following:

```

Reaction :      31s  to      63s  step   :      32s  temp: 950.0C
Mechanics:      31s  to      63s  step   :      32s  temp: 950.0C
Diffusion:      31s  to      63s  step (d):      32s  temp: 950.0C
KMC: Time(s)  Temp(C)      Events Events/s Average step(s)  %Done
      46.416   950.01   3600728007 1877077    4.749174e-08  7.74% (36% V)
Reaction :      1.05min to    2.117min step   :      1.067min temp: 950.0C
Mechanics:      1.05min to    2.117min step   :      1.067min temp: 950.0C
Diffusion:      1.05min to    2.117min step (d):      1.067min temp: 950.0C
KMC: Time(s)  Temp(C)      Events Events/s Average step(s)  %Done
      100.000   950.01   4742533558 1865695    4.692958e-08 16.67% (33% V)
Reaction :      2.117min to    4.25min step   :      2.133min temp: 950.0C
Mechanics:      2.117min to    4.25min step   :      2.133min temp: 950.0C
Diffusion:      2.117min to    4.25min step (d):      2.133min temp: 950.0C
KMC: Time(s)  Temp(C)      Events Events/s Average step(s)  %Done
      215.444   950.01   6881748852 1868310    5.396525e-08 35.91% (34% I)
Reaction :      4.25min to    7.125min step   :      2.875min temp: 950.0C
Mechanics:      4.25min to    7.125min step   :      2.875min temp: 950.0C
Diffusion:      4.25min to    7.125min step (d):      2.875min temp: 950.0C
Reaction :      7.125min to   10min step   :      2.875min temp: 950.0C
Mechanics:      7.125min to   10min step   :      2.875min temp: 950.0C
Diffusion:      7.125min to   10min step (d):      2.875min temp: 950.0C
KMC: Time(s)  Temp(C)      Events Events/s Average step(s)  %Done
      464.159   950.01  11927967061 1864825    4.928753e-08 77.36% (35% I)

Elapsed time for diffuse 7.8672e+03s
      600.000   950.01  14721335445 1882323    4.862968e-08 100.00% (35% I)

```

It is easy to identify the log immediately after the `Diffusion` statement because it is preceded by a “KMC:” header. In the above example, the total simulated (annealed) time is 600 s. The (current) temperature is 950°C. A total of  $1.4 \times 10^{10}$  events has been simulated so far, and the simulator processed 1.9 million events each CPU second. The averaged time step is  $4.9 \times 10^{-8}$  s. Finally, Sentaurus Process KMC writes the particle with the biggest percentage of diffusion jumps. In the example, the diffusion of the neutral interstitial (I) has taken 33 to 36% of the total diffused particles.

This information may change from one simulation to another, and also at different times during the same simulation. The events per second and average step statistics are recomputed between sentences.

## 5: Atomistic Kinetic Monte Carlo Diffusion

Atomistic Diffusion Simulation with Sentaurus Process KMC

### Parallelism and CPU Time

[Table 44](#) lists the CPU times that can be expected when running on different numbers of threads. However, the exact time depends on the particular simulation.

Table 44 Approximate CPU times when using multiple threads

Number of independent threads	Approximate time	Improvement
1	S	1x
2	S/2.3	2.3x
4	S/4.8	4.8x
8	S/8	8x
12	S/9.5	9.5x
16	S/10.5	10.5x

The total simulation time is superlinear for  $n < 8$  and starts saturating for  $n \geq 12$ . The reason for being superlinear for a small number of threads is that the CPU time depends superlinearly on size. Consequently, simulating a size  $XYZ/n$  takes less CPU time than  $S/n$ . Nevertheless, as  $n$  increases, different mechanisms (such as the waiting time of threads to be synchronized) conspire to degrade the total simulation time.

### Snapshots

A snapshot is an interruption of the normal Sentaurus Process KMC simulation flow to print the status of the simulation and to allow you to run a customizable Tcl command (see [Movie on page 395](#)). To control these interruptions, set the `pdb` parameters listed in [Table 45](#).

Table 45 Snapshot parameters

Parameter	Description
<code>Decade &lt;n&gt;</code>	Sets how many snapshots will be generated per decade. 0 disables it.
<code>InitOutputTime &lt;n&gt;</code>	No snapshots per decade are generated when the simulated time is smaller than $n$ .
<code>maxSnapshots &lt;n&gt;</code>	Maximum number of snapshots to be stored. After this limit is reached, the oldest ones are erased to make space for the new ones.

For example:

```
pdbSet KMC Decade 2
```

produces two snapshots per decade, as in:

Time(s)	Temp(C)	Events	Events/s	Average step(s)	%Done
0.000	26.85	0			
548.138	700.00	1		5.481385e+02	0.05% (35% I)
1492.073	700.00	5		2.359835e+02	0.15% (33% I)
3639.863	700.00	7867		2.731862e-01	0.36% (35% I)
10130.431	700.00	14553		9.707701e-01	1.01% (35% I)
31902.727	700.00	35862		1.021742e+00	3.19% (36% I)
100030.228	700.00	205821	169959	4.008467e-01	10.00% (35% I)
317268.817	700.00	668173		4.698554e-01	31.73% (34% I)
1000000.000	700.00	1754838	1086665	6.282812e-01	100.00% (35% I)

## Movie

The Sentaurus Process KMC `Movie` command is similar to the Sentaurus Process `Movie` command and executes the contents of the parameter `KMC Movie` any time a new snapshot is generated. You can use this command interactively to obtain information about the simulation, to add data to the TDR file of Sentaurus Process KMC, and so on.

For example, it can be used to add concentration information and the positions of particles to the TDR file during the simulation:

```
pdbSet KMC Movie {kmc extract tdrAdd concentrations defects}
```

or to plot the evolution of damage while the simulation is still running:

```
pdbSet KMC Movie {  
  kmc deatomize name=ITotal; sel z=log(ITotal+1); plot.ld label=I clear;  
  kmc deatomize name=VTotal; sel z=log(VTotal+1); plot.ld label=V !clear  
}
```

---

## Time Internal Representation and Limitations

In contrast with previous versions, there are no internal limits for the frequencies used in Sentaurus Process KMC. Nevertheless, very high frequencies (typically produced by small migration energies) can lead to slow simulations.

---

## Particles

Particles are represented in Sentaurus Process KMC with three spatial coordinates (x, y, z) and two labels:

- The particle type label identifies the species, charge state, and role of the particle in the simulation.
- The defect type indicates when the particles are agglomerated with others or when they stand alone.

---

## Particle Types

To obtain a list of the standard particles currently defined for Sentaurus Process KMC, use the command:

```
sprocess> kmc particletypes
I V B As C F In P Sb N Nn H IMM IM IP IPP VMM VMMM VM VP VPP VPPP Asi AsiP AsV
AsVP AsVM Bi BiP BiM Ci FV FI Ini IniM InV InVM Pi PiP PV PVM PVP Sbi SbiP SbV
SbVP SbVM NnV
```

Dopants are user defined in Sentaurus Process KMC, while interstitials and vacancies are fixed and cannot be customized. The standard list of interstitials and vacancies defined in Sentaurus Process KMC is:

I	Silicon self interstitial–neutral
IMM	Silicon self interstitial–double negative
IM	Silicon self interstitial–negative
IP	Silicon self interstitial–positive
IPP	Silicon self interstitial–double positive
V	Vacancy–neutral
VMMM	Vacancy–triple negative
VMM	Vacancy–double negative
VM	Vacancy–negative
VP	Vacancy–positive
VPP	Vacancy–double positive
VPPP	Vacancy–triple positive

The dopants are defined in the parameter database. By default, particles for As, B, P, In, C, F, N, Nn (N<sub>2</sub>), H, and Sb are defined. For example, the default particles for As, B, and P are:

As	Substitutional arsenic–positive
Asi	Interstitial arsenic–neutral
AsiP	Interstitial arsenic–positive
AsV	Vacancy arsenic–neutral
AsVM	Vacancy arsenic–negative
AsVP	Vacancy arsenic–positive
B	Substitutional boron–negative
Bi	Interstitial arsenic–positive
BiM	Interstitial arsenic–positive
BiP	Interstitial arsenic–positive
P	Substitutional phosphorus–positive
Pi	Interstitial phosphorus–neutral
PiP	Interstitial phosphorus–positive
PV	Vacancy phosphorus–neutral
PVM	Vacancy phosphorus–negative
PVP	Vacancy phosphorus–positive

**NOTE** Since P at the end of the name means *positive*, to specify a cluster containing P, the P cannot be at the end in any case. This means that AsiP is an arsenic–interstitial positive, while PAsi is a phosphorus arsenic–interstitial cluster. Similarly, AsP will be interpreted as *arsenic positive*, while PAs is phosphorus–arsenic.

**NOTE** These lists show the most commonly used particles, but the list is not exhaustive. An exhaustive list contains all point defects (Is and Vs) with charges from –3 to +3, and all impurity pairs with charges from –2 to +2.

## Particles in Models

The dopants allowed in the simulation are defined in the parameter database under the label `KMC Impurities`. The database lists the impurity name, the charge, and a Boolean parameter indicating whether the particle is allowed in the Sentaurus Process KMC simulation.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Particles

The particle name and the charge must be delimited by a comma without spaces. For example, in the case of arsenic and boron:

```
pdbSet KMC Impurities As,1 true
pdbSet KMC Impurities B,-1 true
```

When the dopant type has been defined, the paired particles (particles with *I* or *V*) can be defined in `KMC Pairs`. The definitions are a string containing the name of the pair, the name of the dopant, the type of pair (*I* or *V*) and the charge. These fields are separated with commas. Finally, a Boolean parameter instructs Sentaurus Process KMC to take the particle into account.

For arsenic and boron:

```
pdbSet KMC Pairs Asi,As,I,0 true
pdbSet KMC Pairs AsiP,As,I,1 true
pdbSet KMC Pairs AsV,As,V,0 true
pdbSet KMC Pairs AsVP,As,V,1 true
pdbSet KMC Pairs AsVM,As,V,-1 true
pdbSet KMC Pairs BV,B,V,0 false
pdbSet KMC Pairs Bi,B,I,0 true
pdbSet KMC Pairs Bi,B,I,0 true
pdbSet KMC Pairs BiP,B,I,0 true
pdbSet KMC Pairs BiM,B,I,-1 true
```

In the previous example, the particle boron vacancy is not defined (set to `false`). A particle is not defined when it does not appear in the `Pairs` list, or when its Boolean variable is `false`.

The following rules must be followed when defining particles:

- The dopants used in the definitions of `Pairs` must exist in the list of impurities
- A charge  $n$  can only be defined when a charge  $n - 1$  or  $n + 1$  is already defined, except for pairs with same charge states as their dopants.
- Charge states without possible pairing reactions cannot be defined.
- The charge must be  $-1$ ,  $0$ , or  $+1$ .
- Pairs with neutral state; and with the charge of its dopant, always must be defined.

For example, when  $\text{As}^+$  is defined as an impurity,  $\text{AsV}^+$  can be defined. The existence of  $\text{AsV}^+$  allows you to define  $\text{AsV}^0$ , and now  $\text{AsV}^-$ .  $\text{AsV}^{--}$  cannot be defined (no charge  $-2$ ). For  $\text{B}^-$ , you can define  $\text{Bi}^-$ ,  $\text{Bi}^0$ , and  $\text{Bi}^+$ .

## Alias

Aliases of particle names are defined in `KMC aliases`, which is a list of particle names and alternative names separated by commas. These aliases are used only when Sentaurus



Process KMC tries to map a name as particles or defects. For example, if there is an alias such as:

```
Bi BoronInt,BI
```

the commands:

```
kmc present defectname=Bi
kmc present defectname=BI
```

are the same, and:

```
sel z=1e19 name=Bi
sel z=1e19 name=BI
sel z=1e19 name=BoronInt
```

create fields with different names, but the atomized particle is the same (Bi).

## Colors

You can change the default visualization color for the atomistic representation of particles and defects in Tecplot SV, or add new colors to existing particles and defects. The list of colors is `KMC colors`, and it is an array of particle names and colors in `#rrggbb` format (red, green, blue).

## Particles and Parameters

New particles need new parameters. For every impurity specified in `Impurities`, a new file must be created for each material folder and surface. The name of these files is obtained using the command `alias` with the name of the Sentaurus Process KMC impurity as a parameter:

```
sprocess> alias B
Boron
```

[Table 46](#) lists the parameters required for materials defined to use the simple model.

Table 46 Nonsilicon material parameters

Parameter	Description
<code>Dm, Em</code>	Diffusion parameters.
<code>VD, VF</code>	Activation volumes for stress.
<code>sinkProbTop, sinkProbBottom, sinkProbLeft, sinkProbRight, sinkProbFront, sinkProbBack</code>	Boundary conditions.

**5: Atomistic Kinetic Monte Carlo Diffusion**  
**Particles**

Table 46 Nonsilicon material parameters

Parameter	Description
Implement_Complex	Parameters for clustering.
ReactionsPointDefect, ReactionsCluster	Binary interactions.

When amorphous materials (where the best example is amorphous silicon) use the dangling bond model (see [Indirect Diffusion on page 445](#)), the parameters listed in the previous table plus those in [Table 47](#) are required.

Table 47 Extra parameters for amorphous materials

Parameter	Description
EmGe, EfGe	Ge correction to migration energies.
gamma	Coefficient for dangling bond creation.
Db, Eb	Binding prefactor and energy.

[Table 48](#) lists the parameters used on interfaces.

Table 48 Parameters used on interfaces

Parameter	Description
EBarrier_Surf?, Eb_Surf?	Interface binding energies for dopants. ? denotes the material. Gas for gas, Si for silicon, Ox for oxide, Ni for nitride, Po for polysilicon, and Unknown for the rest.
Db_Surf	Surface emission prefactor for dopants.
EMax_Surf, C0Max_Surf	Maximum number of particles trapped at the surface.
Evaporation_Surf	Probability to evaporate (annihilate).
VF_Surf?	Activation volume for stress. ? denotes the material.

[Table 49](#) lists the parameters required for materials using full modeling.

Table 49 Full material parameters

Parameter	Description
Dm, Em	Diffusivities.
Db, Eb	Binding prefactors and energies.
VD, VF	Activation volumes for stress.
e0	Electronic levels.
EfGe, EmGe	Corrections for germanium.

Table 49 Full material parameters

Parameter	Description
P_recrysDeposit, E_recrysDeposit, recrysDepositThreshold, C0_recrysMaxActive, E_recrysMaxActive, recrysMaxTotal, recrysMaxSize, recrysDeposit_Complex, E_recrys, E_recrys_exponent, recrysDeposit_Active, e0_Complex	SPER model (recrystallization).
sinkProbTop, sinkProbBottom, sinkProbLeft, sinkProbRight, sinkProbFront, sinkProbBack	Boundary conditions.
ReactionsPointDefect, ReactionsCluster, ReactionsClusterI, ReactionsClusterV, ReactionsClusterIV, ReactionsLoop, ReactionsVoid, Reactions311	Binary interactions.

Finally, amorphous, simple and full materials allow the definition of impurity clusters. These clusters are defined using the parameters listed in [Table 50](#).

Table 50 Parameters used for impurity clusters

Parameter	Description
Implement_Complex	Whether a cluster exists or not.
Etotal_Complex	Cluster potential energy.
e0_Complex	Cluster charge.
VF_Complex	Stress dependency.
CaptVol_Complex	Cluster capture volume used for emission.
D0_Cluster	Cluster emission prefactors.
EbarrierDopant_Complex, EbarrierIV_Complex	Cluster emission barriers.
Dm_Cluster, Em_Cluster	Cluster migration parameters

For further explanations on these parameters, see the comments in the parameter database and the model descriptions.

## Undefining Particles

Particles can be undefined erasing their definition in the parameter database or setting its Boolean to `false`. If an impurity is undefined or erased, Sentaurus Process KMC also undefines all its pairs.

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### Particles

For example, to undefine indium in a simulation, use:

```
pdbSet KMC Impurities In,-1 false
```

To undefine only boron interstitials with a positive charge, use:

```
pdbSet KMC Pairs BiP,B,I,1 false
```

**NOTE** Undefining particles that will not be used in the simulation saves some small memory and CPU time. If an undefined dopant is used (for example, it is implanted or introduced with `select`), it causes an error.

---

## Defect Types

For a list of the defects implemented in Sentaurus Process KMC, use the command:

```
sprocess> kmc defecttypes  
PointDefect AmorphousPocket Amorphous Void ThreeOneOne Loop ImpurityCluster  
Interface
```

Defects implemented in Sentaurus Process KMC include those listed in [Table 51](#).

Table 51 Defects implemented in Sentaurus Process KMC

Defect	Description
Amorphous	Amorphous region inside the crystalline silicon. Only <i>I</i> , <i>V</i> , impurity clusters, and dopants are allowed. See <a href="#">Amorphization and Recrystallization on page 442</a> .
AmorphousPocket	Disordered agglomeration of <i>I</i> s and <i>V</i> s (damage). Only <i>I</i> and <i>V</i> particle types are allowed. See <a href="#">Damage Accumulation Model: Amorphous Pockets on page 420</a> .
ImpurityCluster	Impurity clusters. Agglomeration of dopants with <i>I</i> s or <i>V</i> s. See <a href="#">Impurity Clusters on page 460</a> .
Interface	Dopants trapped in the interfaces (for example, Si/SiO <sub>2</sub> ). See <a href="#">Interfaces and Surfaces on page 495</a> .
LatticeAtom	Atom in the silicon lattice used for SPER or epitaxial deposition. See <a href="#">LKMC: Fully Atomistic Modeling of Solid Phase Epitaxial Regrowth on page 451</a>
Loop	Dislocation loops. Extended <i>I</i> s defect. Only <i>I</i> s are allowed. See <a href="#">Dislocation Loops on page 435</a> .
PointDefect	Single particles (IMM, IM, I, IP, IPP, VMM, VM, V, VP, VPP, AS, and B) or paired ones (Asi, AsiP, ASVM, ASV, ASVP, BiM, Bi, and BiP) that do not belong to any extended defect or particle agglomeration; in other words, impurities, dopants, and impurity-paired point defects.

Table 51 Defects implemented in Sentaurus Process KMC

Defect	Description
ThreeOneOne	{311} rod-like extended defects. Only <i>Is</i> are allowed. See <a href="#">{311} Defects (ThreeOneOne) on page 430</a> .
Void	Vacancy clusters with spherical shape. Only <i>Vs</i> are allowed. See <a href="#">Voids on page 439</a> .

**NOTE** Not all possibilities of particle and defect types are allowed. Some particle types, like the paired ones (*Asi*, *BiM...*), are only allowed as `PointDefect`. Others, like *As* or *B*, can stand alone (`PointDefect`), can be trapped in interfaces (`Interface`), or can belong to an impurity clusters (`ImpurityCluster`). Neutral interstitials, for example, can stand alone (`PointDefect`), can be in damaged clusters (`AmorphousPocket`), {311} defects (`ThreeOneOne`), or dislocation loops (`Loop`). Single particles can be mobile point defects (in other words, interstitials and vacancies), immobile impurity atoms (like substitutional boron and arsenic), and also mobile impurity-defect pairs such as *Bi* or *AsV*. All are considered `PointDefect`.

---

## Point Defects, Impurities, Dopants, and Impurity-paired Point Defects

---

### Interstitials and Vacancies

Interstitials and vacancies in Sentaurus Process KMC perform a diffusion event in each axis *j* (x, y, and z) at a frequency given by the expression:

$$v_m^j = \frac{v_{0,m}}{3} \cdot \exp\left(-\left(E_m + \sigma'_j \Delta V_{par} + \sum_{i \neq j} (\sigma'_i \Delta V_{ort}) + \Delta E_m(Ge)\right) / (k_B T)\right) \quad (650)$$

where:

- $v_m^j$  is the jump frequency for the axis *j*.
- $v_{0,m}$  is the prefactor.
- $E_m$  is the migration energy.
- $\sigma'_i$  are the principal stresses (the stresses in the coordinate system where all the stress tensor nondiagonal components are null).
- $\Delta V_{par}$  is the activation volume for stress-parallel diffusion.

## 5: Atomistic Kinetic Monte Carlo Diffusion

Point Defects, Impurities, Dopants, and Impurity-paired Point Defects

- $\Delta V_{ort}$  is the activation volume for stress-perpendicular diffusion.
- $\Delta E_m(Ge) = \alpha_m[Ge]$  is the correction due to germanium concentration.

These parameters are called  $D_m$  (prefactor),  $E_m$  (energy),  $VD$  (activation volumes), and  $E_{mGe}$  (for  $\alpha_m$ ) in the parameter database. They are defined only in the `full` model materials:

```
sprocess> pdbGet KMC Si I Dm
IMM 5e-2
IM 5e-2
I 5e-2
IP 5e-2
IPP 5e-2
sprocess> pdbGet KMC Si I Em
IMM 0.8
IM 0.8
I 0.8
IP 0.8
IPP 0.8
sprocess> pdbGet KMC Si I VD
IMM 0,0
IM 0,0
I 0,0
IP 0,0
IPP 0,0
sprocess> pdbGet KMC Si I EmGe
0
```

The activation volumes for parallel and perpendicular diffusion, respectively, are separated by a comma (no spaces) in `VD`.

The stresses  $\sigma_{ij}$  are produced by Sentaurus Process and imported by Sentaurus Process KMC. This stress tensor is diagonalized to obtain the principal stresses  $\sigma'_i$ . The directions  $x$ ,  $y$ , and  $z$  used in the equation refer to the system in which the stress tensor is diagonal.

**NOTE** You can calibrate these parameters if necessary to change the point-defect diffusivity and DC product.

Sentaurus Process KMC simulates point-defect migration, modifying the particle coordinates in the orthogonal directions a fixed distance, called  $\lambda$ , which corresponds to the second neighbors distance in the silicon lattice (0.384 nm). Exceptionally, it may change the value of  $\lambda$ , as explained in [Hopping Mode on page 411](#).

After each diffusion event, the charge state of the point defect is updated according to the new local Fermi level (see [Fermi-Level Effects: Charge Model on page 478](#) and [Updating Charged States on page 485](#)). Whenever a jumping point defect encounters another particle, defect, or

interface, the jumping point defect interacts according to the specific situation. These interactions are allowed depending on the following:

- Incoming species—for example, substitutional boron plus interstitial (B + I) is allowed, and the incoming species form a boron interstitial. Boron plus vacancy is not allowed. This interactions can be enabled or disabled in the parameter database.
- Energetics—Sentaurus Process KMC allows interactions for {311} defects, dislocation loops, and pairing because the binding energies are greater than 0. For impurity clusters, if the reaction is unfavourable, the newly formed defect breaks up and dissolves in the original components or is rejected before reacting.
- Charge states—interactions between repulsive species are forbidden, except for the ‘percolation’ model (see [Percolation on page 465](#)).

Mobile particles can interact with other mobile particles or with the particles belonging to extended defects, whenever they enter in the capture radius of the other particle or defect (see [Figure 44](#)). The capture radius for a mobile particle is  $\lambda$ , assumed to be the same as the jumping distance. For extended defects, the capture volume is the sum of the capture volumes of its constituent particles. Mobile particles can interact with surfaces/interfaces as explained in [Interfaces and Surfaces on page 495](#).

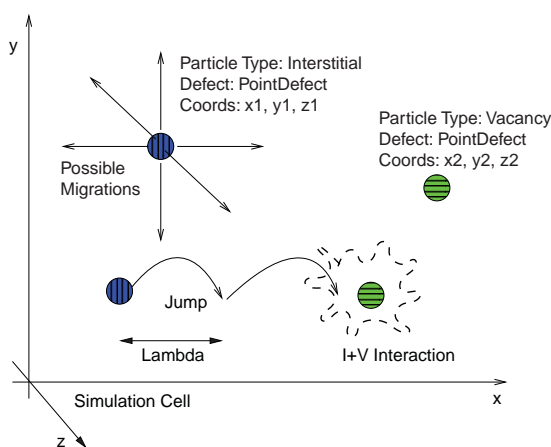


Figure 44 Point defects diffuse by jumping a distance  $\lambda$  in any orthogonal direction and can interact with neighbor particles

---

## Impurities

Isolated impurities in Sentaurus Process KMC can be in a substitutional state or can be paired with interstitials or vacancies. Substitutional impurities are electrically active and typically immobile. The acceptor and donor impurities (Groups III and V of the periodic table, respectively) can move in silicon only by pairing with an interstitial or a vacancy, as shown in the literature [\[4\]\[5\]\[6\]\[7\]\[8\]](#). Other impurities, such as fluorine, may diffuse without the aid of an extra *I* or *V* (see [Impurities Diffusing without Pairing on page 512](#)).

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Point Defects, Impurities, Dopants, and Impurity-paired Point Defects

Impurity atoms are modeled like interstitials or vacancies. They have a position and a defect type and particle type. The defect type is `PointDefect`, and the particle type characterizes the species, charge state, and the presence of a paired *I* or *V*. For example, `BiM` indicates a negatively charged boron paired with an interstitial.

**NOTE** Sentaurus Process KMC assumes interstitial particles and substitutional particles paired with an interstitial as the same configuration; in other words, `Bi` is the same as `IB` or `BI`, and there is only one position (three coordinates) for it.

Paired impurities can perform two possible types of events (see [Figure 45](#)):

- Diffusion jump
- Breakup of the impurity–defect pair



Figure 45 Impurity pairs can diffuse or break up into a substitutional plus an interstitial or a vacancy

**NOTE** Fluorine is modeled as an interstitial particle (in the default parameters, not in Advanced Calibration). Consequently, fluorine diffuses without pairing. See [Impurities Diffusing without Pairing on page 512](#).

## Migration (Diffusion)

The diffusion event is defined as for point defects (see [Eq. 650, p. 403](#)). Nevertheless, the equation defines an *instant* diffusivity that is different from the *effective* diffusivity. Effective diffusivity measured in experiments involves a large number of microscopic migration steps and long times. Microscopically, dopants diffuse using the kick-out mechanism. For example, when an interstitial reacts with a substitutional boron, a boron–interstitial pair is generated:  $B + I \rightarrow B_i$ . In contrast with the boron in substitutional position, the generated pair is mobile. Then,  $B_i$  begins to diffuse, using the diffusivity parameters specified in [Eq. 650](#). After some time, the interstitial boron breaks up, releasing the interstitial. This boron will not move until a new incoming *I* reacts with it. Consequently, the macroscopic diffusivity is related not only with the boron interstitial diffusivity, but also with its breakup frequency as:

$$D^{eff}(B) = D_0^{eff}(B) \exp\left(-\frac{E_{diff}(B)}{k_B T}\right) \quad (651)$$



$D_0^{eff}(B)$  depends on the Bi and I migration prefactors and on the Bi breakup prefactor.

$E_{diff}(B)$  is related with the Bi microscopic migration energy ( $E_m(B_i)$ ), the formation energy of an interstitial ( $E_f(I)$ ) and the Bi binding energy ( $E_b(B_i)$ ) (assuming there are no stress or SiGe corrections):

$$E_{diff}(B) = E_m(B_i) + E_f(I) - E_b(B_i) \quad (652)$$

Finally, the total boron diffusivity is given as the sum of the contribution of all mobile species. For boron interstitial, and assuming there are three mobile species, negative, neutral, and positive:

$$D(B) = D(B_i^-) \frac{[B_i^-]}{[B^-]} + D(B_i^0) \frac{[B_i^0]}{[B^-]} + D(B_i^+) \frac{[B_i^+]}{[B^-]} \quad (653)$$

where  $D(B_i^x)$  represents the microscopic pair diffusivity of charge  $x$ .

## Breakup

The breakup event for an interstitial-impurity pair can be described as:



where  $A_i$  is an interstitial-impurity pair,  $A_s$  is a substitutional impurity atom, and  $I$  is an interstitial silicon atom. This breakup event happens with a frequency given by:

$$v_{bk} = v_{0,bk} \cdot \exp(-E_{bk}/(k_B T)) \frac{1}{3} \sum_i^{x,y,z} \exp(-\Delta E_m^i/(k_B T)) \quad (655)$$

where  $v_{0,bk}$  is the prefactor and  $E_{bk}$  is the activation energy, defined as the binding energy plus the migration energy of the emitted species and the SiGe and stress corrections:

$$E_{bk}(A_i) = E_b(A_i) + E_m(I) + P(\Delta V_f(I) + \Delta V_f(A) - \Delta V_f(A_i)) + [Ge](\alpha_f(I) + \alpha_f(A) - \alpha_f(A_i)) \quad (656)$$

where:

- $P = \left(-\frac{1}{3}\right)(\sigma'_x + \sigma'_y + \sigma'_z)$  is the hydrostatic pressure, computed as the mean value of the principal stresses.
- $\Delta V_f$  are the activation volumes for the formation energies.
- $[Ge]$  is the germanium concentration.
- $\alpha_f$  accounts for the variation of the formation energy with the germanium concentration.

## 5: Atomistic Kinetic Monte Carlo Diffusion

Point Defects, Impurities, Dopants, and Impurity-paired Point Defects

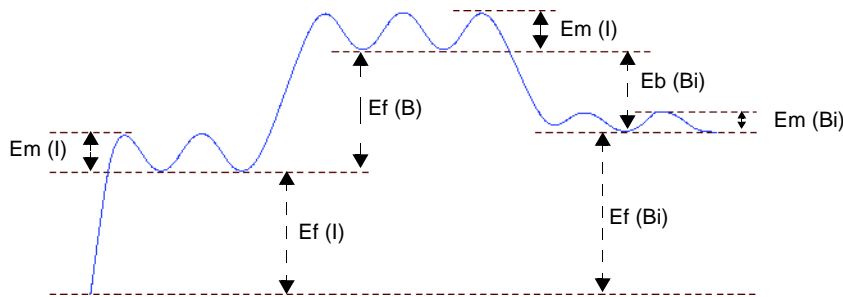
The corrections to the migration energies induced by the stress and SiGe are (as previously explained in [Interstitials and Vacancies on page 403](#)):

$$\Delta E_m^i = \sigma'_j \Delta V_{par} + \alpha_m [Ge] + \sum_{i \neq j} (\sigma'_i \Delta V_{ort}) \quad (657)$$

Sentaurus Process KMC assumes that the activation volume and the SiGe variation for the formation energy do not depend on the charge. All the charge states of the same species share the same activation volume and SiGe dependencies for the formation energy.

[Figure 46](#) shows the energies for boron involved in this mechanism. It is easy to deduce that a change in the formation energies due to stress and SiGe will change the binding energy as:

$$\Delta E_b(B_i) = \Delta E_f(I) + \Delta E_f(B) - \Delta E_f(B_i) \quad (658)$$



**Figure 46** Energies involved in the kick-out mechanism for  $B^- + I^0 = Bi^-$ . Migration energy of the interstitials and boron interstitial are specified in the parameter database as Em. The binding energies are Eb, and the I formation energy is specified as Eform. The formation energy for dopants in pure silicon is assumed to be 0 because the dopants are already in the simulation; the dopants are not created by the system.

## Percolation

In a percolation event, an impurity can react with any other defect in its neighborhood without need for diffusion. In this aspect, it can simulate the reactions that occur through distortions in the lattice but without the need for the migration of particles. The neighborhood of the particle is defined in the same way as for diffusing point defects.

The percolation rate, that is, the frequency at which the particle attempts to interact with any valid defect in its neighborhood, is defined as:

$$v_{per} = P_{per} \exp\left(-\frac{E_{per}}{k_B T}\right) \quad (659)$$

where  $P$  and  $E$  are the prefactors for percolation, specified as input parameters. Percolation only applies to substitutional dopants or impurities. It can provide an extra mechanism for dopant deactivation at very high concentrations.

## Parameters

The dopant diffusion parameters are stored in the parameter database for each material and dopant, under the names  $D_m$ ,  $E_m$  for diffusivities, and  $D_b$ ,  $E_b$  for binding energies.  $D_m$  and  $D_b$  are prefactors,  $E_m$  and  $E_b$  energies. The activation volumes for the formation energies have the name  $V_F$  and  $\alpha_f$  is called  $E_{fGe}$ . The prefactor and the activation energy for percolation are called  $D0\_Percolation$  and  $E0\_Percolation$ , respectively.

The following parameters can be changed:

```
pdbSet KMC <material> <Dopant> Dm <particle type> <value>
pdbSet KMC <material> <Dopant> Em <particle type> <value>
pdbSet KMC <material> <Dopant> Db <particle type> <value>
pdbSet KMC <material> <Dopant> Eb <particle type> <value>
pdbSet KMC <material> <Dopant> VF <particle type> <value>
pdbSet KMC <material> <Dopant> VD <particle type> <value>, <value>
pdbSet KMC <material> <Dopant> EfGe <particle type> <value>
pdbSet KMC <material> <Dopant> D0_Percolation <value>
pdbSet KMC <material> <Dopant> E0_Percolation <value>
```

For the migration energy, the prefactor, the SiGe dependency, and the activation volumes for stresses, the specified material must be modeled as `full` or `simple` (in other words, any material that does not discard particles). For binding energies, only the `full` materials are valid. Percolation parameters are applied to `simple` and `full` materials.

Immobile species (substitutional dopants) have the migration prefactor set to 0, and the migration energy high, to clarify that the species will not perform diffusion steps. Finally, since Sentaurus Process KMC assumes substitutional atoms to be ionized (in other words,  $B^-$  and  $As^+$ ), the binding parameters (both the prefactor and the binding energy) are only defined for pairing reactions with a neutral  $I$  or  $V$ , like  $B^- + I^0 \rightarrow B_i^-$  or  $As^+ + V^0 \rightarrow AsV^+$ . The binding energies for the other breakup reactions are computed automatically using these parameters.

## Parameter Examples

Silicon migration energies of boron particles:

```
sprocess> pdbGet KMC Si B Em
B 5.
BiM 0.5
Bi 0.25
BiP 1.1
```

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Prefactors of the above energies:

```
sprocess> pdbGet KMC Si B Dm
B 0.
BiM 1.e-3
Bi 1.e-3
BiP 1.e-3
```

Migration energies for boron in oxide. The only allowed boron particle is B.

```
sprocess> pdbGet KMC Oxide B Em
B 3.53
```

Binding energy of boron in silicon:

```
sprocess> pdbGet KMC Si B Eb
BiM 0.3
```

and prefactor:

```
sprocess> pdbGet KMC Si B Db
BiM .37
```

Activation volumes for the formation energies of boron interstitial:

```
sprocess> pdbGet KMC Si B VF
BiM -0.0044
```

Variation of formation energy with Ge concentration:

```
sprocess> pdbGet KMC Si B EfGe
0
```

Finally, the binding energy cannot be defined for any material but full model ones, the result should be blank:

```
sprocess> pdbGet KMC PolySilicon B Eb
```

**NOTE** You can change these parameters whenever necessary to calibrate intrinsic and extrinsic dopant diffusivity under equilibrium conditions. For nonequilibrium conditions, you also can change the extended defects if necessary.

**NOTE** Elements are proportional to the volume of the simulation cell.

---

## Hopping Mode

The parameter `KMC HoppingMode` controls the way Sentaurus Process KMC performs diffusion events. This mode accepts the modes `short`, `long`, `double`, and `longdouble`, and it is set by default to `longdouble`. Changing the hopping mode only changes the results statistically (in other words, it is similar to changing the random seed); although, it may change the CPU time significantly. The default hopping mode, `longdouble`, is the fastest one.

### The short Mode

The `short` mode implies that the jumping distance for all the diffusion events  $\lambda$  is the same and is equal to the second neighbor distance. In addition, only one diffusion event is performed at a time.

### The long Mode

The `long` mode implies that the code increases the hopping distance to  $n\lambda$ ,  $n$  being an integer number, in regions where there are no particles with which to interact. This increase improves the performance of the code in this area (in theory, by a factor of  $n^2$ ). In practice, the overall speed improvement is a factor of 2 or smaller, mainly because the empty regions where there are no particles to interact with are limited. The overhead is caused by the `long` mode implementation.

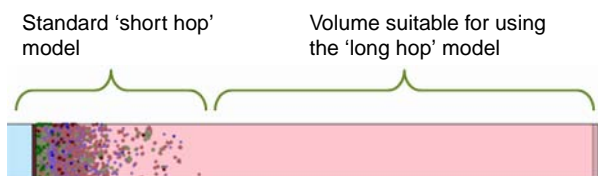


Figure 47 Even if the long hop model is available, it is used only for particles diffusing on empty volumes

### The double Mode

Setting `HoppingMode` to `double` allows Sentaurus Process KMC to perform two diffusion events in one. Nevertheless, to properly account for interactions, the intermediate diffusion event is still simulated by Sentaurus Process KMC. Using this hopping mode saves 10% or less of CPU time.

### The longdouble Mode

The `longdouble` mode is the default mode and enables both long and double hops.

## 5: Atomistic Kinetic Monte Carlo Diffusion

Point Defects, Impurities, Dopants, and Impurity-paired Point Defects

**NOTE** For more information on these models, refer to the literature [9].

---

### Enabling and Disabling Interactions

Interactions between particles are important in Sentaurus Process KMC. Whenever one mobile particle jumps into another particle, Sentaurus Process KMC tries to make both particles interact. These interactions may or may not be possible depending on whether the interaction is allowed and if it is energetically possible.

The interactions allowed between one mobile particle and other particles are specified in the parameter database as the parameter `ReactionsPointDefect`. The interactions between this type of defect are assumed to be always energetically favorable.

Consequently, changing the parameter `ReactionsPointDefect` is the only way to establish whether a moving particle will interact with other (mobile or immobile) particles. To change this parameter, use:

```
pdbSet KMC <material> <dopant> ReactionsPointDefect <string> <true/false>
```

This parameter needs a string and Boolean value. The Boolean value specifies if the interaction is allowed (`true`) or not (`false`). The string contains the name of the two interacting particles, separated by a comma. For example:

```
sprocess> pdbGet KMC Si C ReactionsPointDefect
C,I      true
C,V      false
C,Ci     true
Ci,I     true
Ci,V     true
Ci,Ci    true
```

Therefore, in this example, the interaction between C and V is disabled. To enable it, use the command:

```
pdbSet KMC Si C ReactionsPointDefect C,V true
```

When enabling an interaction, the result does not have to be specified because Sentaurus Process KMC already knows it. The possible interaction results are:

PointDefect	Pairing reactions, in other words, dopants pairing with interstitials or vacancies to generate dopant-interstitial or dopant-vacancy particles. For example, B + I, or As + IM.
-------------	---

AmorphousPocket	Reaction of interstitials or vacancies between them. For example, $I + IM$ , $I + V$ , or $V + V$ . They involve both damage formation (mixed $I$ and $V$ ) and small cluster creation (only $I$ or $V$ ).
ImpurityCluster	Reactions involving the formation of impurity clusters, in other words, when the result has dopants and interstitials or vacancies with two or more of each. For example, $Bi + I$ or $AsV + AsV$ .

The reactions for each single charged state must be introduced, so the charged  $I$  also interacts with  $V$  and with other charged states of  $V$ :

```
sprocess> pdbGet KMC Si I ReactionsPointDefect
I,V      true
I,VM     true
I,VMM    true
I,VP     true
I,VPP    true
IP,V     true
IM,V     true
IM,IP    true
(...)
```

All interactions are listed in the parameter database. With that list of interactions, you can understand which reactions are considered and how they work.

## Interaction Rules

Sentaurus Process KMC does not accept all possible interactions within every two particles, but only interactions with a physical meaning, or with an available model. Consequently, the following rules apply:

- Reactions must include existing particles.
- Some reactions are only allowed in materials with `full` modeling.
- Reactions for a pair must be defined in the file of the involved dopant (for example, a reaction with  $Bi$  must be in the boron file, not in interstitial).
- If the result of a reaction does not exist, the reaction is discarded (in other words, the reaction  $C + V$  is specified, but the particle  $CV$  is not defined).
- Repulsive reactions are not allowed (for example,  $Bi^- + Bi^-$ ) except for ‘percolation’ models such as  $As + As$  or  $B + B$  (see [Percolation on page 465](#)).
- Reactions must satisfy microscopic reversibility. For example, if the reverse reaction is not possible, the reaction is discarded.
- Reactions creating impurity clusters must give a defined cluster. For example,  $Bi + Bi$  is allowed as long as there is a  $B_2I_2$  cluster defined; in this case,  $Bi + BiM$  would also be allowed.

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- Only reactions producing defined `PointDefect`, `ImpurityCluster`, or `AmorphousPocket` are allowed. For example, `Bi + C` will produce an error message if there is no BCI cluster defined.

### Examples

The interactions for boron are:

```
sprocess> pdbGet KMC Si B ReactionsPointDefect
B,I      true
Bi,I     true
Bi,V     true
BiM,V    true
BiP,V    true
B,Bi     false
B,BiP    true
B,IP     true
Bi,Bi    true
Bi,VM    true
Bi,VMM   true
Bi,VP    true
Bi,VPP   true
BiM,VP   true
BiM,VPP  true
BiP,VM   true
BiP,VMM  true
```

B and I can react, giving a mobile Bi particle. B and IP also give a Bi particle. The charge state of the resulting Bi particle is computed automatically by Sentaurus Process KMC depending on the Fermi level, temperature, and Bi levels in the band gap.  $B^- + IM$  is an electrostatically repulsive reaction, and is not allowed.

Bi possible charge states are neutral, positive, and negative. The reactions for these also states should be specified. Bi and its different charges can react with I, V, and Bi.  $Bi + I$  produces an impurity cluster. Only reactions microscopically reversible are allowed. Because a  $BI_2$  cluster breaks up as  $Bi + I$ , any nonrepulsive reaction involving Bi and I is allowed.  $Bi + V$  recombines the IV pair, depositing substitutional boron. All nonrepulsive reactions between  $B_i$  and V are allowed, and all are specified in this example. Finally, there are more ways to produce impurity clusters including  $BiP + B$ , producing  $B_2I$ , and  $B_i^a + B_i^b \leftrightarrow B_2I_2$ , as long as  $a \cdot b \leq 0$  giving  $B_2I_2$ .

The reaction  $B + V$  is not specified here. Typing `B,V false` produces the same effect. Setting this reaction to `true` implies defining a BV particle (and its parameters) and specifying reactions for this BV particle, such as  $BV + I \rightarrow B$ .



**NOTE** Only advanced users should change the default interaction list because improper modifications can drastically change the diffusion models.

---

## Defining Nonstandard Interactions

Sentaurus Process KMC allows you to define a nonstandard interaction. These interactions are intended to provide a mechanism for exceptional models that are not possible to be implemented using the standard models and interactions. These reactions are of the type:



A, B, and C must be single particles (point defects or dopants). They are defined as `SpecialReaction` in the folder including the first species:

```
pdbSet KMC Si A SpecialReaction A,B,C true
```

The reactions defined with this mechanism are not reversible: C will not break into A and B back.

### Interaction Rules

The difference between a regular interaction and a nonstandard one is that the set of rules the latter one obeys is a very reduced subset of the rules for the regular one. In particular, a nonstandard interaction must follow only these rules:

- Reactions must include existing particles. The result is always a point defect, not a cluster or another defect type.
- Reactions are only allowed in materials with `full` modeling.
- Reactions must be defined in the files of the involved dopant (for example, a reaction with Bi must be in the boron file).
- If the result of a reaction does not exist, the reaction is discarded (that is, the reaction  $C + V$  is specified, but the particle CV is not defined).

In particular, these reactions can be nonconservative. For example, you can define a carbon–interstitial interaction giving arsenic ( $C + I \rightarrow As$ ). These reactions are nonstandard because they lack a physical sense, but they are allowed because they offer extra flexibility to define new models.

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### Example

A model for nitrogen diffusion can be defined using a nonstandard interaction, in particular, when you want to model the following:



where  $N_{2,i}$  is mobile but  $N_2V$  is immobile. The second reaction is not a problem. You can define a dopant called Nn to be  $N_{2,i}$ , and make it mobile, and you can define an NnV as the result of Nn + V. These reactions are standard. The problem is that it is impossible to have a N + N reaction giving as Nn using the standard mechanisms. For this exception, you define  $N_i$  as N and use the special reaction:

```
pdbSet KMC Si N SpecialReaction N,N,Nn true
```

**NOTE** Special reactions are printed in the log file:

```
KMC. Using special non-reversible reaction N + N -> Nn
```

---

## Stress Effects on Point Defects, Impurities, Dopants, and Impurity-Paired Point Defects

The stress model for Sentaurus Process KMC is disabled by default, but can be enabled by setting the variable `KMC Stress` to 1:

```
pdbSet KMC Stress 1
```

or by adding the parameter `kmc.stress` in the command line of `diffuse`:

```
diffuse kmc.stress time=...
```

Sentaurus Process KMC uses the stress provided by Sentaurus Process, but Sentaurus Process KMC does not compute it. The stress fields are updated from Sentaurus Process for each `diffuse` step.

Stress local dependency is introduced into Sentaurus Process KMC using the correction of the migration and binding energies of point defects and impurity-paired point defects.

Stress also affects the bandgap narrowing, as explained in [Bandgap Narrowing on page 488](#).

## Migration Energy

An anisotropic correction to the migration energy is introduced as:

$$\begin{bmatrix} \Delta E_m^x \\ \Delta E_m^y \\ \Delta E_m^z \end{bmatrix} = \begin{bmatrix} \Delta V_{par} & \Delta V_{ort} & \Delta V_{ort} \\ \Delta V_{ort} & \Delta V_{par} & \Delta V_{ort} \\ \Delta V_{ort} & \Delta V_{ort} & \Delta V_{par} \end{bmatrix} \begin{bmatrix} \sigma'_x \\ \sigma'_y \\ \sigma'_z \end{bmatrix} \quad (663)$$

where  $\Delta E_m^i$  are the corrections to the migration energy when diffusing in the  $i'$  axis;  $\sigma'_i$  are the principal stresses; and  $\Delta V_{par}$  and  $\Delta V_{ort}$  are the activation volumes for diffusion parallel and perpendicular to stress, respectively. They are included in the PDB as `VD`.

The relation between the  $i'$  axes and the standard ones is established by a rotation  $R$  tensor. This tensor diagonalizes the stresses tensor:

$$[R] \begin{bmatrix} \sigma_{xx} & \sigma_{xy} & \sigma_{xz} \\ \sigma_{xy} & \sigma_{yy} & \sigma_{yz} \\ \sigma_{xz} & \sigma_{yz} & \sigma_{zz} \end{bmatrix} [R]^T = \begin{bmatrix} \sigma'_x & 0 & 0 \\ 0 & \sigma'_y & 0 \\ 0 & 0 & \sigma'_z \end{bmatrix} \quad (664)$$

Setting the parameter `ChangeAxis` to `false` disables this rotation, using the standard `xyz` axis instead of the  $i'$  ones.

**NOTE** Setting `ChangeAxis` to `true` dramatically impacts `{311}` dissolution because the structure is sensitive to the direction of the migrating incoming particles.

For more information, see [Interstitials and Vacancies on page 403](#).

## Binding Energy

The binding energy of an impurity-paired point defect  $A_i$  is corrected by:

$$\Delta E_b(A_i) = \frac{1}{3}(\sigma_{xx} + \sigma_{yy} + \sigma_{zz})(\Delta V_f(I) - \Delta V_f(A_i)) \quad (665)$$

where  $\Delta V_f$  is the activation volume for the formation energy. The activation energy for an impurity-paired point-defect breakup is defined (without stress) as the sum of the binding energy plus the migration energy of the emitted species ( $I$  for  $A_i$ ). Then, an extra correction of the migration energy of the emitted species under stress is needed.

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Since the migration energy corrections depend on the axis, but the breakup of an impurity pair in Sentaurus Process KMC does not, an average of the corrections for all the axes is performed, and the frequency is computed as:

$$v_{bk}^{stress} = v_{bk}^0 \exp(-\Delta E_b / (k_B T)) \frac{1}{3} \sum_i^{x,y,z} \exp(-\Delta E_m^i / (k_B T)) \quad (666)$$

where  $v_{bk}^0$  is the breakup frequency when there is no stress.

For more information, see [Impurities on page 405](#).

---

## Alloys

Alloys are included in Sentaurus Process KMC simulations as a field instead of as a particle. Using Ge as an example of an alloy in Si, it means that Sentaurus Process KMC discards the particular position of Ge (the xyz coordinates) and only keeps track of how many Ge atoms were introduced in each internal element. Doing this saves a huge amount of memory, while allowing Sentaurus Process KMC to account for SiGe effects. Ge works as usual, except for the following limitations:

- There are no Ge particles in the atomistic 3D plot.
- Ge (including implanted Ge) is shown as a field in the atomistic 3D plot.
- There are no events or reports associated with Ge because there are no Ge particles.
- There are no Ge models (for example, no Ge clusters) except for Ge diffusion.

This model can be used to:

- Simulate Ge diffusion.
- Include corrections to the migration and formation energies of point defects and impurity-paired defects when diffusing in SiGe materials.
- Include bandgap corrections due to SiGe.

**NOTE** Sentaurus Process KMC considers the effect of germanium whenever germanium is present. Continuum parameters (such as `Silicon SiliconGermanium.ConversionConc`) do not affect Sentaurus Process KMC simulations.

## Alloy Diffusion

Ge will be used as an example of an alloy in Si material. Here, the Ge model diffusion implemented has been based partially on [10]. This model defines the diffusion of Ge in an indirect way through the use of  $\alpha$  of Is and Vs for a  $\text{Si}_{1-x}\text{Ge}_x$  material as:

$$\alpha_I = \frac{D_I^{Ge}(x)}{D_I^{Si}(x)} \quad (667)$$

where  $D_I^{Ge}(x)$  and  $D_I^{Si}(x)$  are the transport capacity associated with Ge and Si interstitials in  $\text{Si}_{1-x}\text{Ge}_x$ , respectively.

It can be assumed that these  $\alpha$  s follow the equation:

$$\alpha(x) = \alpha_{0, Si}^{1-x} \alpha_{0, Ge}^x \exp\left(-\frac{(1-x)E_{Si} + xE_{Ge}}{k_B T}\right) \quad (668)$$

where  $\alpha_{0, Si}$ ,  $\alpha_{0, Ge}$ ,  $E_{Si}$ , and  $E_{Ge}$  are input parameters specified in the PDB. Both interstitials and vacancies have a different  $\alpha$ .

**NOTE** The Ge diffusion model is switched on by default. To switched it off, set  $\alpha_{0, Si}$  and  $\alpha_{0, Ge}$  to null values.

### Parameters and Parameter Examples

The parameters  $\alpha_{0, Si}$ ,  $\alpha_{0, Ge}$ ,  $E_{Si}$ , and  $E_{Ge}$  are specified in the PDB with the names D0alphaSi, D0alphaGe, EalphaSi, and EalphaGe. In particular:

```
sprocess> pdbGet KMC Si I EalphaSi
0.4
sprocess> pdbGet KMC Si I EalphaGe
0
sprocess> pdbGet KMC Si I D0alphaSi
35
sprocess> pdbGet KMC Si I D0alphaGe
2.2
sprocess> pdbGet KMC Si V EalphaSi
0.25
sprocess> pdbGet KMC Si V EalphaGe
0
sprocess> pdbGet KMC Si V D0alphaSi
30
sprocess> pdbGet KMC Si V D0alphaGe
2.2
```

## Alloy Effects

The following sections discuss alloy effects on point defects, impurities, dopants, and impurity-paired point defects. In the next sections, Ge in silicon is used as an example for these models.

### Migration and Formation Energies

The corrections  $\Delta E_m = \alpha_m[Ge]$  and  $\Delta E_f = \alpha_f[Ge]$  are added to the migration and formation energies, respectively.  $[Ge]$  is the germanium concentration, and  $\alpha_m, \alpha_f$  are the dependencies of energies with Ge concentration for migration and formation.

### Binding Energy

The binding energy of an impurity-paired point defect  $A_i$  is corrected by:

$$\Delta E_b(A_i) = [Ge](\alpha_f(I) + \alpha_f(A) - \alpha_f(A_i)) \quad (669)$$

For more information, see [Impurities on page 405](#).

### Bandgap Narrowing

The Ge inclusion changes the band gap as explained in [Bandgap Narrowing on page 488](#).

## Introducing Alloys in the Simulation

Alloys can be introduced in the simulation by:

- Using implantation.
- Using the `select` command.
- Atomizing a previous continuum structure with the alloy.
- Using `kmc add` to explicitly add it.
- Depositing a layer doped with the alloy.

---

## Damage Accumulation Model: Amorphous Pockets

Damage accumulation evolution, that is, the evolution of small interstitial and vacancy clusters after ion implantations, is a crucial step that affects the subsequent formation of extended defects and impurity clusters. This accumulation generates the transient-enhanced diffusion (TED) of commonly used dopants, such as boron.

Experimentally, electron irradiation and light-ion implantation create isolated point defects inside the silicon. In contrast, heavy ions generate highly disordered regions called *amorphous*

*pockets* (APs) as a consequence of the implanted cascades. Depending strongly on the temperature, ion mass, and dose rate, this disordered region can dissolve as a result of internal recombination or can grow until an amorphous layer is created. The activation energy for annealing this damage varies in the literature, 0.9 eV [11] at room temperature, 1.2 eV for 400°C to 550°C, but it is much less than the 2.7 eV reported for truly amorphized amorphous layers. This means the damage accumulation depends on the dynamic annealing, ripening, and dissolution history of the APs during the implant process. This annealing can have a quasi-continuum range of activation energies.

There is much discussion on how this damage is annealed. Some papers point to an annealing of the disordered region [12]: APs using an internal recombination of *IV* pairs rather than through the emission of point defects. Only when the AP does not contain further *IV* pairs does it begin to emit its remaining *Is* or *Vs*, behaving as a small *I* or *V* cluster.

Sentaurus Process KMC simulates the damage accumulation using APs, disordered collections of point defects (*Is* and *Vs*) stable at low temperatures. APs dissolve fast at higher temperatures, leaving only clusters with the net excess of *Is* or *Vs*. APs can contain *IV* pairs or only *Is* and *Vs*. In the first case, APs try to recombine the pairs; in the second, APs behave as small clusters and can emit their constituent particles. Whenever an AP containing only *Is* or *Vs* (but not *IV* pairs) reaches a threshold size, the AP transforms into an extended defect ( $\{311\}$ s for *Is*, voids for *Vs*).

APs can grow capturing new incoming point defects, and they can dissolve by internal recombination of *IV* pairs or by particle emission when there are no more *IV* pairs (see Figure 48).

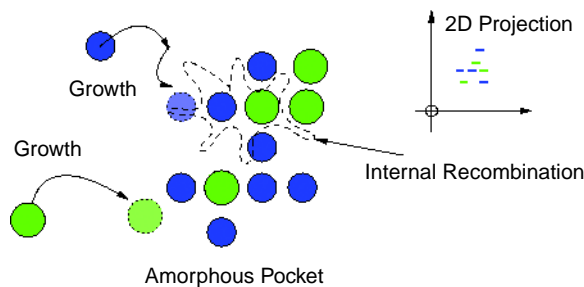


Figure 48 Growth of APs showing their internal recombination

---

## Shape

APs have an irregular shape. Sentaurus Process KMC does not reshape the defect as new; incoming particles join the AP: particles are left in their incoming positions. Figure 49 shows some APs resulting from an implanted cascade.

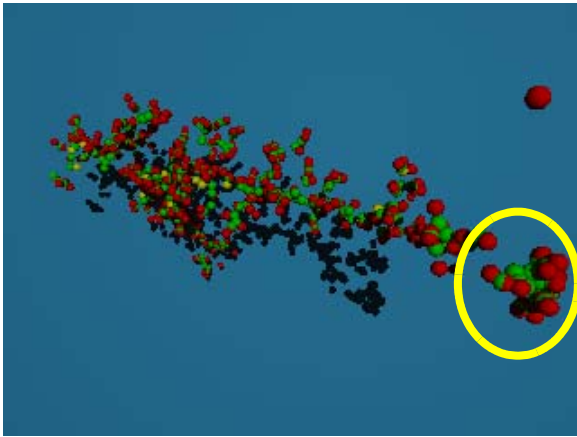


Figure 49 APs formed in Sentaurus Process KMC after some implanted as cascades: interstitials are red, vacancies are green, arsenic is yellow

---

## Growth

APs capture any incoming point defect (*I* or *V*) within their capture radius. The capture radius of APs is the sum of all their constituent particles. Point defects with any charge state are captured by APs containing both *I*s and *V*s. Only neutral *I*s or *V*s are captured when APs contain only *I*s or only *V*s.

---

## Recombination

APs containing *IV* pairs (that is, APs with both interstitials and vacancies) can recombine pairs using a recombination event, which recombines one *I* with one *V* at a time. This event is performed with a frequency given by:

$$v_{diss} = v_{0,diss} \cdot \text{size}^{\beta} \exp(-(E_{diss}(\text{size}) + P\Delta V_{diss} + \alpha_{IV}[Ge])/(k_B T)) \quad (670)$$

where the prefactor  $v_{0,diss}$  is called `D0_AmorphousPocket` in the parameter database, and `size` is the size of the cluster.



The size of a cluster  $I_nV_m$  is a Tcl procedure of  $n$  and  $m$  specified in the file `KMC.tcl` under the name `getAmorphousPocketSize`:

```
fproc getAmorphousPocketSize { sizeI sizeV } {  
    return [expr ($sizeI + $sizeV)/2]  
}
```

It can be modified by users.  $\beta$  is an exponent called `ExponentAmorphousPocket`.  $E_{diss}$  depends on the size of the AP and is specified as a list of energies for each size (`Eb_AmorphousPocket`). The different sizes are specified as  $I_xV_x$ . If some energy is not specified for a size, Sentaurus Process KMC takes the linear interpolation between the last two specified values. For sizes higher than the last specified size, the last specified energy is assigned automatically.  $\alpha_{IV}$  is the Germanium correction to recombination (`Eb_AmorphousPocketGe`) and finally,  $P$  is the hydrostatic pressure and  $\Delta V_{diss}$  is the activation volume for the AP dissolution (`VfAmorphousPocket`).

## Parameters

The parameters needed by the damage accumulation model are specified using:

```
pdbSet KMC Si Damage <Parameter> <value>
```

An example of these parameters is:

```
sprocess> pdbGet KMC Si Damage D0_AmorphousPocket  
0.0005  
sprocess> pdbGet KMC Si Damage ExponentAmorphousPocket  
0.66  
sprocess> pdbGet KMC Si Damage VfAmorphousPocket  
0  
sprocess> pdbGet KMC Si Damage Eb_AmorphousPocket  
IV      0.65  
I199V199 2.4  
sprocess> pdbGet KMC Si Damage Eb_AmorphousPocketGe  
0
```

For the above parameters, the `Eb_AmorphousPocket` values for  $I_xV_x$ , with  $x > 1$  and  $x < 199$  will be generated by Sentaurus Process KMC as a linear interpolation between the points (1, 0.65) and (199, 2.4):

```
Silicon/Damage Eb_AmorphousPocket(IV) = 0.65  
Silicon/Damage Eb_AmorphousPocket Interpolated (2) = 0.658838  
Silicon/Damage Eb_AmorphousPocket Interpolated (3) = 0.667677  
...
```

**NOTE** You can change these parameters to calibrate the damage accumulation model.

**NOTE** The maximum size allowed for IV clusters is  $I_{249}V_{249}$ .

## Emission

When all *IV* pairs have been recombined, APs behave as small *I* or *V* clusters, allowing the emission of their extra constituent particles. These defects emit neutral *Is* or *Vs* particles with a frequency given by:

$$v_{emit} = v_{0, emit} \cdot \exp(-E_{emit}(\text{size})/(k_B T)) \quad (671)$$

The prefactor is proportional to the input parameter `D0_Cluster`, but also includes a dependency on the size of the cluster. The activation energy for emission of an *X* (in other words, either *I* or *V*) is:

$$E_{emit} = E_b(X) + E_m(X) + \Delta E_b(X) + \Delta E_m(X) \quad (672)$$

the sum of the corrected binding energy (that depends on the cluster size) and the migration energy. The cluster size is defined as the number of contained *Is* or *Vs* (see [Figure 50](#)).

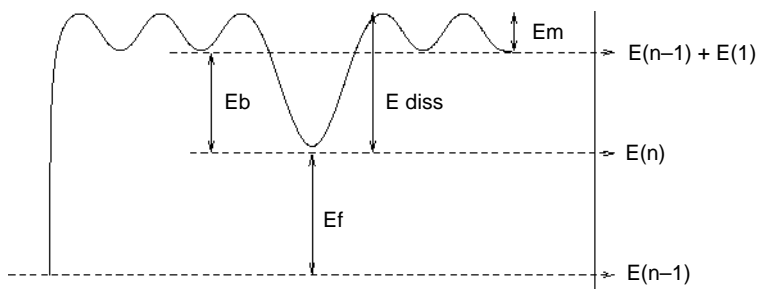


Figure 50 Energies involved in emission of an interstitial from an *n*-size cluster

`D0_Cluster` is the constant proportional to the emission prefactor, and `Eb_Cluster` is the cluster binding energy, where dependency with size is explicitly assigned. For sizes bigger than the last specified cluster, the binding energies are computed using:

$$E_b(\text{size}) = E_{b,L} - (E_{b,L} - E_{b,S}) \frac{\text{size}^a - (\text{size} - 1)^a}{2^a - 1} \quad (673)$$

where:

- $E_{b,L}$  (`Eb_LargeCluster`) is the binding energy for the largest cluster.
- $E_{b,S}$  (`Eb_SmallestCluster`) is the binding energy for the smallest cluster (size 1).
- $a$  (`exponent_Cluster`) is the exponent, usually 2/3 or 3/4.

Figure 51 shows some binding energy values and compares them with the numbers obtained using Eq. 673.

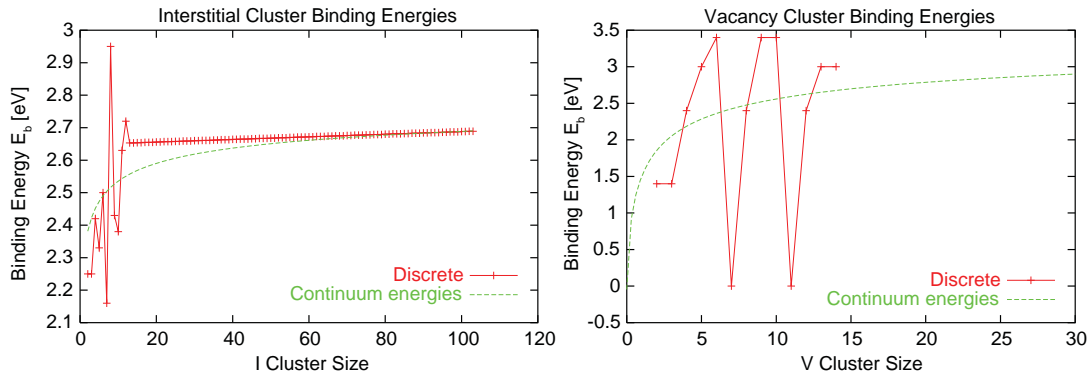


Figure 51 Interstitial cluster (*left*) and vacancy cluster (*right*) binding energies; discrete values are assigned in the parameter database and the continuum energies are computed using Eq. 673

Finally, the correction applied for the migration is the normal one:

$$\Delta E_m(X) = \alpha_m[Ge] + \frac{1}{3} \sum_i^{x,y,z} \exp(-\Delta E_m^i / (k_B T)) \quad (674)$$

and for the binding of the particle to the cluster is:

$$\Delta E_b(X) = P \Delta V_b^{extended}(X) + \alpha_{Cl}[Ge] \quad (675)$$

where  $\Delta V_b^{extended}$  is called `vFCluster` in the PDB and  $\alpha_{Cl}$  is the Germanium correction to binding (`Eb_ClusterGe`).

## Parameters

The parameters for *I*s and *V*s emission are specified only for the silicon material. They can be found in the interstitial and vacancy files included in the parameter database.

### Prefactors

```
sprocess> pdbGet KMC Si I D0_Cluster
150.0
sprocess> pdbGet KMC Si V D0_Cluster
10
```

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Damage Accumulation Model: Amorphous Pockets

### Energies

```
sprocess> pdbGet KMC Si I Eb_Cluster
I2      2.45
I3      2.45
(...)
I13     2.853
I103    2.889
sprocess> pdbGet KMC Si V Eb_Cluster
V2      1.4
V3      1.4
V4      2.4
(...)
```

For sizes between specified sizes (for example, I14 to I102), the parameters are computed as linear interpolations of the specified values:

```
Silicon/I Eb_Cluster(I13) = 2.853
Silicon/I Eb_Cluster Interpolated (14) = 2.8534
(...)
Silicon/I Eb_Cluster Interpolated (102) = 2.8886
Silicon/I Eb_Cluster(I103) = 2.889
```

and parameters for [Eq. 672, p. 424](#):

```
sprocess> pdbGet KMC Si I Eb_SmallestCluster
2.51
sprocess> pdbGet KMC Si I Eb_LargeCluster
3.09
sprocess> pdbGet KMC Si I exponent_Cluster
0.75
sprocess> pdbGet KMC Si V Eb_SmallestCluster
1.5
sprocess> pdbGet KMC Si V Eb_LargeCluster
3.7
sprocess> pdbGet KMC Si V exponent_Cluster
0.6667
```

**NOTE** When changing these parameters, their values affect not only the damage accumulation model, but also the interstitial and vacancy supersaturation and, consequently, the transient-enhanced diffusion (TED). Because the damage accumulation model is the seed for subsequent extended defects or recrystallization, these values also affect the formation of extended defects.

## Amorphous Pockets Life Cycle

Whenever two point defects ( $I + I$ ,  $V + V$  or  $I + V$ ) interact with each other, an AP is generated. When the AP is formed, subsequent incoming  $I$ s or  $V$ s are captured and added to the AP. If the AP contains at least one  $IV$  pair, the AP recombines the  $IV$  pairs. The  $IV$  pair frequency depends on the number of  $IV$  pairs present in the AP. If there is only  $I$ s or  $V$ s in the AP, it emits  $I$ s or  $V$ s.

The evolution of APs can follow three paths:

- APs can dissolve recombining internal  $IV$  pairs, emitting point defects, or both.
- AP containing only  $I$ s or  $V$ s may be transformed into extended defects:  $\{311\}$  defects for  $I$ s and voids for  $V$ s.
- If the concentration of some of the boxes (the internal Sentaurus Process KMC grid elements) containing the AP reaches a concentration threshold, the element is considered amorphous and its particles are removed from the AP. Consequently, APs only exist in crystalline silicon.

For example, assuming there is an AP with two  $V$ s and seven  $I$ s ( $I_7V_2$ ), since the AP contains both  $I$ s and  $V$ s, the only possible event is the recombination of  $IV$  pairs. The first  $IV$  pair recombines with the recombination energy assigned to size 2, leaving an  $I_6V_1$ . The second recombination energy, with a recombination energy assigned to size 1, leaves an  $I_5$  AP. This AP begins to emit  $I$ s, with a frequency associated to its size (5). However, if it captures a  $V$ , it becomes an  $I_5V_1$  and must recombine the  $IV$  pair with an associated recombination size of 1.

An AP must satisfy the following conditions before being transformed into a  $\{311\}$  or void:

- It can contain only  $I$ s or only  $V$ s, but not both.
- It must be bigger than or equal to a threshold size.
- Transition must be enabled.

The threshold size is specified with the parameters `Min311Size` and `MinVoidSize` for  $I$ s and  $V$ s, respectively. The transition is enabled by a value between 0 and 1. This value is computed as:

$$P = E_0 \times \exp((-E + \Delta E)/(k_B T)) \quad (676)$$

The prefactor  $E_0$  is specified as `D0_ApTo311` for  $\{311\}$ s and `D0_ApToVoid` for voids, and the energies as `E_ApTo311` and `E_ApToVoid`. For  $\{311\}$ s  $\Delta E$  are the corrections for pressure and Ge; for voids  $\Delta E = 0$ :

$$\Delta E = PV_{311toLoop} + \alpha_{311toLoop}[Ge]. \quad (677)$$

The volume correction is called `VF311toLoop`, and the Germanium one `VF311toLoop`.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Damage Accumulation Model: Amorphous Pockets

For  $P = 0$ , the transition is disabled; for  $P = 1$ , it is enabled. For  $P > 1$ , the value is rounded to 1. Values between 0 and 1 establish a probability for the transition.

## Parameters

Minimum sizes for the transitions:

```
sprocess> pdbGet KMC Si I Min311Size
33
sprocess> pdbGet KMC Si V MinVoidSize
27
```

Transition probabilities:

```
sprocess> pdbGet KMC Si Damage D0_APto311
200000000.0
sprocess> pdbGet KMC Si Damage E_APto311
1.3
sprocess> pdbGet KMC Si Damage D0_APtoVoid
200000000.0
sprocess> pdbGet KMC Si Damage E_APtoVoid
1.3
```

---

## Interactions of Amorphous Pockets

To change the default AP interactions, use the parameters `ReactionsClusterI`, `ReactionsClusterV`, and `ReactionsClusterIV`. These parameters control the reactions between APs containing only interstitials, only vacancies, or both. APs can react not only with *I*s and *V*s, but also with dopants. In this latter case, the result of the reaction must be specified.

### Interaction with Point Defects: I and V

To customize AP reactions, change the parameters defined for *I*, *V*, and *IV* clusters using the command:

```
pdbSet KMC Si Damage <ReactionsClusterType> <species> <true/false>
```

For example, the command:

```
pdbSet KMC Si Damage ReactionsClusterI I false
```

disables the reaction  $I_n + I \rightarrow I_{n+1}$  for small clusters.

Consequently, it disables the ripening of these clusters. The line:

```
pdbSet KMC Si Damage ReactionsClusterV I false
```

disables the recombination of *I* with small vacancy clusters.

## Parameters

Small interstitial and vacancy clusters may react with neutral interstitials and vacancies. Charged interstitials or vacancies are not allowed due to microscopic reversibility reasons:

```
sprocess> pdbGet KMC Si Damage ReactionsClusterI
           I      true
           V      true
sprocess> pdbGet KMC Si Damage ReactionsClusterV
           I      true
           V      true
```

APs with both *I*s and *V*s accept interstitials or vacancies with any charge. In this case, because they do not emit particles, there are no microscopic reversibility restrictions:

```
sprocess> pdbGet KMC Si Damage ReactionsClusterIV
           I      true
           IP     true
           IM     true
           V      true
           VP     true
           VPP    true
           VM     true
           VMM    true
```

## Interaction with Impurities

APs do not trap impurities, but can interact with them. In this interaction, impurities can lose a point defect, becoming substitutional (for example,  $B_i + I_2V_3 \rightarrow B + I_3V_3$ ) or can gain some of them being transformed into an impurity cluster (for example,  $B_i + I_2V_3 \rightarrow BI_2 + IV_3$ ). Consequently, the interaction within impurities and APs plays a crucial role in deactivating dopants, typically during implantation and low-temperature anneals.

To control these interactions, use:

```
pdbSet KMC Si <impurity> <ReactionsClusterType> <species,result> <true/false>
```

`ReactionsClusterType` can be `ReactionsClusterI` for small *I* clusters, `ReactionsClusterV` for small *V* clusters and `ReactionsClusterIV` for mixed clusters.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Extended Defects

For example, the reaction  $B_i^- + I_n V_m \rightarrow BI_2 + I_{n-1} V_m$  can be disabled for mixed clusters with:

```
pdbSet KMC Si B ReactionsClusterIV BiM,BI2 false
```

**NOTE** A comma must separate the incoming particle from the result, without any space in between.

### Parameters

The reactions between boron (for example) and mixed clusters can be displayed with:

```
sprocess> pdbGet KMC Si B ReactionsClusterIV
BiM,BI2 true
Bi,BI2 true
BiP,BI2 true
B,BI2 true
```

There are no reactions between boron and vacancy clusters:

```
sprocess> pdbGet KMC Si B ReactionsClusterV
```

The reactions between boron and small *I* clusters are disabled:

```
sprocess> pdbGet KMC Si B ReactionsClusterI
Bi,BI2 false
BiM,BI2 false
```

---

## Extended Defects

Small clusters are defined as immobile agglomerations of interstitials or vacancies, and are modeled using the AP defects previously explained. When the number of *I*s or *V*s in these clusters grows above a specified threshold, the small clusters are converted into extended defects ( $\{311\}$  or void types). Finally, when the ripening of  $\{311\}$ s overcomes some limit, the  $\{311\}$ s are transformed into dislocation loops.

---

### $\{311\}$ Defects (ThreeOneOne)

The  $\{311\}$  *rod-like* defects are associated with TED [13]. Consequently, they need a realistic simulation, in both shape and energetic values. Its shape is like rectangular stripes of interstitials lying on a  $\{311\}$  plane along a  $\langle 110 \rangle$  direction. The paper [14] gives an atomic model for its structure, whose stability has been confirmed by theoretical studies [15][16][17].



## Shape

Sentaurus Process KMC models  $\{311\}$  defects as parallel stripes (rows) of  $I$  particles lying in one of the twelve orientations, randomly chosen, of a  $\{311\}$  plane. The  $\{311\}$  shape is modeled as  $N_r$  rows of  $I$ s lying on a  $\langle 01\bar{1} \rangle$  line with a distance of  $a/\sqrt{2}$  between  $I$ s in the same line, and as  $N_c$  columns keeping a distance of  $a\sqrt{22}/4$  between them, with  $a = 0.543$  nm, the silicon lattice constant.

The ratio between length ( $L$ ) and width ( $W$ ) is given by:

$$W \approx \sqrt{CL} \quad (678)$$

being  $C = 0.5$  nm. This ratio is maintained reshaping the  $\{311\}$  defect (that is, changing the number of row and columns) when necessary (see [Figure 52](#)).

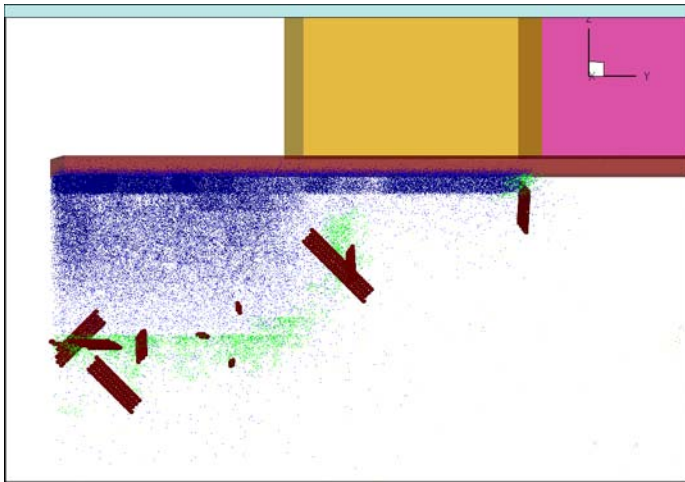


Figure 52  $\{311\}$  defects are simulated by Sentaurus Process KMC as parallel stripes (rows) of  $I$  particles lying in a  $\{311\}$  plane: red is silicon interstitials in  $\{311\}$ ; green is  $I$  and  $V$  in APs; and blue is arsenic

The  $\{311\}$  defects only exist above a size threshold. Smaller defects are assumed to be APs, and they have an irregular shape (see [Amorphous Pockets Life Cycle on page 427](#)).

When  $\{311\}$  defects grow enough, they are transformed into dislocation loop defects (see [Dislocation Loops on page 435](#)). The threshold size (number of interstitials) between  $\{311\}$  defects and dislocation loops is assumed to follow an Arrhenius plot:

$$\text{size} = \text{prefactor} \times \exp(E/(k_B T)) \quad (679)$$

The formation energy of the dislocation loop must be smaller than the  $\{311\}$  formation energy at the threshold size; otherwise, the threshold is taken as the size where both energies are equal.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Extended Defects

Both `prefactor` and `E` are parameters available in the database with names `D0_311toLoop` and `E_311toLoop`, respectively.

### Parameters

The parameters to control the transformation between  $\{311\}$ s and loops are specified for interstitials in silicon:

```
sprocess> pdbGet KMC Si I D0_311toLoop
1.6
sprocess> pdbGet KMC Si I E_311toLoop
0.68
```

**NOTE** These parameters can be changed to fit the  $\{311\}$  to dislocation loop transition size.

### Capture

Each time a neutral  $I$  point defect interacts with an  $I$  belonging to a  $\{311\}$  defect, the  $\{311\}$  captures the point defect. Since  $\{311\}$  defects grow and shrink at their ends, the new particle is attached at the nearest end of the defect. When the end cannot grow because it is too close to a interface or a boundary, the other end is used.

When `311DopantModel` is set to 1, impurities also can be trapped. These trapped impurities will remain in the captured location until they are re-emitted. Only neutral impurities (or neutral impurity pairs) are captured and re-emitted.

### Emission

To preserve microscopic reversibility between the capture and the emission processes, emitted particles (neutral interstitials) are taken randomly from one of the two ends and released from a random point at the  $\{311\}$  surface (see [Figure 53 on page 433](#)).

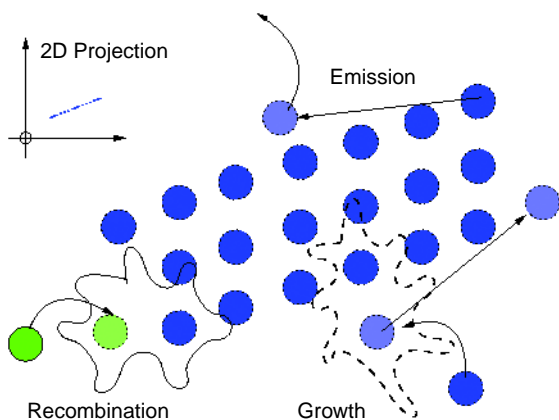


Figure 53 Recombination of defects in a {311} defect

The emission frequency is computed as in APs by:

$$v_{emit} = v_{0,emit} \times \exp((-E_{emit}(size) + P\Delta V_{311} + \alpha_{311}[Ge])/(k_B T)) \quad (680)$$

where the considerations for the AP emission, including all the corrections, apply. The binding energies are taken from the list supplied with the `Eb_Cluster` parameter. These energies are shared with the APs. As explained above, for sizes less than a threshold value, defects are considered APs. Otherwise, they are rearranged as {311} defects. Consequently, only binding energies for sizes equal or bigger than APs-{311} threshold applies for {311} defects. Corrections are applied for both pressure and Germanium content. These corrections are specified as `VF311` and `Eb_311Ge`, respectively.

{311}s may also emit captured dopants if the `311DopantModel` is set to 1. The emission frequency for them is:

$$v_{emit}(A_i) = v_{0,emit}(A_i) \times \exp(-E_{emit}((A_i)/(k_B T))) \quad (681)$$

being the prefactor and activation energy called `D0_311` and `Eb_311`, respectively, in the PDB.

## Parameters

For impurity re-emission, the parameters are:

```
sprocess> pdbGet KMC Si In D0_311
200.0
sprocess> pdbGet KMC Si In Eb_311
2.0
```

## Recombination

The {311} defects recombine incoming Vs with any charge by annihilation of the Is at the nearest {311} defect end. When {311} defects dissolve, they do not become APs when the threshold AP-{311} size is reached. The emission frequency depends on the binding energy, and the binding energy only depends on the size of the defect. Since a interstitial cluster and a small {311} defect have the same binding energy when they have the same size, the defect shape affects only the capture volume, but not the emission frequency. Consequently, rearranging {311} as small defects and vice versa only changes the capture volume, and these changes are negligible for small clusters. Nevertheless, the capture volume differences between small {311} defects and irregular clusters are negligible, and there is no information about the shape of dissolving {311} defects.

Finally, when a {311} reaches size 2, it releases the particles as two interstitials and the {311} disappears.

## Interactions

Interactions between {311} defects and mobile particles can be modified with:

```
pdbSet KMC Si <I/V/Impurities> Reactions311 <species> <true/false>
```

Growth reactions ( $I_n + I$ ) are controlled with  $I$ , and recombination reactions ( $I_n + V$ ) with  $V$ . {311} defects can break up paired dopants capturing the interstitial or recombining the vacancy (for example,  $B_i + I_n \rightarrow B + I_{n+1}$ ). The remaining dopant will be immediately released or captured (and re-emitted later) by the defect depending on the value of the parameter 311DopantModel (0 releases dopants, 1 traps it). A captured dopant can be re-emitted. These reactions enable the {311} to decrease the impurity diffusion.

Only neutral Is react with {311} defects and, consequently, only paired dopants with the same charge as the substitutional dopant react with {311} defects. Any charge state is allowed for the recombination of vacancies.

## Parameters

Use the following for growth and recombination:

```
sprocess> pdbGet KMC Si I Reactions311
I         true
sprocess> pdbGet KMC Si V Reactions311
V         true
```

For paired impurity breakup (boron, for example), use:

```
sprocess> pdbGet KMC Si B Reactions311
BiM      false
sprocess> pdbGet KMC Si I 311DopantModel
0
```

You can define the parameter `311DopantModel` globally as a default for all dopants, but define it locally with a different value that overwrites the global value for a particular dopant. For example:

```
pdbSet KMC Si I 311DopantModel 0
pdbSetDouble KMC Si B 311DopantModel 1
```

sets the model for all the impurities as ‘release dopant,’ except for boron.

---

## Dislocation Loops

Dislocation loops are planar defects lying on  $\{111\}$  planes [18]. A dislocation loop can be either a faulted dislocation loop (FDL) or perfect dislocation loop (PDL). FDLs are circular stacking faults surrounded by a dislocation line. PDLs are not implemented in Sentaurus Process KMC.

$\{311\}$  defects are the precursors of dislocation loops. When the implant conditions (available concentration of  $I$ , distance to the free surface) are appropriate,  $\{311\}$  defects grow until they reach the threshold size and transform into dislocation loops. Dislocation loops are more stable than  $\{311\}$  defects; consequently, the supersaturation created by dislocation loops is lower.

### Shape

The shape of dislocation loops is computed as a filled circle in a  $\{111\}$  orientation (see Figure 54). All  $\{111\}$  orientations are allowed, and one is randomly chosen.

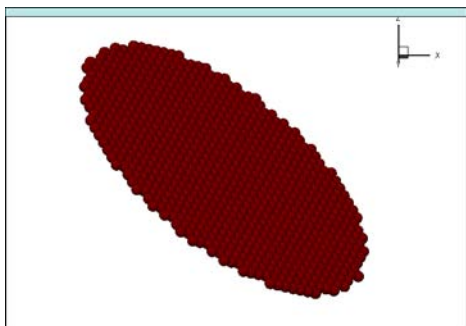


Figure 54 A dislocation loop taken from a Sentaurus Process KMC simulation

## Capture

Dislocation loops capture any incoming neutral interstitial. The original position is lost, and the particle is moved to the proper position in the disk. The capture radius is the sum of the capture radius of the constituent particles.

When the `ReactionsLoop` is set and `LoopDopantModel` is `true`, dislocation loops capture incoming impurities. When `LoopDopantModel` is `false`, the impurity is not captured. However, when it carries a point defect (in other words, is an impurity pair), the pair is broken; the impurity is deposited as a substitutional impurity; and the point defect reacts with the loop.

## Emission

Dislocation loops emit neutral interstitials with a frequency given by:

$$v_{emiss} = v_{0,emiss} \times \exp\left(-\frac{E_{b,loop}(\text{size}) + E_m(I) + \Delta E_m(I) + \Delta E_{b,loop}}{k_B T}\right) \quad (682)$$

$v_{0,emiss}$  includes both a prefactor and a linear dependency with the dislocation loop size, and  $E_{b,loop}(\text{size})$  is the binding energy of the dislocation loop, which only depends on the size. Sentaurus Process KMC computes the binding energies as:

$$E_{b,loop}(\text{size}) = E_f(I) + E_{f,loop}(\text{size} - 1) - E_{f,loop}(\text{size}) \quad (683)$$

The dislocation loop formation energies are taken from [19] as:

$$E_{f,loop}(\text{size}) = \pi\gamma R^2 + \frac{a^2\mu}{6(1-\nu)} \cdot R \cdot \log\left(\frac{8R}{b}\right) - nE_f(I) \quad (684)$$

where:

- $R = \sqrt{\text{size}/(\pi d_{111})}$  is the loop radius.
- $\gamma$  is the stacking fault energy per unit area.
- $\mu$  is the shear modulus.
- $\nu$  is the Poisson ratio.
- $b$  is Burger's vector modulus.
- $a$  is the silicon lattice parameter.
- $d_{111}$  is the atomic density in a {111} plane, in  $\text{nm}^{-2}$ .

The above parameters are specified in the parameter database.  $\gamma$  is called `gamma`,  $\mu$  is `mu`,  $\nu$  is `nu`, and  $b$  is named `burgVectMod`. The emission prefactor is called `D0_Loop`.

The corrections applied to the migration energy of interstitials are the usual ones:

$$\Delta E_m(I) = \alpha_m[Ge] + \frac{1}{3} \sum_i^{x,y,z} \exp(-\Delta E_m^i / (k_B T)) \quad (685)$$

and for the binding of the particle to the loop is:

$$\Delta E_{b,loop} = P \Delta V_b^{loop} + \alpha_{loop}[Ge] \quad (686)$$

where  $\Delta V_b^{loop}$  is called VFLoop, and  $\alpha_{loop}$  is called Eb\_LoopGe in the PDB.

Captured impurities (when LoopDopantModel is true) re-emit impurities into the bulk with a frequency given by:

$$v_{emit}(A_i) = v_{0,emit}(A_i) \times \exp(-E_{emit}(A_i) / (k_B T)) \quad (687)$$

being the prefactor and activation energy called D0\_Loop and Eb\_Loop in the PDB, respectively.

## Parameters

The parameters needed for the simulation of dislocation loops are defined for interstitials in silicon:

```
sprocess> pdbGet KMC Si I D0_311toLoop
1.6
sprocess> pdbGet KMC Si I E_311toLoop
0.68
sprocess> pdbGet KMC Si I D0_Loop
1000000.0
sprocess> pdbGet KMC Si I gamma
0.4375
sprocess> pdbGet KMC Si I mu
472
sprocess> pdbGet KMC Si I nu
0.3
sprocess> pdbGet KMC Si I burgVectMod
0.3135
sprocess> pdbGet KMC Si I VFLoop
0
sprocess> pdbGet KMC Si Eb_LoopGe
0
```

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Extended Defects

For impurity re-emission, the parameters are:

```
sprocess> pdbGet KMC Si In D0_Loop
200.0
sprocess> pdbGet KMC Si In Eb_Loop
2.0
```

**NOTE** These parameters can be changed to fit the dislocation loop formation and dissolution.

Figure 55 shows how a dislocation loop grows capturing interstitials, and how it shrinks recombining incoming vacancies or emitting interstitials.

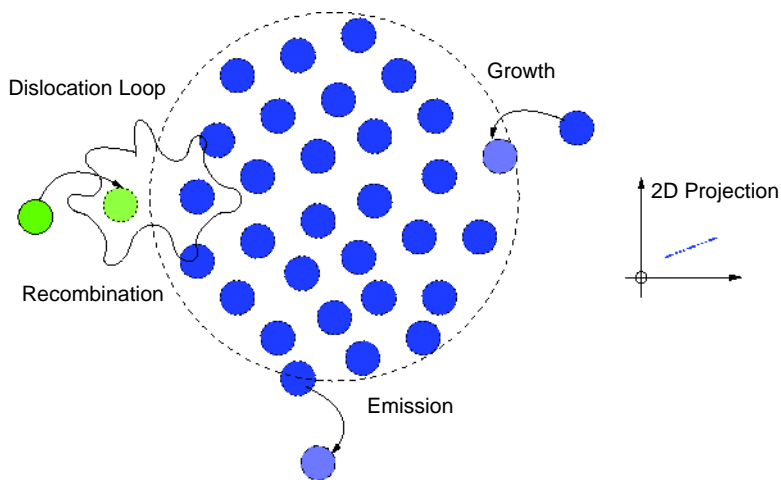


Figure 55 Emission, capture, and recombination of point defects in a dislocation loop

## Interactions

The interactions between dislocation loops and mobile particles are:

- Growth reactions. Only with neutral Is:

```
pdbSet KMC Si I ReactionsLoop I <true/false>
```

- Recombination reactions. Any vacancy:

```
pdbSet KMC Si I ReactionsLoop <V/VM/VP/VMM/VPP> <true/false>
```

- Impurity pairs break up and interact with the associated point defect (I or V). Only with pairs with the substitutional charge state the same as the substitutional dopant (for example,  $B_i^-$  for  $B^-$ ). The interstitial or vacancy is trapped or recombined, and the dopant is released (0) or trapped (1) depending on the model used. The model is specified for all dopants (default value) using the parameter `LoopDopantModel` for interstitials.



This particular default can be overwritten for one particular dopant.

```
pdbSet KMC Si I LoopDopantModel <true/false>  
pdbSetDouble KMC Si <dopant> LoopDopantModel <true/false>
```

## Parameters

Loops trap interstitials, but the recombination of vacancies is disabled:

```
sprocess> pdbGet KMC Si I ReactionsLoop  
I      true  
sprocess> pdbGet KMC Si V ReactionsLoop  
V      false
```

Loops can break up some paired dopants, for example, boron:

```
sprocess> pdbGet KMC Si B ReactionsLoop  
BiM    true  
sprocess> pdbGet KMC Si I LoopDopantModel  
0
```

---

## Voids

Small vacancy defects have been reported (using paramagnetic resonance and photoluminescence) [20][21][22][23]. Theoretical studies [24][25] indicate that some of these small clusters can be particularly stable. Sentaurus Process KMC models these small clusters as APs and, consequently, they have irregular shapes. Nevertheless, size-dependent binding energies are considered for their *V* emission (see [Damage Accumulation Model: Amorphous Pockets on page 420](#)).

Vacancy clusters appear as spheroidal voids when they are big enough to be seen by TEM [26]. Tight-binding molecular dynamics studies show that the binding energies are a function of the cluster size [27] (see [Figure 56 on page 440](#)).

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Extended Defects

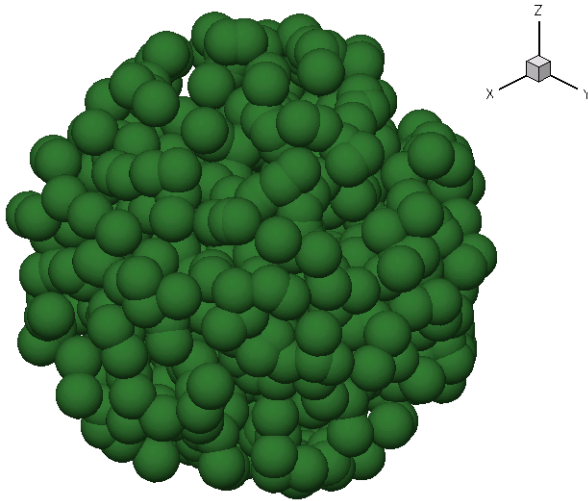


Figure 56 Voids are simulated with a spherical shape; this one contains 654 vacancies

## Shape

The threshold size between irregular small vacancy clusters (APs) and voids is specified with the parameter `MINVOIDSIZE`. Another parameter, `MAXVOIDSDIAM`, is used to set up the maximum-allowed diameter (in nanometers) for these defects.

Reshaping the small clusters into voids above the mentioned limit is necessary to maintain the right volume/surface ratio, as the `V` cluster grows. A large cluster of `n` vacancies is reshaped to be spheroidal, occupying the volume corresponding to the same number of silicon lattice sites. Sentaurus Process KMC manages the void shape to assert that its density is correct.

## Parameters

The parameters for voids are specified for silicon material and vacancy as species:

```
sprocess> pdbGet KMC Si V MinVoidSize
27
sprocess> pdbGet KMC Si V MaxVoidDiam
5.0
```

## Capture

Voids capture neutral vacancies, rearranging them to have a spheroidal shape. Figure 57 shows the possible interactions between voids and point defects.

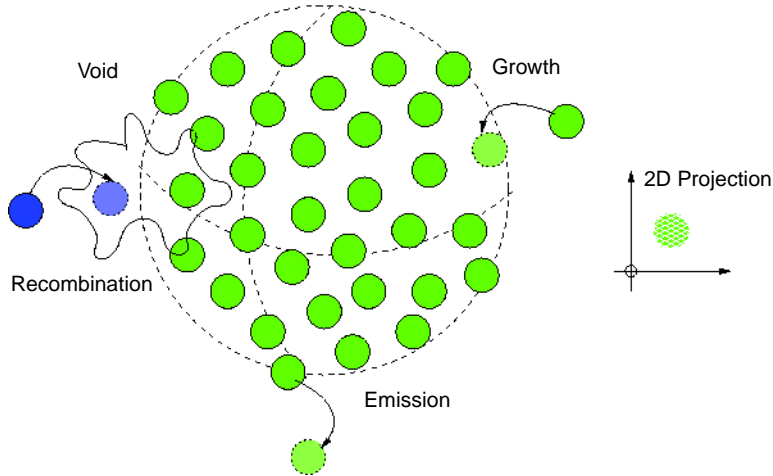


Figure 57 Voids are big cluster vacancies with a spherical shape that grow trapping neutral vacancies and shrink by recombination and vacancy emission

## Emission

Voids emit neutral vacancies with a frequency:

$$v = v_0 \times \exp(-(E_{b, void}(\text{size}) + \Delta E_{b, void} + E_m(V) + \Delta E_m(V))/(k_B T)) \quad (688)$$

$v_0$  is a prefactor which includes a constant and a dependency with the surface of the void, and  $E_{b, void}(\text{size})$  is the binding energy of a void. These binding energies are assigned in the parameter database together with the small vacancy cluster binding energies. For information on how to locate and modify them, see [Amorphous Pockets Life Cycle on page 427](#). For voids, only the values for sizes bigger than the AP-Void threshold apply.

Finally, corrections to the migration energy of vacancies and the binding of them to the void are applied. The migration correction is the usual one:

$$\Delta E_m(V) = \alpha_m [Ge] + \frac{1}{3} \sum_i^{xy,z} \exp(-\Delta E_m^i / (k_B T)) \quad (689)$$

and for the binding energy, it is corrected using the parameter for small vacancy clusters:

$$\Delta E_{b, void} = P \Delta V_b^{cluster}(V) + \alpha_{void} [Ge] \quad (690)$$

where  $\alpha_{void}$  is Eb\_VoidGe.

## Recombination

Voids recombine incoming interstitials with any charge.

## Interactions

Interactions between void defects and other particles fall into these categories:

- Trapping of neutral vacancies (growth):

```
pdbSet KMC Si V ReactionsVoid V <true/false>
```

- Recombination of interstitials:

```
pdbSet KMC Si V ReactionsVoid <I/IM/IP> <true/false>
```

- Impurity pair breakup. Voids do not trap impurities, but they can trap or recombine the interstitial or vacancy associated with a paired impurity. (For example,  $B_i + V_n \rightarrow B^- + V_{n-1}$ ). The pair must have the same charge as the substitutional dopant (in other words,  $B_i^-$  for  $B^-$ ,  $AsV^+$  for  $As^+$ ).

```
pdbSet KMC Si <impurity> ReactionsVoid <species> <true/false>
```

## Parameters

Voids trap vacancies and recombine interstitials:

```
sprocess> pdbGet KMC Si V ReactionsVoid  
V      true  
sprocess> pdbGet KMC Si I ReactionsVoid  
I      true
```

Voids may break up some pairs. For example,  $B_i^-$  is disabled:

```
sprocess> pdbGet KMC Si B ReactionsVoid  
BiM    false
```

---

## Amorphization and Recrystallization

A predictive atomistic process simulator must include an amorphization model. Nevertheless, accounting for each particle and position during the amorphization, although possible [28], is not convenient for the sizes, times, and computer resources involved in process modeling. Despite this, amorphization involves the destruction of the lattice structure. Without a lattice, the KMC method, which discards the lattice and tracks only defects, is opened to a quasiautomistic approach, as explained in this section.

Figure 58 shows a generic damage concentration profile after an implant.

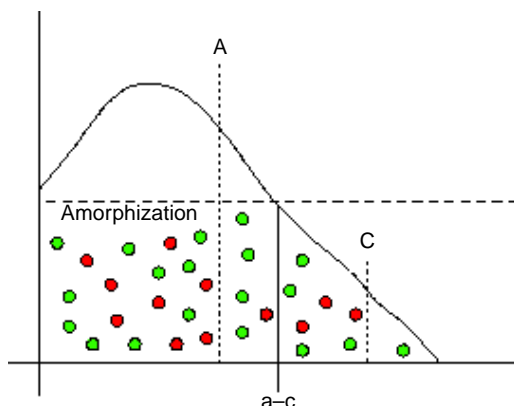


Figure 58 Damage concentration profile after an implant

There are two different concentrations in Figure 58 (A and C) and one concentration threshold called Amorphization. This threshold is stored in the parameter database in the damage section as AmorphizationThreshold:

```
sprocess> pdbGet KMC Si Damage AmorphizationThreshold
1.5e+22
```

**NOTE** You can change this limit if necessary. The damage accumulation model is dependent on the AmorphizationThreshold.

The behavior of the simulator while adding new point defects (damage) differs depending on the local concentration of the internal grid elements. A new point defect is inserted into a box depending on the concentration of that box. If the concentration is smaller than the Amorphization threshold (C, crystalline region), the point defect is inserted as it is. In other words, a particle is placed inside the simulator with its three coordinates, the defect, and particle type. Finally, the damage concentration can be higher than the amorphization threshold (region A (amorphous) in Figure 58). In this case, if a particular crystalline volume (specified by the parameter minAmorphousVol) has an averaged damage concentration larger than the threshold, the entire internal volume is assumed to be amorphous. The atomistic 3D coordinates for  $I_s$  and  $V_s$  are discarded for amorphous boxes because the definition of a point defect is now meaningless in an amorphous region, and only their concentration is stored. Finally, the material of the internal box changes from crystalline (such as silicon) to amorphous (such as amorphous silicon) and an interface, which is capable of simulating a three-phase segregation model, is created between them.

**NOTE** For amorphous regions, the atomistic 3D information is discarded, and only the number of particles is stored. When asking Sentaurus Process KMC for the atomistic information (the 3D coordinates for each particle), you should not expect to obtain  $I_s$  and  $V_s$  in amorphous regions.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Amorphization and Recrystallization

**NOTE** To obtain the amorphous–crystalline interface, use the command:  
`kmc extract acinterface`

---

## Amorphous Defects

An amorphous defect is a special defect assigned to each grid element of Sentaurus Process KMC with a damage level above the amorphization threshold.

### Material

Amorphous defects are always associated with amorphous materials. Each amorphous internal element is paired with an amorphous defect.

### Shape

The shape of an amorphous defect coincides with the element containing it. Amorphous layers are created as a set of several amorphous defects. Consequently, amorphous layers can follow any complicated amorphous geometry, but always as a set of Sentaurus Process KMC elements.

### Growth

Amorphous defects do not grow because they are limited to the size of the element. Amorphous layers grow when new elements are amorphized and become amorphous. These amorphous elements capture any incoming particle.

### Recombination

These defects can recombine their damage and become crystalline silicon. Amorphous defects do not emit particles; recrystallization is the only event they can perform.

---

## Diffusion in Amorphous Materials

Two models are available for diffusion in amorphous materials:

- A simpler, direct diffusion model
- An indirect diffusion model that uses dangling bonds as an intermediate species

To select the model to use, set `KMC <material> Damage amorphous.bonds to true`, where `<material>` is the crystalline material.

## Direct diffusion

Dopants can diffuse in amorphous materials using direct diffusion. The implemented diffusivity is:

$$D_m(X) = D_{m,0}(X) \exp(-E_m((X)/(k_B T))) \quad (691)$$

where the parameters  $D_{m,0}$  and  $E_m$  are input parameters.

## Parameters

The parameters  $D_{m,0}$  and  $E_m$  needed for diffusion in amorphous materials are specified in the PDB as `Dm` and `Em`, respectively, under the amorphized material:

```
pdbSet KMC <amorphous material> <dopant> Em <dopant> <value>
```

For example:

```
pdbSet KMC AmorphousSilicon B Em B 0.8  
pdbSet KMC AmorphousSilicon B Dm B 1e-3
```

**NOTE** The alias `aSi` can be used for `AmorphousSilicon`.

## Indirect Diffusion

The observed boron diffusion in amorphous silicon does not seem to obey a standard Fick's law with constant diffusivity prefactors and activation energy, thereby making the direct diffusion model in amorphous silicon inaccurate. A different model has been proposed [29][30] that relies on the presence and distribution of dangling bonds and floating bonds and that interacts with the boron atoms. In this model, an initial number  $n_0$  of dangling bonds (threefold-coordinated atoms) and floating bonds (fivefold-coordinated atoms) is created during amorphization.

These dangling bonds and floating bonds are allowed to evolve using a simple direct diffusion  $D_d$  for dangling bonds and  $D_f$  for floating bonds. Dangling bonds and floating bonds can interact with them, annihilating each other. Dangling bonds also can interact with boron (or any other user-defined impurity) with a proportionality constant  $\alpha$ .

In this model, boron in amorphous silicon can exist in two different states: an immobile fourfold-coordinated  $B^4$  state and a highly mobile threefold-coordinated  $B^3$  state. Boron changes between these two states by capturing and releasing a dangling bond. The threefold

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Amorphization and Recrystallization

mobile boron is allowed to diffuse with a simple Arrhenius plot. Boundary conditions can be set at the `AmorphousSilicon_Silicon` and `AmorphousSilicon_Oxide` interfaces for dangling bond (DB) and floating bond (FB) recombination. Finally, despite the initial concentration  $n_0$  of dangling bonds produced by amorphization, an extra contribution of  $\gamma[B]$  is added to produce a total DB concentration of:

$$n_B = n_0 + \gamma[B] \quad (692)$$

where  $\gamma$  is a coefficient relating to the presence of boron atoms in amorphous silicon with an excess of dangling bonds, and  $[B]$  is the concentration of boron in amorphous silicon.

Consequently, the following reactions are allowed:



### Implementation

To minimize the number of species and physical mechanisms, the implementation of indirect diffusion through dangling bonds and FBs has been done by renaming:

- Dangling bonds as *interstitials in amorphous silicon*
- Floating bonds as *vacancies in amorphous silicon*
- $B^4$  as *substitutional boron in amorphous silicon*
- $B^3$  as *interstitial boron in amorphous silicon*

In this way, all that is needed is to allow  $I$  and  $V$  inclusion, and the following reactions in amorphous silicon:



The  $B$  interaction with  $I$  and further emission by  $B_i$  are modeled as a regular kickout mechanism. Consequently, the parameter  $\alpha$  is modeled indirectly through the binding energy and prefactor of the  $B_i$  pair.

When amorphizing an element with volume  $\Delta V$ , an initial number of  $n_0 \Delta V \delta$   $I$ s and  $V$ s will be created inside, where  $\delta$  is the silicon density. If there are boron atoms inside or boron atoms are introduced through implantation or any other means (for example, using the `select` or `profile` commands), an extra number of  $\gamma$   $I$ s will be introduced per boron atom.



## Parameters

The parameters needed for this model are introduced in different places. If you want to model the indirect diffusion of boron in amorphous silicon (other impurities or amorphous materials are accepted also), you can use `aSi` as an alias for `AmorphousSilicon`.

Table 52 Parameters used for indirect diffusion in amorphous silicon

Parameter	Description	Symbol
KMC aSi amorphous.bond true	Model activation.	None
KMC aSi I Dm I <value> KMC aSi I Em I <value>	Dangling bond diffusion.	$D_d$
KMC aSi V Dm V <value> KMC aSi V Em V <value>	Floating bond diffusion.	$D_f$
KMC aSi B Dm Bi <value> KMC aSi B Em Bi <value>	$B_3$ diffusion.	None
KMC aSi B Eb Bi <value> KMC aSi B Eb Bi <value>	$B_3$ - $B_4$ reaction rate.	$\alpha$
KMC aSi B ReactionsPointDefect B,I true	$B^4 + DB \leftrightarrow B^3$ .	None
KMC Si Damage amorphous.n0 <value>	Initial dangling bond and floating bond percentage (versus silicon density).	$n_0$
KMC aSi B gamma <value>	Number of dangling bonds created per boron atom.	$\gamma$

---

## Impurity Clusters in Amorphous Materials

Impurities diffusing in amorphous materials can interact with each other and form impurity clusters. In contrast with impurity clusters in crystalline volumes, the amorphous impurity clusters do not contain interstitials or vacancies, and are only an agglomeration of impurities. Consequently, they can only re-emit the trapped impurities. With this exception, they behave as regular impurity clusters. For further information, see [Impurity Clusters on page 460](#).

## Recrystallization

Two recrystallization models are implemented:

- The simple KMC quasiautomistic model assigns a recrystallization rate to each amorphous defect for recrystallization simulations. No orientation dependencies are allowed.
- The fully atomistic model uses a lattice kinetic Monte Carlo (LKMC) method to simulate the evolution of the amorphous–crystalline interface. This model includes orientation-dependent solid phase epitaxial regrowth (SPER) and facet formation.

The recrystallization model is set up with:

```
pdbSet KMC <material> Damage Model.SPER <model>
```

where <material> is the crystalline material (typically, silicon), and <model> is one of the following:

- LKMC model
- Simple KMC quasiautomistic model

### KMC: Quasiautomistic Solid Phase Epitaxial Regrowth

Recrystallization is implemented as a special event performed by the amorphous defects. At a given temperature, every amorphous defect can recombine all its internal damage, in other words, recrystallize, with a frequency  $\nu_{recryst}$ . The recrystallization of several amorphous defects with different recrystallization frequencies, depending on their recrystallization axis and the number of amorphous neighbors, generates an advancing recrystallization front, as can be seen in [Figure 59 on page 449](#).

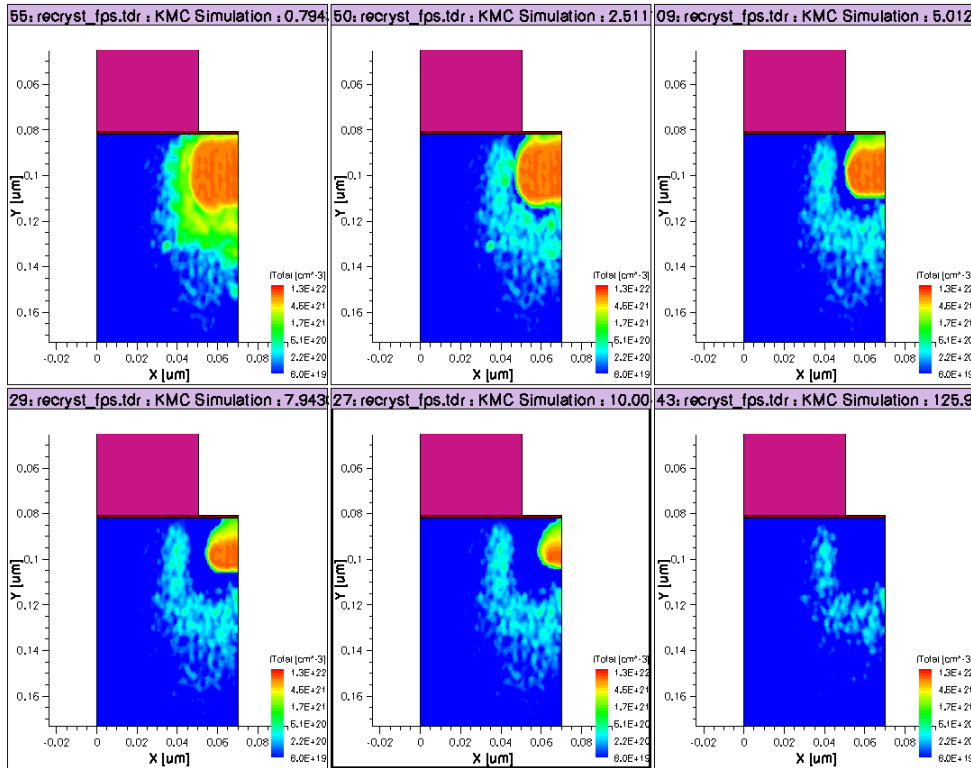


Figure 59 Source and gate of a transistor during SPER, as simulated by Sentaurus Process KMC. The total concentration of interstitials is represented. The time evolution is shown while the recrystallization front (a consequence of the recrystallization of isolated amorphous defects) is moving. At the end, there is only damage near the a-c interface. This remaining damage may form end-of-range (EOR) defects.

Therefore, if  $w$  is the length of an amorphous defect in the recrystallization direction, the frequency associated with the recrystallization is  $v/w$ . This recrystallization velocity  $v$  is computed as an Arrhenius function that includes dependencies on both the local Fermi level and the presence of impurities [31]:

$$V(n) = V_0^{Fermi}(n) \times \exp(-(E_{recryst}(n) + P\Delta V^{SPER} + c)/(k_B T)) \quad (697)$$

$E_{recryst}(n)$  parameters are specified as  $E_{recryst}$ .  $\Delta V^{SPER}$  is the activation volume for SPER (dependency on hydrostatic pressure) called  $vF_{Recryst}$ , and  $n$  is the percentage of amorphous material around a given element. The time it takes to recrystallize an amorphous cell depends on the number of amorphous neighbors; the more neighbors that are amorphous, the longer it takes. The longer recrystallization takes, the more stable the amorphous defect, so

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Amorphization and Recrystallization

its activation energy is bigger.  $V_0^{Fermi}$  accounts for the prefactor, including dependency on the Fermi level. This dependency is introduced as:

$$V_0^{Fermi}(n) = V_0(n)(1 + |K \times \text{Doping}|) \quad (698)$$

being  $V_0(n)$  and the input parameter called `v0_recryst`. `Doping` is the local amorphous element doping, and  $K$  is a calibration parameter (different for n-type and p-type materials) called `v0_recrys_ntype` and `v0_recrys_ptype`, respectively.

Finally,  $c$  takes into account the changes in SPER regrowth due to local impurity concentration. This correction term is modeled as:

$$c = \sum_{\text{Impurities}} \left( 1 - \left\{ \frac{[\text{Impurity}]}{5 \times 10^{22}} \right\}^x \right) E_{\text{recrys}}(50) + \left( \frac{[\text{Impurity}]}{5 \times 10^{22}} \right)^x E_f(\text{Impurity}) \quad (699)$$

$E_f(\text{Impurity})$  is the parameter controlling how much each impurity changes the planar recrystallization activation energy (assumed to have 50% amorphous neighboring elements).  $x$  is an exponent to control how this correction depends on the dopant concentration. A null impurity concentration gives a zero correction, while an impurity concentration of  $5 \times 10^{22}$  produces  $c = E_f(\text{Impurity}) - E_{\text{recrys}}(50)$ . Consequently,  $E_f(\text{Impurity})$  represents the planar recrystallization activation energy if the sample contains only the impurity, while  $x$  allows it to control the transition between these two opposite situations. These parameters are called `E_recrys` and `E_recrys_exponent`, respectively in the PDB.

This model, in which elements with fewer amorphous neighbors recrystallize faster, extends the ideas described in the literature [28] for amorphous elements. This simple method can simulate the faster recrystallization of amorphous corners or thin amorphous panhandlers embedded in crystalline silicon.

Finally, if a recrystallization event that will break the compactness of the amorphous layer is detected, its recrystallization will be retarded by the parameter `CompactFactor`. This prevents the formation of amorphous isolated islands and ensures a better compactness of the amorphous material.

### Parameters

The parameters for the recrystallization model are:

```
sprocess> pdbGet KMC Si Damage VFRecrys
0
sprocess> pdbGet KMC Si Damage V0_recrys
0      1.7e8
99     1.7e8
100    0
sprocess> pdbGet KMC Si Damage E_recrys
0      1.72
```

15	1.72
40	2.7
70	2.7
95	3.3
99	5

**NOTE** To produce consistent notation, the suffix has changed from `recryst` to `recrys`.

The unspecified values between two specified ones are computed by linear interpolation.

The parameters controlling the Fermi level and impurity concentration dependencies are specified for each dopant (and material). For example, for boron, they are:

```
sprocess> pdbGet KMC Si B E_recrys
2.7
sprocess> pdbGet KMC Si B E_recrys_exponent
1
```

## LKMC: Fully Atomistic Modeling of Solid Phase Epitaxial Regrowth

It is well known that the SPER velocity depends on the substrate orientation with approximate ratios of 20:10:1 for orientations (100), (110), and (111), respectively. In addition, the recrystallization of thin layers in fin transistors is shown as an ‘arrow tip’ shape formed by two (111) planes that slow down the SPER, leading to the formation of polycrystalline silicon in regions still not recrystallized.

This model, based on the literature [32], introduces the lattice in the amorphous–crystalline interface and assigns a recrystallization event to each of the atoms there. When an internal mesh element is detected to be amorphous as explained in [Amorphization and Recrystallization on page 442](#), the silicon lattice is recreated around it. This lattice takes into account the wafer orientation specified in the `init` command. Those lattice atoms belonging to crystalline elements are assigned a “crystalline” flag, while those belonging to the amorphous element are assigned an “amorphous” flag. This produces the initial amorphous–crystalline interface. At this point, even when the amorphous–crystalline interface still follows the contour of the internal mesh, it is formed by a set of individual lattice atoms.

From this point, different recrystallization rates are assigned to each atom at the interface. The interface is defined as the set of lattice atoms that, having an amorphous state, has at least one first neighbor with a crystalline state. Any other lattice atom that does not belong to this interface has a recrystallization rate of 0. This means that crystalline-lattice atoms have a zero probability of recrystallizing (because they are already crystalline).

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Amorphization and Recrystallization

In some cases where regular SPER is very slow, random nucleation and growth can produce polysilicon material [33] not simulated here. Inclusion of defective silicon created during SPER also is not simulated.

For amorphous lattice atoms belonging to the interface (in other words, surrounded by at least one crystalline lattice atom), a SPER rate is assigned. The model assumes that an atom in the amorphous phase must form two undistorted bonds with its first neighbors in the silicon phase to become crystalline. For amorphous atoms close to a (001) surface, this happens naturally. For (011) surfaces, two adjacent amorphous atoms have to *cluster* together so that each atom has two undistorted bonds. Finally, for (111) orientations, three atoms are needed to cluster together.

Consequently, there will be three different recrystallization prefactors – K(1), K(2), and K(3) – depending on the number of amorphous atoms needed to complete two undistorted bonds. These K(1), K(2), and K(3) prefactors will be related but not proportional to the different (001), (011), and (111) SPER velocities. In particular, K(2) and K(3) are probabilities for two and three atoms, respectively, to come together in an amorphous phase and form spontaneously undistorted crystalline bonds between them. Consequently, K(2) is expected to be smaller than K(1), and K(3) is expected to be smaller than K(2), by several orders of magnitude.

Each of these lattice atoms is given a recrystallization frequency of:

$$v^{\text{LKMC}} = v_0^{\text{Fermi}} \times K(n) \times \exp\left(-\frac{(E_{\text{recryst}}^{\text{LKMC}} + (|\epsilon_{xy}| + |\epsilon_{xz}| + |\epsilon_{yz}|)\lambda + P\Delta V^{\text{SPER}} + c)}{k_B T}\right) \quad (700)$$

$K_{(n)}$  are the K(1), K(2), and K(3) prefactors explained above where:

- $v_0^{\text{Fermi}} = 1 + |K \times \text{Doping}|$  is a Fermi-level correction similar to [Eq. 698](#).
- $E_{\text{recryst}}^{\text{LKMC}}$  is taken as  $E_{\text{recryst}}(50)$  in [Eq. 697](#).
- $|\epsilon_{xy}|$ ,  $|\epsilon_{xz}|$ , and  $|\epsilon_{yz}|$  are the absolute value of the shear stresses.
- $\lambda$  is a parameter coupling the shear stresses.
- $P\Delta V^{\text{SPER}}$  and  $c$  are the same terms as those defined in [Eq. 697](#).

[Figure 60 on page 453](#) shows the evolution of an amorphized fin during SPER when this model is used, after 2-, 4-, and 6-minute annealing at 550°C. When the arrow tip is formed by the two lateral 111 planes, the recrystallization is almost stopped (*middle* and *right* images). The planes are formed by the presence of the oxide–silicon interface. Since the oxide does not provide the needed undistorted bonds for silicon recrystallization, it is used as a starting point for the (111) plane formation.

A similar model using LKMC for epitaxial regrowth can be read in [Epitaxial Deposition on page 507](#).

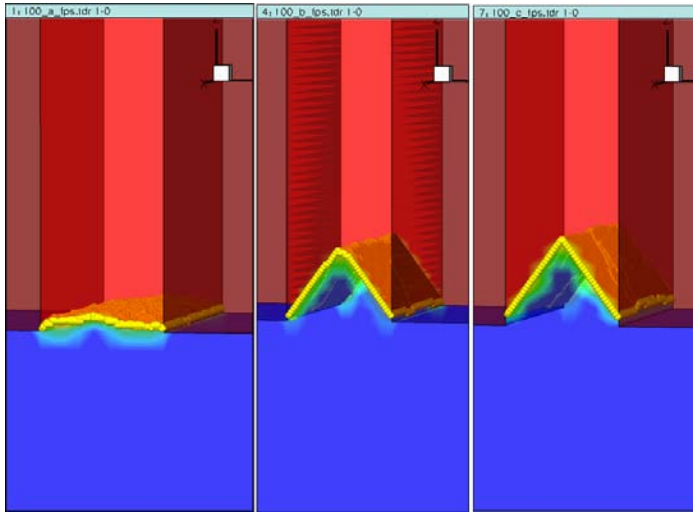


Figure 60 SPER evolution (blue is crystalline silicon; red is amorphous one) with time (left to right) 2, 4, and 6 minutes at 550°C of a thin (20 nm) silicon fin. The oxide (brown material) does not provide the correct template for the lattice atoms to form undistorted bonds, stopping the recrystallization and leading the way to the (111) planes. When the two (111) planes are formed, no further fast (100) SPER is possible, and the SPER occurs through the very slow and defect-prone (111) recrystallization.

Several corrections are applied to the recrystallization rate of a lattice atom. Three of them – the pressure correction ( $P\Delta V^{\text{SPER}}$ ), the impurity correction (through the term  $c$ ), and the Fermi-level correction ( $v_0^{\text{Fermi}}$ ) – are the same in both this model and the simple KMC model (see [KMC: Quasiatomistic Solid Phase Epitaxial Regrowth on page 448](#)).

### Shear-Strain Correction

The correction for shear strain,  $(|\epsilon_{xy}| + |\epsilon_{xz}| + |\epsilon_{yz}|)\lambda$ , is unique to this model. Its inclusion allows the LKMC model to successfully simulate the evolution of line-shaped amorphized regions. The experimental rate at the corners of line-shaped amorphized regions is very small, producing a pinching of the SPER interface at the corners [34]. This can be simulated with the inclusion of this shear stress term [32]. The shear strain is generated during amorphization due to the different density of the amorphous phase. The expansion of the amorphous phase is not possible in embedded amorphous regions. The compression of the amorphous phase leads to a sharp gradient of shear stress at the corners. The model uses the shear strain to simulate the anomalous regrowth patterns and facet formation experimentally seen in rectangular-shaped amorphized regions, as shown in [Figure 61 on page 454](#).

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Amorphization and Recrystallization

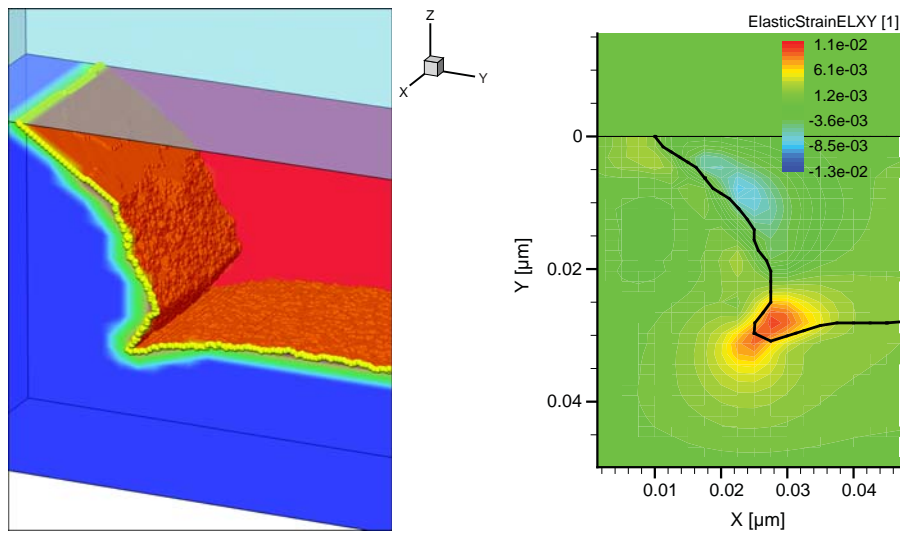


Figure 61 Recrystallization of a rectangular-shaped amorphous region using the LKMC model in Sentaurus Process KMC

Figure 61 (left) shows the distribution of lattice atoms at the amorphous interface side. A (111) plane, featuring a small nano-island, can be observed close to the interface. The trench formed at the corner is due to the perturbation introduced by shear strain. Figure 61 (right) shows the xy shear strain distribution; its maximum intensity occurs at the corner.

Since this model relies on the strain created by the different density of the amorphous material versus the silicon one, some extra commands must be introduced in the script to account for it.

First, a new material to account for amorphous silicon in the mechanics simulator must be introduced:

```
mater add name = Amorph
```

Mechanics properties for this new material must be defined:

```
pdbSetDoubleArray Silicon Amorph Conc.Strain {0 0 1 0.02}  
pdbSetBoolean Silicon Mechanics UpdateStrain 1
```

and Sentaurus Process KMC must be instructed that stress is being taken into account:

```
pdbSet KMC Stress 1
```

Finally, the synchronization between the atomistic and the mechanics simulator is automatic. After every mechanics step, the KMC Stress 1 parameter instructs Sentaurus Process KMC to update the stress and strain fields. After each diffusion (atomistic diffusion) step, Sentaurus Process KMC updates the “Amorph” distribution by automatically calling the procedure KMCsync written in KMC.tcl. This procedure, which can be modified by the user but, in



principle, does not need to be, contains the lines responsible for updating the amorphous region in mechanics to properly account for the strain and stress:

```
LogFile IL2 "A/C synchronization: KMC -> PDE"
kmc deatomize name=AC
sel Silicon z=1e22*AC name=Amorph store
```

## Parameters

Table 53 lists the parameters used in this model. It is assumed that silicon (Si) is the crystalline material and amorphous silicon (aSi) is the amorphous material.

Table 53 Parameters for LKMC model

Parameter name as typed in parameter database	Description	Symbol
KMC Si Damage Model.SPHER <model>	Use LKMC to set the model, KMC to unset.	None
KMC Si Damage prefactor.SPHER.100 <value>	Value for the prefactor associated with 100 SPHER.	K(1)
KMC Si Damage prefactor.SPHER.110 <value>	Value for the prefactor associated with 110 SPHER.	K(2)
KMC Si Damage prefactor.SPHER.111 <value>	Value for the prefactor associated with 111 SPHER.	K(3)
KMC Si Damage Shear.Coupling <value>	Shear-strain coupling parameter.	$\lambda$
KMC Si Damage VFRecrys <value>	SPHER pressure correction (same as the KMC model).	$\Delta V^{\text{SPHER}}$
KMC Si Damage E_recrys 50 <value>	Activation energy for recrystallization (same as the KMC model).	$E_{\text{recryst}}^{\text{LKMC}}$
KMC Si Damage V0_recrys_ntype <value> KMC Si Damage V0_recrys_ptype <value>	Fermi-level corrections (same as the KMC model).	$v_0^{\text{Fermi}}$
KMC Si Damage E_recrys <value> KMC Si Damage E_recrys_exponent <value>	Impurity corrections (same as the KMC model).	$c$
KMC Si Damage Lattice.Constant <value>	Lattice constant.	None

## Defect Generation during SPHER

It is known that when (111) planes have formed in a simulation, the recrystallization beyond these planes is defective, and silicon of low quality, or even polysilicon, is formed. A simple predictive LKMC model for defect formation during SPHER based on [35] and [36] is included.

Such modeling is performed by assigning two tags after every recrystallization event in the lattice: a *normal* tag for sites sharing the substrate configuration, and a *defective* tag for sites assumed not to bond to their neighbors and that form twin defects. Although this modeling does not physically set the atoms in twin positions, but only assigns them a *tag* while remaining

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Amorphization and Recrystallization

in a perfect crystalline position, it is sufficient to predict the defective regions in silicon and to slow down SPER in a similar way to experiments [35][36].

The new defective sites are produced by two mechanisms:

- Recrystallization of (111) sites, having a probability  $P_{def}$  of becoming defective.
- Recrystallization of atoms in the neighborhood of defective sites, inheriting such tags and becoming also defective.

The definition of a coordination number, a keystone in this model to identify the microscopic configurations, also is modified to distinguish between normal and defective sites. In this way, the formation of defects slows down the recrystallization of neighboring sites.

The formed defects are represented in the non-LKMC module as an *IV twin defect* in the TDR file. No actions are associated with them in the regular KMC simulator. Consequently, when they are formed, twin defects do not disappear and do not interact with other particles. They are created for users to identify the regions predicted to have highly defective silicon.

The only new parameter needed for the model is the probability of (111) recrystallizations to produce twin defects. This parameter is specified in:

```
pdbSet KMC Si Damage probability.SPHER.defect <0-1>
```

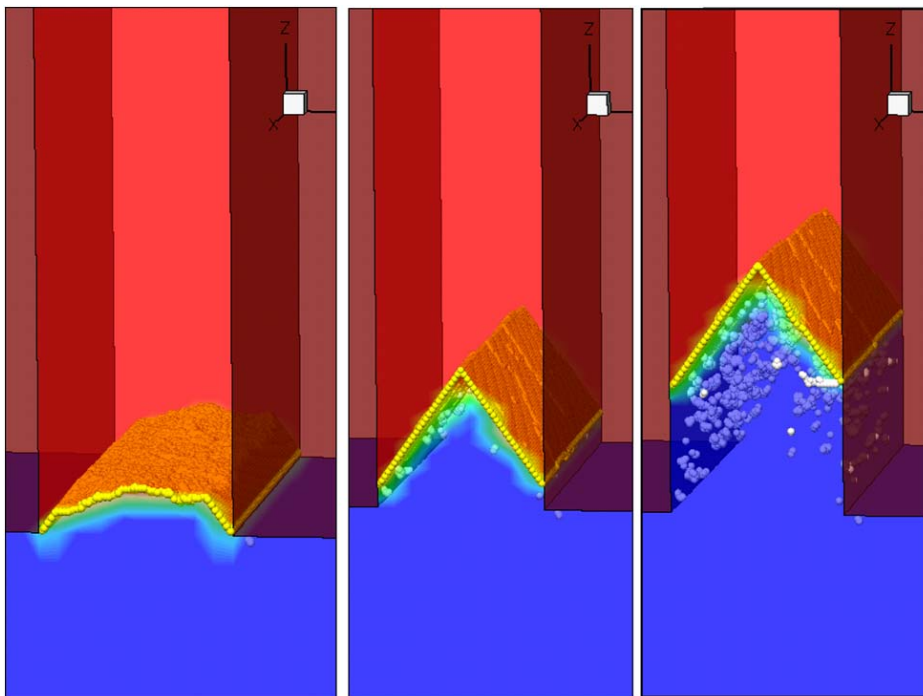


Figure 62 Evolution of a thin (20 nm width) amorphized silicon fin (amorphous is red, crystalline is blue) annealed at 600°C; arrow-shaped a/c interface is represented by yellow atoms and formation of defects (twins) is shown as white spheres

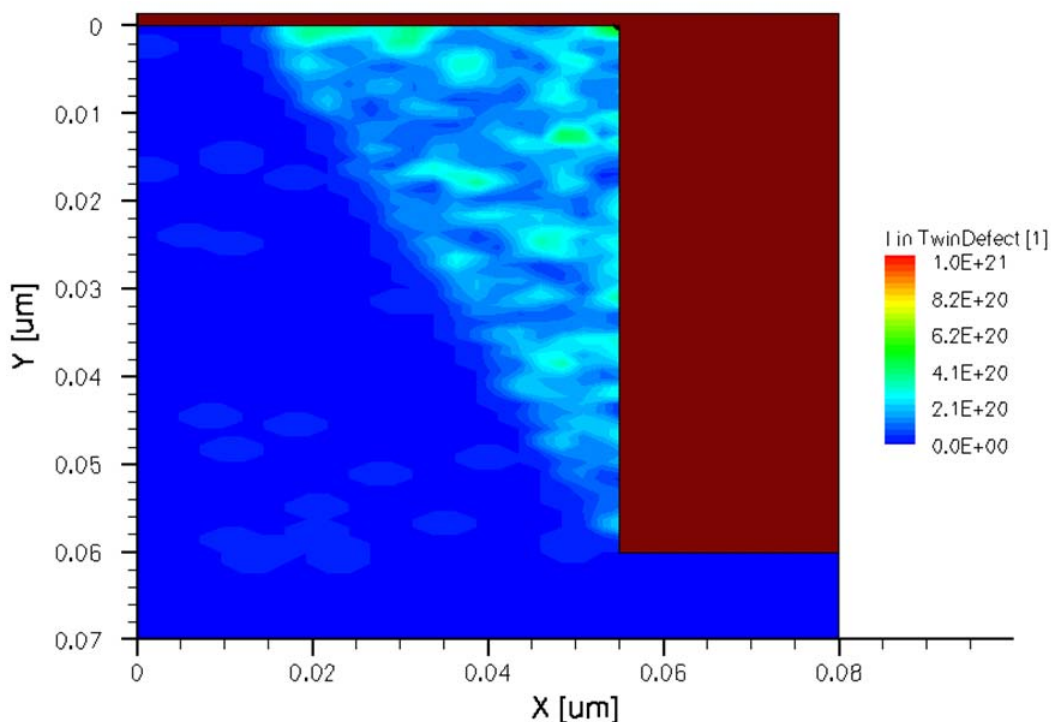


Figure 63 Concentration of twin defects representing defective silicon formation when SPER is in an amorphous region close to  $\text{SiO}_2$  (silicon is blue,  $\text{SiO}_2$  is brown)

Figure 62 on page 456 and Figure 63 show two examples where twin-defect formation is involved. Figure 62 represents the formation of defects during the SPER of a thin silicon fin. Figure 63 shows the defective triangular-shaped region, bounded by a (111) plane, typical of SPER close to  $\text{SiO}_2$ -filled trenches.

## Redistributing Damage

The recrystallization event forces all  $IV$  pairs inside an amorphous defect to recombine. The  $I$  or  $V$  excess is redistributed to the neighboring amorphous boxes if any. Otherwise, the excess is recombined at the surface. If there is no free surface/interface neighboring amorphous boxes, it is left as point defects. If the recrystallization front has crossed several elements, the amount of excess point defects can be high. When the defects are deposited in the crystalline silicon, they grow and ripen into extended defects depending on the annealing conditions.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Amorphization and Recrystallization

#### Parameters

The parameter `depositExcessDamage` controls whether to redistribute the excess or to discard it. In simulations with buried amorphous layers, setting this parameter to `true` is suggested:

```
sprocess> pdbGet KMC Si Damage depositExcessDamage
0
```

#### Impurity Sweep/Deposit

The recrystallization process may affect the impurity concentration. The recrystallization front moves indium and other dopants away, changing the concentration profiles [37][38]. To model this effect, the amorphous defects transfer impurities during recrystallization:

- Dopants usually (`recrysDeposit`) remain in the box or move away with the recrystallization front (see [Figure 64 on page 459](#)). The two available models for this movement are `Elements` and `Hops`, chosen by the `RedistributionModel` parameter:
  - The `Elements` model takes all the  $n$  particles in one internal element and moves  $n \times \text{recrysDeposit}$  to the adjacent one. If moving the dopant with the recrystallization front increases the concentration of the neighboring element more than a limit (`recrysMaxTotal`), it will be deposited in the current element, no matter what its moving probability.
  - The `Hops` model goes particle-by-particle inside the affected element and decides whether the particle should be displaced a second neighbor distance, depending on `recrysDeposit`. If the particle is not displaced, it remains where it was. The algorithm continues with the next particle (which may still be the same one, pushing it again through the adjacent element little by little) until no more particles remain. To prevent the concentration of displaced particles being too high, the algorithm forces the deposit probability to be 1 when a particle has 25 or more dopant neighbors. The algorithm corrects this probability by linear interpolation starting when the number of neighbors is a given a percentage of 25. This percentage is controlled by the parameter `recrysDepositThreshold`.
- When the box is recrystallized, if the remaining dopant concentration is bigger than the solubility limit (`C0_recrysMaxActive`, `E_recrysMaxActive`) after SPER, the extra dopants are deposited as impurity clusters. These clusters have a limited size, and there are two different models to deposit these clusters depending on whether `recrysMaxSize` is defined.

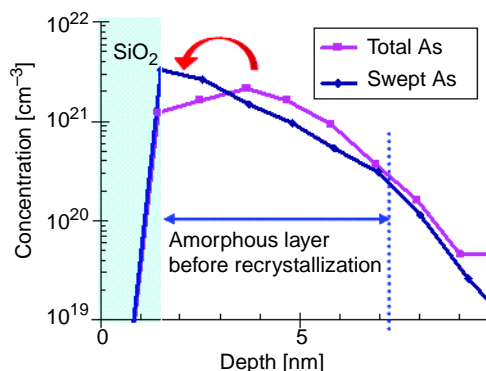


Figure 64 Impurity sweep example showing that arsenic has been pushed through the surface during recrystallization or SPER

The parameters for the recrystallization model are defined only for impurities in silicon (or other full material). `P_recrysDeposit` and `E_recrysDeposit` define (prefactor and energy) the probability for a dopant remaining in the same box after the recrystallization front passes. Setting this value to 1 disables the swept of impurities. `recrysMaxTotal` establishes the maximum concentration piled up during SPER. `recrysMaxActive` is the maximum allowed concentration of an active dopant in the recrystallized areas. Finally, if `recrysMaxSize` is defined (and it is by default), the old model to limit the maximum size of the deposited impurity clusters will be used. To undefine this parameter, use:

```
sprocess> pdbUnSetDouble KMC Si B recrysMaxSize
```

This instructs Sentaurus Process KMC to use the new model to deposit impurity clusters after SPER. This model deposits the clusters specified in `recrysDeposit_Complex` with the probabilities defined there.

Finally, the active dopants after SPER are deposited as substitutional impurities, but you can change this default using `recrysDeposit_Active`. This parameter accepts a list of impurities and impurity pairs with the probability to be deposited. For example:

```
sprocess> pdbSet KMC Si F recrysDeposit_Active F .1
sprocess> pdbSet KMC Si F recrysDeposit_Active Fi .9
```

This deposits 90% of the ‘active’ fluorine as `Fi`, and 10% as `F`.

**NOTE** Specifying a high probability for a cluster with a number of dopants greater than 1 does not necessarily means that you will obtain only that cluster. For example, if you specify that `B2I` should be 100% of the deposited clusters, but Sentaurus Process KMC finds only one boron particle in an element, Sentaurus Process KMC will not form a `B2I`.

## Parameters

The recrystallization parameters for dopants can be obtained as:

```
sprocess> pdbGet KMC Si As P_recrysDeposit
0.3
sprocess> pdbGet KMC Si As E_recrysDeposit
0.0
sprocess> pdbGet KMC Si As recrystMaxActive
1e+21
sprocess> pdbGet KMC Si As recrystMaxSize
4
sprocess> pdbGet KMC Si B recrystDeposit_Complex
B3I3 .40 B2I3 .30 BI2 .30
sprocess> pdbGet KMC Si B recrystDeposit_Active
B 1.0
```

To see which model is being used, use:

```
sprocess> pdbGet KMC Si Damage RedistributionModel
Elements
```

The concentration thresholds associated with each model are:

```
sprocess> pdbGet KMC Si B recrystMaxTotal
2e+22
sprocess> pdbGet KMC Si B recrystDepositThreshold
75
```

---

## Impurity Clusters

At certain concentrations, dopants are electrically inactive in crystalline silicon [7]. At the same time, high  $I$  concentration can make a fraction of boron electrically inactive even when its concentration is below its solubility [39]. This phenomena can be explained by a  $B_mI_n$  clustering mechanism [15][40] or dopant precipitation [7]. Sentaurus Process KMC considers these mechanisms, implementing the impurity clusters.

Recent studies [41] show that boron precipitation in amorphous silicon occurs through formation of a boron complex, thereby making the inclusion of impurity clusters in amorphous materials necessary. Consequently, pure dopant clusters,  $B_n$ , are allowed in amorphous materials and other materials modeled as `simple`.

The  $A_nB_o...X_m$  impurity clusters allow powerful modeling of the interaction of several impurities between them. For example, fluorine–boron clusters ( $F_nB_oI_m$  and  $F_nB_oV_m$ ) can be tried to explain the effects of boron coimplanted with fluorine, or  $As_nP_oV_m$  clusters to allow a satisfactory explanation, as seen in [52]. Nevertheless, the most common use of impurity

clusters is the traditional one where only one dopant is present. Consequently, except where indicated, the description of impurity clusters that follows assumes that the clusters are in the more common form  $A_nX_m$  with only one impurity involved. Starting with Version H-2013.03, impurity clusters have a simple model for diffusion, that is, they can migrate. For more information, see [Diffusion on page 462](#).

Finally, impurity clusters do not need to be neutral. Consequently, the charge state of each impurity cluster can be defined by using the parameter `e0_Complex`. When needed, an impurity cluster with a particular charge as  $A_nX_m^{\text{charge}}$  will be denoted. In addition, clusters can react with charged particles, as long as the reaction is not between a cluster and a particle with the same sign, in other words, it is not an electrostatic repulsive reaction.

To simplify the following descriptions, this section describes, the  $A_nX_m$  clusters with only one impurity, and neutral reactions (in other words, reactions similar to  $A_nX_m^a + AX^b \leftrightarrow A_{n+1}X_{m+1}^c$ ,  $a + b = c$ ). To see how the model works when this is not the case, see [Charge Dependency on page 473](#).

**NOTE** Since P is used both for *positive* and *phosphorus*, clusters containing phosphorus cannot have the P at the end of the cluster name. For example, AsIP will be interpreted as a positive interstitial arsenic, while AsPI or PAsI will be a phosphorus–arsenic–interstitial cluster; the same is true for AsP, PAs, and so on.

---

## Shape

An impurity cluster is an irregular agglomeration of impurities (A, B, ...) with or without interstitials and vacancies (X) that can be written as  $A_nB_o...X_m$ , with n impurity atoms of type A, o of type B, and so on, and m Is or Vs. If  $m = 0$ , it is a pure impurity cluster (the only ones allowed in `simple` materials).

For Sentaurus Process KMC, the notation  $A_nB_o...X_m$  means any possible configurations with n impurities of type A, o of type B, and so on, and m interstitial (vacancy) atoms. The interstitial (vacancy) atoms can be both silicon self-interstitials or dopant atoms in an interstitial position. Since Sentaurus Process KMC assumes all the  $A_nB_o...X_m$  configurations to be the same with only one effective formation energy, A,B, ... are represented always as a substitutional but inactive dopant or impurity, and X as a silicon interstitial or vacancy.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Impurity Clusters

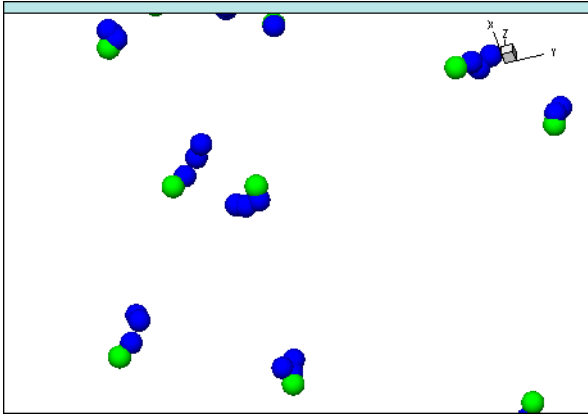


Figure 65 AsV impurity clusters simulated with Sentaurus Process KMC; blue is arsenic and green is vacancy

---

## Diffusion

A diffusion mechanism has been added to impurity clusters. This means that impurity clusters can perform migration hops similar to the ones performed by point-defects, impurities, and dopants. An impurity cluster migration event involves all its constituent particles: The whole cluster is displaced. The particle coordinates are modified isotropically at a fixed distance of  $\lambda = 0.384$  nm in the orthogonal direction (parallel to the x-axis, y-axis, or z-axis).

The migration rate for impurity clusters is assumed to be:

$$v_m = v_{0,m} \times \exp(-E_m/k_B T) \quad (701)$$

where  $v_{0,m}$  is the prefactor for each cluster, called `Dm_Cluster` in the parameter database, and  $E_m$  is the migration energy for each cluster, specified as `Em_Cluster` in the PDB.

## Parameters

As previously stated, the names of the diffusion parameters for impurity clusters are `Dm_Cluster` and `Em_Cluster`:

```
sprocess> pdbGet KMC Si As Dm_Complex As2V  
1e-3
```

```
sprocess> pdbGet KMC Si As Em_Complex As2V  
1.5
```



## Limitations

The migration events for impurity clusters, although similar to the ones for *single* particles, do not share all their features. In particular, the following limitation applies:

- The diffusivity for impurity defects is global, isotropic, and constant. There are no SiGe, stress, strain, or charge dependencies on diffusivity.
- Impurity defects do not interact with interfaces at all (Si–SiO<sub>2</sub> and so on). All interfaces are considered mirrors.
- Periodic boundary conditions or mirror conditions are correctly applied to the limits of the simulation box.
- There is no recombination probability at the boundaries. This means that the parameters `sinkProbTop`, `sinkProbBottom`, `sinkProbBack`, `sinkProbFront`, `sinkProbLeft`, and `sinkProbRight` do not apply to diffusing impurity clusters.
- Speedup migration does not apply to impurity cluster diffusion: no long hops or double hops.

## Growth

Impurity clusters grow trapping neutral mobile particles (see [Figure 66](#)).

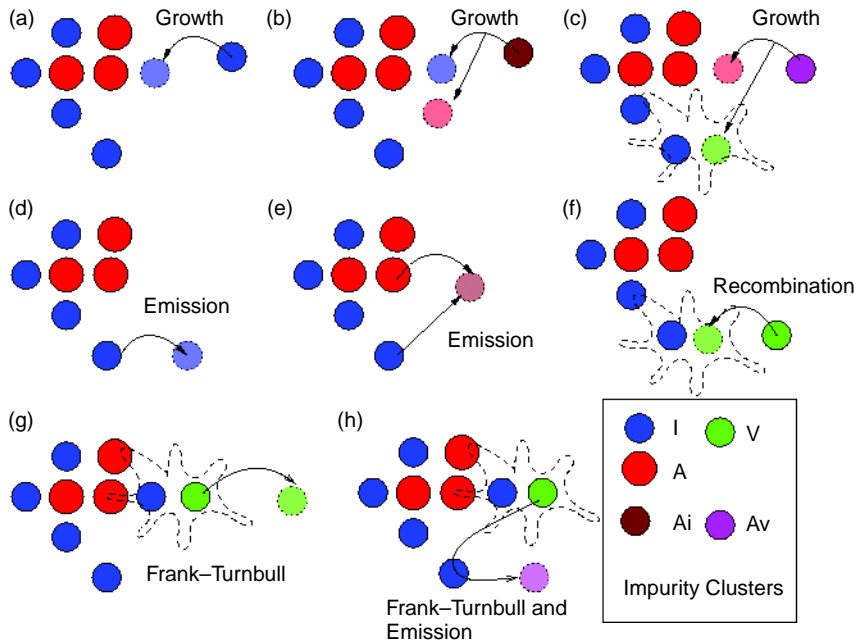


Figure 66 Impurity clusters are disordered agglomerations of dopants and silicon point defects that trap and emit particles. FT mechanisms and IV recombinations are also possible.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Impurity Clusters

For an  $A_nI_m$  cluster, both  $I$  and  $A_i$  particles can be trapped:



The trapping is not automatic as it was for extended defects. In extended defects, the binding energy is always positive, so the trapping is always allowed. For impurity clusters, the cluster can grow in both  $I$ s ( $V$ s) or dopants. The energy between the initial and final states is not always favorable. Sentaurus Process KMC computes the probability for an impurity cluster  $A_nI_m$  to trap an  $I$  or  $A_i$  as:

$$P_{capture} = \exp\left(-\frac{E_{capture}}{k_B T}\right) \quad (703)$$

where:

$$E_{capture}^{AnIm} = E_{barrier}(A_nI_m) + \max(0, -E^{AnIm}_b) \quad (704)$$

and  $E_{barrier}(A_nI_m)$  is an optional energy barrier.

The binding energies  $E^{AnIm}_b$  are computed using the potential impurity cluster energies:

$$E^{AnIm}_b(I) = E_{pot}(A_nI_{m+1}) - E_{pot}(A_nI_m) \quad (705)$$

$$E^{AnIm}_b(A_i) = E_{pot}(A_{n+1}I_{m+1}) - E_{pot}(A_nI_m) + E_{pot}(A_i) \quad (706)$$

The potential energy for the neutral  $A_i$ , assuming that the substitutional  $A$  is negative, is given by  $-E_b(A_i^-) - e(-, 0)(A_i)$ , where the binding energy includes the pressure and Ge corrections. The minus sign accounts for the fact that the binding must have a sign that is opposite that of the potentials.

These potentials energies are computed as:

$$E_{pot}(A_nI_m) = E_{pot}^0(A_nI_m) + P\Delta V_{pot}(A_nI_m) \quad (707)$$

where  $E_{pot}^0(A_nI_m)$  is specified in the parameter database for each impurity in silicon as `Etotal_Complex`.  $\Delta V_{pot}(A_nI_m)$  is the activation volume to take into account the hydrostatic pressure dependency, also defined for each impurity cluster size as `VF_Complex`. The energy barriers are called `EbarrierIV_Complex` and `EbarrierDopant_Complex`. The `EbarrierIV` is defined for emission and capture of interstitials and vacancies, and `EbarrierDopant` for dopants or paired dopants. For example, to set the potential energy of a BIC, such as  $BI_2$  to some value:

```
pdbGet KMC Si B Etotal_Complex BI2 <n>
```

and, for As<sub>4</sub>V:

```
pdbGet KMC Si As Etotal_Complex As4V <n>
```

## Initial Seeds

The clusters  $A_2I$ ,  $AI_2$ ,  $A_2I_2$ , and  $A_2$  are the initial seeds for the impurity cluster ripening. The formation of  $A_2$  is discussed in [Percolation on page 465](#). The others are formed by the reactions:

- $A^a + A_i^b \leftrightarrow A_2I^c$
- $A_i^a + I^b \leftrightarrow AI_2^c$
- $A_i^a + A_i^b \leftrightarrow A_2I_2^c$
- $A^a + A^a \leftrightarrow A_2^c$

where  $a$  and  $b$  are the charge states for the reactants, and  $c$  for the result. All these reactions provide a cluster starting with impurities or impurity pairs. In the cases where  $a + b \neq c$  for the first reactions or  $2a \neq c$  for the last one, the reaction is not neutral, and the special considerations of [Charge Dependency on page 473](#) should be taken.

These initial seeds can be enabled and disabled independently by the parameter `ReactionsPointDefect`, as explained in [Enabling and Disabling Interactions on page 412](#).

## Percolation

Some dopants deactivate without visible diffusion when they are in high concentrations [\[42\]](#). They also can form impurity clusters [\[43\]](#). Sentaurus Process KMC models this deactivation allowing the substitutional dopants to interact with impurity clusters or with other dopants right after its inclusion in the simulation (for example, after being implanted or selected).

As can react with As giving As<sub>2</sub>. Substitutional As does not migrate, so this reaction is only possible when two arsenic are close enough to each other. The higher the arsenic concentration, the higher this possibility. An As + As<sub>2</sub> reaction and As<sub>3</sub> + As reaction also are possible. These species also are immobile. They react only when they are close enough. Consequently, the probability of forming an As<sub>4</sub> cluster using this mechanism is low because it needs four As atoms close enough to each other. This probability increases with the concentration. With high concentration, the probability is not negligible, and the substitutional As react with each other forming As clusters and becoming inactive.

**NOTE** The reaction between two substitutional dopants to give an impurity cluster is the only exception to the rule that two particles with the same charge will not interact.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Impurity Clusters

In simple materials, such as amorphous silicon, this ‘percolation’ model is the only one allowing impurity clusters to be formed. Since all particles are neutral in simple materials, the percolation reaction does not constitute an exception there.

## Parameters

The potential and binding energies for impurity clusters are defined only in materials with full and simple modeling, including amorphous. They are defined in arrays whose index is the cluster name. For example, for F clusters:

```
sprocess> pdbGet KMC Si F Etotal_Complex
FV2      -4.20
F2       -0.5    F2V      -4.63    F2V2     -7.07
F3       -1     F3V      -7.08    F3V2     -9.04
F4       -1.5   F4V      -7.12    F4V2     -11.47
F5       -3     F5V      -8.5     F5V2     -13.29
F6       -4.5   F6V      -9.7     F6V2     -16.09
          F7V      3
          F12     -4.20
          F2I     -4.63    F2I2     -7.07
          F3I     -7.08    F3I2     -9.04
          F4I     -7.12    F4I2     -11.47
          F5I     -8.5     F5I2     -13.29
          F6I     -9.7     F6I2     -16.09
          F7I      3
```

A particular value for only one element also can be obtained. The current potential energy for As<sub>4</sub>V is:

```
sprocess> pdbGet KMC Si As Etotal_Complex As4V
-5.4
```

The barriers are, by default, not defined:

```
sprocess> pdbGet KMC Si F EbarrierIV_Complex
sprocess> pdbGet KMC Si F EbarrierDopant_Complex
```

The charge value for the clusters is retrieved with:

```
sprocess> pdbGet KMC Si F e0_Complex
sprocess> pdbGet KMC Si B e0_Complex
B3  0      B3I  0      B3I2  0      B3I3  0
B2  0      B2I  0      B2I2  0      B2I3  0
          BI2  0
```

No value means that they are neutral.

**NOTE** The impurity cluster model and the activation or deactivation of clusters can be calibrated further fitting the potential energies. For further accuracy, Advanced Calibration also can be used.

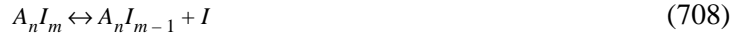
When a particular energy for a particular configuration is not specified (in other words, when input in the parameter file exists for an  $A_n I_m$  or  $A_n V_m$  impurity cluster), Sentaurus Process KMC assumes this configuration to be unstable. When a barrier energy is not specified, a value of 0 eV (no barrier) is assigned.

All impurities are allowed to form impurity clusters with  $I$ ,  $V$ , or both. If an impurity does not form impurity clusters, the default can be changed, modifying the parameters and the interactions (see [Interactions on page 475](#)).

---

## Emission

Impurity clusters can emit both neutral interstitials (vacancies) or mobile dopants:



Sentaurus Process KMC computes the emission frequencies as:

$$v_{emission} = v_{0,emission} \times \exp\left(-\frac{E_{emission}}{k_B T}\right) \quad (710)$$

The emission energies are:

$$E_{emission}(I) = E_m(I) + E_{barrier}(A_n I_m) + \max(0, E^{AnIm_b}(I)) \quad (711)$$

$$E_{emission}(A_i) = E_m(A_i) + E_{barrier}(A_n I_m) + \max(0, E^{AnIm_b}(A_i)) \quad (712)$$

$E_m$  is the migration energy of the emitted species, and both  $E^{AnIm_b}(I)$  and  $E^{AnIm_b}(A_i)$  have been shown above. The emission prefactors for dopant and I or V emission depend on the model used.

When `UseCaptVol_Complex` is set to `true`, the emission prefactors are proportional to the capture volumes of the impurity clusters:

- $v_{0,emission}(A_i) = K(A_i) V_{capt}(A_n I_m)$
- $v_{0,emission}(I) = K(I) V_{capt}(A_n I_m)$

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Impurity Clusters

$V_{capt}(A_nI_m)$  is the capture volume for each impurity cluster, defined in the PDB as `CaptVol_Complex`, and the constant  $K$  is a parameter named `D0_Cluster` in the PDB.

**NOTE** The unit of the capture volumes is the capture volume of one single point defect.

If `UseCaptVol_Complex` is set to `false`, Sentaurus Process KMC uses the default old model, in which the capture volumes are internally fixed to be  $m$  for  $I$  emission and  $\min(n, m)$  for  $A_i$  emission. The use of this default model is not suggested, since it does not lead to microscopic reversibility.

When a particle is emitted, the impurity cluster tests if the number of remaining particles is enough to maintain the cluster. If there is only an interstitial (vacancy) or an interstitial and a dopant, the cluster dissolves leaving an interstitial or a mobile, paired dopant, respectively.

## Parameters

The prefactor constants are:

```
sprocess> pdbGet KMC Si As D0_Cluster
As,AsV 2.1
As,V 10
sprocess> pdbGet KMC Si B D0_Cluster
B,Bi 3
B,I 150
```

The notation for these prefactors is as follows: two strings are needed, separated by a comma. The second string represents the emitted particle for which the parameter is being defined. The first string represents the type of cluster. This first string is needed to define a different prefactor for emitting a  $B_i$  from a B cluster rather than from a hypothetical BF cluster. For example, the emission of  $B_i$  from a  $B_2I_2$  will use `B,Bi`, while from a  $B_2F_3I_2$  will use `BF,Bi`. This last one can be defined in `KMC Si B` and `KMC Si F`, but if defined in both of them with different values, it will produce an error.

The capture volume parameters are:

```
sprocess> pdbGet KMC UseCaptVol_Complex
0
sprocess> pdbGet KMC Si B CaptVol_Complex
B3 1 B3I 1 B3I2 2 B3I3 3
B2 1 B2I 1 B2I2 2 B2I3 2
BI2 1
```

The notation for capture volumes is as following: if only the cluster is specified, that applies to all emissions for that particular size, but if a cluster size and a particular particle are specified,

separated by a comma, that applies to that cluster emitting only that particle. For example, the following applies only to emission if I by B<sub>2</sub>I<sub>2</sub>:

```
pdbSet KMC Si B CaptVol_Complex B2I2,I 6
```

The rest of the parameters needed for emission are the same as in [Growth on page 463](#).

---

## Recombination

Impurity clusters can trap incoming neutral Vs (*I*s) and recombine them with internal Is (*V*s):



The capture probability is:

$$P_{capture} = \exp\left(-\frac{E_{capture}}{k_B T}\right) \quad (714)$$

The associated energies are:

$$E^{AnIm}_{capture} = E^{AnIm}_b - E_{pot}(V) - E_{pot}(I) \quad (715)$$

and:

$$E^{AnIm}_b = E(A_n I_{m-1}) - E(A_n I_m) \quad (716)$$

After the *IV* pair recombination, the cluster size is tested and, if necessary, dissolved, as previously explained.

## Parameters

The parameters used for recombination of point defects are the same as in [Growth on page 463](#).

---

## Frank–Turnbull Mechanism

A generalized Frank–Turnbull (FT) mechanism is the emission of a neutral *V* (*I*) from an *A<sub>n</sub>I<sub>m</sub>* (*A<sub>n</sub>V<sub>m</sub>*) impurity cluster by the formation of a Frenkel pair (*IV*):



## 5: Atomistic Kinetic Monte Carlo Diffusion

### Impurity Clusters

or:



Sentaurus Process KMC includes the FT mechanism to maintain microscopic reversibility. Since impurity clusters recombine incoming *I*s or *V*s, the opposite mechanism (FT) also is needed. Usually, this mechanism is unfavorable, but for some particular configurations, the energetic differences between them can enable the formation of *IV* pairs and, therefore, the emission of particles using the FT mechanism (see [Figure 67](#)).

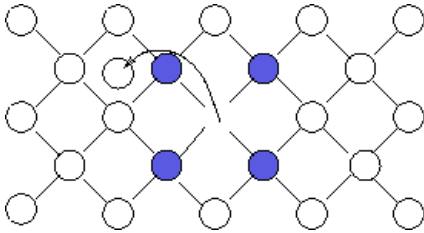


Figure 67 Example of FT mechanism: an  $As_4$  cluster can emit an interstitial to become an  $As_4V$  impurity cluster: blue is arsenic and white is silicon

The vacancy (interstitial) emission frequency is computed as:

$$v_{emission} = v_{0,emission} \times \exp\left(-\frac{E_{emission}}{k_B T}\right) \quad (719)$$

being:

$$E_{emission}(V) = E_m(V) + \max(0, E^{AnIm_b}(V)) \quad (720)$$

and:

$$E^{AnIm_b}(V) = E_{pot}(I) + E_{pot}(V) + E_{pot}(A_n I_{m+1}) - E_{pot}(A_n I_m) \quad (721)$$

where the potential energies for the clusters and the point defects include pressure and Ge corrections.

## Parameters

The parameters used are the same as in [Growth on page 463](#). The potential energies for interstitial and vacancies are specified for the material as *Ef*:

```
sprocess> pdbGet KMC Si I Ef
4.0
sprocess> pdbGet KMC Si V Ef
3.8
```



The corrections to the potential energies for I and V are  $\nu_F$  and  $E_fGe$  for pressure and Ge, respectively:

```
sprocess> pdbGet KMC Si I EfGe
I 0.0
sprocess> pdbGet KMC Si I VF
I 0.0
```

The prefactor for I and V emission is computed automatically for impurity clusters with only one dopant (for example,  $B_nI_m$  or  $As_nV_m$  clusters) and must be specified for other cases. For example, in a case with  $AsPV$  clusters, the prefactors for Frank–Turnbull emission are specified as follows:

```
pdbSet KMC Si As D0_Cluster AsP,V 50
pdbSet KMC Si As D0_Cluster AsP,I 50
```

The following is also valid:

```
pdbSet KMC Si P D0_Cluster AsP,V 50
pdbSet KMC Si P D0_Cluster AsP,I 50
```

---

## Complementary Recombination

Some impurities diffuse using both the interstitial and vacancy mechanisms. For these cases, the impurity clusters can react with both of them. For example, an  $A_nV_m$  impurity cluster can grow trapping  $AsV$ , as previously explained, and can interact with an incoming  $As_i$ , trapping the  $As$  and recombining the  $I$  with one internal vacancy. This implies to take into account the reaction:



These complementary recombinations of neutral particles are allowed with a probability of:

$$P_{capture} = \begin{cases} \exp(-E_{capture}/(k_B T)) & E_{capture} > 0 \\ 1 & E_{capture} \leq 0 \end{cases} \quad (723)$$

The capture energies are computed as:

$$E_{capture} = \begin{cases} E_{pot}(A_{n+1}V_{m-1}) - E_{pot}(A_nV_m) - E_f(V) - E_f(I) - E_{pot}(A_i) & m > 0 \\ E_{pot}(A_{n+1}V_m) - E_{pot}(A_nV_m) - E_{pot}(A_i) + E_m(I) - E_m(A_i) & m \equiv 0, n > 1 \\ E(A_i \rightarrow A) & m \equiv 0, n \equiv 1 \end{cases} \quad (724)$$

where  $E(A_i \rightarrow A)$  is an internal parameter that cannot be changed.

## Parameters

The parameters used are the same as in [Frank–Turnbull Mechanism on page 469](#). The potential energy for the paired dopant is the binding energy of the pair corrected with the Fermi-level dependency.

## Complementary Emission

To maintain microscopic reversibility, the reaction reverse to the complementary recombination must be defined (see [Figure 68](#)).

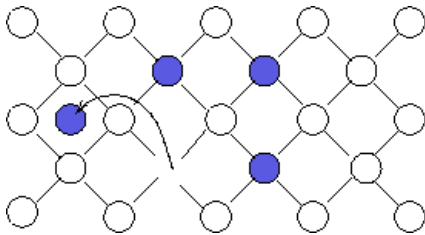
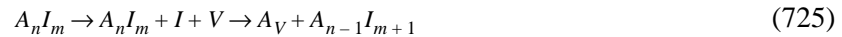


Figure 68 Example of complementary emission: the cluster emits an interstitial that takes an impurity and generates a vacancy; blue is arsenic and white is silicon

The equation for this process is:



Its emission frequency is computed using the emission frequency equation:

$$E_{emission} = E_m(A_V) + \max(0, E^{A_n I_m}_b(A_V)) \quad (726)$$

where:

$$E^{A_n I_m}_b(A_V) = E_f(I) + E_f(V) + E_{pot}(A_{n-1} V_{m+1}) - E_{pot}(A_n I_m) \quad (727)$$

## Parameters

The parameters used are the same as in [Recombination on page 469](#).

For simple impurity clusters, those with only one impurity ( $B_n I_m$ ,  $As_n V_m$ , and so on), the prefactor for emission is calculated automatically. For complex impurity clusters, ( $As_n P_o V_m$  and so on), the prefactor must be written explicitly:

```
pdbSet KMC Si As D0_Cluster AsP,Asi 50
```

---

## Charge Dependency

### Neutral Reactions

In the previous discussions, all the impurity clusters are assumed to be neutral and, consequently, there are no explicit charge Fermi-level dependencies. Nevertheless, there are nonexplicit dependencies. In particular, for clusters emitting impurity-paired dopants, the emission energy depends on the binding of the paired dopants, which, in turn, contains a Fermi-level dependency.

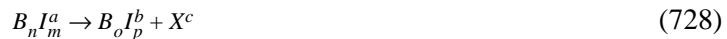
The Fermi-level dependency of the binding energy is related to the level of the neutral-paired dopant in the band gap. This level also depends on the temperature and the bandgap narrowing.

All the previous dependencies are included by default, except the indirect dependency on the bandgap narrowing, which can be switched off and on using:

```
pdbSet KMC <material> BandGap Correct_Complex <true/false>
```

### Nonneutral Reactions

Assume the following reaction:



The potential energy for  $B_n I_m^a$  is defined with respect to a ground state that produces the impurity cluster in a neutral reaction. This means that:

$$nB^- + mV^0 + \begin{cases} -(a+n)e^- \Rightarrow a+n < 0 \\ (a+n)h^+ \Rightarrow a+n > 0 \end{cases} \quad (729)$$

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Impurity Clusters

is the ground state for  $As_nV_m^a$ . Consequently, an account of holes and electrons must be followed during the reaction. In particular, calling the initial cluster  $i$  and the final one  $f$ , these accounts are:

$$\begin{aligned} \blacksquare \quad h_i^+ &= \begin{cases} a+n \Rightarrow a+n > 0 \\ 0 \Rightarrow a+n < 0 \end{cases}, \quad e_i^- = \begin{cases} 0 \Rightarrow a+n > 0 \\ -a-n \Rightarrow a+n < 0 \end{cases} \\ \blacksquare \quad h_{f1}^+ &= \begin{cases} b+o \Rightarrow n+o < 0 \\ 0 \Rightarrow b+a < o \end{cases}, \quad e_{f1}^- = \begin{cases} 0 \Rightarrow b+o > 0 \\ -b-o \Rightarrow b+o < 0 \end{cases} \end{aligned}$$

The final state must account for the charge in the emitted particle. Calling  $d$  the charge of the substitutional dopant of the emitted species  $X$  (in other words,  $d = -1$  if  $X^c = B_f^-$  or  $d = 0$  if  $X^c = I^c$ ), the final accounts for holes and electrons are:

$$\begin{aligned} \blacksquare \quad h_f^+ &= h_{f1}^+ + \begin{cases} c-d \Rightarrow c-d > 0 \\ 0 \Rightarrow c-d < 0 \end{cases} \\ \blacksquare \quad e_f^- &= e_{f1}^- + \begin{cases} 0 \Rightarrow c-d > 0 \\ d-c \Rightarrow c-d < 0 \end{cases} \end{aligned}$$

This allows writing the first energetic term for the binding energy as:

$$E_{charges} = (e_i^- - e_f^-)(E_g - e_F) + (h_i^+ - h_f^+)e_F \quad (730)$$

The second term is the obvious difference in potential energies:

$$E_{clusters} = E_{pot}(B_nI_m) - E_{pot}(B_oI_p) \quad (731)$$

The binding energy of the emitted particle is also needed, including the transition from the *neutral* state  $d$  to the current emitted state:

$$E_b(X^c) = E_b(X^d) + E \left( X^d + \begin{cases} (d-c)e^- \Rightarrow d-c > 0 \\ (c-d)h^+ \Rightarrow c-d > 0 \end{cases} \rightarrow X^c \right) \quad (732)$$

In addition, only in cases where a Frank–Turnbull emission is involved ( $X^c = V^c$  or  $X^c = BV^c$ ), the pair recombination energy is:

$$E_{recom} = E_f(I) + E_f(V) \quad (733)$$

This gives a binding energy of:

$$E^{BnIm_b}(X^c) = -E_{charges} - E_{clusters} - E_b(X^c) + E_{recom} \quad (734)$$

That finally allows computing the emission energy:

$$E_{emission}(X^c) = E_m(X^c) + E_{barrier}(B_nI_m) + \max(0, E^{BnIm_b}(X^c)) \quad (735)$$

**NOTE** All the previous energies (potential, binding, migration, and so on) are computed including hydrostatic pressure, SiGe, and bandgap narrowing local corrections.

---

## Interactions

You can modify all the interactions involved in the impurity cluster model. The impurity clusters can be enabled or disabled with the Boolean parameter `Implement_Complex`. For example, to disable the  $F_n V_m$  impurity clusters, use:

```
pdbSet KMC Si F Implement_Complex 0
```

When the impurity clusters are enabled, you can set and unset the particular reactions using the `ReactionsCluster` parameter:

```
pdbSet KMC Si <dopant> ReactionsCluster <reaction> <true/false>
```

where `reaction` is a string with two fields, separated by a comma. The first field is the name of the impurity cluster, and the second is the name of the reacting particle. Spaces are not allowed between these fields. The setting or unsetting of these reactions enables or disables the specified reactions and its reverse ones. This is performed to maintain the microscopic reversibility. For example, to disable the capture of a vacancy by  $As_2$  to growth to  $As_2V$ :

```
pdbSet KMC Si As ReactionsCluster As2,V false
```

This also disables the inverse reaction, in other words, the emission of  $V$  by  $As_2V$ . To enable the recombination of  $I$  by an  $As_4V$  cluster:

```
pdbSet KMC Si As ReactionsCluster As4V,I true
```

This reaction also enables the FT emission of  $I$  by  $As_4$ , that is,  $As_4 \rightarrow As_4V + I$ .

Enabling a reaction does not mean that the reaction will happen; it depends on the energetics. If the reaction is unfavorable, it will not occur (but the inverse will). Disabling a reaction will forbid the reaction to occur, even if it is described by the parameters as favorable. Any reaction not listed in `ReactionsClusters` is disabled.

## Complex Impurity Clusters

To enable impurity clusters with more than one dopant (for example, an  $As_2PV$ ), the switches for both the As and P clusters should be on:

```
pdbSetBoolean KMC Si As Implement_Complex 1
pdbSetBoolean KMC Si P Implement_Complex 1
```

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Impurity Clusters

To enable the cluster reaction  $As_2 + PV \leftrightarrow As_2PV$  (assuming  $As_2$  is predefined), use the `As` or the `P` to define the reaction. If both are used with different values, an error message will be displayed. In this example, they are defined in `As`:

```
pdbSet KMC Si As ReactionsCluster As2,PV true
```

The energy and capture volume of this new cluster must be defined as usual:

```
pdbSet KMC Si P Etotal_Complex PAs2V -3.0
pdbSet KMC Si P CaptVol_Complex PAs2V 1.3
```

The `I`, `V`, and `PV` emission prefactors are:

```
pdbSet KMC Si P D0_Cluster PAs,I 0.5
pdbSet KMC Si P D0_Cluster PAs,V 0.5
pdbSet KMC Si P D0_Cluster PAs,PV 0.1
```

Finally, for `AsV` emission from the cluster  $As_2PV$ , allow the reaction  $AsP + AsV \leftrightarrow As_2PV$  by defining:

```
pdbSet KMC Si P ReactionsClusters PAs,AsV true
```

This also enables the formation of the clusters through the reaction of these particles.

## Parameters

To show the parameters involved in the impurity cluster reactions, arsenic is used as an example. `AsV` clusters are allowed:

```
sprocess> pdbGet KMC Si As Implement_Complex
1
```

Since `AsV` clusters are allowed in the Sentaurus Process KMC simulation, they require some enabled reactions. The reactions are explained in [Percolation on page 465](#) and allow deactivation without arsenic diffusion:

```
sprocess> pdbGet KMC Si As ReactionsCluster
As2,As true
As3,As true
```

Reactions to grow capturing `V` and to shrink emitting them are:

```
As2,V true
As3,V true
As4,V true
```

Capture or emission of AsV is:

```
As2,AsV true
As3,AsV true
```

Recombination of interstitials and Frank–Turnbull emission of interstitials are:

```
As2V,I true
As3V,I true
As4V,I true
```

Recombination of interstitials, capture of arsenic, and emission of As<sub>i</sub> are:

```
As2V,Asi true
As3V,Asi true
```

The following rules must be satisfied to allow a reaction between a particle and an impurity cluster:

- The first field must be a correct impurity cluster, and the second must be a defined particle.
- The particle must be an interstitial or a vacancy of a paired dopant. The resulting cluster must be defined (in `Etotal_Complex` and `CaptVol_Complex`).
- Only nonrepulsive interactions are allowed, except for percolation. The reactions do not need to conserve the charge.

Impurity clusters require an initial impurity cluster or ‘seed’ to begin the ripening. This initial cluster is formed with the reactions of two particles. These reactions are explained in [Enabling and Disabling Interactions on page 412](#).

---

## Setting Up Impurity Clusters in a Material

To set up an impurity cluster in a material (for example,  $B_n$  in amorphous silicon), the following PDB parameters must be created:

- First, the cluster must be allowed:

```
pdbSetBoolean KMC aSi B Implement_Complex true
```

- Second, an emission prefactor for the cluster, cluster potential energies, barriers, capture volumes, and stress corrections must be defined:

```
pdbSetDoubleArray KMC aSi B D0_Cluster { B 3.0 }
pdbSetDoubleArray KMC aSi B Etotal_Complex { B2 -0.45 B3 -2.5 }
pdbSetDoubleArray KMC aSi B EbarrierDopant_Complex { }
pdbSetDoubleArray KMC aSi B CaptVol_Complex { B2 1.5 B3 2.0 }
pdbSetDoubleArray KMC aSi B VF_Complex { }
```

## 5: Atomistic Kinetic Monte Carlo Diffusion

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- Third, for these clusters to form, you must introduce a reaction path:

```
pdbSetArray KMC aSi B ReactionsPointDefect { B,B true }
pdbSetArray KMC aSi B ReactionsCluster      { B2,B true }
```

- None of this will happen without a mobile particle allowing for growing and emission:

```
pdbSet KMC aSi B Dm B 3.0e-3
pdbSet KMC aSi B Em B 2.1
```

**NOTE** The impurity cluster parameters (energies, barriers, capture volumes, stress corrections) must be specified in the PDB only when the cluster is implemented (with `Implement_Complex true`). This saves many parameters in the description of impurities without impurity clusters.

---

## Fermi-Level Effects: Charge Model

Point defects ( $I$ ,  $V$ ) and impurity atoms ( $B$ ,  $As$ ) can appear in different charge states in silicon, while extended defects and impurity clusters have a fixed charge state in Sentaurus Process KMC. Impurity atoms are neutral in materials using the `simple` model.

For example, interstitials and vacancies can be triple negative, double negative, double positive, triple positive, neutral, positive, or negative. Some species and charged states are listed in [Table 54](#). You can customize these definitions. The maximum charge state for point defects is  $\pm 3$  and for impurity paired defects  $\pm 2$ .

Table 54 Species and charged states of Sentaurus Process KMC

I	$I^{+++}$ , $I^{++}$ , $I^+$ , $I^0$ , $I^-$ , $I^{--}$ , $I^{---}$ IPPP, IPP, IP, I, IM, IMM, IMMM
V	$V^{+++}$ , $V^{++}$ , $V^+$ , $V^0$ , $V^-$ , $V^{--}$ , $V^{---}$ VPPP, VPP, VP, V, VM, VMM, VMMM
As	$As^+$ , $As_i^+$ , $As_i^0$ , $AsV^+$ , $AsV^0$ , $AsV^-$ As, AsiP, Asi, AsVP, AsV, AsVM
B	$B^-$ , $B_i^+$ , $B_i^0$ , $B_i^-$ B, BiP, Bi, BiM
C	$C^0$ , $C_i^0$ C, Ci
F	$F^0$ , $FI^0$ , $FV^0$ F, FI, FV
Sb	$Sb^+$ , $Sb_i^0$ , $Sb_i^+$ , $SbV^-$ , $SbV^0$ , $SbV^+$ Sb, Sbi, SbiP, SbVM, SbV, SbVP



Table 54 Species and charged states of Sentaurus Process KMC

In	In <sup>-</sup> , In <sub>i</sub> <sup>0</sup> , In <sub>i</sub> <sup>-</sup> , InV <sup>0</sup> , InV <sup>-</sup> In, Ini, IniM, InV, InVM
P	P <sup>+</sup> , P <sub>i</sub> <sup>0</sup> , P <sub>i</sub> <sup>+</sup> , PV <sup>0</sup> , PV <sup>-</sup> , PV <sup>+</sup> P, Pi, PiP, PV, PVM, PVP

Charge states can be modeled using different approaches. The most intuitive approach is adding a charge ‘label’ to each particle. Nevertheless, because the migration energy (and maybe some other parameters) change with the charged state, each of these states requires a full set of parameters.

---

## Sentaurus Process KMC Approach

No charge label is defined for the particles. The charge is implicitly assumed in each particular particle, and there are different particles for each charged state. This implies the necessity of defining the interactions one by one, according not only with the particle type, but also with its charge state.

The charge is represented in a quasiatomistic approach to account for the fact that the electron transport is several orders of magnitude faster than the atomic transport. The charge magnitudes (for example, Fermi level and bandgap width) are associated with each internal box in the simulation. Consequently, there can be local changes between different boxes, but the charge magnitudes are considered to be homogenous in each Sentaurus Process KMC internal element.

---

## Assumptions

Sentaurus Process KMC takes the energy reference in the valence band. The following assumptions also are taken:

- Charge reactions are faster than structural reactions [44]. Consequently, the charges are updated instantaneously.
- Formation energy for neutral species (for example,  $E_f(I^0)$ ) are not dependent on the Fermi level. Sentaurus Process KMC takes the formation energies for neutral species as parameters using them to compute the energies for the nonneutral species.
- Potential energies for impurity clusters are not dependent on the Fermi level. For example, Sentaurus Process KMC defines the potential energy for  $As_n V_m^a$  as the energy returned by the system in the reaction  $nAs^+ + mV^0 + (n - a)e^- \rightarrow As_n V_m^a$  (assuming that  $n - a > 0$ ).
- The electronic level dependency with temperature is proportional to the bandgap temperature dependency. The same applies for the bandgap narrowing. This assumption allows Sentaurus Process KMC to establish proportionality relations to compute the

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Fermi-Level Effects: Charge Model

electronic levels and bandgap narrowing at different temperatures using a known value for one particular temperature.

- Substitutional dopants are always ionized; that is, substitutional boron is always  $B^-$  and substitutional arsenic  $As^+$ .
- The properties inside each Sentaurus Process KMC element are constant. Properties can change between internal elements.

For further references on similar KMC charge models, see [1][45][46].

---

## Formation Energies for Charged Species

Taking  $I^+$  as an example, in the reaction:



the energy needed to take an electron from an  $I^0$  and obtain  $I^+ + e^-$  is denoted as  $e(+,0)$ , and is measured from the valence band. The formation energy for a positive interstitial is:

$$E_f(I^+) = E_f(I^0) + e_F - e(+,0) \quad (737)$$

where  $e_F$  is the Fermi level. Consequently, the concentration between different interstitial charge species using as a reference the neutral concentration is:

$$\frac{[I^0]}{[I^+]} = \exp\left(\frac{e_F - e(+,0)}{k_B T}\right) \quad (738)$$

$$\frac{[I^-]}{[I^0]} = \exp\left(\frac{e_F - e(0,-)}{k_B T}\right) \quad (739)$$

The electronic levels (for  $T = 0$  K) are specified in the parameter database as  $e0$ . They are defined only for silicon. They can be changed with:

```
pdbSet KMC Si <I/V/impurity> e0 <species> <n>
```

for example:

```
pdbSet KMC Si I e0 IP 0.35
```

## Parameters

The bandgap levels for interstitials and vacancies can be retrieved with:

```
sprocess> pdbGet KMC Si I e0
IM 1.0
IP 0.35
sprocess> pdbGet KMC Si V e0
VMM 1.06
VM 0.6
VP 0.03
VPP 0.13
```

They also are specified for dopants, like As:

```
sprocess> pdbGet KMC Si As e0
AsVM 0.77
AsVP 0.3
AsiP 0.1
```

**NOTE** The modification of these parameters affects both extrinsic and intrinsic diffusion.

---

## Binding Energies for Particles

The binding energy needed for pairing and breakup reactions is only specified for the reaction with the neutral interstitial or vacancy. For example, for boron, the binding energy is specified for the reaction  $B^- + I^0 = B_i^-$ . The other binding energies (for example,  $B^- + I^+ = B_i^0$ ) are computed using the binding energy for the above reaction and the energy levels associated to the charge transitions [46]:

$$E_b(B_i^0) = E_b(B_i^-) + e(B_i)(0, -) - e(I)(+, 0) \quad (740)$$

The activation energy for the  $B_i^0$  breakup is  $E_b(B_i^0) + E_m(I^+)$ . Because electronic levels scale with  $E_g$  (as shown below), a slight dependency with  $T$  is introduced in these calculated binding energies.

---

## Binding Energies for Impurity Clusters

For an example of how to compute the binding energy for an impurity cluster, see [Nonneutral Reactions on page 473](#).

## Temperature Dependency

The bandgap width used in Sentaurus Process KMC is given by the expression [47]:

$$E_g(T) = E_g(T=0) - \frac{AT^2}{B+T} \quad (741)$$

Using the assumption of proportionality with the band gap, Sentaurus Process KMC assumes that the electronic levels at different temperatures can be computed as:

$$e(j+1,j)(T) = e(j+1,j)(0) \times \frac{E_g(T)}{E_g(0)} \quad (742)$$

Effective state density of conduction and valence bands follows similar expressions:

$$N_c(T) = N_c(300) \times \left(\frac{T}{300}\right)^{\exp N_c} \quad (743)$$

$$N_v(T) = N_v(300) \times \left(\frac{T}{300}\right)^{\exp N_v} \quad (744)$$

Finally, Sentaurus Process KMC uses the values to compute the intrinsic levels and intrinsic carrier densities:

$$e_i(T) = \frac{E_g(T)}{2} + \left(\frac{k_B T}{2}\right) \ln\left(\frac{N_v}{N_c}\right) \quad (745)$$

$$n_i(T) = \sqrt{N_c N_v} \times \exp\left(-\frac{E_g(T)}{2k_B T}\right) \quad (746)$$

## Parameters

The needed parameters are specified in the parameter database under the folder BandGap:

Eg0	Bandgap width at 0 K ( $E_g(0)$ ).
Agap	Bandgap width temperature dependency parameter ( $A$ ).
Bgap	Bandgap width temperature dependency parameter ( $B$ ).
Nc300	Effective state density for the conduction band, at 300 K ( $N_c(300)$ ).
Nv300	Effective state density for the valence band, at 300 K ( $N_v(300)$ ).

`expNc` Effective state density temperature dependency parameter (conduction).

`expNv` Effective state density temperature dependency parameter (valence).

They can be changed using `pdbSet`. For example, to set the bandgap width at 0 K, use:

```
pdbSet KMC Si BandGap Eg0 1.17
```

The parameters for the bandgap temperature dependency are defined for silicon in the `BandGap` folder:

```
sprocess> pdbGet KMC Si BandGap Eg0
1.17
sprocess> pdbGet KMC Si BandGap Agap
0.000473
sprocess> pdbGet KMC Si BandGap Bgap
636.0
sprocess> pdbGet KMC Si BandGap Nc300
3.2e+19
sprocess> pdbGet KMC Si BandGap Nv300
1.8e+19
sprocess> pdbGet KMC Si BandGap expNc
1.5
sprocess> pdbGet KMC Si BandGap expNv
1.5
```

---

## Charge Attractions and Repulsions

The short-range repulsions between charged particles have been implemented forbidding the interactions between particles in the same charge state (except for the percolation reactions; see [Percolation on page 465](#)). Long-range forces are considered automatically due to the bias induced in the particle migration by the local Fermi level.

---

## Fermi-Level Computation

Sentaurus Process KMC computes the Fermi level assuming charge neutrality and Fermi-Dirac statistics. It simply makes the number of charges in each cell element equal to the concentration of substitutional dopants and charged impurity clusters in the box. The presence of mobile charged particles is neglected.

The charge concentration for each element is an average of the charge concentration in the neighborhood. The averaging radius is taken as the parameter `smoothRadius`. The power of

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### Fermi-Level Effects: Charge Model

this average is controlled with the parameter `smoothPower`. This average is important because of the atomistic nature of the simulation.

Without this averaging, a medium-dose doped sample, with some elements filled up with particles and some empty ones, could be considered as a set of intrinsic (empty) boxes and a few boxes with a very high concentration.

For example, a dopant concentration of  $1 \times 10^{20} \text{ cm}^{-3}$  corresponds to one particle in  $10 \text{ nm}^3$ . The volume of an internal element may be as small as  $1 \text{ nm}^3$ . This means one particle per 10 boxes. Without any charge averaging, a moving interstitial would diffuse intrinsically in nine empty boxes and extrinsically in one box. With the average, the interstitial ‘sees’ the right concentration of  $1 \times 10^{20} \text{ cm}^{-3}$  and diffuses according to this concentration (see [Figure 69](#)).

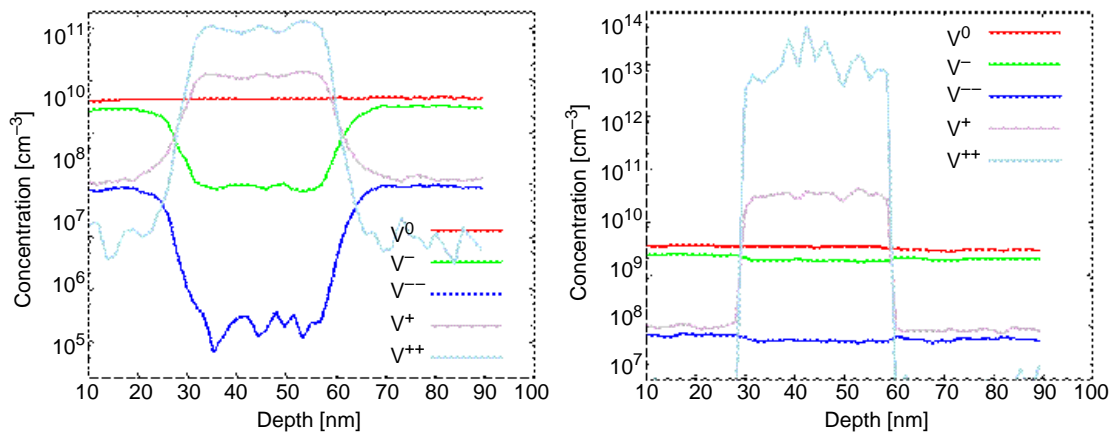


Figure 69 Simulated vacancy profiles for a p-sample (from 30 to 60 nm) for different vacancy charged states: (*left*) smoothing out the charge concentration and (*right*) incorrect results without smoothing

## Parameters

This smoothing is a default Sentaurus Process KMC feature performed by an ultrafast algorithm and is controlled only by the cutoff radius (in nanometers) specified in the parameter database:

```
sprocess> pdbGet KMC Si BandGap smoothRadius  
7
```

**NOTE** To switch off this local computation and to set up a constant, user-defined dopant concentration, experienced users may want to use:

```
pdbSetDouble KMC setDopantConc <dopant concentration>
```

where dopant concentration is a positive quantity for n-type devices and a negative one for p-type devices.

---

## Updating Charged States

The charge model of Sentaurus Process KMC assumes that the electronic transport and reactions are faster than the atomic transport and reactions. Therefore, it is necessary to implement mechanisms to update the charge distribution (and the local Fermi level) that follows the structural changes. Since the equilibrium ratios depend only on the Fermi level, it is necessary to update them each time the Fermi level varies.

There are two reasons for local changes in the Fermi level:

- Mobile particles diffusing between elements with different Fermi levels
- Change of the electronic concentration in one element

Besides, each time a new particle appears or disappears because of pairing or breakup reactions, it is necessary to ensure that the charge state of the new particle is consistent with its local Fermi level.

Different mechanisms are implemented to maintain the right charge ratios. All are performed at the same time, but they apply to different scenarios.

## Electronic Concentrations and Charge-State Ratios

An update algorithm periodically reviews all the particles and updates the Fermi level and the proportions of charged particles in each element. The algorithm:

- Smooths the charge distribution.
- Computes the Fermi level for each box using the charge neutrality assumption.
- Establishes the appropriate charge ratios.

**NOTE** This update algorithm slows down the simulation. It is crucial to follow the changes in the Fermi level, but without spending too much CPU time.

## Mobile Particles

Mobile particles see different Fermi levels when they move from one element to another. Therefore, it is needed to update its charge each time it crosses the boundaries between boxes. At the same time, particles change their charge state to maintain the proper charge distribution; consequently, they need extra updates. This is implemented with an algorithm that updates the charge of mobile particles each time they perform a migration jump. This algorithm also considers the migration frequency of each particle, as explained in [46], to avoid artificial concentration increases in the slow diffusing species concentration.

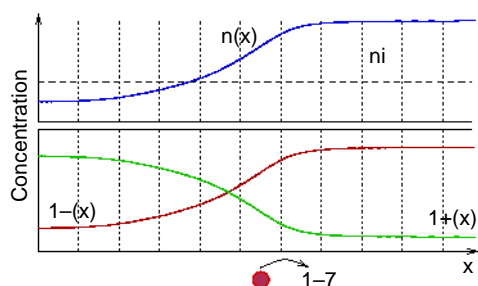


Figure 70 A mobile particle ( $I^-$ ) sees different electronic properties when jumping from one element to a different one. Its charge state must be updated to reproduce the expected macroscopic concentration.

## Pairing and Breakup Reactions

After pairing or breakup reactions, some species appear and disappear in the Sentaurus Process KMC elements. To ensure that the concentration of these species maintains the correct proportions, a breakup, pairing charge update mechanism is implemented. It computes the probability of the new particles to be in a particular charge state.

### Parameters

The charge update algorithm only uses one external parameter in the database called `ChargeVarPercent` and accounts for the maximum relative error allowed for the Fermi-level updates. This parameter is a compromise between accuracy and efficiency.

Decreasing its value leads to more accurate but slower simulations, and the charge model can overload your computer resources.

Increasing its value speeds up the simulation at the cost of accuracy:

```
sprocess> pdbGet KMC ChargeVarPercent
0.25
```

**NOTE** Only small modifications to this parameter are recommended.



## Electric Drift

The charge model of Sentaurus Process KMC considers the:

- Introduction of an electric field, related to the local charge variations.
- Existence of forces acting over the charged species; these forces generate a bias in the diffusion – the *electric drift*.

Sentaurus Process KMC models electric bias modifying the jump probabilities to account for the space anisotropy produced when an electric field is present.

A particle inside the electric field can jump in both directions, but the probability of jumping following the electric field is higher. Consequently, a ‘migration barrier’ is implemented. The barriers are related to the relative concentration of each species. For example, for an  $I^+$  jumping from a position  $x_2$  in a box to a position  $x_1$  in a different box, if  $P(x_2) > P(x_1)$ , where  $P$  is the probability of an interstitial having a positive charge, the jump is always possible. Otherwise, there is a probability of  $1 - [P(x_2)]/[P(x_1)]$  of being rejected.

For an  $I^+$  particle, the jump is accepted with a probability of:

$$\frac{P(x_2)}{P(x_1)} = \exp\left(\frac{[e_F - e(+,0)]_2 - [e_F - e(+,0)]_1}{k_B T}\right) \quad (747)$$

where typically, if there is no bandgap narrowing effects,  $e(+, 0)_2 = e(+, 0)_1$  and:

$$\frac{P(x_2)}{P(x_1)} = \exp\left(\frac{e_{F2} - e_{F1}}{k_B T}\right) \quad (748)$$

The subscripts 1 and 2 refer to magnitudes in different elements. [Figure 71](#) shows an energy diagram of this process. The number of rejected jumps for each axis is shown in a report at the end of the annealing.

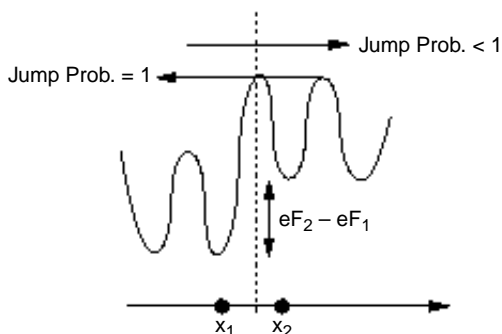


Figure 71 Energy diagram showing the jump process

## Bandgap Narrowing

### Narrowing due to Dopant Concentration

Sentaurus Process KMC includes doping-induced energy shifts of the conduction band minimum and the valence band maximum. The narrowing of the fundamental band gap is presented as the function [48] for n-type semiconductors:

$$\Delta E_{gdc} = A_{cn1/4} \left( \frac{N^+}{10^{18}} \right)^{1/4} + A_{cn1/3} \left( \frac{N^+}{10^{18}} \right)^{1/3} + A_{cn1/2} \left( \frac{N^+}{10^{18}} \right)^{1/2} \quad (749)$$

$$\Delta E_{gdv} = A_{vn1/4} \left( \frac{N^+}{10^{18}} \right)^{1/4} + A_{vn1/3} \left( \frac{N^+}{10^{18}} \right)^{1/3} + A_{vn1/2} \left( \frac{N^+}{10^{18}} \right)^{1/2} \quad (750)$$

and for p-type semiconductors:

$$\Delta E_{gdc} = A_{cp1/4} \left( \frac{N^-}{10^{18}} \right)^{1/4} + A_{cp1/3} \left( \frac{N^-}{10^{18}} \right)^{1/3} + A_{cp1/2} \left( \frac{N^-}{10^{18}} \right)^{1/2} \quad (751)$$

$$\Delta E_{gdv} = A_{vp1/4} \left( \frac{N^-}{10^{18}} \right)^{1/4} + A_{vp1/3} \left( \frac{N^-}{10^{18}} \right)^{1/3} + A_{vp1/2} \left( \frac{N^-}{10^{18}} \right)^{1/2} \quad (752)$$

The total bandgap narrowing is:

$$\Delta E_{gd} = E_{gdc} - E_{gdv} \quad (753)$$

Since the distance between bands shrinks, Eq. 753 gives negative values.

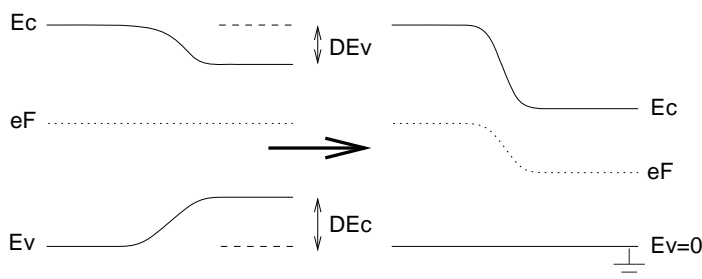


Figure 72 Bandgap narrowing; Sentaurus Process KMC assumes the valence band has zero energy

## Parameters

The parameters  $A_{cn1/4}$  and so on are extracted from [47] and are listed in the parameter database for BandGap in silicon. For the conduction band:

```

pdbGet KMC Si BandGap Acn1_4
0
sprocess> pdbGet KMC Si BandGap Acn1_3
-0.01484
sprocess> pdbGet KMC Si BandGap Acn1_2
0.00078
sprocess> pdbGet KMC Si BandGap Acp1_4
-0.01627
sprocess> pdbGet KMC Si BandGap Acp1_3
0
sprocess> pdbGet KMC Si BandGap Acp1_2
-0.00018

```

For the valence band:

```

sprocess> pdbGet KMC Si BandGap Avn1_4
0.01508
sprocess> pdbGet KMC Si BandGap Avn1_3
0
sprocess> pdbGet KMC Si BandGap Avn1_2
0.00074
sprocess> pdbGet KMC Si BandGap Avp1_4
0
sprocess> pdbGet KMC Si BandGap Avp1_3
0.01846
sprocess> pdbGet KMC Si BandGap Avp1_2
-0.00263

```

## Narrowing due to Strain

There are two models available for modeling the narrowing due to stress. A simple one and a full narrowing model.

The full narrowing model is chosen setting the pdb parameter FullNarrowing to true. This model is the same as in [Bandgap Narrowing on page 268](#):

$$\Delta E_{ci} = D_{ci}(\epsilon_{xx} + \epsilon_{yy} + \epsilon_{zz}) + D_{cxi}\epsilon_{xx} + D_{cyl}\epsilon_{yy} + D_{czi}\epsilon_{zz} \quad (754)$$

$$\begin{aligned} \Delta E_{vi} = & D_{vi}(\epsilon_{xx} + \epsilon_{yy} + \epsilon_{zz}) \pm 0.5D_{vbi}((\epsilon_{xx} - \epsilon_{yy})^2 + (\epsilon_{yy} - \epsilon_{zz})^2 + (\epsilon_{zz} - \epsilon_{xx})^2) \\ & + D_{vdi}(\epsilon_{xy}^2 + \epsilon_{xz}^2 + \epsilon_{yz}^2) \end{aligned} \quad (755)$$

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Fermi-Level Effects: Charge Model

Sentaurus Process KMC also uses the averaged values of conduction and valence bands energies:

$$\Delta E_{cs} = -kT \log \left( \frac{1}{3} \sum_{i=1}^3 e^{-\frac{\Delta E_{ci}}{kT}} \right) \quad (756)$$

$$\Delta E_{vs} = kT \log \left( \frac{1}{2} \sum_{i=1}^2 e^{-\frac{\Delta E_{vi}}{kT}} \right) \quad (757)$$

defining the narrowing due to strain effects as:

$$\Delta E_{gs} = \Delta E_{cs} - \Delta E_{vs} \quad (758)$$

The simple model computes the narrowing as:

$$\Delta E_{gs} = K |\epsilon_x + \epsilon_y + \epsilon_z| \quad (759)$$

where the parameter  $K$  is called `DiScalar`.

When Ge is present, the narrowing is computed as a linear interpolation between the narrowing produced by strain for pure Si ( $\Delta E_{gs}^{\text{Si}}$ ), and the one for pure Ge ( $\Delta E_{gs}^{\text{Ge}}$ ). In this way, the total narrowing for  $\text{Si}_{1-x}\text{Ge}_x$  is:

$$\Delta E_{gs} = \Delta E_{gs}^{\text{Si}} + x(\Delta E_{gs}^{\text{Ge}} - \Delta E_{gs}^{\text{Si}}) \quad (760)$$

where  $x$  is the relative Ge concentration specified in  $\text{Si}_{1-x}\text{Ge}_x$ .

### Parameters

The parameters used for the `full` model for pure Si are defined in the Sentaurus Process KMC dataset as:

```
sprocess> pdbGet KMC Si BandGap EcDilatational
          1 -8.6
          2 -8.6
          3 -8.6
sprocess> pdbGet KMC Si BandGap EvDilatational
          1 -2.1
          2 -2.1
sprocess> pdbGet KMC Si BandGap EcDeviatoric(1)
          1 9.5
          2 0.0
          3 0.0
```

```
sprocess> pdbGet KMC Si BandGap EcDeviatoric(2)
1 0.0
2 9.5
3 0.0
sprocess> pdbGet KMC Si BandGap EcDeviatoric(3)
1 0.0
2 0.0
3 9.5
sprocess> pdbGet KMC Si BandGap EvDeviatoric(1)
1 0.5
2 4.0
sprocess> pdbGet KMC Si BandGap EvDeviatoric(2)
1 0.5
2 4.0
```

The parameter for the simple model for pure Si is:

```
sprocess> pdbGet KMC Si BandGap DiScalar
1.75
```

The parameters used for pure Ge are similar to the ones for pure Si, but with the Ge. prefix:

```
sprocess> pdbGet KMC Si BandGap Ge.EcDilatational
1 0.59 2 0.59 3 0.59
sprocess> pdbGet KMC Si BandGap Ge.EvDilatational
1 -1.24 2 -1.24
sprocess> pdbGet KMC Si BandGap Ge.EcDeviatoric(1)
1 -9.42 2 0.0 3 0.0
sprocess> pdbGet KMC Si BandGap Ge.EcDeviatoric(2)
1 0.0 2 -9.42 3 0.0
sprocess> pdbGet KMC Si BandGap Ge.EcDeviatoric(3)
1 0.0 2 0.0 3 -9.42
sprocess> pdbGet KMC Si BandGap Ge.EvDeviatoric(1)
1 2.55 2 5.50
sprocess> pdbGet KMC Si BandGap Ge.EvDeviatoric(2)
1 2.55 2 5.50
sprocess> pdbGet KMC Si BandGap Ge.DiScalar
1.75
```

Finally, the simple (0) or full (1) narrowing models are selected:

```
sprocess> pdbGet KMC Si BandGap FullNarrowing
0
```

## Narrowing due to Presence of an Alloy

The narrowing due to an alloy concentration is computed as (assuming, in this example, that Ge is the alloy in Si material):

$$\Delta E_{gGe} = -[Ge](\beta_1 + \beta_2[Ge]) \quad (761)$$

where  $[Ge]$  is the germanium concentration, and  $\beta_1, \beta_2$  are the parameters needed for the quadratic interpolation between the silicon gap (1.12 eV) and the Ge gap (0.78 eV). They are respectively called `GeNarrowing` and `GeNarrowing2`.

### Parameters

```
sprocess> pdbGet KMC Si BandGap GeNarrowing
6.8e-24
sprocess> pdbGet KMC Si BandGap GeNarrowing2
0
```

This is simply  $(1.12-0.78)/5e22$ .

## Bandgap Narrowing Use

The value of  $\Delta E_g$ , computed as:

$$\Delta E_g = \Delta E_{gdop} + \Delta E_{gs} + \Delta E_{gGe} \quad (762)$$

is used to correct  $e_i, n_i, e_F$ , and the dopant levels in the gap,  $e(j, j+1)(A)$ . For these last ones, they are assumed to be proportional to the band gap. This means that these new values, after applying the bandgap narrowing correction, are:

$$e(j, j+1)(A)^{corrected} = e(j, j+1)(A) \left( 1 + \frac{\Delta E_g}{E_g} \right) \quad (763)$$

It is interesting to note that  $\Delta E_g < 0$ .

Whenever a Sentaurus Process KMC model needs a bandgap level, the bandgap narrowing-corrected value is used. The only exception is the activation energy for the impurity pair emission from impurity clusters where the narrowing correction can be controlled by:

```
pdbSet KMC <material> BandGap Correct_Complex <false/true>
```

**NOTE** The bandgap narrowing due to doping, stress, and SiGe is always switched on by default. To disable it, set the proper parameters to zero.

## Charge Model and Boron Diffusion Example

The known charged states of  $B_i$  are  $B_i^-$ ,  $B_i^0$ , and  $B_i^+$  [21][22]. The three states are included in Sentaurus Process KMC, although the inclusion of  $B_i^+$  is only important for systems far from equilibrium. The pairing, breakup, and charge reactions related to  $B_i$  are represented in the current Sentaurus Process KMC model by the reactions:



Direct breakup of  $B_i^+$  is not included because  $I^{++}$  is not implemented. Boron effective diffusivity  $D(B)$  is given by the sum of the contribution of all mobile species:

$$D(B) = D(B_i^-) \frac{[B_i^-]}{[B^-]} + D(B_i^0) \frac{[B_i^0]}{[B^-]} + D(B_i^+) \frac{[B_i^+]}{[B^-]} \quad (768)$$

Using the Maxwell–Boltzmann approximation, the previous equation is usually written as:

$$D(B) = S_I \left[ D_X(B) + D_P(B) \frac{p}{n_i} + D_{PP}(B) \left( \frac{p}{n_i} \right)^2 \right] \quad (769)$$

where  $S_I$  is the interstitial supersaturation, and  $p$  and  $n_i$  are the hole concentration and the intrinsic concentration, respectively.

The relations between the above diffusivity components and the microscopic parameters are [46]:

$$D_X(B) = v_{capt} D(I^0) [I^0]^* \frac{v_m(B_i^-)}{v_{break}(B_i^-)} \quad (770)$$

$$D_P(B) = v_{capt} D(I^0) [I^0]^* \frac{v_m(B_i^0)}{v_{break}(B_i^0)} \exp\left(\frac{e(B_i)(0, -) - e_i}{k_B T}\right) \quad (771)$$

**5: Atomistic Kinetic Monte Carlo Diffusion**  
 Fermi-Level Effects: Charge Model

$$D_{PP}(B) = v_{capt} D(I^0) [I^0]^* \frac{v_m(B_i^-)}{v_{break}(B_i^-)} \exp\left(\frac{e(B_i)(0, -) + e(B_i)(+, 0) - 2e_i}{k_B T}\right) \quad (772)$$

$e_i$  is the intrinsic level.

These expressions can be used as a bridge between the parameters of continuum simulators and those used by Sentaurus Process KMC. The above continuum expression assumes Maxwell–Boltzmann and quasi-equilibrium conditions, which are not needed in Sentaurus Process KMC.

---

## Charge Model and Arsenic Diffusion Example

A similar analysis can be performed for arsenic, which has both vacancy and interstitial contributions, related to  $AsV$  and  $As_i$  defects. The arsenic reactions are:



and:





All the previously mentioned contributions are included in KMC. Consequently:

$$D(As) = D(AsV^+) \frac{[AsV^+]}{[As^+]} + D(As_i^+) \frac{[As_i^+]}{[As^+]} + D(AsV^0) \frac{[AsV^0]}{[As^+]} + D(As_i^0) \frac{[As_i^0]}{[As^+]} + D(AsV^-) \frac{[AsV^-]}{[As^+]} \quad (782)$$

which in continuum models is usually reduced to:

$$D(As) = [f_I S_I - (1 - f_I) S_V] \times \left[ D_X(As) + D_M(As) \frac{n}{n_i} + D_{MM}(As) \left( \frac{n}{n_i} \right)^2 \right] \quad (783)$$

$f_I$  is the fraction of interstitial-assisted diffusion. Note, however, that this last continuum description conveys several simplifying assumptions compared with the model included in Sentaurus Process KMC. The common assumption that  $D_X$  and  $D_M$  fit an Arrhenius plot is only true if the contributions of  $AsV^+$  and  $As_i^+$  have the same activation energy. The same applies for the  $AsV^0$  and  $As_i^0$  contributions. The continuum equation also assumes that the interstitial fraction,  $f_I$ , is independent of the Fermi level (the same for the three charged states) and is independent of the temperature.

---

## Interfaces and Surfaces

An interface is the extension between two regions with different materials. The most common interface is the silicon–oxide interface. Sentaurus Process KMC allows for modeling all interfaces between two different materials.

As explained in [Materials and Space on page 386](#), Sentaurus Process KMC divides the space in small rectangular elements and assigns to each of them a material. The interfaces are the set of element faces between different materials.

The element faces are independent. The interface behaves as the sum of all of its faces, but such an ‘interface’ does not really exist. What exists are the element faces, all of them emitting and trapping with different rates depending on its area, local stress, and so on. In the following sections, these element faces are called *interface*.

Interfaces set the equilibrium concentration for self-silicon point defects and the solubility concentration for impurities. Sentaurus Process KMC models the interfaces differently for silicon point defects than for impurities.

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### Interfaces and Surfaces

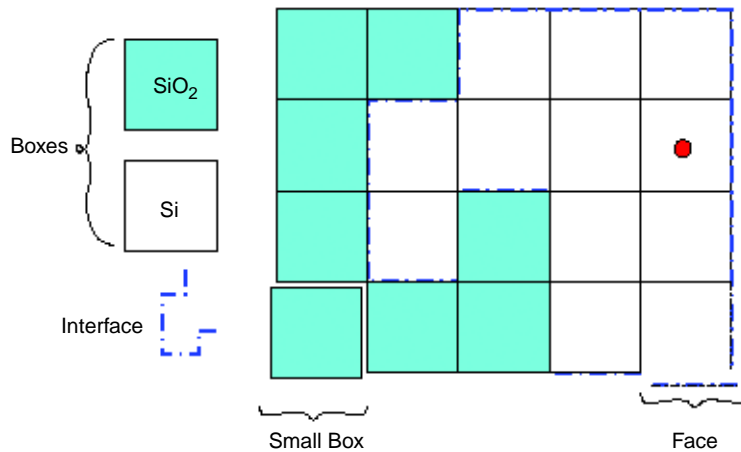


Figure 73 Sentaurus Process KMC interfaces are the set of element faces between different materials

---

## Different Interface Models

The parameter `Model` specifies the behavior of an interface:

```
pdbSet KMC Oxide_Silicon Model Allcharges
```

The different models are:

<code>Allcharges</code>	Three-phase segregation model for dopants. Emission and capture of all the charge states of point defects on materials with <code>full</code> modeling. Capture of all the charge states of impurity-paired defects on materials with <code>full</code> modeling.
<code>Amorphous</code>	When one material is <code>full</code> and the other is <code>simple</code> , this interface acts as an asymmetric mirror. Particles going from the <code>simple</code> to the <code>full</code> material are reflected, while particles going from the <code>full</code> to the <code>simple</code> material are allowed to pass. No trapping or emission of particles on either side.
<code>Interface</code>	Three-phase segregation model for dopants. Emission and capture of neutral point defects on materials with <code>full</code> modeling.
<code>none</code>	No interface between materials. This model is only possible when the model of the materials involved in the interface is the same; that is, both are <code>simple</code> or <code>full</code> .
<code>Reflective</code>	The interface acts as a mirror. Particles are not trapped. No emission of particles on either side.

## Interfaces for Self-Silicon Point Defects

It is common to define a recombination length  $L_r$  as the distance from the surface needed to obtain the equilibrium concentration (see Figure 74).

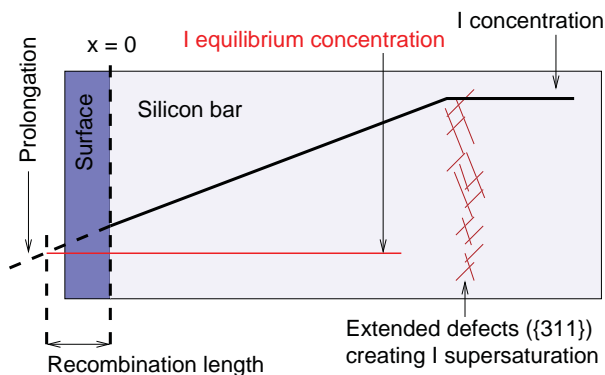


Figure 74 Recombination length is the distance between the interface and the point in which the prolongation of the point-defect concentration joins its equilibrium concentration

The microscopic meaning of  $L_r$  can be associated with the probability of a point defect being trapped at the surface:

$$P_{trap} = \frac{\lambda}{L_r} \quad (784)$$

where  $\lambda$  is the point-defect jumping distance. The smaller  $L_r$ , the better sink is the surface. For interstitials in the silicon-oxide interface, it is close to a perfect sink with  $L_r < 5 \text{ nm}$  [49][50].

### Capture

Interfaces capture neutral interstitials and vacancies with the probability set in Eq. 784. When  $L_r$  is set to zero, the probability is set to 1, a perfect sink.

### Emission

In [1], the point-defect (for example, interstitials) equilibrium concentration is related to the interface frequency emission prefactor and energy as:

$$[I]^* = \frac{2}{\lambda} \times \frac{D_0 FS}{a^2} \exp\left(-\frac{E_f(I)}{k_B T}\right) \quad (785)$$

## 5: Atomistic Kinetic Monte Carlo Diffusion Interfaces and Surfaces

where the surface frequency emission is:

$$v = \text{sites} \times P_{\text{trap}} \times D_0 FS \frac{6}{\lambda^2} D_{0,m} \times \exp\left(-\frac{E_m + \Delta E_m^{\text{stress}} + \Delta E_m^{\text{Ge}} + E_f + \Delta E_f^{\text{stress}} + \Delta E_f^{\text{Ge}}}{k_B T}\right) \quad (786)$$

where:

- `sites` is the number of capture sites in the interface (proportional to its surface and equal to  $\frac{2}{a^2}YZ$ ).
- `D0FS` is the surface emission prefactor.
- `Em` and `Ef` are the migration and formation energies of the point defects, respectively.
- `ΔEmstress`, `ΔEfstress` are the regular corrections to migration and formation due to stress.
- `ΔEmGe`, `ΔEfGe` are the corrections to migration and formation due to Ge concentration, explained below.

The point defects are emitted from a randomly chosen position at the surface. Only neutral `Is` or `Vs` are emitted when the interface model is `Interface`. All charge states are emitted and captured when using `Allcharges`. In equilibrium, these two models give the same results.

## Stress

The presence of stress changes the migration and formation energy of interstitial and vacancies and, consequently, the emission frequency. Each interface (where, as previously stated, interface was called to the independent element faces) is oriented in a unique axis ‘j’, and the projections of the principal axes into ‘j’ should be accounted. Then, the total emission frequency is:

$$v = \sum_{axis}^{x', y', z'} P_{axis}^j v_{axis} \quad (787)$$

where  $P_{axis}^j$  are the projections of the principal axis into the surface axis. Finally, for each axis, the migration and formation energies including stress effects are computed as:

$$E_m^{\text{stress}} + E_f^{\text{stress}} = E_m + E_f + \sigma'_{axis} \Delta V_{par} + \sum_{i \neq axis} \sigma'_i \Delta V_{ort} + \frac{1}{3} \Delta V^f \sum_i \sigma'_i \quad (788)$$

where  $\Delta V_{ort}$ ,  $\Delta V_{par}$ , and  $\Delta V^f$  are the perpendicular and parallel activation volumes for diffusion and the activation volume for formation, respectively.

For more information on these parameters and the stress models, see [Stress Effects on Point Defects, Impurities, Dopants, and Impurity-Paired Point Defects on page 416](#).

## Alloys

The presence of an alloy (assumed to be Ge in this example) changes the migration and formation energy of point defects in the following way:

$$\Delta E_m^{Ge} = \alpha[Ge] \quad (789)$$

$$\Delta E_f^{Ge} = \beta[Ge] \quad (790)$$

where  $[Ge]$  is the germanium concentration, and  $\alpha$ ,  $\beta$  are the dependencies of migration and formation with germanium, specified as  $E_{mGe}$  and  $E_{fGe}$  in the PDB.

## Parameters

The parameters that control the point-defect interface model can be found in the PDB by looking in the `Oxide_Silicon` folder. By default, interfaces, other than the oxide–silicon interface, have their point-defect interface model set to `None` and do not require any parameters. The formation energies are listed for the material, not for the interface.

For example, the formation energy of interstitials in silicon is under `Silicon`, not in `Oxide_Silicon` or any other interface.

<code>D0FS_Mat</code>	Surface emission prefactor, $D_0FS(I)$ . <code>Mat</code> is the short name of the material.
<code>Ef</code>	Formation energy, $E_f(I)$ .
<code>RecLnm_Mat</code>	Recombination length, $L_r$ . <code>Mat</code> is the short name of the material.

The migration energies are displayed in the point defect section of the file (see [Point Defects, Impurities, Dopants, and Impurity-paired Point Defects on page 403](#)). The surface values can be easily obtained using the command line.

For example, for interstitials and vacancies in the silicon–oxide interface:

```
sprocess> pdbGet KMC Oxide_Silicon I D0FS_Si
5000.0
sprocess> pdbGet KMC Silicon I Ef
4.0
sprocess> pdbGet KMC Oxide_Silicon I RecLnm_Si
0
sprocess> pdbGet KMC Oxide_Silicon V D0FS_Si
800.0
sprocess> pdbGet KMC Silicon V Ef
3.8
```

## 5: Atomistic Kinetic Monte Carlo Diffusion Interfaces and Surfaces

```
sprocess> pdbGet KMC Oxide_Silicon V RecLnm_Si
0
```

and for vacancies in the silicon–gas interface:

```
sprocess> pdbGet KMC Gas_Silicon V D0FS_Si
800.0
sprocess> pdbGet KMC Gas_Silicon V RecLnm_Si
0
sprocess> pdbGet KMC Si V Ef
3.8
```

**NOTE** You can modify these values. Changes in the formation energy or surface emission prefactor will modify the DC equilibrium product of point defects and the diffusivity of all the species. A change, both in the formation and migration parameters, that maintains the DC product constant will not produce this undesirable effect, but may change the extended defects dissolution times.

### Oxidation-enhanced Diffusion (OED) Model

The current flux of I (V) across an outer surface in Sentaurus Process KMC is described in the previous model as:

$$\vec{j} \cdot \vec{n} = K_s([I] - [I^*]) \quad (791)$$

being:

$$K_s = \frac{1}{6} v_m(I) \lambda^2 / L_r \quad (792)$$

and  $\lambda$  the jumping distance. An extra term is included to account for oxidation:

$$\vec{j} \cdot \vec{n} = K_s([I] - [I^*]) - G_{ox} \quad (793)$$

This term  $G_{ox}$  tries to combine the Sentaurus Process continuum model (see [Surface Recombination Model: PDependent on page 345](#)) with an atomistic implementation. In particular, its definition is:

$$G_{ox} = (\vec{\theta} \cdot \vec{n}) \|\vec{V}_{ox}\| G_{scale} \left( \frac{\|\vec{V}_{ox}\|}{V_{scale}} \right)^{G_{pow}} \exp\left(-\frac{E_{\theta} + P\Delta V_{\theta}}{k_B T}\right) \quad (794)$$

where  $\vec{\theta}$  is a vectorial prefactor and  $\vec{n}$  is the normal to the interface, so that  $(\vec{\theta} \cdot \vec{n})$  gives the proper component for a planar, axis-oriented, interface in an internal element.

$\|\vec{V}_{ox}\|$  is the `ReactionSpeed` computed by the PDE solver in Sentaurus Process and used here by Sentaurus Process KMC.  $V_{scale}$  and  $G_{pow}$  are additional model parameters to adjust the interstitial injection.  $G_{scale}$  is a term defined to account for Fermi-level effects, and defined similarly to the continuum one as:

$$G_{scale} = \frac{mm + m + 1 + p + pp}{mm \left(\frac{n}{n_i}\right)^{2PotOx} + m \left(\frac{n}{n_i}\right)^{PotOx} + 1 + p \left(\frac{n}{n_i}\right)^{-PotOx} + pp \left(\frac{n}{n_i}\right)^{-2PotOx}} \quad (795)$$

$E_\theta$  is the activation energy for point-defect injection and, finally,  $\Delta V_\theta$  is a parameter to include a hydrostatic dependency for OED.

Consequently, this is a hybrid model in which the continuum solver computes and generates a `ReactionSpeed` value to be used by Sentaurus Process KMC to compute the point-defect injection prefactor.

**NOTE** Boundary movement is allowed in this model and is switched on by default. This implies that the model serves to generate a more adequate point-defect injection from the interface during oxidation processes, while a remeshing mechanism changes the oxide thickness. If you do not want the oxide thickness to change, set `Grid Reaction.Modify.Mesh` to 0.

## Parameters

Table 55 lists the parameters defined for the oxide–silicon interface only.

Table 55 Parameters used in OED model

Parameter name	Description
ox_Etheta	Activation energy $E_\theta$ .
ox_xtheta, ox_ytheta, ox_ztheta	Components for the $\vec{\theta}$ vector used as a prefactor.
ox_VFtheta	Pressure correction $\Delta V_\theta$ .
ox_Vscale, ox_Gpow	<code>ReactionSpeed</code> control: $V_{scale}$ and $G_{pow}$ .
ox_pp, ox_p, ox_Ep, ox_m, ox_mm, ox_Em, ox_pot	Parameters used to compute the Fermi-level dependencies introduced by $G_{scale}$ . In particular, prefactor and activation energies for $pp$ , $p$ , $m$ , and $mm$ terms, and exponent.

To use this model, call `diffuse` with any oxidation parameter (for a list of oxidation parameters for `diffuse`, see [diffuse on page 875](#)).

## Interfaces for Impurities

The interface model of impurities in Sentaurus Process KMC follows a three-phase segregation model. Particles can be emitted to both sides of the interface or can stay trapped at the interface. [Figure 75](#) shows the atomistic mechanisms and energies for trapping and detrapping impurities.

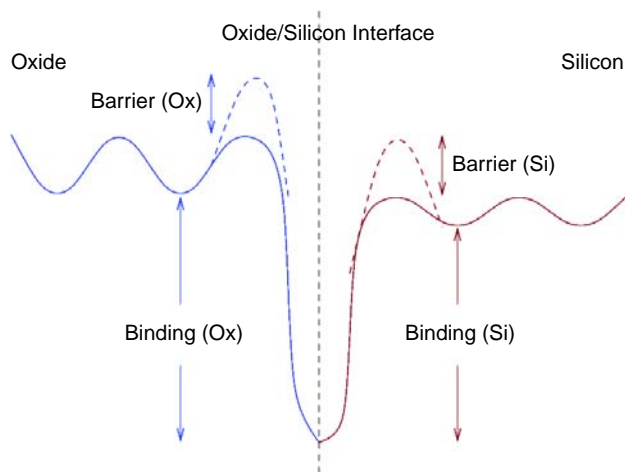


Figure 75 Dopants reaching the interface may be trapped by it with a different binding energy for each interface side. Energy barriers for capture and emission also can be present.

These interfaces are modeled between any two materials; however, depending on the material model, the interface will behave differently.

### Simple Material Side

The simple material side faces a material using the `simple` model. In these materials, only direct diffusion of dopants is allowed. Since there are no paired dopant impurity point defects, the model is as follows: Dopants arriving at the nonsilicon side may be captured with certain probability, and they can be remitted later.

#### Capture

The capture probability is:

$$P^{\text{non-Si}}_{\text{cap}}(A) = \exp(-\text{Barrier}(A)/(k_B T)) \left( 1 - \frac{\text{Trapped}(A)}{\text{MaxTrapped}(A)} \right) \quad (796)$$



where  $A$  is the dopant being trapped,  $Barrier$  is the barrier energy,  $Trapped$  is the number of particles trapped at the interface, and  $MaxTrapped$  is the maximum number of them that can be trapped.

If the particle is trapped, there is a probability to evaporate (annihilate) the just-trapped dopant.

## Emission

Interfaces emit particles to the nonsilicon side with a frequency given by:

$$v^{\text{non-Si}}_{emiss}(A) = Trapped(A)Prefexp(-Ener/(k_B T)) \quad (797)$$

The emission is proportional to the number of trapped dopants and to a parameter  $Pref$  that acts as a prefactor. The emission energy is:

$$Ener(A) = Barrier(A) + E_m(A) + Binding(A) \quad (798)$$

The migration energy contains stress and Ge corrections. The binding energy contains a pressure correction:

$$\Delta E_b^{surface}(A) = P\Delta V_b^{surface}(A) \quad (799)$$

## Parameters

The energy barrier to a nonsilicon interface is introduced as  $E_{Barrier\_Surf}<mat>$ , where  $<mat>$  is Si, aSi, Ox, Ni, Po Gas, and Unknown, or any other user-defined material short name:

Si	Silicon
aSi	Amorphous silicon
Ox	Oxide
Ni	Nitride
Po	PolySilicon
Gas	Gas
Unknown	Unknown

The values are always specified in the interface parameter file:

```
sprocess> pdbGet KMC Oxide_Silicon B EBarrier_SurfOx
B 0.1
```

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### Interfaces and Surfaces

The probability to evaporate a trapped particle is called `Evaporation_Surf`:

```
sprocess> pdbGet KMC Oxide_Silicon B Evaporation_Surf
B 0 Bi 0
```

The pressure correction to the binding energy of the dopants to the surface is given by the parameter `VF_Surf<mat>`:

```
sprocess> pdbGet KMC Oxide_Silicon B VF_SurfOx
```

The maximum number of trapped particles per cubic centimeter follows an Arrhenius plot with prefactor `C0Max_Surf`:

```
sprocess> pdbGet KMC Oxide_Silicon B C0Max_Surf
2e+14
```

and energy `EMax_Surf`:

```
sprocess> pdbGet KMC Oxide_Silicon B EMax_Surf
0
```

The prefactor for emission is called `Db_Surf`:

```
sprocess> pdbGet KMC Oxide_Silicon B Db_Surf
B 1e-3
```

Finally, the binding energy of dopants is `Eb_Surf<mat>`:

```
sprocess> pdbGet KMC Oxide_Silicon B Eb_SurfOx
B 0.28
```

## Full Material Side

The particles transporting dopants (or impurities) in materials with full modeling are not typically the dopants themselves, but impurity-paired point defects. In other words, an impurity plus an interstitial or a vacancy. When these *pairs* reach the interface, if they are trapped, the accompanying interstitial or vacancy is recombined, and the dopant itself is piled at the surface. Consequently, the dopant cannot be emitted unless an incoming interstitial or vacancy reacts with it, carrying it away from the interface.

### Capture

Neutral (or charged, if the model `Allcharges` is selected) impurity-paired point defects are trapped at the surface with a probability given by:

$$P_{cap}^{Si}(A_i) = \exp(-Barrier(A_i)/(k_B T)) \left( 1 - \frac{Trapped(A)}{MaxTrapped(A)} \right) \quad (800)$$

Different barriers can be assigned to  $A_i$  and  $AV$  and, consequently, different recombination probabilities. The number of trapped particles and maximum trapped particles is assigned to the interface and is shared between both sides.

## Emission

Particles are not emitted by themselves, but the interface allows particles to be moved to the material bulk. Point defects (interstitials and vacancies) can react with the dopants trapped at the surface, forming mobile impurity-paired point defects. The probability of these reactions being successful depends on the binding of the dopant to the surface and the barrier energy:

$$P_{emiss}^{Si}(A_i) = \exp(-Ener(A_i)/(k_B T)) \quad (801)$$

where:

$$Ener(A_i) = Binding(A_i) + Barrier(A_i) \quad (802)$$

The binding is corrected with a pressure-dependent term:

$$\Delta E_b^{surface}(A_i) = P \Delta V_b^{surface}(A_i) \quad (803)$$

## Parameters

The parameters that control the maximum number of trapped particles have already been discussed in [Simple Material Side on page 502](#). The barrier energy is called EBarrier\_SurfSi:

```
sprocess> pdbGet KMC Oxide_Silicon As EBarrier_SurfSi
Asi 0.0
AsV 0.0
```

and the binding energy is Eb\_SurfSi:

```
sprocess> pdbGet KMC Oxide_Silicon As Eb_SurfSi
Asi 0.1
AsV 0.1
```

The stress correction is given by:

```
sprocess> pdbGet KMC Oxide_Silicon B VF_SurfSi
```

---

## Oxidation

Sentaurus Process KMC is fully coupled with oxidation. Consequently, any oxidation conditions issued in the `diffuse` command of Sentaurus Process are transferred to Sentaurus Process KMC. Setting `Grid DoNotMove.Reaction` to 1 (it is 0 by default) disables boundary movement at the oxide–silicon interface. Otherwise, the Sentaurus Process oxidation algorithm is allowed to work during the *reaction* step, and the new structure (with expanded oxide) is imported into Sentaurus Process KMC immediately before the atomistic diffusion step. The velocities at which the interfaces and the oxide move are used to compute the displacement of the particles.

Sentaurus Process KMC uses the displacement to relocate the displaced particles and finishes the remeshing. After this, regular atomistic diffusion occurs. Since there are several interpolations performed in this process, minor inaccuracies in the final position of particles can be introduced during remeshing, especially during large oxidations. Regular diffusion occurring at the same time as oxidation should make these interpolation inaccuracies negligible.

In principle, Sentaurus Process KMC can be used successfully for 1D, 2D, and 3D oxidation. In particular, since the precision of the Sentaurus Process KMC solution does not depend on a fine continuum mesh, a coarse Sentaurus Process mesh can be specified, increasing the stability of oxidation, while the Sentaurus Process KMC part takes care of the position of particles. The example in [Figure 76](#) shows the results of such an approach.

Sentaurus Process KMC also allows OED (see [Oxidation-enhanced Diffusion \(OED\) Model on page 500](#)).

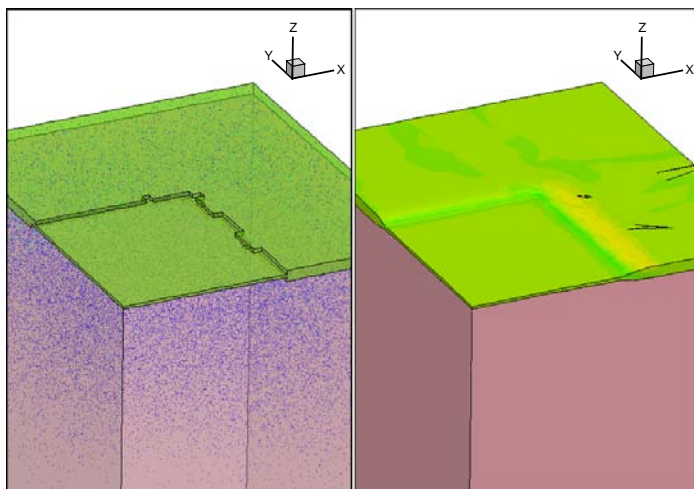


Figure 76 Example of Sentaurus Process KMC coupled with an oxidation in 3D: (*left*) KMC simulation in which the internal mesh is coupled to (*right*) continuum oxidation simulation

## Epitaxial Deposition

Epitaxial deposition can be performed by using one of the following:

- Regular Sentaurus Process epitaxy
- Native epitaxial deposition using an LKMC model based on [51]

This section describes the native epitaxy model only. The model is switched off by default and must be switched on for the native epitaxy:

```
pdbSet KMC Epitaxy true
```

The model shares many features with LKMC (to fully understand this model, see [LKMC: Fully Atomistic Modeling of Solid Phase Epitaxial Regrowth on page 451](#)).

The model introduces the silicon lattice and assigns a flag to each lattice position. This flag is switched on for lattice positions that match the silicon material and is switched off for positions lying in the gas. The simulator assigns a frequency to all the off positions to become on, that is, to accept a silicon atom (coming from the gas). Only off lattice positions that have an on lattice in the neighborhood have a frequency different from zero. Consequently, the silicon grows slowly, simulating an epitaxial deposition.

The frequency for an off position at the silicon–gas interface to accept a silicon atom and become on is:

$$v_{\text{Epi}} = K' \times v_{\text{SEG}}^{\text{LKMC}} \quad (804)$$

where  $v_{\text{SEG}}^{\text{LKMC}}$  is the frequency for selective epitaxial growth (SEG), very similar to the one written in [Eq. 700, p. 452](#):

$$v_{\text{SEG}}^{\text{LKMC}} = K_{\text{SEG}}^{\text{LKMC}}(\text{site}) \times \exp\left(-\frac{E_{\text{SEG}}^{\text{LKMC}} + \Delta E(\text{site})}{k_{\text{B}}T}\right) \quad (805)$$

$K_{\text{SEG}}^{\text{LKMC}}(\text{site})$  is a prefactor that accounts for the local microscopic growth for each configuration. This prefactor depends on two variables:  $n$  and  $m$ .  $n$  can be 100, 110, or 111 defined very similarly to  $K(1)$ ,  $K(2)$ , and  $K(3)$  in [LKMC: Fully Atomistic Modeling of Solid Phase Epitaxial Regrowth on page 451](#).  $m$  is used to distinguish between configurations with the same  $n$  but different second neighbor coordination numbers. In this model, also published in [51], 100 configurations only are split into three different ones: 100, 100.7, and 100.8 for 100 configurations with six or fewer, seven, and 8 or more second neighbor coordination numbers.

$\Delta E(\text{site})$  is a correction energy applied to special sites. It is used to simulate the formation of {311} facets during SEG. As such, only 1 site is defined to have a non null correction: the

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Epitaxial Deposition

{311} local configuration. This configuration is in two different situations a) and b). a) is a (100) generic site that lacks half of its third neighbors, and b) is a (110) where the second atom in the chain needed to define the place as 110 would have first coordination number equal to 2. Assigning a slower rate to configuration a) prevents the {311} facet becoming a {111} facet. The slower rate for configuration b) assures that the local {311} configuration is not broken by a lateral (110) regrowth.

$K'$  is an empirical factor to fit the epitaxial deposition thickness to the specified thickness. This empirical factor is computed automatically by Sentaurus Process KMC trying to match the thickness specified in the processing conditions. In particular:

$$K' = K_{\text{thickness}} \times \text{thickness} / (v_{\text{SEG}}^{\text{LKMC}}(100) \times \text{time} \times K_{\text{nanolayer}}) \quad (806)$$

where:

- `thickness` is the specified thickness.
- `time` is the annealing time.
- $K_{\text{nanolayer}}$  is the length of a nanolayer of recrystallized silicon. A nanolayer is assumed to be half the lattice constant.
- $v_{\text{SEG}}^{\text{LKMC}}(100) = K(100) \times \exp(-E_{\text{SEG}}^{\text{LKMC}} / (k_B T))$  is the frequency for recrystallization in a pure (100) substrate.
- $K_{\text{thickness}}$  is an empirical constant, available in the PDB as `Damage prefactor.thickness`, that relates the microscopic growth of a lattice atom in a (100) local neighborhood with the macroscopic growth of a (100) substrate.

This epitaxial deposition can create {111} facets and maintain the same (100):(110):(111) growth rate as SPER. Under regular selective epitaxial conditions, the shapes generated agree with experimental ones.

At the end of the LKMC epitaxial deposition, the simulator smooths the generated atomistic interface and reinserts it into Sentaurus Process. The algorithm used to mesh the atomistic shape uses the parameter `KMC Simplify.Geometry`. A bigger value provides a faster and more stable insertion, but with a loss of surface details.

The inclusion of doping is possible during LKMC epitaxy. If a doping profile with a linear change is indicated, the included doping will be linear with time, and not with thickness.

Finally, the generation of an LKMC starting surface from Sentaurus Process and the reinsertion after LKMC epitaxy are delicate and time-consuming operations if they are performed only once at the start of the `diffuse` command and at the end. This means that the state of the simulator at intermediate steps during the `diffuse` command may not be synchronized with the KMC simulator.

**NOTE** To avoid problems, the `KMC Movie` command is disabled during LKMC epitaxy. In addition, the `diffuse movie` command must not be used during LKMC epitaxial deposition.

## Parameters

The parameters needed for this model are defined in the parameter database under `KMC Si Epitaxy`. [Table 56](#) lists the parameters for the site prefactors.

Table 56 Parameters for site prefactors

Parameter	Description
<code>prefactor.SEG.100.8</code>	For (100) sites with 8 or more second neighbor coordination number
<code>prefactor.SEG.100.7</code>	For (100) sites with 7 second neighbor coordination number
<code>prefactor.SEG.100</code>	For (100) sites with 6 or fewer second neighbor coordination number
<code>prefactor.SEG.110</code>	For (110) sites
<code>prefactor.SEG.111</code>	For (111) sites

[Table 57](#) lists the parameters for the activation energies.

Table 57 Parameters for activation energies

Parameter	Description
<code>energy.SEG</code>	Overall activation energy for SEG
<code>energy.SEG.311</code>	Correction for 311 planar SEG

[Table 58](#) lists the parameters for the thickness.

Table 58 Parameters for the thickness

Parameter	Description
<code>prefactor.thickness</code>	Empirical factor to fit the thickness in epitaxial growth

As an example, some of these parameters can be obtained as:

```
sprocess> pdbGet KMC Si Epitaxy prefactor.SEG.100
3.3e+15
sprocess> pdbGet KMC Si Epitaxy prefactor.SEG.100.8
1.8e+18
sprocess> pdbGet KMC Si Epitaxy prefactor.SEG.111
3.5e+14
sprocess> pdbGet KMC Si Epitaxy energy.SEG
2.7
```

Figure 77 shows an example of epitaxial deposition using LKMC.

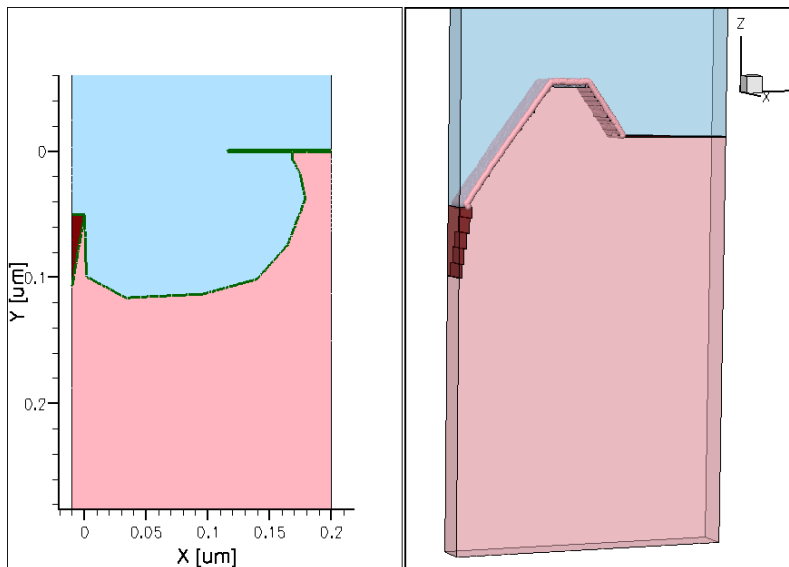


Figure 77 (Left) Initial shape and (right) final shape after LKMC epitaxial deposition with thickness of 175 nm

---

## Including New Impurities

You can customize Sentaurus Process KMC to include other impurities not supported by default. The modifications affect the parameter database and the file `KMC.tcl`. Nevertheless, it is not necessary or recommended to modify the files included in the Sentaurus Process distribution. All the modifications can be included in the input file.

For the parameter database, the `pdbSet` family of commands allows overwriting previous values or defining new ones. For the procedures written in the file `KMC.tcl`, defining the new procedure in the input file is enough; the new one will be executed instead of the old one.

The modifications include the following:

1. Include the new impurity `x` in Sentaurus Process KMC under the label named `KMC Impurities`.
2. Include the impurity-related particle pairs (`Xi` or `XV` or both) in `KMC Pairs` (see [Particles in Models on page 397](#)). If your model does not have impurity pairs (in other words, simple material), you do not need to specify them, including `Dm` and `Em`.
3. Be careful about which charge states you include because not all are allowed; you must specify parameters for all those included.



4. Include possible aliases for the particle in `KMC Aliases`. If the particle already exists for Sentaurus Process, include this name as an alias in Sentaurus Process KMC (see [Alias on page 398](#)).
5. You can customize the colors for this particle (although it is optional) in Tecplot SV in `KMC Colors` (see [Colors on page 399](#)).
6. To create parameters for the new particle, define the parameters explained in [Particles and Parameters on page 399](#) under `KMC <mat> X`, where `<mat>` is every material defined in your simulation, and `X` is the name of the new defined dopant. Be sure to include all of them. Parameters for the impurity cluster model are not needed if `Implement_Complex` is set to `false`. All others require values since they specify how the surface and amorphous regions interact with the new dopant `X`.
7. Specify the reactions for `KMC <mat> X` in `ReactionsPointDefect`. Typical reactions here include the pair formation (such as `X,I true`) and impurity cluster formation (such as `Xi,X true`). These reactions only need to be defined in materials with the full model.
8. Specify also the reactions with damage and extended defects if there are any. You can leave these fields empty. See [Interaction with Impurities on page 429](#), [Interactions on page 434](#), [Interactions on page 438](#), and [Interactions on page 442](#).

If you include impurity clusters, ensure the following:

1. Define reactions that create impurity clusters from two isolated particles.
2. Enable the right impurity clusters for your simulation with `Implement_Complex` (see [Impurity Clusters on page 460](#)).
3. Fill the parameters for the impurity clusters. You can leave the energy barriers empty, but you must specify `Etotal_Complex` energies and `CaptVol_Complex` capture volumes.
4. Write the reactions for your impurity clusters. If you have specified an energy for a particular impurity cluster, then that impurity cluster should be reachable through some reactions. Include the reactions with dopants and point defects in `ReactionsCluster` (see [Interactions on page 475](#)).
5. If you need dopant deactivation without diffusion for high concentrations, see [Percolation on page 465](#).

Finally, you must define some variables set in the `KMC.tcl` file placed in `TclLib`. This can (and should) be performed locally in your input file:

1. Add the names of your new impurities and pairs to the `nameOf` array.
2. Complete the map of MC implantation to Sentaurus Process KMC with `MCnameOf`.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Including New Impurities

If you need to transfer information back and forth from continuum to KMC, you also must modify the procedures `PDE2KMCUser` and `KMC2PDEUser`:

- Add the new particles and clusters to the lists in `PDE2KMCUser`. The first field is the field name in Sentaurus Process (continuum models), the second is the name in Sentaurus Process KMC, and the third is the conversion factor. For example:

```
fproc PDE2KMCUser { } {  
    return "Dopant X 1 \  
    DopantInt Xi 1 \  
    DopantVac XV 1 \  
    DopantCluster X2 .5 \  
    DopantCluster X3 .3333"  
}
```

- Add the new particles in `KMC2PDEUser`. The first name is the name in Sentaurus Process KMC, the second is the Sentaurus Process field, and the third is the factor. For example:

```
fproc KMC2PDEUser { } {  
    return "X Dopant 1\  
    Xi DopantInt 1\  
    XV DopantVac 1\  
    X2 DopantCluster 1\  
    X3 DopantCluster 1.5\  
    X4 DopantCluster 2"  
}
```

**NOTE** `MCnameOf` can be used to manipulate some KMC species without actually implementing them. For example, an unknown implant can be performed to simulate preamorphization. If Sentaurus Process KMC does not support the unknown dopant, use `set MCnameOf(dopant) "I"` to instruct the MC implantation code to pass the dopant atoms as interstitials to Sentaurus Process KMC. This way, all of the damage generated by an unknown dopant implant will be correctly calculated and passed, and the dopant ions will be considered to be silicon interstitials by Sentaurus Process KMC.

---

## Impurities Diffusing without Pairing

Sentaurus Process KMC allows impurities to diffuse using two different mechanisms:

- Normal diffusion
- Diffusion without pairing

## Normal Diffusion

For impurities with +1 or -1 charge, in other words, dopants, the substitutional dopant is active, but it does not diffuse. The substitutional dopant reacts with interstitials or vacancies, forming a pair that diffuses. These pairs break up with a given frequency, releasing the dopants back into the substitutional positions.

## Diffusion without Pairing

For neutral impurities, the normal diffusion is still available. An alternative diffusion mechanism is migration without pairing. In these cases, the impurity diffuses as it is, that is, the substitutional impurity has a nonzero diffusivity and continues forming pairs with point defects.

Diffusion without pairing has the following characteristics:

- The impurity has nonzero diffusivity. The pairs can exist, but they do not have to diffuse:

```
sprocess> pdbGet KMC Silicon F Dm
      F 5e-3
      FV 0
      FI 0
sprocess> pdbGet KMC Silicon F Em
      F .8
      FV 5
      FI 5
```

- When a pair (for example, FI) breaks up, [Eq. 655](#) and [Eq. 656, p. 407](#) still apply. The migration energy of the impurity is not accounted for.
- The impurities cannot interact with extended defects, but their pairs can, as explained in [Extended Defects on page 430](#).
- Impurities interact with interfaces. Interfaces re-emit impurities.
- Impurity clusters are possible with some variations:
  - Reactions within the impurities (for example,  $F + F$ ) apply to the moving particles and not only the percolation model.
  - Impurity clusters emit point defects and impurities, as explained in [Emission on page 424](#), but the capture and emission reactions for impurities are:



- Consequently, the binding energies involved in the capture and emission of impurities will be:

$$E^{AnI_m}_b(A) = E_{pot}(A_{n+1}I_m) - E_{pot}(A_nI_m) \quad (808)$$

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Reports

- Recombination, FT, and complementary FT mechanism are implemented as well. The binding energies for them are not changed since the emission recombination of  $A_i$  (for  $A_n I_m$  clusters) or AV (for  $A_n V_m$  clusters) is not involved.

---

## Reports

Sentaurus Process KMC prints several reports in the log file including:

- Models used
- Particle distribution
- Cluster distribution
- Defect activity
- Interactions
- Event

---

## Models Used Report

Sentaurus Process KMC reports the models used immediately after being initialized. A summary is printed for each impurity, dopant, and point defect:

KMC models	Silicon
Interstitial	
DiffModel	Direct(I)
ChargeModel	I( -1 0 1 )
ClusterModel	I+I AmorphousPocket Void ThreeOneOne Loop
SPERModel	Clean
Vacancy	
DiffModel	Direct(V)
ChargeModel	V( -2 -1 0 1 2 )
ClusterModel	V+V AmorphousPocket Void ThreeOneOne
SPERModel	Clean
Arsenic	
DiffModel	Kick-out(Asi) Kick-out(AsV)
ChargeModel	Asi( 0 1 ) AsV( -1 0 1 )
ClusterModel	As+As AsnVm
SPERModel	As4Vm 30% deposited 70% moved
Boron	
DiffModel	Kick-out(Bi)
ChargeModel	Bi( -1 0 1 )
ClusterModel	BnIm AmorphousPocket Loop
SPERModel	B3Im 100% deposited 0% moved

Fluorine	
DiffModel	Direct(F)
ChargeModel	FI( 0 ) FV( 0 )
ClusterModel	F+F FnIm FnVm
SPERModel	F2Im F2Vm 30% deposited 70% moved
-----	
Stress model	Disable
-----	
SPER model	Non-Lattice KMC
-----	

Table 59 Sentaurus Process KMC models

Model	Description
ChargeModel	The particles and their allowed charged states are displayed.
ClusterModel	The interactions between the impurity or point defect and extended defects and clusters are displayed.
DiffModel	The diffusion model can be direct or kick-out. Kick-out means that the particle does not diffuse unless paired with an interstitial or vacancy.
SPERModel	Recrystallization model shows the percentage of dopant being deposited, and the bigger deposited cluster, if any. Point defects are just cleaned during the recrystallization.
Stress model	Disabled or enabled.
SPER model	The algorithm for SPER can be non-lattice KMC (isotropic) or lattice KMC (anisotropic).

This summary is printed for any particle allowed in the simulation, even if this particle is not going to be used.

---

## Particle Distribution Report

The activation report lists how many dopants exist per material and the state of the material:

```
--          KMC Particle distribution report
Material      Dopant   Total   State
Nitride       As       28604   100.00% mobile
Oxide         As        759   100.00% mobile
Oxide_Silicon As       1777   100.00% trapped
PolySilicon   As      21986   100.00% mobile
Silicon       As      58394   41.55% active
Oxide         B         25   100.00% mobile
PolySilicon   B        283   100.00% mobile
Silicon       B        828   99.52% active
```

## 5: Atomistic Kinetic Monte Carlo Diffusion Reports

The different states depend on the material:

full material	Particles can be active (substitutional dopant) or inactive (anything else).
simple material	Particles can be mobile (single impurity) or immobile (impurity in a cluster).
Interface	Number of particles trapped at the interface.

---

## Cluster Distribution Report

This report shows the distribution of clusters versus size for each material and reports how many clusters are in the simulation and their types:

```
--          KMC impurity cluster distribution report      --
Name      #number
--- Silicon ---
As4I      4889 As2      4062 As4      1110 As2V      571
As3I      121 As2I      95 As3      56 As3V      19
As4V      9 As4I2      6 B2I2      2
```

For example, in the above report, all the BICs are  $B_2I_2$ . The As–vacancy clusters are distributed between different types, but the most common one is  $As_4I$ .

---

## Defect Activity Report

Sentaurus Process KMC displays the point defects, impurities, dopants, extended defects, clusters, amorphous areas, recrystallizations, and surface emission accounted for during the simulation:

```
--          KMC defect activity report      --
First:  Time Events  Temp | Last: Time  Events Temp Label
      0.000 0.00e+00  27 |      3e-01 2.86e+09  672 PointDefect (I)
      0.000 0.00e+00  27 |      2e-01 2.86e+09  772 PointDefect (V)
2.285897e-02 1.04e+06  27 |      75610 here      PointDefect (As)
      0.000 0.00e+00  27 |      1132 here      PointDefect (B)
      9.639 1.47e+06  27 |      4e-01 2.86e+09  572 PointDefect (IM)
1.657462e-01 1.08e+03  27 |      3e-01 2.86e+09  672 PointDefect (IP)
      11.025 1.52e+06  27 |      2e-01 2.86e+09  722 PointDefect (VMM)
2.849592e-02 3.60e+01  27 |      2e-01 2.86e+09  722 PointDefect (VM)
      103.606 2.99e+06  27 |      2e-01 2.86e+09  772 PointDefect (VP)
2.352941e-04 1.19e+07  650 |      1e-03 1.85e+09 1230 PointDefect (VPP)
6.114947e-01 1.08e+06  27 |      2e-01 2.86e+09  722 PointDefect (AsV)
      13.397 1.60e+06  27 |      2e-01 2.86e+09  722 PointDefect (AsVM)
```

6.057627e-01	1.08e+06	27		2e-01	2.86e+09	772	PointDefect (AsVP)
0.000	1.04e+06	27		8e-01	2.86e+09	222	PointDefect (Asi)
8.988	1.45e+06	27		33 here			PointDefect (AsiM)
9.790420e-01	1.10e+06	27		4e-01	2.86e+09	622	PointDefect (AsiP)
9.143608e-01	2.14e+04	27		6e-04	2.55e+07	1000	PointDefect (BV)
1.154401e-01	5.63e+02	27		1e-03	1.68e+09	1230	PointDefect (BVM)
1.501662e-01	9.14e+02	27		7e-04	3.78e+07	1040	PointDefect (BVP)
0.000	0.00e+00	27		3e-01	2.86e+09	672	PointDefect (Bi)
7.337895e-03	2.00e+00	27		3e-01	2.86e+09	672	PointDefect (BiM)
1.501662e-01	9.14e+02	27		1e-03	7.36e+08	1300	PointDefect (BiP)
0.000	0.00e+00	27		3e-02	2.85e+09	862	AmorphousPocket (I)
5.772006e-03	1.00e+00	27		1e-03	2.07e+09	1180	AmorphousPocket (V)
0.000	0.00e+00	27		2e-03	2.43e+09	1030	AmorphousPocket (IV)
3.254430e-04	1.29e+07	720		8e-04	1.36e+08	1130	Void
2.241841e-03	1.04e+07	950		1 here			ThreeOneOne
0.000	1.04e+06	27		5111 here			ImpurityCluster (AsI)
7.615	1.40e+06	27		599 here			ImpurityCluster (AsV)
7.573	1.40e+06	27		5228 here			ImpurityCluster (As)
1.154401e-02	6.00e+00	27		2 here			ImpurityCluster (BI)
17.278	4.97e+06	27		7e-04	5.66e+07	1070	ImpurityCluster (B)
0.000	0.00e+00	27		1464 here			Elements emitting I
0.000	0.00e+00	27		1464 here			Elements emitting V
3.300695e-04	1.29e+07	730		936 here			Elements emitting As
7.478722e-04	6.83e+07	1080		1e-03	2.15e+09	1130	Elements emitting Asi
47.284	2.31e+06	27		7e-04	6.21e+07	1110	amorphous (Recryst.)
0.000	0.00e+00	27		23025 here			LatticeAtom

The report contains two columns with three subcolumns each. The first report shows when the model was first used; the last report shows when the model was last used. If the model is still being used, the number of particles or defects using it is displayed followed by “here.” The three subcolumns report the time, number of simulated events, and temperature.

For example, the previous report shows the first {311} defect (ThreeOneOne) was formed at  $2.2 \times 10^{-3}$  s, with a temperature of 950°C, and with one {311} still in the simulation. There was silicon amorphous, from 47 s, 27°C to  $6.7 \times 10^{-4}$  s at 1110°C. Since any anneal resets the time to zero, the first time applies to a previous anneal or implant (since there is damage accumulation, in other words, room temperature annealing, during implants).

For the interface models, the report shows how many interfaces are in the simulation (*I* and *V*), and how many of them contain trapped dopants (936 for As). It also lists the first and last time the interfaces let As go in the form of As<sub>i</sub>.

This information shows how the different models were used during the simulation and when the damage was annealed.

## Interactions Report

This reports shows, for each material and interface, all the reactions between a mobile particle (point defect or impurity-pair point defect) and the number of times they happened.

The first column lists the name of the interacting defect, the second the interaction itself, and the third the number of times it happened from the beginning of the simulation. Columns 4, 5, 6, and 7 are the same as 2 and 3. This report explains which reactions may be important and which are not. For example, in the report below, the reaction I+VP (31 times) is negligible in comparison with I+V (111848 times) and does not play a significant role in this simulation for the formation of AP.

Finally, depending on the defect reported, the output can be slightly different.

### PointDefect

```

--          KMC interactions report          --
          Reaction  #Times  Reaction  #Times  Reaction  #Times---
Silicon ---
PointDefect  I+I          278778  I+V          111848  I+As          1435719
PointDefect  I+B          644803  I+IM          862      I+IP          7856
PointDefect  I+VMM           83      I+VM          3316     I+VP          31
PointDefect  I+AsV          273     I+AsVP        2480     I+AsVM        35
PointDefect  I+Bi          2809
PointDefect  V+V          56907  V+As          25324   V+IM          103
PointDefect  V+IP          3541   V+VMM         288     V+VM          4248
PointDefect  V+VP          77     V+Asi        12480   V+AsiP       3405
PointDefect  V+Bi          433     V+BiP        1924   V+BiM         44
PointDefect  As+As          243     As+IM        1313602  As+VMM       38966
PointDefect  As+VM          30332  As+AsVM      2666
PointDefect  B+IP          285066  B+BiP        203

```

It includes the reaction between two mobile particles.

### Indirect Diffusion

When using the indirect diffusion model for amorphous materials, the results are similar to crystalline ones, but *I* and *V* mean *dangling* bond and *floating* bond, respectively.

```

          Reaction  #Times  Reaction  #Times  Reaction  #Times
--- AmorphousSilicon ---
PointDefect  I+V          40475  I+B          30707

```



## AmorphousPocket

AmorphousPocket	Ix+I	713391	Ix+V	210933	Ix+VMM	305
AmorphousPocket	Ix+VM	4575	Ix+VP	25		
AmorphousPocket	Vx+I	31202	Vx+V	43040	Vx+IM	126
AmorphousPocket	Vx+IP	11372	Vx+Bi	1281	Vx+BiM	47
AmorphousPocket	IxVy+I	312602	IxVy+V	910338	IxVy+B	204
AmorphousPocket	IxVy+IM	154	IxVy+IP	15555	IxVy+VMM	110
AmorphousPocket	IxVy+VM	4930	IxVy+VP	5	IxVy+Bi	4683
AmorphousPocket	IxVy+BiP	618	IxVy+BiM	106		

It includes the reaction between small interstitial clusters (Ix), small vacancy clusters (Vx), and APs including both Is and Vs (IxVy). To keep the report small, all the sizes are condensed into only one Ix, Vx, or IxVy.

## ThreeOneOne

ThreeOneOne Ix+I 1035217

All the {311} sizes are condensed under the term Ix.

## Loop

Loop Ix+I 177885 Ix+BiM 10

All the dislocation loop sizes are written under the term Ix.

## ImpurityCluster

ImpurityCluster	B2+I	31	B2+Bi	6		
ImpurityCluster	B3+I	3				
ImpurityCluster	B2I+I	463	B2I+V	25	B2I+Bi	21
ImpurityCluster	B3I+I	27591	B3I+V	1148		
ImpurityCluster	BI2+V	3835	BI2+Bi	278		
ImpurityCluster	B2I2+I	1518	B2I2+V	86	B2I2+Bi	1314
ImpurityCluster	B3I2+I	26				
ImpurityCluster	B2I3+V	26				
ImpurityCluster	As2+V	1728	As2+As	5	As2+AsV	1251
ImpurityCluster	As3+V	100	As3+AsV	69		
ImpurityCluster	As4+V	3				
ImpurityCluster	As2V+I	56605	As2V+Asi	20411		
ImpurityCluster	As3V+I	87723	As3V+Asi	18437		
ImpurityCluster	As4V+I	1973488				

Since impurity clusters are important for the correct activation and deactivation of dopants, and their sizes are small numbers, all are written in the report.

## Interface

```

--- Oxide_Silicon ---
Interface      I          11364  I+As          73  V          1141
Interface      AsV         410   Asi          1440

```

The name of each particle interacting with any interface, and the number of times it happened, is reported last.

---

## Event Report

The event report is the reverse of the reaction report. The reaction report shows the forward reactions; the events report shows the reverse ones. Since the reactions and other events depend strongly on the defects, this report changes from defect to defect.

## PointDefect

```

--          KMC event report          --
          Name      Jump X      Jump Y      Jump Z      Break-up
PointDefect  I       2921360317  2921305233  2921406601
PointDefect  V       1285293026  1285290404  1285265687
PointDefect  As        1120        1071        1163
PointDefect  B          7          23          15
PointDefect  IM      228653836  228646801  228625103
PointDefect  IP      1074734274  1074760443  1074719693
PointDefect  VMM     86102860   86115025   86090069
PointDefect  VM      846251937  846307626  846269323
PointDefect  VP      7881794   7875672   7878359
PointDefect  Asi     1144728   1144688   1142864   832840
PointDefect  AsiP    51512    52143    51812   1894402
PointDefect  AsV     18255    17863    17967    30572
PointDefect  AsVP    3544     3436     3438    22783
PointDefect  AsVM    3585     3586     3460    37804
PointDefect  Bi     13459181  13453297  13458878  257929
PointDefect  BiP     94930    95115    95524
PointDefect  BiM    124899   123825   124860   670411

```

The second column shows the name of the mobile particle. The 3rd, 4th, and 5th columns show how many diffusion events (hops or jumps) have every particle perform in the x-, y-, and z-axis, respectively. In the absence of anisotropies, these three numbers must be approximately the same. Finally, the last column shows the number of breakups. Since not all the mobile particles can break up (for example,  $B_i$  will break in  $B + I$ , but  $I$  cannot break up), some of the particles will have an empty column there. The relative number between the number of diffusion steps and the number of breakups gives an estimation of the stability of the particle. The more stable the particle (more diffusion events and less breakups), the larger its long-hop distance.

When using the double-hop model, the report looks like:

Name	Jump ><	Jump >>	Jump >^	Break-up	
PointDefect	I	288583696	288599278	1154233402	
PointDefect	V	524892	527369	2103188	
PointDefect	IM	32935856	32946513	131772254	
PointDefect	IP	153307399	153285675	613169175	
PointDefect	VMM	373744	374963	1498954	
PointDefect	VM	256003	255776	1022437	
PointDefect	VP	309	260	1111	
PointDefect	VPP	4	4	10	
PointDefect	AsV	14570	14473	58109	47289
PointDefect	AsVM				223313
PointDefect	AsVP	348	371	1464	3547
PointDefect	Asi	102330	102738	411863	839856
PointDefect	AsiP	8695	8669	34730	843920
PointDefect	BV	41	30	157	3
PointDefect	BVM	166	181	682	280
PointDefect	BVP				1
PointDefect	Bi	26231	25952	104499	21468
PointDefect	BiM	9798	9735	39016	42747

In this report, the third column reports the number of jumps in opposite directions. The fourth column reports the number of jumps in the same direction, and the fifth column lists jumps in orthogonal directions. For further information, see [Hopping Mode on page 411](#).

## AmorphousPocket

	Name	IV Recom	I Emis	V Emis
AmorphousPocket	Ix		300905	
AmorphousPocket	Vx			59627
AmorphousPocket	IxVy	802007		

I<sub>x</sub> are small interstitial clusters. They can only emit interstitials. V<sub>x</sub> are small vacancy clusters that can only emit vacancies. Finally, I<sub>x</sub>V<sub>y</sub> are APs. They can recombine (destroy) an internal IV pair.

## ThreeOneOne

	Name	I Emis
ThreeOneOne	Ix	1038899

{311}s can only emit neutral interstitials.

## 5: Atomistic Kinetic Monte Carlo Diffusion Reports

### Loop

	Name	I	Emis
Loop	Ix		181927

Dislocation loops, like the {311}s, can only emit neutral interstitials.

### ImpurityCluster

Name	Emis		
ImpurityCluster B3		10	V
ImpurityCluster B3I3		913	I 14203 Bi
ImpurityCluster B2I3		4710	I
ImpurityCluster B3I2		13570	I
ImpurityCluster B2I2		656	I
ImpurityCluster BI2		1	I 32 Bi
ImpurityCluster B2I		578	BiP

An impurity cluster (for example, a BIC) emits  $B_i$  and  $I$ .  $B_2I$  also can emit  $B_iP$  particles. Finally, an internal Frenkel pair can be created, trapping the  $I$  and emitting the  $V$ . This has been the case in this simulation for 10  $B_3$  ( $B_3 \rightarrow B_3I + V$ ). Since  $BV$  is not defined by default, it cannot be emitted.

Name	Emis			
ImpurityCluster B3		1	V	
ImpurityCluster B2		10	V	
ImpurityCluster B3I2		6	I	
ImpurityCluster C2I		3	I	1 V 32 Ci
ImpurityCluster B3I		1	V	6 Bi
ImpurityCluster B2I		107	Bi	
ImpurityCluster CB2I		84	Bi	2 Ci
ImpurityCluster CBI		42	I	1 Bi

In this case, apart from more or less standard boron and carbon clusters, there is a hypothetical carbon–boron–interstitial (CBI) cluster. Two members of this CBI cluster are present here,  $CB_2I$ , emitting  $B_i$  and  $C_i$ , and  $CBI$ , emitting  $I$  and  $B_i$ .

### Amorphous Defects

	Name	Recryst.		
Amorphous	Ele.	4932 B3I3	4598 B2I3	7087 BI2

This is an example of recrystallization depositing inactive boron in different cluster configurations. In this case, the simulator tries to deposit the impurity clusters with a proportion of 30%, 30%, and 40% for  $B_3I_3$ ,  $B_2I_3$ , and  $BI_2$ , respectively.

## Lattice Atoms

	Name	SPER
LatticeAtom	I	2070434

Example of output related with epitaxial growth, showing the number of atoms that were incorporated into crystalline silicon.

## Simple Materials

An event report is written for simple materials as well:

```

--- AmorphousSilicon ---
      Name      Jump ><      Jump >>      Jump >^      Break-up
PointDefect    B           4           2           16
      Name      Recryst.
amorphous      I           7575
      Name      Jump ><      Jump >>      Jump >^
Rejected PD    As           9           42

```

## Indirect Diffusion

The report for amorphous materials with indirect diffusion is similar to the one of crystalline materials, but the *I* and *V* mean *dangling* bond and *floating* bond, respectively.

```

--- AmorphousSilicon ---
      Name      Jump ><      Jump >>      Jump >^      Break-up
PointDefect    I          408765      409824      1637334
PointDefect    V          244177      244724      975635
PointDefect    Bi         456685      457074      1824373      30707
      Name      Jump ><      Jump >>      Jump >^
Rejected PD    I           141130
Rejected PD    V           85422
Rejected PD    Bi          155922

```

## Extracting KMC-related Information

You can request Sentaurus Process KMC information in one of the following ways:

- Using the Sentaurus Process interface (in some cases, the information must be translated to Sentaurus Process fields using `kmc deatomize` before calling the Sentaurus Process commands):
  - `struct` command
  - With the `select`, `print`, `WritePlx`, and `plot` commands
- Calling directly the Sentaurus Process KMC kernel:
  - Writing Sentaurus Process KMC TDR files
  - Extracting atomistic information with the `kmc extract` command (see [kmc on page 954](#))

Calling Sentaurus Process KMC directly has the following advantages:

- More information can be obtained than using the regular interface.
- The atomistic continuum conversions needed to compute the concentrations are more accurate.
- The atomistic information (in other words, 3D coordinates and shape of defects) can be displayed.
- Simulations can be saved and loaded.

---

## Transferring Fields from KMC to Continuum Information: `deatomize`

Sentaurus Process KMC is independent of the mesh and fields of Sentaurus Process. Consequently, after a diffusion in atomistic mode (see [Atomistic Mode on page 371](#)), there are no Sentaurus Process fields to visualize. You can instruct Sentaurus Process KMC to create fields with KMC information. For example, to deatomize the simulation and convert the 3D positions into concentrations, use:

```
kmc deatomize name=<field>
```

When the field is created, Sentaurus Process KMC will not modify it unless there is a new `deatomize` command. This means that the field is synchronized with the Sentaurus Process KMC simulation when it is created. However, after that, if the simulation changes (for example, performing another diffusion), the field will conserve the initial values.

The fields created by `kmc deatomize` are:

- Concentration of particles (number of particles per volume unit). It could be substitutional (B, As, ...), paired (AsV, Bi), and the charge state is included (AsV is neutral; AsVM is negative). If these particles are mapped as *mobile* in the `KMC.tcl` file (see [Including New Impurities on page 510](#)), the field will be computed as an average of time. Otherwise, the field will contain the instantaneous concentration.
- Total concentration of impurities (number of particles in any defect per volume unit): `ITotal`, `BTotal`, ...
- Concentration in the interface (number of particles in the interface per volume unit): `BInterface`, `AsInterface`...
- Concentration in amorphous material (number of particles in amorphous layers per volume unit): `AsAmorphous`, `BAmorphous`...
- Concentration of a particular extended defect (number of defects, where one defect contains more than one particle, per volume unit): `I54`, `V23`, `I1026`...
- Concentration of a particular AP (number of APs, where an AP contains more than one particle): `IV`, `I3V4`...
- Concentration of a particular impurity cluster (number of impurity clusters, where an impurity cluster contains more than one particle): `B2I3`, `As4V`...
- Active concentrations (active number of dopants per volume unit, net, p-type, n-type, and total): `NetActive`, `pNetActive`, `nNetActive`, and `tNetActive`.
- Germanium concentration: `Ge`.

Some fields compute the defect concentration (concentration of APs, impurity clusters, and extended defects). You can transform them into particle concentrations multiplying by the size of the defect.

For example, you can obtain the concentration of boron particles in  $B_2$ ,  $B_3$ ,  $BI_2$ , and  $B_2I_2$  in the field BICs with the following set of commands:

```
kmc deatomize name=B2; kmc deatomize name=B3
kmc deatomize name=BI2; kmc deatomize name=B2I2
select z="2*B2 + 3*B3 + BI2 + 2*B2I2" name=BICs
```

## Smoothing Out Deatomized Concentrations

The direct deatomization of Sentaurus Process KMC quantities into continuum mesh elements produces values with strong gradients between neighboring elements. This is especially true for small concentrations, where Sentaurus Process KMC contains a few particles that are deatomized as an “all or nothing” distribution; that is, some cells may contain one particle, and this is a concentration of  $1/(\Delta V)$ , while others contain no particles, thereby having a zero concentration.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Extracting KMC-related Information

In some cases, especially when the Sentaurus Process KMC output is used as a device simulation input, a smoother concentration is desirable, as seen in [Figure 78](#). This can be performed by setting the PDB parameter:

```
KMC Smooth.Field <field> <number>
```

where:

- <field> is the field name to be smoothed (for example, `NetActive`).
- <number> is an integer.

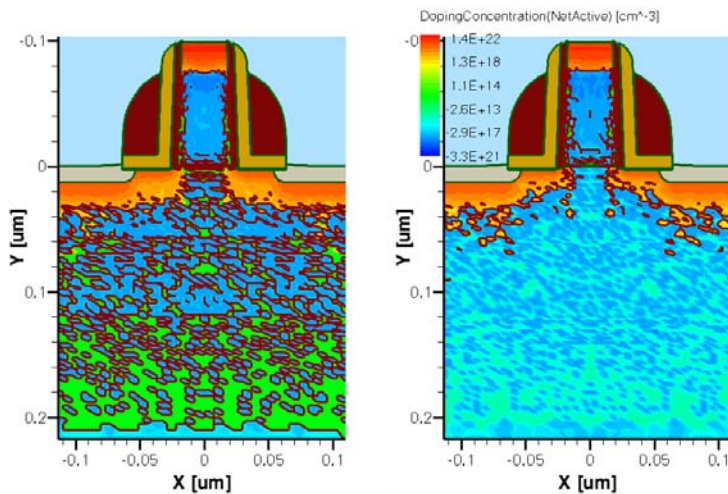


Figure 78 Comparison of NetActive concentration in simulations performed with (*left*) Smooth.Field equal to 0 (disabled) and (*right*) equal to 1

A value of 0 produces no smoothing; larger numbers produce more smoothed profiles. The smoothing algorithm works as follows:

- For each node in the standard Sentaurus Process mesh, the number of particles  $N$  associated with the node is counted.
- The concentration set to that node is, in principle,  $N/V^{\text{Voronoi}}$ , where  $V^{\text{Voronoi}}$  is the Voronoi volume associated with the node.
- $N$  is compared to  $M$ , where  $M$  is the number specified in `Smooth.Field` for this field.
- If the field name does not exist in `Smooth.Field`, 0 is assumed.
- If  $N < M$ , the smoothing algorithm applies. Starting at the node, the algorithm looks for particles not associated with the Voronoi volume of the node, with an increasing radius.
- When  $M - N$  particles are found in a radius  $R$ , it stops searching. At this point, there are  $M$  particles inside the radius,  $M - N$  outside the Voronoi volume, and  $N$  inside the Voronoi volume.



- Then, the concentration of the node will be:

$$N/V^{\text{Voronoi}} + (\text{weight}(N-M))/V_R \quad (809)$$

where  $V_R$  is the volume associated with a segment (1D), circle (2D), or circumference (3D) of radius  $R$ , and `weight` is the PDB value `Smooth.Weight`:

```
pdbSet KMC Smooth.Weight 0.01
```

This technique is not intended to perfectly conserve the total dose, but to fill the nodes with low concentrations with values depending on the distance to the nearest particles. The factor `weight` is included to limit the extra dose introduced in those nodes.

The `Smooth.Field` parameter is used whenever a deatomization is performed. This includes calling directly `kmc deatomize` from the command line or indirectly through `KMC2PDE` or another procedure.

**NOTE** The algorithm to smooth atomistic concentrations can be extremely slow in simulations with a large number of nodes.

The smooth algorithm can be relatively slow for simulations with a large number of nodes or a large number of particles. This can be resolved by calling it in parallel mode with the following option:

```
math numThreadsDeatomize=<n>
```

This option is independent from the KMC parallel mode and does not interfere with it. It applies to the smooth algorithm only, not to the whole deatomization.

---

## Adding and Obtaining Defects in Simulations: `add`, `defects.add`, and `defects.write`

Sentaurus Process KMC allows you to add defects to the simulation using the commands:

```
kmc add queue name=<defect name> coordx=<x> coordy=<y> coordz=<z> [amorphous]
      [crystalline]
kmc add
```

First, the defects are queued in the creation queue with the command:

```
kmc add queue
```

You can queue as many defects as you want. Queueing a defect does not actually introduce it in the simulation. You must use the command `kmc add` alone to empty all of the queue by generating defects in the simulation.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Extracting KMC-related Information

The option name specifies the defect to be created (examples are B, B2I4, I54, and BInterface). The options `coordx`, `coordy`, and `coordz` provide the place where the defect (or the center of mass of the defect) will be created. Finally, the optional arguments `amorphous` and `crystalline` provide a way to tell the simulator whether this defect should be created in an amorphous or a crystalline material. For example, if the current material is crystalline, but the option `amorphous` is specified, the simulator not only creates a defect, but also changes the material from crystalline to amorphous phase.

An alternative way to add defects to the simulation is using the `defects.read` command, which requires the name of a text file to be specified with `defects.read`, for example:

```
kmc defects.read=my_filename
```

This command takes all the defects specified in the file and adds them consecutively in a very similar way to the `add` command. Similar to the `add` command, only the center of mass is specified for defects having more than one particle.

One line specifies one defect. The format of each line is:

```
defect_type defect_name coord_x coord_y coord_z
```

where:

- `defect_type` is the generic name of the defect, for example, `PointDefect`, `Loop`, `ThreeOneOne`, `Interface`, `ImpurityCluster`.
- `defect_name` is the particular name of the defect, for example, B, P, I50, BiM, B3I2.
- `coord_x`, `coord_y`, `coord_z` are the coordinates (in nanometers) for the center of mass of the defect.

For example:

Interface	P	1.000000	11.250000	13.000000
PointDefect	As	5.032000	5.320000	1.032000
ThreeOneOne	I50	10.000000	10.222565	9.777436
PointDefect	B	10.000000	5.000000	6.000000
PointDefect	BiM	30.000002	5.000000	14.000000
ThreeOneOne	I100	19.554871	20.445129	20.000000
Loop	PI59	13.000000	13.000000	13.000000
PointDefect	Bi	26.000000	26.000000	26.000000
ImpurityCluster	B2I	6.235641	7.115777	7.077633
ImpurityCluster	B3I2	4.287220	7.497602	4.604665
PointDefect	Ge	6.696747	7.492962	0.834044

Similarly, the command `kmc defects.write` writes all the defects currently in the simulation into a file with the above format. The name of the file must be specified as:

```
kmc defects.write=my_filename
```

Files written with `defects.write` can be read later with `defects.read`. Since only the center of mass of the particle is written, this is an inaccurate way to save a simulation. To save a simulation, use instead `struct` or `kmc extract tdrWrite`.

---

## Using the Sentaurus Process Interface

### The select, print, WritePlx, and plot Commands

The commands `select`, `print`, `WritePlx`, and `plot` work as expected. If you need a field for them, create it using `kmc deatomize` (see [Transferring Fields from KMC to Continuum Information: deatomize on page 524](#)).

In particular, `select` creates particles inside Sentaurus Process KMC whenever the name of the field is recognized as a particle or defect. These names are:

Dopants	As, B, ...
Impurities	C,F, ...
Paired particles	Bi, AsV, Ci, ...
Point defects	I,V
Any of the above particles with a different charge	IM, VPP, BiM, AsVP, ...
Amorphous	BAmorphous, AsAmorphous, ...
Amorphous pockets	IV, I4V5, ...
Dopants or impurities in an interface	BInterface, AsInterface, ...
Extended defects	I43, V21, ...
Impurity clusters	AsV4, BI2, ...

### Example

For a typical situation with a 1D SIMS-like simulation (implant and anneal), the 1D profiles can be extracted in a `.plx` file using `WritePlx`:

```
SetPlxList BTotal B
WritePlx file
```

Calling `WritePlx` without selecting the list with `SetPlxList` also works. It generates a list of the most common fields:

```
WritePlx file
```

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Extracting KMC-related Information

In nonatomistic mode, the fields must be deatomized first:

```
kmc deatomize name=BTotall
kmc deatomize name=B
```

## The init Command

The `init` command works as expected. Background dopings can be assigned. A TDR file to be loaded can also be assigned with:

```
init tdr=filename
```

and, if the file has been saved with Sentaurus Process KMC and contains atomistic information (see the option `defects` for `tdrAdd`, [kmc on page 954](#)), Sentaurus Process will load it, and the simulation can be continued.

**NOTE** Loading a file and continuing a simulation with `init` will give results similar, but not identical, to performing the simulation without the save/load process. The differences between the results are only statistical; in other words, both represent possible solutions.

## The struct Command

The `struct` command works as expected, except that by default it creates some extra fields to be saved. It generates these extra fields by calling the function `preKMC` with the argument `struct`. You can modify or customize this function in the `KMC.tcl` file. By default, `preKMC` tries to generate and store fields similar to a five-stream model from the KMC information.

The `struct` command also saves restart information, allowing the Sentaurus Workbench `#split` command to work properly with Sentaurus Process KMC.

## The load Command

The `load` command accepts the options `kmc` and `replace` only. It is intended to load a TDR Sentaurus Process KMC simulation to replace the existing one. It performs the necessary conversions between the existing internal Sentaurus Process KMC and the one read from the TDR file, conserving the existing one.

## The deposit Command

The `deposit` command works as expected, including depositing doped layers.

## The diffuse Command

The `diffuse` command works as expected with Sentaurus Process KMC, except that the diffusion is done with the atomistic solver. In particular, the options for oxidation and silicidation are supported (see [Oxidation on page 506](#)). Epitaxial options also are supported. For lattice LKMC epitaxy, see [Epitaxial Deposition on page 507](#).

## Nonatomistic Mode

When Sentaurus Process KMC operates in the nonatomistic mode (see [Nonatomistic Mode on page 374](#)), it transforms the five-stream model fields into atomistic information before every annealing and converts the atomistic information to five-stream model information after any annealing. Sentaurus Process KMC is disabled between annealings; consequently, all information should be accessed using the standard Sentaurus Process interface. The only way to access atomistic information is by using the `Movie` option during the Sentaurus Process KMC annealings.

The transformation from five-stream to atomistic information is performed in the function `preKMC` with the argument `diffuse` in the `KMC.tcl` file. The function `preKMC` is called automatically before a Sentaurus Process KMC diffusion in nonatomistic mode. After the diffusion, the function `postKMC`, with argument `diffuse`, is invoked to convert the atomistic information into five-stream fields. You can modify and customize both functions.

## Atomistic Mode

When operating in atomistic mode, Sentaurus Process KMC does not automatically perform any transformation from atomistic to continuum, or vice versa, except if the command `struct` is called (see [Atomistic Mode on page 371](#)).

---

## Calling Directly the Sentaurus Process KMC Kernel

The best way to access the atomistic information is by calling directly the Sentaurus Process KMC kernel using the `kmc` command. The option `extract` of this command accesses the KMC raw information directly and returns it in different formats, or creates a TDR file to be opened with Sentaurus Workbench Visualization.

## Writing and Displaying TDR Files with KMC Information

The command:

```
kmc extract tdrWrite filename=<filename>
```

creates files to be displayed by Sentaurus Workbench Visualization. This file contains a collection of states or snapshots. Each snapshot is taken at a particular time during the simulation; the collection of snapshots gives information about the time evolution during the simulation. Each snapshot can contain concentrations and histograms, atomistic information, or both. These snapshots are created with the command:

```
kmc extract tdrAdd [concentrations] [defects] [stress] [histogram]  
[visual={<fields>} [list={<fields>}]
```

The parameter `concentrations` includes a list of standard fields. These fields are the total concentration for each particle, the time-averaged concentrations of mobile particles, NetActive, the electronic concentration, the concentration of impurities in the surface, amorphous and impurity clusters, and the concentration of point defects in APs, amorphous layers, impurity clusters, and extended defects. These concentrations are displayed with the same dimension as the simulation.

Since Sentaurus Process KMC always works in 3D, for 1D simulations, the displayed concentrations are averaged for yz planes and, for 2D simulations, they are averaged in z-lines. An extra A/C field also is stored to let you know whether the material is amorphous or crystalline.

The `histogram` option includes a 2D graph representing the APs and impurity cluster histograms. These histograms give the number of defects existing in the simulation for each different size (*I* and *V* for APs, impurities, and point defects for impurity clusters). One-dimensional histograms, giving the number of extended defects versus its size, are included as well when using the `histogram` option. Stress and strain information can be added to these concentrations and histograms with the `stress` option.

[Figure 79 on page 533](#) shows one snapshot saved with the `concentrations` and `histogram` options for a 2D simulation.

Regarding NetActive, the parameter `KMC tdr smoothDopingConcentration` controls whether this concentration is smoothed. By default, it is not smoothed because smoothing it artificially decreases the channel length. On the other hand, the smooth algorithm partially removes irregularities and other atomistic features that may appear on the p-n junctions. This smoothing is different than the one controlled by `Smooth.Field` and is explained in [Smoothing Out Deatomized Concentrations on page 525](#).

While `smoothDopingConcentration` controls the smoothing of only `NetActive` in the Sentaurus Process KMC TDR file, `Smooth.Field` controls the smoothing of any field when translating the atomistic information into the continuum mesh concentration.

The parameter `defects` includes atomistic information about the defects in the simulation. This atomistic information can be used to obtain an atomistic 3D plot that is independent of the simulation dimensions. It offers the most realistic representation of the simulation.

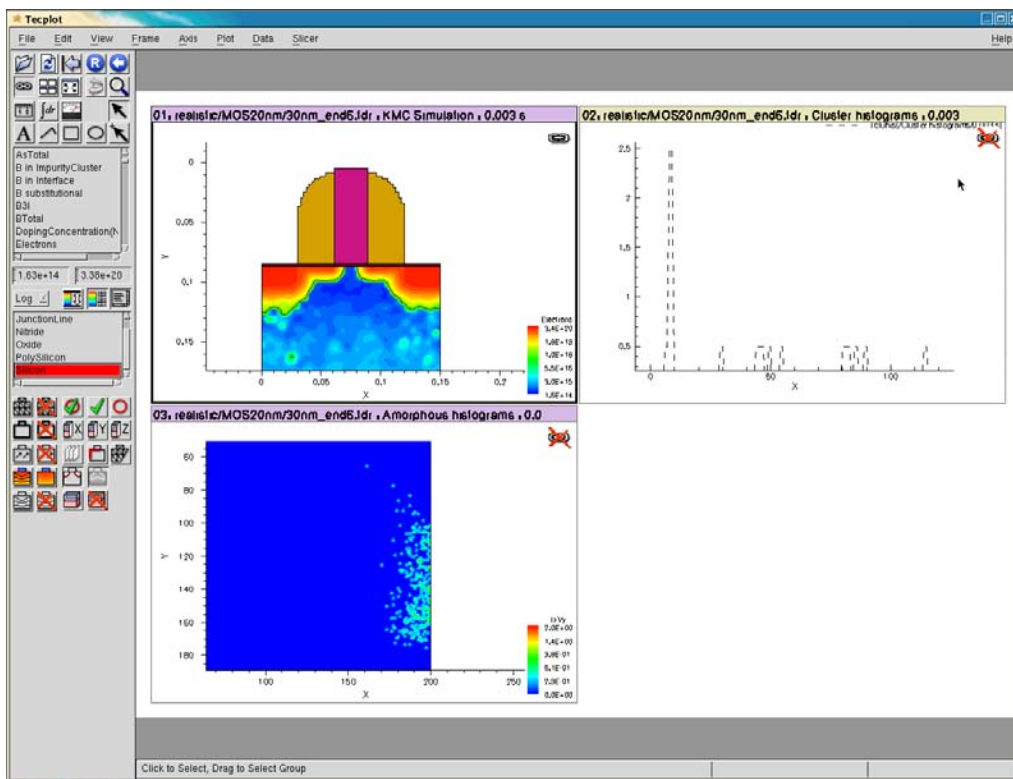


Figure 79 Example of a TDR file of Sentaurus Process KMC displayed with Sentaurus Workbench Visualization. The concentrations and histogram options have been used; 1D histograms for clusters and 2D histograms for APs and impurity clusters are included. The concentration (in this case, for a 2D simulation) for several fields is included with this option.

## 5: Atomistic Kinetic Monte Carlo Diffusion

### Extracting KMC-related Information

Figure 80 shows an example of the information saved with the `defects` option.

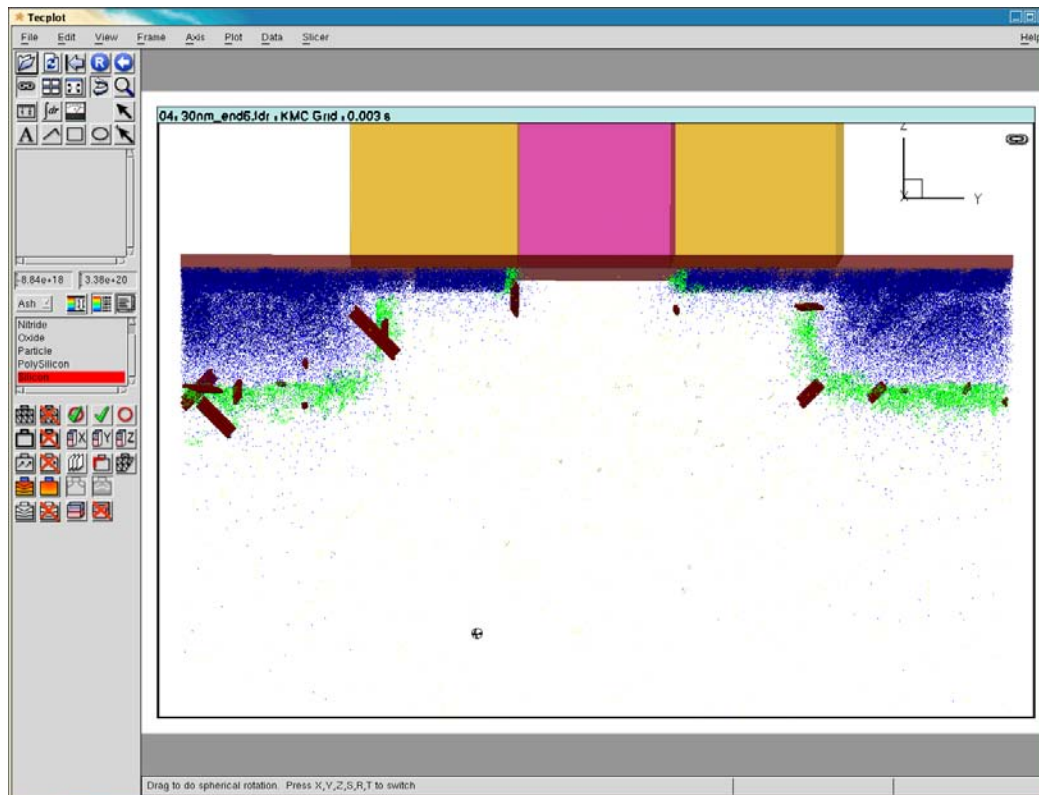


Figure 80 Example of TDR file of Sentaurus Process KMC including atomistic information; the `defects` option has been used

The `defects` option also includes extra information necessary to restart or load the simulation. A file saved with this parameter can be reloaded into Sentaurus Process KMC, and the simulation can be continued. To load the simulation, use the command `init`.

Using the `KMC Movie` option, you can include the command `kmc extract tdrAdd` to view the evolution of the simulation with time.

Finally, the option `visual` stores atomistic 3D information in a way similar to `defects`. The differences between using `visual` and `defects` are:

- Files saved with `visual` cannot be restarted.
- The `visual` option produces smaller file sizes than `defects`. In particular, `visual` stores the defects, but it does not store the information needed to restart. The `visual` files are intended for visualization purposes only.
- The `visual` option requires a list of defects, separated by commas, to be saved. The `all` option saves all the defects.



- Other valid defects include defect names (such as `BiM` or `B2I3`), general defect names (such as `ThreeOneOne`), and material names (`Silicon`). This lets you control which defects will be saved and visualized later, making it easier to visualize information without saving a large file with all the 3D information.

### Plotting Only Some Particles

Sentaurus Process visualization does not represent all the particles inside APs. Since the number of particles (interstitials and vacancies) in APs can be large after an implant, only 1 in 50 particles is visualized by default. This default behavior is written in the TDR file as set by the parameter `VisualizeDamage`:

```
sprocess> pdbGet KMC VisualizeDamage  
50
```

Sentaurus Process visualization can overwrite the default set for each file using the option:

```
-s:psf n
```

where `n` is the new value of `VisualizeDamage`:

**NOTE** Setting `VisualizeDamage` to 1 causes Sentaurus Workbench Visualization to plot all the particles present in the simulation. This number can be very large immediately after an implant.

### Time-averaged Concentration Name

The default field name for time-averaged concentrations in the TDR file is ‘mobile’, but it can be defined with the parameter `KMC tdr averageTag`.

---

## Inquiring about KMC Profiles, Histograms, and Defects

Besides the `select` command and the TDR files, you can access Sentaurus Process KMC information using the `kmc extract` command (see [kmc on page 954](#)):

- `kmc extract histogram`—extracts histograms for extended defects, impurity defects, and APs.
- `kmc extract profile`—extracts concentrations and stresses in 1D, 2D, and 3D.
- `kmc extract supersaturation`—extracts the concentration relative to the equilibrium concentration for point defects.
- `kmc extract defects`—obtains the atomistic information of the defects.
- `kmc extract dose`—extracts doses, that is, concentrations in  $\text{cm}^{-2}$ .

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- `kmc extract materials`—obtains information about the different materials in the simulation.
- `kmc extract acinterface`—obtains the position of the amorphous–crystalline interfaces in the simulation.

### The histogram Option

```
kmc extract histogram name= {
                             IV
                             BI
                             I
                             ...
                             [meansize [minsize=<n>]]
                             [materialname=<material>]
```

Sentaurus Process KMC includes several models where the defects are not isolated, but agglomerated in extended defects that can contain many particles. The `histogram` option allows you to extract information about the sizes (number of particles) of these extended defects.

The `histogram` option needs a valid name to compute the following available histograms:

Interstitial-extended defects	Set <code>name=I</code> to extract information about the small I clusters, {311} defects, and dislocation loops.
Vacancy-extended defects	Set <code>name=V</code> to extract information about the small V clusters and voids.
B interstitial clusters or other clusters with I	Set <code>name=XI</code> to extract information about the dopant named 'X'. For example, for boron impurity clusters (BICs), <code>name=BI</code> .
As vacancy clusters or other clusters with V	Set <code>name=XV</code> . For example, set <code>name=AsV</code> to extract information about the arsenic–vacancy clusters.
Cluster with multiple impurities	For example, set <code>name=PAAs</code> for clusters with both P and As.
Amorphous pockets	Set <code>name=IV</code> .

The optional parameter `meansize` displays the average size of clusters instead of displaying the whole list of clusters when using this parameter. Without specifying `minsize`, the average size begins with size 0.

Finally, the parameter `materialname` restricts the output to the material specified instead of the whole simulation.

## Interstitial Histograms

These histograms extract the number of defects in the simulation for each size. The histograms contain information about the small, irregular clusters (see [Amorphous Pockets Life Cycle on page 427](#)), {311} defects (for size bigger than the established limit), and dislocation loops. For example:

```
LogFile [kmc extract histogram name=I]
```

gives a list of extended defects with *I*. In this example:

```
sprocess> LogFile [kmc extract histogram name=I]
I2 302
I3 104
I4 42
I5 12
I6 4
I72 1
I677 1
sprocess> LogFile [kmc extract histogram name=I meansize]
4.11373
sprocess> LogFile [kmc extract histogram name=I meansize minsize=10]
374.5
```

## Vacancy-extended Defects Histogram

These histograms are similar to the interstitial-extended defects histogram, except that the extracted number of particles versus size is for vacancies:

```
sprocess> LogFile [kmc extract histogram name=V]
V5 1
V7 2
V8 5
V9 2
V10 5
(...)
sprocess> LogFile [kmc extract histogram name=V meansize]
12.9143
sprocess> LogFile [kmc extract histogram name=V meansize minsize=10]
15
```

## Amorphous Pockets Histogram

The AP histograms contain the number of cluster versus *I* and *V* size. APs with null *I*s or *V*s can be considered as APs or small *I* or *V* clusters.

```
sprocess> LogFile [kmc extract histogram name=IV]
I2 367
I3 69
```

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```
I4 22
I5 1
IV 823
I2V 249
I3V 61
I4V 23
I5V 2
V2 408
IV2 251
I2V2 111
(...)
```

The average size can be requested for these clusters. It will return values for both *I* and *V*:

```
sprocess> LogFile [kmc extract histogram name=IV meansize]
I2.3501V0.796781
```

The parameter `meansize` applies here and specifies the minimum size to begin the average for both species.

### Boron–Interstitial Clusters

The boron–interstitial cluster histogram offers information about the number of BICs for each BIC configuration ( $B_nI_m$ ).

```
sprocess> LogFile [kmc extract histogram name=BI]
B2I 16
B3I 347
sprocess> LogFile [kmc extract histogram name=BI meansize]
B2.95592I1
```

### Arsenic–Vacancy Clusters

The arsenic–vacancy cluster histogram offers information about the number of arsenic and vacancies in impurity clusters for each configuration ( $As_nI_m$ ):

```
sprocess> LogFile [kmc extract histogram name=AsV]
As2 277
As3 109
As4 3
As2V 752
As3V 281
As4V 178
sprocess> LogFile [kmc extract histogram name=AsV meansize]
As2.47V0.756875
```

## The profile Option

Sentaurus Process KMC computes the profiles concentration versus size as a convenient way to directly obtain useful data.

```
kmc extract profile [timeaveraged] name={
    holes
    electrons
    particles(B, Asp, ...)
    clusters(InVm, BnIm, ...)
    stress
    strain
    GapNarrowing
    dopants
    totals(BTotal, AsTotal)
}
```

```
[defectname={
    ThreeOneOne
    Interface
    Loop
    ...
}] [materialname=] [coordx=] [coorcy=] [coordz=]
```

For example, 1D profiles can be compared with SIMS experiments. The profiles are an average of the concentration of particles. For 3D, Sentaurus Process KMC takes a volume to be averaged equal to an element defined by the parameters `extractDeltaX`, `extractDeltaY`, and `extractDeltaZ`. For 2D and 1D, this volume includes all the elements in *y* and *z*, respectively.

The parameter `name` chooses the profiles to be obtained. `holes` and `electrons` return the concentration of holes and electrons, respectively. `GapNarrowing` returns the bandgap narrowing, in eV. Stress can be `stressXX`, `stressYY`, and `stressZZ`, and strain is one of `strainXX`, `strainXY`, `strainXZ`, `strainYX`, `strainYZ`, or `strainZY`. A particle name (like `Bi`, `IM`, or `AsVP`) returns the concentration of all the particles in the simulation matching the given one. A cluster name (for example, `As4V`) will return the concentration of that cluster in the simulation. For particles, the concentration of particles is returned; for clusters, the concentration of clusters is returned. For example, an `As4` cluster is considered to be four `As` particles when you request the concentration of `As`, but only one defect when you request the concentration of `As4` clusters. An impurity name followed by the word “Total”, like `BTotal`, will return the total profile of that impurity (active, inactive, in pairs, clusters and so on) in the simulation.

When a particle profile is specified, the optional parameter `defectname` can be used to further specify the kind of particle. For example, the command:

```
kmc extract profile name=I
```

computes the concentration of interstitials in any kind of defect, in other words, the total interstitial concentration.

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### Extracting KMC-related Information

The command:

```
kmc extract profile name=I defectname=ImpurityCluster
```

computes the concentration of interstitials in impurity clusters.

The parameter `defectname` should not be specified with cluster concentration, electrons, holes, `GapNarrowing`, stresses or strains.

Finally, the parameter `materialname` restricts the output to the material specified instead of the whole simulation.

The returned concentration has the same dimensionality as the performed simulation. Use the optional parameters `coordx`, `coordy`, and `coordz` to change this default. These parameters specify cutlines. For example, in a 3D simulation the command:

```
kmc extract profiles name=I
```

returns the concentration for all the volume elements in the simulation. The command:

```
kmc extract profiles name=I coordx=20<nm> coordz=10<nm>
```

returns a 1D profile with concentrations in the plane  $x = 20$  <nm> and  $z = 10$  <nm>.

Finally:

```
kmc extract profiles name=I coordx=20<nm> coordy=15<nm> coordz=10<nm>
```

returns only one value, the concentration at the specified point.

The use of the parameters `coordx`, `coordy`, and `coordz` depends on the simulation dimensions. As previously explained, specifying `coordx` for 1D, 2D, or 3D simulations, `coordy` for 2D or 3D, or `coordz` for 3D, returns the concentrations only on elements including the specified cutlines. On the other hand, the use of `coordy` or `coordz` in 1D simulations, or `coordz` in 2D, is quite different. In this case, the result returned is not averaged for the whole remaining dimensions ( $y$  and  $z$  for 1D,  $z$  for 2D), but only calculated in the specified cutlines. In other words, specifying `coordy` in a 3D simulation returns all the concentrations in the  $x, z$  volumes for the  $y$  specified in `coordy`; while specifying `coordy` in a 1D simulation returns concentrations versus the  $x$ -axis, but instead of being averaged for every  $y$  and  $z$ , they will be averaged only for every  $z$  in the plane marked by `coordy`. In 3D, it will reduce the size of the output (since only the output for the specified plane  $y$  is written). In 1D, the output has the same number of lines (one for each  $x$  position), but the concentration displayed is different because it is averaged into  $z$  only, and not into  $y$  and  $z$ .

Sentaurus Process KMC returns the instantaneous concentration by default. For mobile particles the instantaneous concentration does not usually contain any information rather than noise. The parameter `timeaveraged` instructs Sentaurus Process KMC to return the average

concentration of mobile particles between the current time and the last time Sentaurus Process KMC created a snapshot (see [Snapshots on page 394](#)).

For example, [Figure 81](#) has been produced with the input script:

```

pdbSet KMC MaxYum 40e-3
pdbSet KMC MaxZum 40e-3
SetAtomistic
pdbSet KMC Movie ""
pdbSet IncrementalHops 0
line x loc=0.0 tag=xleft spacing = 0.002
line x loc=1.5e-3 tag=xmed spacing = 0.002
line x loc=5e-3 tag=xright spacing = 0.002
region oxide xlo=xleft xhi=xmed
region silicon xlo=xmed xhi=xright

init
diffuse time=1e7<s> temp=700 info=1
kmc extract tdrClear
kmc extract tdrAdd concentrations
kmc extract tdrWrite filename=equil

```

The concentrations of neutral, positive, and negative interstitials also can be obtained with:

```

sprocess> kmc extract profile timeaveraged name=IP coordx=2.5<nm>
162487
sprocess> kmc extract profile timeaveraged name=I coordx=2.5<nm>
1.0276e+06
sprocess> kmc extract profile timeaveraged name=IM coordx=2.5<nm>
18170.5

```

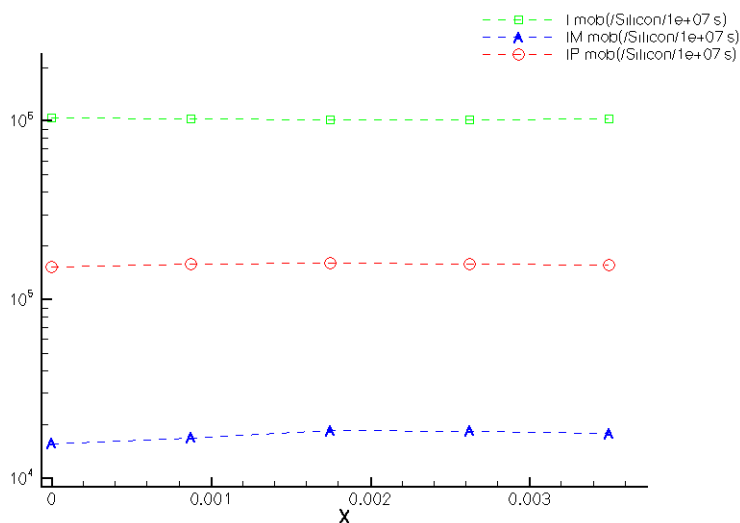


Figure 81 Equilibrium concentrations of neutral (green), positive (red), and negative (blue) interstitials at 700°C

## The supersaturation Option

```
kmc extract supersaturation name= $\begin{cases} I \\ V \end{cases}$ 
```

Supersaturation is the current concentration relative to the equilibrium concentration:

$$\text{supersaturation}(X) = \frac{[X]}{[X]^*} \quad (810)$$

Sentaurus Process KMC computes the supersaturation for *I*s and *V*s. The current global concentration is calculated involving a time average between the current time and the last snapshot:

```
sprocess> LogFile [kmc extract supersaturation name=I]  
1.00555
```

To obtain the supersaturation evolution with time, use the KMC *Movie* parameter as shown in the following example:

```
SetAtomistic  
set kmcSupersat ""  
pdbSet KMC MaxYum 30e-3  
pdbSet KMC MaxZum 30e-3  
pdbSet KMC Movie {lappend kmcSupersat $time [kmc extract \  
    supersaturation name=I]}  
pdbSet KMC automaticRampUp 1  
line x loc=0.0          tag=xleft spacing = 0.002  
line x loc=1.5e-3      tag=xmed  spacing = 0.002  
line x loc=350e-3     tag=xright spacing = 0.002  
region oxide  xlo=xleft xhi=xmed  
region silicon xlo=xmed xhi=xright  
  
init  
implant Silicon energy=40 dose=2e13 tilt=7  
diffuse time=100000<s> temp=600  
LogFile $kmcSupersat
```

produces the results:

```
10.0007 4.29101e+07  
21.5462 2.51728e+07  
46.4218 1.58636e+07  
100.004 1.41889e+07  
215.493 7.67109e+06  
464.238 3.44625e+06  
1000.26 1.86513e+06  
2156.46 477255  
4645.69 322049
```



```
10002.8 113849
21551.6 132116
46419.1 110329
100006 81506.4
```

Figure 82 shows a comparison with experimental results.

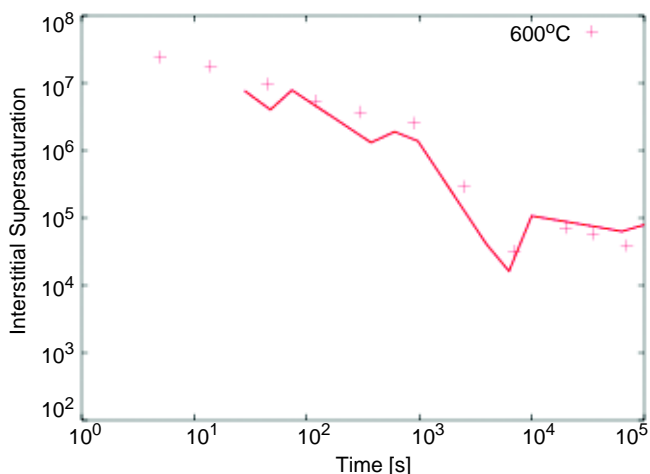


Figure 82 Supersaturation evolution with time, after a silicon implant ( $2 \times 10^{13}$  dose, 40 keV energy) annealed  $1 \times 10^5$  s at 600°C. (Experimental points modified from [50] to use the same B diffusivity.) Points are experiments, lines are KMC.

## The defects Option

The `defects` option allows access to the raw atomistic information of any simulation. The obtained information must match the parameters `name` and `defectname` when they are specified.

```
kmc extract defects [name = { particles(B, Ap, ...)
                           clusters(InVm, BnIm, ...) } ] [defectname = { ThreeOneOne
                                                                    Interface
                                                                    Loop
                                                                    ... } ]
```

```
[countparticles] [countdefects] [materialname=<material>]
[acinterface]
```

When there are no restrictions, all defects are accessed. For example, for the following added defects:

```
kmc add queue name=BI2 coordx=2<nm> coordy=2<nm> coordz=3<nm>
kmc add queue name=I2 coordx=3<nm> coordy=2e-3 coordz=4e-3
kmc add queue name=I3 coordx=4<nm> coordy=3<nm> coordz=1<nm>
kmc add
```

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The obtained defects are:

```
sprocess> kmc extract defects
0.00201273      0.00238963 0.00298179   I ImpurityCluster 0
0.00196125      0.00204962 0.00249501   I ImpurityCluster 0
0.00177392      0.00225923 0.00247647   B ImpurityCluster 0
0.00320253      0.00162722 0.00466375   I AmorphousPocket 1
0.00222551      0.00139856 0.004411     I AmorphousPocket 1
0.0044946       0.00317389 0.00130069   I AmorphousPocket 2
0.00441116      0.00353071 0.000842549  I AmorphousPocket 2
0.00403856      0.00351353 0.00084327   I AmorphousPocket 2
sprocess> kmc extract defects name=I
0.00201273      0.00238963 0.00298179   I ImpurityCluster 0
0.00196125      0.00204962 0.00249501   I ImpurityCluster 0
0.00320253      0.00162722 0.00466375   I AmorphousPocket 1
0.00222551      0.00139856 0.004411     I AmorphousPocket 1
0.0044946       0.00317389 0.00130069   I AmorphousPocket 2
0.00441116      0.00353071 0.000842549  I AmorphousPocket 2
0.00403856      0.00351353 0.00084327   I AmorphousPocket 2
sprocess> kmc extract defects name=I defectname=ImpurityCluster
0.00201273      0.00238963 0.00298179   I ImpurityCluster 0
0.00196125      0.00204962 0.00249501   I ImpurityCluster 0
sprocess> kmc extract defects name=BI2
0.00201273      0.00238963 0.00298179   I ImpurityCluster 0
0.00196125      0.00204962 0.00249501   I ImpurityCluster 0
0.00177392      0.00225923 0.00247647   B ImpurityCluster 0
```

The six columns present in the output are:

- X-coordinate of the defect
- Y-coordinate of the defect
- Z-coordinate of the defect
- Particle name
- Defect name.
- Number of defect. Particles with the same number belong to the same defect.

**NOTE** The command `kmc extract defects` can produce large outputs.

When there are amorphous defects in the simulation, the result may not be the expected. Amorphous defects do not store the damage, but only its concentration (see [Amorphous Defects on page 444](#)). Consequently, amorphous defects will not report any interstitial or vacancy inside them. Impurities are stored and displayed. Nevertheless, if the indirect diffusion model is used in amorphous silicon, the dangling bonds, floating bonds, and mobile and immobile impurities will be obtained as I, V, Bi and B (for boron) (see [Indirect Diffusion on page 445](#)).

The parameter `materialname` restricts the output to the material specified instead of the whole simulation.

The options `countparticles` and `countdefects` do not display the atomistic information, but they count the number of particles and defects, respectively, for the given conditions. For example, this example shows how to count the particles and defects listed in the last example:

```
sprocess> kmc extract defects countparticles
8
sprocess> kmc extract defects countdefects
3
sprocess> kmc extract defects name=I countparticles
7
sprocess> kmc extract defects name=I defectname=AmorphousPocket countdefects
2
```

The parameter `acinterface` displays the lattice atoms belonging to the amorphous–crystalline interface. All the lattice atoms can be obtained by using `acinterface detailed`. This parameter generates an output only when the LKMC model is used for recrystallization (see [LKMC: Fully Atomistic Modeling of Solid Phase Epitaxial Regrowth on page 451](#)).

## The dose Option

The `dose` option extracts the concentration per surface unit (in other words,  $\text{cm}^{-2}$ ) for the whole simulation cell. `dose` can be used to look at the evolution of the species with the time.

$$\text{kmc extract dose} \left[ \text{name} = \begin{cases} \text{Particles}(I, AsV, B_i, \dots) \\ \text{Defects}(I_n, V_n, I_n V_m, B_n I_m, \dots) \\ \text{Totals}(AsTotal, BTotal, \dots) \end{cases} \right]$$

$$\left[ \text{defectname} = \begin{cases} \text{ImpurityCluster} \\ \text{ThreeOneOne} \\ \dots \end{cases} \right] [\text{countdefects}] [\text{materialname}=\langle\text{material}\rangle]$$

The parameters `name` and `defectname` restrict the species to compute the dose. `name` can be any particle or defect. `defectname` can be specified only when `name` is a particle, and it restricts the particles to be of the specified type. A list of defect types is obtained with `kmc defecttypes`. A “total” name: the name of an impurity followed by the work “Total”, like `BTotal`, applies to all the circumstances where the specified impurity is present, that is, in clusters, substitutional, pairs, and so on.

This command counts the number of particles (such as `kmc extract defects` with the same restrictions and the `countparticles` option) and it divides this number by the surface area. Finally, the parameter `materialname` restricts the output to the material specified

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instead of the whole simulation. For interfaces, instead of specifying a material name, specify a particle name such as `AsInterface`, `BInterface`.

As an example, the following input file implants silicon into silicon and extracts the dissolution of {311} during annealing:

```
set silicon_depth 350e-3
set size 50e-3
set SiO2gate 1.5e-3
SetAtomistic
set sol ""
pdbSet KMC Movie {lappend sol $time [kmc extract dose name=I \
    defectname=ThreeOneOne]}
pdbSet KMC MaxZum $size
pdbSet KMC MaxYum $size
pdbSet KMC GasUm $SiO2gate
pdbSet KMC automaticRampUp true
line x loc=0.0          tag=xtop    spacing = 0.002
line x loc=$silicon_depth tag=xbottom spacing = 0.002
region silicon xlo=xtop xhi=xbottom

init
deposit oxide fill coord=[expr -$SiO2gate]
implant silicon energy=40 dose=5e13 tilt=7
diffuse time=3100 temp=670
LogFile $sol
```

This example produces the results:

```
46.4176 2.88e+12
100.01 9.56e+12
215.464 1.104e+13
464.175 1.596e+13
1000 2.172e+13
2154.45 3.144e+13
4641.63 3.736e+13
10000 3.044e+13
21544.5 1.388e+13
46417.4 9.6e+11
100233 0
```

Figure 83 shows the comparison with experimental data [8].

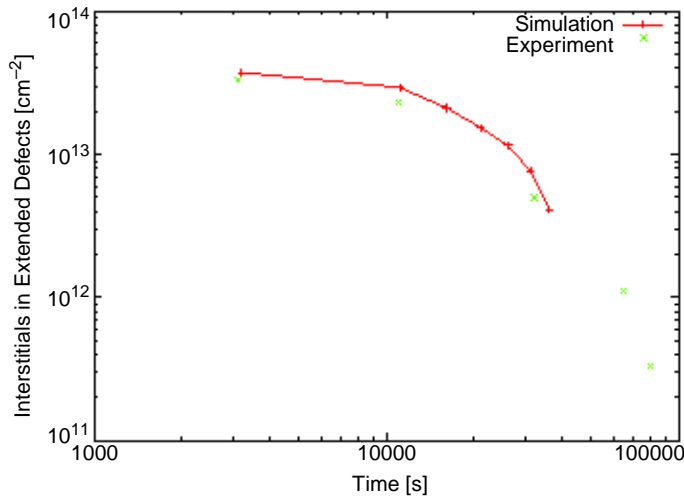


Figure 83 Dissolution of {311} extended defects at 670°C after a silicon into silicon implant of 40 keV,  $5 \times 10^{13} \text{ cm}^{-2}$

## The materials Option

```
kmc extract materials [detailed] [coordx=] [coorxy=] [coordz=]
```

The command `kmc extract materials` produces the list of materials currently in the simulation:

```
sprocess> kmc extract materials
Silicon Oxide Gas
```

The option `detailed` produces a list of coordinates and materials. This list contains the same number of dimensions as the simulation (except if you use `coordx`, `coorxy`, or `coordz`). For example, in a 1D simulation:

```
sprocess> kmc extract materials detailed
-0.002 Gas
-0.000625 Oxide
0.00075 Oxide
0.002125 Oxide
0.0035 Oxide
0.004875 Oxide
0.00625 Oxide
0.007625 Oxide
0.009 Oxide
0.010375 Silicon
0.01175 Silicon
0.013125 Silicon
0.0145 Silicon
```

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```
0.015875 Silicon
0.01725 Silicon
```

The parameters `coordx`, `coordy`, and `coordz` affect the output of `detailed` by changing its dimensionality. They work exactly the same as in `kmc extract profile` (see [The profile Option on page 539](#)).

### The `acinterface` Option

```
kmc extract acinterface [coordx=] [coordy=] [coordz=]
```

The command `kmc extract acinterface` produces the list of amorphous–crystalline interfaces found in the simulation given a 1D cutline. No extra options are needed in 1D. In 2D, you must specify `coordx` or `coordy`. In 3D, you must specify two of three parameters `coordx`, `coordy`, and `coordz`. For example, in 1D:

```
sprocess> kmc extract acinterface
Silicon Amorphous/Crystalline 0.0165
```

When the KMC model for SPER is detected, the option `acinterface` displays all the places where the amorphous–crystalline field crosses the threshold specified in `KMC ACInterfaceAt`. A value of 1 means perfectly amorphous and 0 means perfectly crystalline. The default value is 0.9. The output also displays the materials at both sides of the interface, displaying first the material with a smaller coordinate value. In this case, the interface is at 0.0165  $\mu\text{m}$ , and the transition is from Amorphous to Crystalline as the x-coordinate increases. When the LKMC model is used for SPER, the parameter `ACInterfaceAt` is ignored, and a more precise interface is extracted directly from the LKMC atomistic information.

---

## Common Dopant and Point-Defect Names

Several KMC commands contain a `name=<particlename>` parameter. [Table 60 on page 549](#) lists several of these names and the commands where they are applicable. Since dopants can be defined as needed, the names depend on the simulation parameters. In particular, they contain names defined when using Advanced Calibration. A list of the names can be obtained using `kmc particletypes`. Clusters also are included in the list. Since the number of different clusters is large, only a partial cluster list is included as an example (see [Table 61 on page 552](#)).

The commands considered for the referenced tables, and the symbols used to represent them, are:

- `kmc add queue` (Add)
- `kmc extract profile` (Pro)
- `kmc extract histograms` (His)

- `kmc extract dose (Dos)`
- `kmc extract defects (Def)`
- `kmc extract supersaturation (Sup)`
- `kmc deatomize (Dea)`
- `kmc present (Pre)`

The defects used in the descriptions are:

- Point defects, self-silicon point defects like interstitials and vacancies.
- Extended defects, agglomeration of self-silicon point defects.
- Clusters, agglomeration of impurities or dopants, with or without point defects.
- Substitutional dopants or impurities.
- Paired dopants or impurities, paired with point defects.
- Amorphous pockets, agglomeration of point defects (also sometimes called *damage*).
- Defects attached to interfaces.

Table 60 Names used in Sentaurus Process KMC

Name	Description	Used in
I	Neutral interstitial in point defects, clusters, and extended defects	Sup, His, Add, Pro, Dos, Def, Dea, Pre
IMM	$I^-$ , point defect	Add, Pro, Dos, Def, Dea, Pre
IM	$I^+$ , point defect	Add, Pro, Dos, Def, Dea, Pre
IP	$I^+$ , point defect	Add, Pro, Dos, Def, Dea, Pre
IPP	$I^{++}$ , point defect	Add, Pro, Dos, Def, Dea, Pre
ITotal	Total interstitial concentration; similar to $I + IMM + IM + IP + IPP$	Dea, Pre, Pro, Dos
V	Neutral vacancy in point defects, clusters, and extended defects	Sup, His, Add, Pro, Dos, Def, Dea, Pre
VMMM	$V^{--}$ , point defect	Add, Pro, Dos, Def, Dea, Pre
VMM	$V^-$ , point defect	Add, Pro, Dos, Def, Dea, Pre
VM	$V^+$ , point defect	Add, Pro, Dos, Def, Dea, Pre
VP	$V^+$ , point defect	Add, Pro, Dos, Def, Dea, Pre
VPP	$V^{++}$ , point defect	Add, Pro, Dos, Def, Dea, Pre
VPPP	$V^{+++}$ , point defect	Add, Pro, Dos, Def, Dea, Pre
VTotall	Total vacancy concentration; similar to $V + VMMM + VMM + VM + VP + VPP + VPPP$	Dea, Pre, Pro, Dos

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 Extracting KMC-related Information

Table 60 Names used in Sentaurus Process KMC

Name	Description	Used in
B	Boron, substitutional, at interfaces or in clusters	Add, Pro, Dos, Def, Dea, Pre
BV	Neutral-paired defect, boron vacancy	Add, Pro, Dos, Def, Dea, Pre, His
BVM	BV <sup>-</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
BVP	BV <sup>+</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
Bi	Neutral-paired defect, boron interstitial	Add, Pro, Dos, Def, Dea, Pre, His
BiM	Bi <sup>-</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
BiP	Bi <sup>+</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
BTotal	Total boron concentration; similar to B + BV + BVM + BVP + Bi + BiM + BiP	Dea, Pre, Pro, Dos
BInterface	Boron at interfaces	Add, Pro, Dos, Def, Dea, Pre
As	Arsenic, substitutional at interfaces or in clusters	Add, Pro, Dos, Def, Dea, Pre
AsV	Neutral-paired defect of arsenic and a vacancy	Add, Pro, Dos, Def, Dea, Pre, His
AsVM	AsV <sup>-</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
AsVP	AsV <sup>+</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
Asi	Neutral-paired defect of arsenic and an interstitial	Add, Pro, Dos, Def, Dea, Pre, His
AsiM	Asi <sup>-</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
AsiP	Asi <sup>+</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
AsTotal	Total arsenic; similar to As + AsV + AsVM + AsVP + Asi + AsiM + AsiP	Dea, Pre, Pro, Dos
AsInterface	Arsenic attached at interfaces	Add, Pro, Dos, Def, Dea, Pre
C	Carbon, substitutional, at interfaces or in clusters	Add, Pro, Dos, Def, Dea, Pre
CV	Neutral-paired defect of carbon and a vacancy	Add, Pro, Dos, Def, Dea, Pre, His
Ci	Neutral-paired defect of carbon and an interstitial	Add, Pro, Dos, Def, Dea, Pre, His
CInterface	Carbon attached at interfaces	Add, Pro, Dos, Def, Dea, Pre
CTotal	Total carbon; similar to C + CV + Ci	Dea, Pre, Pro, Dos
F	Fluorine, substitutional at interfaces or in clusters	Add, Pro, Dos, Def, Dea, Pre
FI	Neutral-paired defect of fluorine with an interstitial	Add, Pro, Dos, Def, Dea, Pre, His
FV	Neutral-paired defect of fluorine with a vacancy	Add, Pro, Dos, Def, Dea, Pre, His
FTotal	Total fluorine; similar to F + FI + FV	Dea, Pre, Pro, Dos



Table 60 Names used in Sentaurus Process KMC

Name	Description	Used in
FInterface	Fluorine attached at interfaces	Add, Pro, Dos, Def, Dea, Pre
In	Indium, substitutional, at interfaces or in clusters	Add, Pro, Dos, Def, Dea, Pre
InV	Neutral-paired defect of indium and a vacancy	Add, Pro, Dos, Def, Dea, Pre, His
InVM	InV <sup>-</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
InVP	InV <sup>+</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
Ini	Neutral-paired defect of indium and an interstitial	Add, Pro, Dos, Def, Dea, Pre, His
IniM	Ini <sup>-</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
IniP	Ini <sup>+</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
InTotal	Total indium; similar to In + InV + InVM + InVP + Ini + IniM + IniP	Dea, Pre, Pro, Dos
InInterface	Indium attached at interfaces	Add, Pro, Dos, Def, Dea, Pre
P	Phosphorus, substitutional, at interfaces or in clusters	Add, Pro, Dos, Def, Dea, Pre
PV	Neutral-paired defect of phosphorus and a vacancy	Add, Pro, Dos, Def, Dea, Pre, His
PVM	PV <sup>-</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
PVP	PV <sup>+</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
Pi	Neutral-paired defect of phosphorus and an interstitial	Add, Pro, Dos, Def, Dea, Pre, His
PiM	Pi <sup>-</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
PiP	Pi <sup>+</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
PTotal	Total phosphorus; similar to P + PV + PVM + PVP + Pi + PiM + PiP	Dea, Pre, Pro, Dos
PInterface	Phosphorus attached at interfaces	Add, Pro, Dos, Def, Dea, Pre
Sb	Antimony, substitutional, at interfaces or in clusters	Add, Pro, Dos, Def, Dea, Pre
SbV	Neutral-paired defect of antimony and a vacancy	Add, Pro, Dos, Def, Dea, Pre, His
SbVM	SbV <sup>-</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
SbVP	SbV <sup>+</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
Sbi	Neutral-paired defect of antimony and an interstitial	Add, Pro, Dos, Def, Dea, Pre, His
SbiP	Sbi <sup>+</sup> , paired defect	Add, Pro, Dos, Def, Dea, Pre
SbTotal	Total antimony; similar to Sb + SbV + SbVM + SbVP + Sbi + SbiP	Dea, Pre, Pro, Dos

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Table 60 Names used in Sentaurus Process KMC

Name	Description	Used in
SbInterface	Antimony at interfaces	Add, Pro, Dos, Def, Dea, Pre
N	Nitrogen, substitutional, at interfaces or in clusters	Add, Pro, Dos, Def, Dea, Pre
NTotal	Total nitrogen, same as N	Dea, Pre, Pro, Dos
NInterface	Nitrogen at interfaces	Add, Pro, Dos, Def, Dea, Pre
Nn	N <sub>2</sub> , substitutional, at interfaces or in clusters	Add, Pro, Dos, Def, Dea, Pre
NnV	Moving N <sub>2</sub> V particle	Add, Pro, Dos, Def, Dea, Pre, His
NnTotal	Similar to Nn + NnV	Dea, Pre, Pro, Dos
NnInterface	N <sub>2</sub> stored at the interface	Add, Pro, Dos, Def, Dea, Pre
H	Hydrogen, substitutional, at interfaces or in clusters	Add, Pro, Dos, Def, Dea, Pre
HTotal	Total hydrogen, only H	Dea, Pre, Pro, Dos
HInterface	Hydrogen at interfaces	Add, Pro, Dos, Def, Dea, Pre
Ge	Germanium (stored as a field, not as a particle)	Add, Pro, Dos, Def, Dea, Pre

Table 61 Some cluster names used in Sentaurus Process KMC

Name	Comment	Used in
IV	Interstitial–vacancy amorphous pocket.	His, Add, Pro, Dos, Def, Dea, Pre
I3V2	Amorphous pocket. Any other I <sub>x</sub> V <sub>y</sub> with x and y integers is also valid.	Add, Pro, Dos, Def, Dea, Pre
I8	Extended defect formed by eight interstitials. Any other I <sub>x</sub> , where x is an integer, is also valid.	Add, Pro, Dos, Def, Dea, Pre
V4	Extended defect formed by four vacancies. Any other V <sub>x</sub> , with x an integer, is valid.	Add, Pro, Dos, Def, Dea, Pre
B2I3	Boron–interstitial cluster. Other integers are also valid.	Add, Pro, Dos, Def, Dea, Pre
As4V	Arsenic–vacancy cluster. Other integers are also valid.	Add, Pro, Dos, Def, Dea, Pre
B2IC3	Dopant cluster. Any combination of dopants with (or without) interstitials or vacancies is valid.	Add, Pro, Dos, Def, Dea, Pre
P2As2I	Another example for dopant cluster	Add, Prod, Dos, Def, Dea, Pre

---

## Advanced Calibration for Sentaurus Process KMC

The default parameters used in Sentaurus Process KMC are inherited from previous versions of Sentaurus Process KMC and may not be accurate for modern processing conditions. A more accurate calibration for Sentaurus Process KMC has been performed by the Advanced Calibration team and is available using the command:

```
AdvancedCalibration
```

This command includes the calibration of point-defect diffusivity, extended defects formation and dissolution, boron diffusivity, boron–interstitial clustering process (activation and deactivation of boron), surface trapping and re-emission of boron, and so on.

This command must be written after `SetAtomistic` since it detects the presence of an atomistic simulation to load the Advanced Calibration parameters related to Sentaurus Process KMC:

```
SetAtomistic  
...  
AdvancedCalibration
```

In cases where Advanced Calibration for Sentaurus Process KMC must be loaded, but it is not possible to call it after `SetAtomistic`, the following workaround can be used. In particular, this is the preferred mode to call Advanced Calibration for Sentaurus Process KMC in hybrid simulations, and the only way to do it when using the `kmc` option in the `diffuse` command:

```
pdbSet AtomisticData 1  
AdvancedCalibration  
pdbSet AtomisticData 0
```

**NOTE** For more information on the Advanced Calibration parameters and methodology, refer to the *Advanced Calibration for Process Simulation User Guide*.

**NOTE** The use of Advanced Calibration is strongly recommended.

---

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References



## CHAPTER 6 Alagator Scripting Language

---

*This chapter discusses the Alagator scripting language, which is used to specify partial differential equations and boundary conditions for use with diffusion simulations.*

The equations are expressed in a Newton iteration–ready form. They are specified as text strings that are assumed to be equal to zero. Most mathematical operators are supported to specify equations, and various operators for differential terms are available. For terms that include the gradient (`grad`) operator, Sentaurus Process automatically calculates the divergence. It is not necessary to specify the divergence in the equations.

Binary operators, functions, constants, and parameters are supported. Care must be exercised with Tcl expansion of variables and strings, as usually users want variables to be evaluated at run-time, not when they are read.

---

### Operators

The Alagator language operators and variables consist of binary operators, simple functions, differential functions, string names, solution names, subexpressions, constants, and parameters.

---

### Binary and Unary Operators

Most common binary algebraic operators are supported. Addition (+), subtraction (–), multiplication (\*), and division (/) are included. Unary negation is also supported with the usual mathematical rules applying. Typical precedence rules apply (see [Table 62 on page 560](#)). Parentheses are supported for grouping operations. In addition to the basic four mathematical operators, power (^) is also supported; for example,  $a^b$  raises  $a$  to the  $b$  power.

**NOTE** The Tcl command `expr pow(a,b)` is not supported in the Alagator language when  $a$  and  $b$  do not evaluate to an integer or double value.

Many comparison operators are implemented. These do not support derivative operations, so they cannot be used in the gradient expression. However, they can be used in the `select` command (see [select on page 1053](#)). The operators `>`, `<`, `>=`, `<=`, `==`, and `!=` are implemented

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### Operators

with their usual meanings. Care must be used with equals and not equals, since a comparison of floating point values in this way can be problematic.

Table 62 Operator precedence

Operator	Description	Operator	Description
$\wedge$	Power	$\&\&$	Logical <i>and</i>
$-$	Unary minus	$\ \ $	Logical <i>or</i>
$*, /$	Multiplication, division	$?:$	Conditional operator
$+, -$	Addition, subtraction	$,$	Comma operator for lists
$<, <=, >=, >, ==, !=$	Equality, inequality		

Logical operators *and* ( $\&\&$ ) and *or* ( $\|\|$ ) are also provided for use with callbacks and initialization. When these operators are used as part of a differential equation, care must be taken as the Newton method does not ensure convergence for problems that are not first-order continuous.

In addition to these, a conditional operator ( $?:$ ) is provided, which takes three operands. The first operand is a condition, the second operand is the value of the entire conditional expression if the condition is true, and the third operand is the value of the entire conditional expression if the expression is false. For example, the command:

```
sel z = "(Vac>1e15) ? (1e15) : (Vac)" name = Vac
```

sets the value of  $Vac$  to  $1 \times 10^{15}$  on mesh points where  $Vac$  is greater than  $1 \times 10^{15}$  and does not change  $Vac$  on mesh points where  $Vac$  is smaller than  $1 \times 10^{15}$ . Since the `select` command works on mesh nodes, the conditional operator is very useful for truncating profiles.

---

## Simple Functions

All simple functions take one argument that must be enclosed in parentheses. The argument can be any expression. Most common functions are available, including 'exp' natural exponentiation, 'log' natural log, 'log10' log base 10, and 'sqrt' square root. Additionally, the complementary error function 'erfc' and error function 'erf' are provided to help build initial doping profiles. All of these functions have supported derivatives and can be used in the specification of partial differential equations (PDE).

'abs' and 'sign' provide an absolute value and sign operation. The sign operation is positive if the argument is greater than zero and minus one for less than zero. These functions do not provide derivatives and cannot be used as part of a differential equation.

---

## Differential Functions

The differential functions are used in partial differential equations only and are not evaluated with the `select` command. There are two differential operators: `ddt` and `grad`. Time derivatives are supported with the `ddt` operator. It takes a single argument and computes the first-time derivative of the argument for use in a partial differential equation. Time-step integration is provided automatically using the Bank–Rose TRBDF method [1].

Spatial derivatives are supported in two ways. A simple gradient is supported with `grad`. Implied is the evaluation in a discrete sense and the integral around a control volume. For this reason, `div` is not required. For example, `A*B*grad(C)` is treated as `div(A*B*grad(C))`.

---

## Special Functions

### The `diag` Operator

The special operator `diag` provides the modeling of anisotropic diffusion. The special operator (anisotropic diffusion matrix) has the form:

$$\text{diag}(a, b, c) \equiv \begin{bmatrix} a & 0 & 0 \\ 0 & b & 0 \\ 0 & 0 & c \end{bmatrix} \quad (811)$$

where `a`, `b`, and `c` are any valid Alagator expression. It also can include diffusion solution variables. For discretization, the `diag` operator projects the vector to the edge direction. For 1D structures, `a` must be specified. For 2D structures, `a` and `b` must be specified. For 3D structures, `a`, `b`, and `c` must be defined.

The following expressions are valid:

```
ddt(C1)-D1*diag(a,b,c)*grad(C1)
ddt(C1)-D1*diag(a,b,c)*grad(C1)-D2*diag(g,h,i)*grad(C2)
ddt(C1)-D1*diag(a,b,c)*grad(C1)-D2*grad(C2)
# Addition of two diag operators (diag(...)+diag(...))
ddt(C1)-(D1*diag(a,b,c)+D2*diag(g,h,i))*grad(C1)
```

The following expressions are not valid:

```
# Multiplication of two diag operators (diag(...)*diag(...))
ddt(C1)-(D1*diag(a,b,c)*diag(g,h,i))*grad(C1)
# Division of two diag operators (diag(...)/(diag(...))
ddt(C1)-(D1*diag(a,b,c)/diag(g,h,i))*grad(C1)
```

## 6: Alagator Scripting Language

### Operators

```
# Addition of a diag operator with a constants (diag(...)+C)
ddt(C1)-(D1*diag(a,b,c,d,e,f)+D2)*grad(C1)
```

You can use built-in functions to define anisotropy. For example:

$$\text{diag}\left(e^{\frac{3\sigma_x}{kT}}, e^{-\frac{2\sigma_y}{kT}}, 1\right) \equiv \begin{bmatrix} e^{\frac{3\sigma_x}{kT}} & 0 & 0 \\ 0 & e^{-\frac{2\sigma_y}{kT}} & 0 \\ 0 & 0 & 1 \end{bmatrix} \quad (812)$$

```
term name=BoronDiffFactor Silicon add eqn = "diag(exp(3.0*ElasticStrainKK_x \
* [simDelayDouble Diffuse Vt]),exp( -2.0 * ElasticStrainKK_y * \
[simDelayDouble Diffuse Vt]),1.0)"
```

The above command makes the effective diffusivity of boron anisotropic. If `<dopant>DiffFactor` (see [Alagator for Diffusion on page 563](#)) is already defined (that is, `AdvancedCalibration`), perform the following:

```
set locterm [term name=BoronDiffFactor Silicon print]
term name=BoronDiffFactor Silicon add eqn = "($locterm) * \
(diag(exp(3.0*ElasticStrainKK_x * [simDelayDouble Diffuse Vt]), \
exp( -2.0 * ElasticStrainKK_y * [simDelayDouble Diffuse Vt]),1.0))"
```

---

## String Names

Strings that are not recognized as real numbers, operators, or functions are handed to the resolution phase of the parser. These strings are compared to four sets of possible matches. The first set is valid solution names created with the `solution` command (see [solution on page 1076](#)). The second set is the data field name. The third set is named subexpressions created with the `term` command (see [term on page 1099](#)). Finally, any remaining strings are passed to the Tcl expression function to see if they can be parsed to a real number constant. This allows parameters from the parameter database to be used in differential equations.

---

## Solution Names and Subexpressions: Terms

Solution names (for example, `Boron, 311`) must match the string exactly as specified in the `solution` command (see [solution on page 1076](#)). These are the most important resolutions since they allow linking of the equations to the variables to be solved. Derivatives are automatically taken of all equations with respect to each solution name found in the equation. Terms are useful for common subexpressions. The string used in the equations must match exactly the name given in the `term` command (see [term on page 1099](#)).

---

## Constants and Parameters

Anything that does not match a term or solution is handed to the Tcl expression parser to see if it evaluates as a valid expression. The result is treated as a constant. The evaluation of the expression is performed again in the code if the temperature or time changes, so that parameters can have explicit dependencies on these values.

When defining parameters, care must be given to the nested declaration. Especially when parameters are derived using the `pdbDelayDouble` command from other parameters, the Tcl expression parser may be unable to expand the whole expression and evaluate it correctly. For example:

```

pdbSetDouble Si Test Param1 {[Arr 1 2]} (1)
pdbSetDouble Si Test Param2 {2.0*[pdbDelayDouble Si Test Param1]}(2)
pdbSetDouble Si Test Param3 {2.0*[pdbGetDouble Si Test Param1]}(3)
pdbGet Si Test Param2 (4)
pdbGet Si Test Param3 (5)

```

The first three lines set `Param1`, `Param2`, and `Param3`. `Param2` and `Param3` are derived parameters from `Param1`. While `Param2` uses `pdbDelayDouble` to obtain the value of `Param1`, `Param3` uses `pdbGetDouble`. When retrieving data, line 4 will return an error message and line 5 will return a valid double number without an error message. The error message is issued because `pdbDelayDouble` returns an expression of `Param1`, which is treated as a string by the Tcl parser during the evaluation of `Param2`. To prevent such errors, `Param2` can be encapsulated with the `expr` command:

```

pdbSetDouble Si Test Param2 {[expr 2.0*[pdbDelayDouble Si Test Param1]]}

```

**NOTE** If Sentaurus Process cannot evaluate an expression correctly, it assumes that it is zero.

---

## Alagator for Diffusion

In this section, an example is used to illustrate how to specify equations using the Alagator scripting language. The general expression for diffusion of species  $C_X$  is given by:

$$\frac{\partial C_X}{\partial t} = \nabla \cdot D \nabla C_X \quad (813)$$

and will be translated to Alagator language as:

```

ddt(CX)-D*grad(CX) = 0

```

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where `CX` is the solution variable and `D` is the diffusivity term (see [Solution Names and Subexpressions: Terms on page 562](#)).

**NOTE** Do not specify the `div` operator in front of `D*grad(CX)`; `div` is implied.

**NOTE** The `grad` operator must work on function of solution variable.

**NOTE** Since the examples given in this chapter use parameters that are not in the PDB, long-hand `pdbSet` commands are used (see [pdbSet and Related Functions on page 1005](#)).

---

## Basics

The simplest diffusion equation uses a constant diffusivity and can be described by Fick's first law and second law. Two main steps are required to initialize and solve this equation. First, a solution must be defined (see [solution on page 1076](#)). Second, the equation must be entered into the parameter database.

A minimum of two commands can be used to accomplish this, for example:

```
solution name=CX add !negative !damp solve
pdbSetString Silicon CX Equation "ddt(CX) - 1e-15*grad(CX)"
```

The first line creates a new solution named `CX` and adds it to the solution list. The solution cannot take negative values and numeric damping is not applied to the updates of the Newton iteration. The solution is always to be solved.

**NOTE** Aliases are defined only for `pdb` commands. In the above example, the solution name used in the definition of partial differential equations must match the one defined with the `solution` command.

The second line makes an entry into the parameter database. This is created for the material `Silicon` and the solution variable `CX`. An entry is made for an `Equation`, which is the predefined entry that Alagator looks for to find a differential equation. The string value set is the differential equation that will be solved for this variable in this material. The equation uses a time operator (`ddt`) and gradient operator (`grad`) to implement a simple diffusion equation. The divergence operator is implied and computed as part of the discretization of the equations. Whenever a gradient operator `grad` is in an Alagator script, it is assumed that the divergence will be taken of that term during assembly.

In this example, the equation to be solved is  $d(CX)/dt - \text{div}(1.0e-15 * \text{grad}(CX)) = 0$ . The solution name in the equation (`CX`) must also be identical to the name in the `solution` command. The diffusivity in this example is hard wired to be  $10^{-15} \text{ cm}^2/\text{s}$ .

In this first example, the diffusivity does not depend on the temperature. To use a temperature-dependent diffusivity, use the following command lines:

```
set diff {[Arrhenius 0.138 1.37]}  
pdbSetString Silicon CX Equation "ddt(CX) - $diff * grad(CX)"
```

In the first line, a local Tcl variable is created to hold a string representing the diffusivity. The braces are necessary to prevent immediate evaluation of the Arrhenius function (see [Arrhenius on page 857](#)). The Arrhenius function is a predefined helper function that allows for the simple creation of Arrhenius expressions. It uses the temperature set by the `diffusion` command or the `SetTemp` command (see [SetTemp on page 1062](#)). The presence of braces means that the Arrhenius function is inserted directly into the parameter database equation and is evaluated *during* the diffusion. For each diffusion time-step, the Arrhenius function will then be evaluated at the current temperature.

A further enhancement can be made by adding the diffusivity to the parameter database. This allows other users to change the value in the equation by accessing the properties directly. The following changes make the equation dependent on the stored value in the database:

```
pdbSetDouble Silicon CX D {[Arrhenius 0.1 3.62]}  
set diff [pdbDelayDouble Silicon CX D]  
pdbSetString Silicon CX Equation "ddt(CX) - $diff * grad(CX)"
```

The first line sets the diffusivity in the database. This can be made permanent by directly editing the hierarchy files. The second line uses `pdbDelayDouble` to return the expression stored in the database. This is necessary so that the evaluation of the expression does not occur until the `diffuse` command is executed. Now, the equation depends on the database entry. (You can change this entry to observe the effect of different diffusivities on the final profile.)

In addition, it is possible to solve for CX only after it is introduced into the structure or otherwise present in the material. This is performed by modifying the `solution` command:

```
solution name=CX !negative !damp ifpresent=CX add
```

The `ifpresent` option enables the solution as a variable for the diffusion equation only if a real data field exists with that name. This means that only structures already having CX defined (with the `select` command, for example) will solve the differential equation. This is useful for controlling CPU time and matrix size by not requiring solutions of systems that do not have that species present.

---

## Setting Boundary Conditions

### Dirichlet Boundary Condition

The previous example can be enhanced by adding a boundary condition to allow in-diffusion of this species from a gas source. For simplicity, it is assumed that the gas source fixes the surface concentration of species CX at  $5 \times 10^{19} \text{ cm}^{-3}$ .

The following two commands create this boundary condition:

```
pdbSetBoolean Gas_Silicon CX Fixed_Silicon 1
pdbSetString Gas_Silicon CX Equation_Silicon "CX_Silicon - 5.0e19"
```

Both commands work on the gas–silicon interface for the CX variable. The first command states that the value is to be fixed on the silicon side, that is, a Dirichlet boundary condition is to be applied. The keyword `Fixed` is used only with the Dirichlet boundary condition.

Fluxes will be ignored at this node and the boundary condition will control the concentration. The `_Silicon` option on `Fixed` indicates the value is to be set on the silicon side. This is critical because there can be three components on any interface, one for each material and one for the interface. The second command sets the boundary condition equation on the silicon side to be the concentration of  $5 \times 10^{19} \text{ cm}^{-3}$ .

**NOTE** Equations are set to zero by definition. The CX variable also has `_Silicon` appended to indicate that the concentration is set on the silicon side.

**NOTE** The interface names are lexically ordered. Most interface names are set to the right order using the `alias` command (for example, `Silicon_Gas` will be interpreted as `Gas_Silicon`). If a new interface name is introduced, the order must be followed.

### Segregation Boundary Condition

If a segregation-type boundary condition is needed, for example, at the oxide–silicon interface, the following two commands will create this boundary condition:

```
pdbSetString Oxide_Silicon CX Equation_Oxide "(1.6e-7*(CX_Oxide - \
CX_Silicon/0.28))"
pdbSetString Oxide_Silicon CX Equation_Silicon "-(1.6e-7*(CX_Oxide - \
CX_Silicon/0.28))"
```

Of course, this boundary condition assumes that the diffusion equation for CX is solved in the oxide region as well. Otherwise, the diffusion equations would be unbalanced at this interface.



Both of the commands work on the oxide–silicon interface. The `_Silicon` and `_Oxide` options on `Equation` indicate the side of the interface to which the given flux will be applied. The same options on the solution variable `CX` indicate whether the solution variable value at this interface is taken from the oxide side or the silicon side. It should also be noted that the fluxes have opposite signs. The first number ( $1.6 \times 10^{-7}$ ) in the flux equation is the transfer coefficient and the second number (0.28) is the segregation coefficient.

## Natural Boundary Condition

If a natural boundary condition is needed, the following three commands will create this boundary condition:

```
set Ksurf {[Arrhenius 1.17e6 1.37]}
set CXStar {[Arrhenius 3.6e27 3.7]}
pdbSetString Gas_Silicon CX Equation_Silicon "- $Ksurf * (CX_Silicon - \
$CXStar)"
```

The first two lines set the surface recombination rate and the equilibrium concentration, and the third line sets the equation. In this case, a flux is added to the equation on the silicon side, so there is no need for the `Fixed` flag. Recombination at an interface obtains a negative sign and generation obtains a positive sign. The variable again needs to have `_Silicon` appended to indicate the value on the silicon side of the interface.

## Interface Traps

Interfaces can act like traps for diffusing species. It is also possible that the trapped species may diffuse along the interface and segregate into neighboring materials.

The following commands create this boundary condition:

```
set diff {[Arrhenius 5.e-14 1.2]}
set Ktrap {[Arrhenius 1.17e-2 1.37]}
set CXStar {[Arrhenius 3.6e27 3.7]}

pdbSetString Gas_Silicon CX Equation "ddt(CX) -$diff * grad(CX) - $Ktrap * \
(CX_Silicon - $CXStar)"
pdbSetString Gas_Silicon CX Equation_Silicon "-$Ktrap * (CX_Silicon - \
$CXStar)"
```

The first three lines set the diffusivity, trapping rate, and equilibrium concentration of `CX` at the gas–silicon interface, respectively. The fourth line sets the trapping equation at the gas–silicon interface. The solution variable name (`CX`) without the suffix `_Silicon` indicates the value at this interface. The variable with `_Silicon` appended indicates the value on the silicon side of the interface. The `grad()` operator has the usual meaning as previously explained (see [Basics](#)

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[on page 564](#)). The last term in the equation is the flux, which depends on the trapping rate. The last line adds the corresponding flux to the equation on the silicon side.

### External Boundary Condition

To set a boundary condition at the outer sides, use the command:

```
pdbSetString <material> <solution> Equation_<boundary> <string>
```

where:

- <material> is the material name.
- <solution> is the solution name.
- <boundary> is specified with one of the following: LeftSide, RightSide, FrontSide, BackSide, or Bottom.

The specified equation is added to the bulk equation of the solution at the nodes on the specified side.

---

## Using Terms

It is possible to extend the previous example by introducing a new solution variable, CY, and the following recombination reaction between CX and CY:



$$R_{CXCY} \equiv K_f(CXCY - CX^*CY^*) \quad (815)$$

The reaction states that two species (CX and CY) annihilate each other when they react.  $K_f$  is the forward reaction rate, and  $CX^*$  and  $CY^*$  are the equilibrium values of the solution variables. The new solution variable is assumed to diffuse according to Fick's law of diffusion. Building on the previous example, the above equation can be implemented by the following command lines:

```
solution add name=CX !damp !negative solve
solution add name=CY !damp !negative solve

set Kf {[Arrhenius 4.2e-11 0.1]}
set CXStar {[Arrhenius 3.6e27 3.7]}
set CYStar {[Arrhenius 4.0e26 3.97]}

set RCXCX "$Kf * (CX * CY - $CXStar * $CYStar)"

set diff {[Arrhenius 0.138 1.37]}
```

```

pdbSetString Silicon CX Equation "ddt(CX) - $diff * grad(CX) + $RCXCY"
set diff {[Arrhenius 0.02 0.3]}
pdbSetString Silicon CY Equation "ddt(CY) - $diff * grad(CY) + $RCXCY"

```

The first two lines create solutions for CX and CY. The third line is the forward reaction rate. The next two lines set the equilibrium concentrations of CX and CY. The sixth line sets the RCXCY variable to be a subexpression for the recombination reaction. Any excess of CX and CY is annihilated until the concentrations are at the equilibrium product. Finally, the diffusivity is obtained and the equation is set, similar to the previous example. The recombination reaction is added to both solution variable equations.

A common error is *not* to add reaction terms to all affected equations. When the recombination is positive, it forces the time derivative to become negative to make the equation equal to zero.

The implementation cited above is difficult to read. The RCXCY variable is used more than once and may need to be used in other equations. To reduce the maintenance of the code, a term can be created and used everywhere, not only in the local scope where the term is defined (see [term on page 1099](#)).

A term is a common subexpression that can be used in multiple instances. When the term appears in multiple equations, the values are easily retrieved from memory and accumulated, for example:

```

solution add name=CX !damp !negative solve
solution add name=CY !damp !negative solve

set Kf {[Arrhenius 4.2e-11 0.1]}
set CXStar {[Arrhenius 3.6e27 3.7]}
set CYStar {[Arrhenius 4.0e26 3.97]}

term name=RCXCY Silicon eqn = "$Kf * (CX * CY- $CXStar * $CYStar)"

set diff {[Arrhenius 0.138 1.37]}
pdbSetString Silicon CX Equation "ddt(CX) - $diff * grad(CX) + RCXCY"
set diff {[Arrhenius 0.02 0.3]}
pdbSetString Silicon CY Equation "ddt(CY) - $diff * grad(CY) + RCXCY"

```

This is almost identical to the previous example, except that a term was created, not a local variable. Due to this change, the dollar sign (indicative of a Tcl variable) is no longer needed in the equation. It has become a simple text string, which will be resolved to the term. The terms are kept until you exit the simulator, so it can be used in other equations or in a `select` command (if you want to monitor the recombination rates).

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### Alagator for Diffusion

A further enhancement can be made by adding the diffusivity, equilibrium concentrations, and reaction rate to the parameter database as previously. The following changes make the equation dependent on the stored values in the database:

```
pdbSetDouble Silicon CX D {[Arrhenius 0.138 1.37]}
pdbSetDouble Silicon CY D {[Arrhenius 0.02 0.3]}
pdbSetDouble Silicon CX Kf {[Arrhenius 4.2e-11 0.1]}
pdbSetDouble Silicon CX Cstar {[Arrhenius 3.6e27 3.7]}
pdbSetDouble Silicon CY Cstar {[Arrhenius 4.0e26 3.97]}

solution add name=CX !damp !negative solve
solution add name=CY !damp !negative solve

set Kf [pdbDelayDouble Silicon CX Kf]
set CXStar [pdbDelayDouble Silicon CX Cstar]
set CYStar [pdbDelayDouble Silicon CY Cstar]

term name = RCXCY Silicon eqn = "$Kf * (CX * CY- $CXStar * $CYStar)"

set diff [pdbDelayDouble Silicon CX D]
pdbSetString Silicon CX Equation "ddt(CX) - $diff * grad(CX) + RCXCY"
set diff [pdbDelayDouble Silicon CY D]
pdbSetString Silicon CY Equation "ddt(CY) - $diff * grad(CY) + RCXCY"
```

As stated in the previous section, the first five lines use `pdbDelayDouble` to return the expression stored in the database. This is necessary so that the evaluation of the expression does not occur until the `diffuse` command is executed.

---

## Callback Procedures

Callbacks allow additional ‘intelligence’ to be built into the equations by allowing procedures to be called at run-time. These procedures build the Alagator equation strings according to user-specified options. By selecting model switches, you can choose between different physical models to be represented in the equation strings. By having callback procedures that use a material name, a dopant name, or a defect name as arguments, the same type of equation can be built for several materials, dopants, and defect species. In Sentaurus Process, all frequently used equations are built-in callback procedures.

The callback procedure–related keywords in Alagator are:

- `InitGrowth`
- `InitSolve`
- `InitProc`
- `EquationGrowthProc`

- `EquationInitProc`
- `EquationProc`
- `GrowthRateProc`

`InitGrowth` and `EquationGrowthProc` are used to define generic growth equations (see [Alagator for Generic Growth on page 584](#)), and `GrowthRateProc` is used with the `epi` model (see [Epitaxy on page 270](#)). Using the `pdbSet` command, you can point Alagator to use various Tcl callback procedures.

This section focuses on the remaining keywords. All of these keywords provide a Tcl callback procedure name to Sentauros Process:

<code>EquationInitProc</code>	Provides the Tcl callback procedure name that sets up the initialization equations.
<code>EquationProc</code>	Provides the Tcl callback procedure name that sets up diffusion equations.
<code>InitProc</code>	Provides the Tcl callback procedure name that is usually used to reset or delete existing parameter database equations or terms at the beginning of a diffusion simulation.
<code>InitSolve</code>	Provides the Tcl callback procedure name that is used to reset or delete existing parameter database equations or terms.

## Callbacks during Execution of `diffuse` Command

The Tcl callback procedures are called at various stages during the execution of a `diffuse` command. In addition to the callback procedures, Sentauros Process calls the `diffPreProcess` Tcl procedure before executing the `diffuse` command and the `diffPostProcess` Tcl procedure after executing the `diffuse` command. The default behavior is described in [Ion Implantation to Diffusion on page 340](#).

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Figure 84 shows the flowchart of this process. Sections relating to generic growth are omitted. They are explained in [Alagator for Generic Growth on page 584](#).

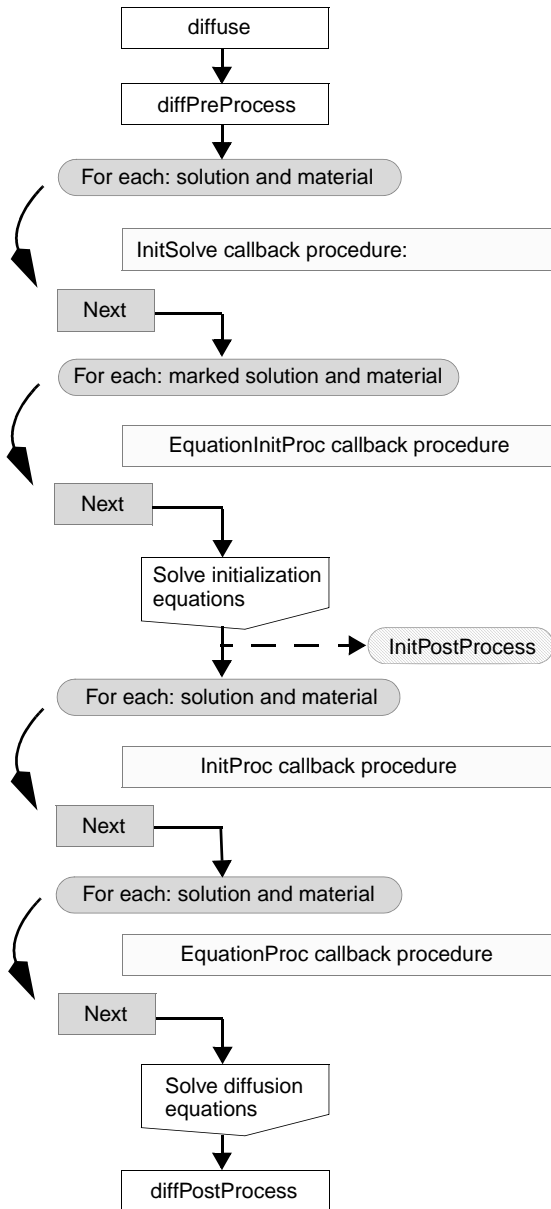


Figure 84 Flowchart with calls to the callback procedures during the execution of a diffuse command by Sentaurus Process; callbacks related to material growths are omitted

## The diffPreProcess Procedure

The execution of every `diffuse` command starts with a call to the `diffPreProcess` Tcl procedure. The `diffPreProcess` Tcl procedure is used to initialize various data fields or to preprocess the existing data fields. For example, the truncation of interstitial and vacancy profiles in the amorphous regions is performed in this procedure. In `diffPreProcess`, the point-defect equations are switched on or off according to the diffusion models selected.

### Initialization

After the execution of `diffPreProcess`, Sentaurus Process checks for all materials and solution names, and whether a procedure name is specified for the keyword `InitSolve` for the material and solution names. If a procedure name is defined, the procedure will be called, using the material name and solution name as arguments.

Subsequently, Sentaurus Process checks for all marked materials and solutions to see if a procedure name is specified with the keyword `EquationInitProc` for the solution variable that needs to be initialized. If this is the case, the procedure will be executed with the material name and solution name as arguments. Typically, in this procedure, the equation string is built, which is to be solved at `time=0` in the diffusion solver. Alternatively, if no callback procedure name is defined for the keyword `EquationInitProc` for a material and solution, the equation string to be used for the initialization can be specified directly on the command line.

After that, Sentaurus Process will solve the initialization equations for all materials and solutions that need to be initialized. The initialization equations are solved for the initial temperature of the temperature ramp specified in the `diffuse` statement. Such an initialization is usually not required for all solutions. It is typically necessary for solutions whose initial value depends in a complex way on the data fields (see [Complex Initialization Procedures: InitSolve and EquationInitProc on page 580](#)).

If initialization is not required at all, it can be omitted using the `!isolve` option with the `diffuse` command.

A Tcl procedure called `InitPostProcess` is provided for convenience. It is called after the initialization is completed. It can be used to plot or save the solution variable profiles after the initialization. By default, `InitPostProcess` is an empty procedure.

### Building and Solving Diffusion Equations

After the initialization, Sentaurus Process checks for all materials and solution names to see whether a procedure name is specified for the keyword `InitProc`. If the procedure is defined, it will be called for the specified material name and solution name. These procedures are usually used to set the equation strings to empty strings and to remove terms defined in previous diffusion steps. By having empty equation strings, the equations and terms can be built up piecewise, by adding expressions for each selected model that contributes to an

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### Alagator for Diffusion

equation or a term. This is necessary because different diffusion models may be used for different diffusion steps, and because additional species may be added between diffusion steps, which may require terms to be added to the equations for existing species.

In the next step, Sentaurus Process checks for all materials and solution names to see whether a procedure name is specified for the keyword `EquationProc`. If the procedure is defined, it will be called with the material name and the solution name as parameters. These procedures are used to set the diffusion equations for the solution variable. Alternatively, if no callback procedure is defined for a material and a solution, the equation string can be set in a command line without specifying any callback procedures.

**NOTE** If the callback procedure `EquationProc` is provided for a material name and solution name, it will typically overwrite any equation specified on the command line for this material and solution.

After the diffusion equations are set, Sentaurus Process solves the equations for the whole temperature cycle specified in the `diffuse` statement.

### The `diffPostProcess` Procedure

Finally, the procedure `diffPostProcess` will be called. The main purpose of the procedure is to delete the data fields that are no longer needed and to store the total concentration of point defects. The procedures `diffPreProcess`, `diffPostProcess`, and `InitPostProcess` can be found in the Tcl library (see [Ion Implantation to Diffusion on page 340](#)) in the file `DiffProcess.tcl`.

---

## Using Callback Procedures

In this section, the previous examples will be implemented using callback procedures. First, the callback procedure keywords `InitProc` and `EquationProc` will be explained since they are the most widely used. Then, the examples will be expanded to include the use of other keywords and procedures.



## Setup Procedure: InitProc

The keyword `InitProc` is used to clean up equation strings. It specifies the name of the callback procedure to be called by Sentaurus Process. For example, the first command below:

```

pdbSetString Silicon CX InitProc ResetEquations

```

```

proc ResetEquations { Mat Sol } {
  LogFile "This callback procedure unsets $Sol equation in $Mat."
  pdbUnSetString $Mat $Sol Equation
}

```

defines the `ResetEquations` procedure as the callback procedure of the solution variable `CX` in silicon. The callback procedure itself takes two arguments: a material name and a solution name. In this example, Sentaurus Process will call the `ResetEquations` procedure with two arguments. The first argument `Mat` will be `Silicon` and the second argument `Sol` will be `CX`. The argument names `Sol` and `Mat` are arbitrary, and they can be any valid Tcl variable but the first argument is always the material name and the second argument is always the solution name.

The procedure is called every time the solutions are checked during the diffusion. The procedure prints the message 'This callback procedure unsets CX equation in Silicon' and removes the `pdb` equation if it was defined.

Note that neither the solution name `CX` nor the material name `Silicon` is used in the implementation of the `ResetEquations` callback procedure. Therefore, the callback procedure is a generic procedure and can be used for several materials and solutions. This example can be extended with the following commands:

```

pdbSetString Silicon CX InitProc ResetEquations
pdbSetString Silicon CY InitProc ResetEquations
pdbSetString Oxide CX InitProc ResetEquations
pdbSetString Oxide CY InitProc ResetEquations

```

In this case, the same callback procedure, `ResetEquations`, is used for the solution variables `CX` and `CY` in the materials oxide and silicon. Sentaurus Process will print the following messages:

```

This callback procedure unsets CX equation in Oxide.
This callback procedure unsets CX equation in Silicon.
This callback procedure unsets CY equation in Oxide.
This callback procedure unsets CY equation in Silicon.

```

The advantage of using callback procedures is clear. With four new command lines, the equations for `CX` and `CY` in both oxide and silicon can be unset. At the same time, there is only



In this case, the same callback procedure, `SetEquations`, is used for the solution variables `CX` and `CY` in silicon. Sentaurus Process will print the following messages:

```
This callback procedure sets CX equation in Silicon.
This callback procedure sets CY equation in Silicon.
```

The advantage of using callback procedures is clear. With two new command lines, you can set the diffusion equations for `CX` and `CY` in silicon. At the same time, there is only one callback procedure to maintain. If you change the callback procedure, the changes will apply to both settings.

The above implementation uses the same diffusivity for both `CX` and `CY`. In order to use different diffusivities for each solution variable, the callback procedure `SetEquations` needs to be modified and diffusivities for each solution variable should be set as follows:

```
pdbSetString Silicon CX EquationProc SetEquations
pdbSetString Silicon CY EquationProc SetEquations

pdbSetDouble Silicon CX D {[Arrhenius 0.138 1.37]}
pdbSetDouble Silicon CY D {[Arrhenius 0.02 0.3]}

proc SetEquations { Mat Sol } {
  LogFile "This callback procedure sets $Sol equation in $Mat."
  set diff [pdbDelayDouble $Mat $Sol D]
  pdbSetString $Mat $Sol Equation "ddt($Sol) - $diff * grad($Sol)"
}
```

The first change above is the setting of `CX` and `CY` diffusivities in the database. The second change is in the `SetEquations` callback procedure. Instead of having a hard-wired diffusivity number, `pdbDelayDouble` is used to obtain the expression stored in the database. Now, the diffusivities depend on the database entry. You can change these entries to observe the effect of different diffusivities on the final profile.

The example given in [Using Terms on page 568](#) can be enhanced further by using both terms and callback procedures as follows:

```
pdbSetDouble Silicon CX D {[Arrhenius 0.138 1.37]}
pdbSetDouble Silicon CY D {[Arrhenius 0.02 0.3]}
pdbSetDouble Silicon CX Kf {[Arrhenius 4.2e-11 0.1]}
pdbSetDouble Silicon CY Kf {[Arrhenius 4.2e-11 0.1]}
pdbSetDouble Silicon CX Cstar {[Arrhenius 3.6e27 3.7]}
pdbSetDouble Silicon CY Cstar {[Arrhenius 4.0e26 3.97]}
pdbSetString Silicon CX Recomb "CY"
pdbSetString Silicon CY Recomb "CX"

solution add name=CX !damp !negative solve
solution add name=CY !damp !negative solve
```

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```
pdbSetString Silicon CX EquationProc SetEquations
pdbSetString Silicon CY EquationProc SetEquations

proc SetEquations { Mat Sol } {
    LogFile "This callback procedure sets $Sol equation in $Mat."

    set diff [pdbDelayDouble $Mat $Sol D]
    set Kf    [pdbDelayDouble $Mat $Sol Kf]
    set Recomb [pdbGetString $Mat $Sol Recomb]

    set CXStar [pdbDelayDouble $Mat $Sol Cstar]
    set CYStar [pdbDelayDouble $Mat $Recomb Cstar]

    term name = RCXCY $Mat eqn = "$Kf * ($Sol * $Recomb- $CXStar * $CYStar)"

    pdbSetString $Mat $Sol Equation "ddt($Sol) - $diff * grad($Sol) + RCXCY"
}
```

First, the diffusivity, equilibrium concentration, and forward reaction rate for the recombination of CX and CY are stored in the parameter database. Since CX and CY recombine with each other, this information (Recomb) is also stored in the database. Then, the callback procedure is modified to read these database entries. The Tcl variable Recomb in the callback procedure will have the value of CY for CX and CX for CY. The forward recombination rate RCXCY is the same for both solution variables. The callback procedure will be called once for CX and once for CY. During each call, the term RCXCY will be created. Since the term name does not depend on the solution name, the first term created during the CX equation setup will be deleted during the CY equation setup. This is performed intentionally for this example since both equations use exactly the same term. If you want to create a unique term for each call, the callback procedure must be modified as follows:

```
proc SetEquations { Mat Sol } {
    LogFile "This callback procedure sets $Sol equation in $Mat."

    set diff [pdbDelayDouble $Mat $Sol D]
    set Kf    [pdbDelayDouble $Mat $Sol Kf]
    set Recomb [pdbGetString $Mat $Sol Recomb]

    set CXStar [pdbDelayDouble $Mat $Sol Cstar]
    set CYStar [pdbDelayDouble $Mat $Recomb Cstar]

    term name = R${Sol}${Recomb} $Mat eqn = "$Kf * ($Sol * $Recomb- $CXStar * \
    $CYStar)"

    pdbSetString $Mat $Sol Equation "ddt($Sol) - $diff * grad($Sol) + \
    R${Sol}${Recomb}"
}
```

In this case, two terms will be created: RCXCY and RCYCX.

## Preprocessing and Postprocessing Data: diffPreProcess, UserDiffPreProcess, diffPostProcess, UserDiffPostProcess

Sentaurus Process can initialize solution variable fields on the command line using various commands, such as `select` (see [select on page 1053](#)) and `profile` (see [profile on page 1033](#)). If the initialization can be standardized, it is better to use the `diffPreProcess` callback procedure. By default, `diffPreProcess` is used to initialize the data fields for interstitials, vacancies, dopants, dopant clusters, dopant-defect clusters, and defect clusters (see [Ion Implantation to Diffusion on page 340](#)). The procedure also switches on and off point-defect solutions and various cluster solutions.

You can overwrite the procedure `diffPreProcess`. For example:

```
proc diffPreProcess { } {
    LogFile "This procedure is used to initialize data fields CX and CY"

    sel z = "CX + 2.0e18 * exp( -(x-0.5)*(x-0.5) / (0.01 * 0.01) ) + 1.0" \
        name=CX store
    sel z = "CY + CX * 0.1" name=CY store
}
```

This procedure will create a Gaussian profile for the solution variable `CX` with a peak at the depth  $x = 0.5$  and a maximum concentration of  $2 \times 10^{18} \text{ cm}^{-3}$ . Ten percent of the `CX` profile will be added to the existing data field `CY`.

More complex examples can be created by combining `pdb` commands and the Tcl callback procedures, for example:

```
pdbSetDouble Silicon CY minDose 1e10

proc diffPreProcess { } {
    LogFile "This procedure is used to initialize data fields CX and CY"

    sel z = "CX + 2.0e18 * exp( -(x-0.5)*(x-0.5) / (0.01 * 0.01) ) + 1.0" \
        name=CX store

    sel z = CY
    set dose [FindDose]
    if { $dose > [pdbGetDouble Silicon CY minDose] } {
        solution add name=CX !damp !negative solve
    } else {
        solution add name=CX !damp !negative nosolve
    }
}
```

In this example, a parameter called `minDose` is created for `CY` in the database to set the minimum allowed dose for diffusion to occur. In the callback procedure `diffPreProcess`,

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### Alagator for Diffusion

the `CX` profile is set as previously explained. The second and fourth lines calculate the dose of `CY` in silicon. The ‘if-else’ statement retrieves the minimum dose value from the database. If the existing dose of `CY` is below the minimum dose, the solution for `CY` is switched off; otherwise, it is switched on.

To enforce additional actions to be performed upon diffusion preprocessing, it is not necessary to overwrite the default implementation of the procedure `diffPreProcess`. Instead, to preserve the default initialization of data fields, it is recommended to redefine the procedure `UserDiffPreProcess`. By default, `UserDiffPreProcess` is an empty procedure and is called from the procedure `diffPreProcess` as one of the last commands.

The callback procedure `diffPostProcess` is called at the end of diffusion. By default, it is used to store the total concentrations of point defects and to delete some temporary data fields such as `Int_Implant` and `Vac_Implant`. In the last command line of `diffPostProcess`, the procedure `UserDiffPostProcess` is called, which is empty by default. If you want to add commands to be executed after diffusion, it is recommended to redefine the procedure `UserDiffPostProcess`.

## Complex Initialization Procedures: InitSolve and EquationInitProc

In some cases, the initialization of solution variables can be very complex and cannot be accomplished by using the `select` command (see [select on page 1053](#)). In these cases, Sentaurus Process defines the initialization equations using the Alagator language and callback procedures.

Assume that the `CX` solution variable is initialized by solving the following equation:

$$CX_{Total} = CX + (\alpha CX)^\beta \quad (816)$$

where  $CX_{Total}$  is the total concentration of `CX`, and  $\alpha$  and  $\beta$  are user-defined initialization parameters. Depending on the value of  $\alpha$  and  $\beta$ , you need to solve [Eq. 816](#).

To initiate the initialization setup procedure, the solution name must be defined as:

```
solution add name=CX !damp !negative solve InitStep
```

The keyword `InitStep` allows this solution variable to be initialized.

The keyword `InitSolve` determines which callback procedure name will be called by Sentaurus Process. For example, the first command below:

```

pdbSetString Silicon CX InitSolve ResetInitEquations

```

```

proc ResetInitEquations { Mat Sol } {
    LogFile "This callback procedure unsets $Sol equation in $Mat during initialization."
    pdbUnSetString $Mat $Sol Equation
}

```

defines the `ResetInitEquations` procedure as the callback procedure of the solution variable `CX` in silicon. The callback procedure itself takes two arguments: a material name and a solution name. In this example, Sentaurus Process will call the `ResetInitEquations` procedure with two arguments. The first argument `Mat` will be `Silicon` and the second argument `Sol` will be `CX`. In this example, the solution variable `CX` is marked to be initialized in silicon. If there is no such setting for the solution variable `CX`, `CX` will not be initialized.

After calling the callback procedures defined by `InitSolve`, Sentaurus Process will look for an equation string for the solution variable. This is performed by defining a callback procedure using the keyword `EquationInitProc`.

In this procedure, the equation string for initialization is constructed. For example, the first command below:

```

pdbSetString Silicon CX EquationInitProc SetInitEquations

```

```

proc SetInitEquations { Mat Sol } {
    LogFile "This callback procedure sets $Sol equation in $Mat during initialization."

    set alpha [pdbDelayDouble $Mat $Sol Alpha]
    set beta  [pdbDelayDouble $Mat $Sol Beta]
    pdbSetString $Mat $Sol Equation "${Sol}_Implant - $Sol - ($alpha * $Sol)^$beta"
}

```

defines the `SetInitEquations` procedure as the callback procedure of the solution variable `CX` in silicon. The callback procedure itself takes two arguments: a material name and a solution name. In this example, Sentaurus Process will call the `SetInitEquations` procedure with two arguments. The first argument `Mat` will be `Silicon` and the second argument `Sol` will be `CX`. The argument names `Sol` and `Mat` are arbitrary, and they can be any valid Tcl variable, but the first argument is always the material name and the second argument is always the solution name.

The `EquationInitProc` and `EquationProc` keywords work in the same way. The callback procedure defined with the keyword `EquationInitProc` is called only during initialization.

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### Alagator for Diffusion

The callback procedure defined with the keyword `EquationProc` is called only during diffusion. It is assumed that `Alpha` and `Beta` are already entered into the database and `CXTotal` is defined.

---

## Diffusion Summary: pdb, TclLib, SPROCESS.models

So far, it has been shown how to set up diffusion equations and boundary equations, and how to initialize solution variables. The complete example can be divided into three major parts. The first part is the `pdb` entries as follows:

```
pdbSetDouble Silicon CX D      {[Arrhenius 0.138 1.37]}
pdbSetDouble Silicon CY D      {[Arrhenius 0.02 0.3]}
pdbSetDouble Silicon CX Kf     {[Arrhenius 4.2e-11 0.1]}
pdbSetDouble Silicon CY Kf     {[Arrhenius 4.2e-11 0.1]}
pdbSetDouble Silicon CX Cstar {[Arrhenius 3.6e27 3.7]}
pdbSetDouble Silicon CY Cstar {[Arrhenius 4.0e26 3.97]}
pdbSetString Silicon CX Recomb "CY"
pdbSetString Silicon CY Recomb "CX"
pdbSetDouble Silicon CX Alpha  {[Arrhenius 1.03103e-17 -0.4]}
pdbSetDouble Silicon CX Beta   {4.0}
```

This part corresponds to the parameter database (see [Parameter Database on page 53](#)). All default Sentaurus Process model parameters are stored in the parameter database. The second part is the definition of the names of the solution variables and the names of the callback procedures:

```
solution add name=CX !damp !negative solve
solution add name=CY !damp !negative solve

pdbSetString Silicon CX EquationProc SetEquations
pdbSetString Silicon CY EquationProc SetEquations

pdbSetString Silicon CX InitProc ResetEquations
pdbSetString Silicon CY InitProc ResetEquations

pdbSetString Gas_Silicon CY InitProc ResetEquations
pdbSetString Gas_Oxide CX InitProc ResetEquations

pdbSetString Silicon CX InitSolve ResetInitEquations
pdbSetString Silicon CX EquationInitProc SetInitEquations
```

The information for the default Sentaurus Process models are stored in the `TclLib` directory (see [Environment Variables on page 46](#)) in the file `SPROCESS.models`, which is read by Sentaurus Process as soon as the simulation starts. The file also contains information with regard to solver types, implant directories, and material names.



The third part is the definition of diffusion and initialization models. The models are stored in the TclLib directory (see [Environment Variables on page 46](#)):

```

proc UserDiffPreProcess { } {
    LogFile "This procedure is used to initialize data fields CX and CY"
    sel z = "CX + 2.0e18 * exp( -(x-0.5)*(x-0.5) / (0.01 * 0.01) ) + 1.0" \
        name=CXTotal store
    sel z = "CY + CXTotal * 0.1" name = CY store
}

proc ResetEquations { Mat Sol } {
    LogFile "This callback procedure resets $Sol equation in $Mat."
    pdbUnSetString $Mat $Sol Equation
}

proc SetEquations { Mat Sol } {
    LogFile "This callback procedure sets $Sol equation in $Mat."
    set diff [pdbDelayDouble $Mat $Sol D]
    set Kf [pdbDelayDouble $Mat $Sol Kf]
    set Recomb [pdbGetString $Mat $Sol Recomb]

    set CXStar [pdbDelayDouble $Mat $Sol Cstar]
    set CYStar [pdbDelayDouble $Mat $Sol Recomb Cstar]

    term name = RCXCY $Mat eqn = "$Kf * ($Sol * $Recomb- $CXStar * $CYStar)"
    pdbSetString $Mat $Sol Equation "ddt($Sol) - $diff * grad($Sol) + RCXCY"
}

proc ResetInitEquations { Mat Sol } {
    LogFile "This callback procedure unsets $Sol equation in $Mat during \
        initialization."
    pdbUnSetString $Mat $Sol Equation
}

proc SetInitEquations { Mat Sol } {
    LogFile "This callback procedure sets $Sol equation in $Mat during \
        initialization."
    set alpha [pdbDelayDouble $Mat $Sol Alpha]
    set beta [pdbDelayDouble $Mat $Sol Beta]
    pdbSetString $Mat $Sol Equation "${Sol}_Implant - $Sol
        - (($alpha*$Sol)^$beta)"
}

```

---

## Alagator for Generic Growth

The generic growth scheme uses most of the standard definitions used in diffusion. Read [Alagator for Diffusion on page 563](#) before continuing with this section.

---

### Basics

In this section, examples of varying complexity are used to illustrate how to specify growth equations using the Alagator scripting language. Most of the definitions are identical to those of the diffusion equation. However, the keywords used to define the callback procedures and the definition of solution variables differ. In addition, the reaction equations interact with the reaction command.

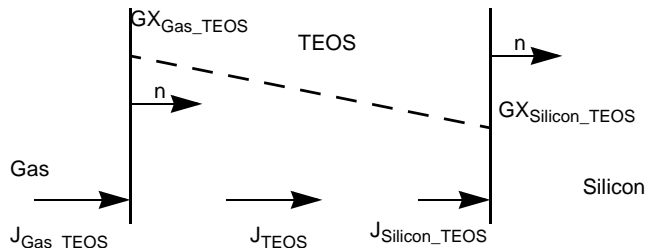


Figure 85 Flux, ambient concentration, and motion of the growth front during the growth process

Consider a reaction where the ambient  $GX$  reacts with silicon and forms a new material called TEOS. The schematic in [Figure 85](#) shows the ambient concentration at each interface and the motion of the growth during the process.  $J$  represents the fluxes towards the `Gas_TEOS` and `Silicon_TEOS` interfaces, and the flux of  $GX$  inside TEOS.

Since TEOS is a new material, first, it must be entered into the existing material list using the command:

```
mater add name=TEOS
```

Then, the reacting materials must be defined using the `reaction` command (see [reaction on page 1038](#)).

It is possible to create a reaction based on existing ambients, but in this case, a new `react` type (named  $GX$ ) ambient is created:

```
ambient name=GX react add  
reaction name=TEOSreaction mat.l=Silicon mat.r=Gas mat.new=TEOS \  
new.like=oxide ambient.name=GX diffusing.species=GX
```

Silicon (mat.l) is on the left side of the reacting interface and Gas (mat.r) is the material on the right side of the reacting interface. The newly formed material (mat.new) at the reacting interface is TEOS. The new material and its interfaces with other materials also are defined to be like Oxide and Oxide interfaces (for example, TEOS = Oxide, PolySilicon\_TEOS = Oxide\_PolySilicon). For the GX reaction, it requires an ambient, and the ambient name is GX. The reaction will not occur unless the ambient GX is present in a gas flow or directly in the diffuse command. (For more information about how to specify ambients, see [Ambients and Gas Flows on page 605](#).) Reactions that require a react-type ambient cannot have more than one diffusing species name. If the reaction does not require an ambient, it can have multiple names of diffusing species. In this case, the reaction occurs if the reacting interfaces exist in the structure.

The reaction command automatically adds the diffusing species GX to the general solution list. This is performed internally by using the command:

```
solution name=GX add !negative GrowthStep solve
```

where GrowthStep identifies this solution name as a reaction solution name. When the solution name and the new material are defined, the reaction and diffusion equations are written as follows:

```
pdbSetString TEOS GX Equation "ddt(GX)- \[Arrhenius 0.2 1.86\]*grad(GX)"
pdbSetString Gas_TEOS GX Equation_TEOS "-(GX_TEOS - 1e17)"
pdbSetString Silicon_TEOS GX Equation_TEOS "-5e-2*(GX_TEOS)"
pdbSetString Silicon_TEOS GX GrowthReaction " 5e-2*(GX_TEOS)"
```

The first line sets the diffusion equation of GX in TEOS. The next two lines set the boundary fluxes at the Gas\_TEOS and Silicon\_TEOS interfaces. One of the commands works on the Gas\_TEOS interface and the other one works on the Silicon\_TEOS interface. The \_TEOS option on Equation indicates the side of the interface to which the given flux will be applied. The same option on the solution variable GX indicates that the solution variable value at this interface is taken from the TEOS side. These settings are identical to the ones described in [Setting Boundary Conditions on page 566](#).

The last line is unique to the generic growth equations. The keyword GrowthReaction is used to define the growth reaction flux at the reacting interface. In this example, the growth reaction flux is identical to the diffusion flux at the reacting interface. In addition, the sign of the growth reaction flux is the opposite of the sign of the diffusion flux.

Finally, it is necessary to specify the ambient in a gas flow (see [gas\\_flow on page 901](#)) and use it with the diffuse command or specify it directly in the diffuse command in order for the reaction to occur. For example:

```
gas_flow name=gxflw partial_pressure = { GX = 1.0 }
diffuse time=100 temp=1000 gas_flow = gxflw
```

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### Alagator for Generic Growth

or:

```
diffuse time=100 temp=1000 GX
```

will both switch on reactions involving the ambient GX and will set the partial pressure of GX to 1. Using the `gas_flow` command is more flexible in that the partial pressure can be set to any value (not just 1.0) or the partial pressure can be computed from gas flows and gas reactions.

## Epi Reactions

This is an example of using the `reaction` command to create a new epitaxial growth mode:

```
ambient name=MyEpi epi add
# Now, create the new temporary material to be used during epi growth
# the name <Ambient>On<Material> is not necessary, it is just
# the same convention as used internally
mater name=MyEpiOnNitride add
reaction name= MyEpiOnNiReact mat.l=Nitride mat.r=Gas mat.new=MyEpiOnNitride \
  ambient.name=MyEpi new.like=PolySilicon mat.final=PolySilicon
```

In this example, there is an additional parameter `mat.final`, which is the final name of the epi material. There is a conversion from `mat.new` to `mat.final` at the end of the `diffuse` command. For details on how to set up epi reactions and growth rates, see [Epitaxy Growth Rate: GrowthRateProc on page 593](#).

The model can be enhanced by adding the model parameters to the PDB. This allows other users to change the values in the equations by accessing the properties directly. The following changes make the equations dependent on the stored value in the database:

```
pdbSetDouble TEOS GX Dstar "\[Arrhenius 0.2 1.86\]"
pdbSetDouble Gas_TEOS GX Cstar "1e17"
pdbSetDouble Silicon_TEOS GX Kfd "5e-2"
pdbSetDouble Silicon_TEOS GX Kfg "5e-2"

set diff [pdbDelayDouble TEOS GX Dstar]
pdbSetString TEOS GX Equation "ddt(GX)- $diff * grad(GX)"

set GXStar [pdbDelayDouble Gas_TEOS GX Cstar]
pdbSetString Gas_TEOS GX Equation_TEOS "-(GX_TEOS - $GXStar)"

set GKfd [pdbDelayDouble Silicon_TEOS GX Kfd]
pdbSetString Silicon_TEOS GX Equation_TEOS "-$GKfd*(GX_TEOS)"

set GKfg [pdbDelayDouble Silicon_TEOS GX Kfg]
pdbSetString Silicon_TEOS GX GrowthReaction " $GKfg*(GX_TEOS)"
```

The first lines set the diffusivity, equilibrium value of GX, and forward reaction rates for the diffusion and growth fluxes in the database. This can be made permanent by directly editing the hierarchy files. The `pdbDelayDouble` command is used to return the expression stored in the database. This is necessary so that the evaluation of the expression does not occur until the `diffuse` command is executed. Now, the equation depends on the database entry.

It is possible to use terms with the generic growth equations. For example:

```

pdbSetDouble TEOS      GX Dstar "\[Arrhenius 0.2 1.86\]"
pdbSetDouble Gas_TEOS GX Cstar "1e17"
pdbSetDouble Silicon_TEOS GX Kfd "5e-2"
pdbSetDouble Silicon_TEOS GX Kfg "5e-2"

set diff [pdbDelayDouble TEOS GX Dstar]
pdbSetString TEOS GX Equation "ddt(GX)- $diff * grad(GX)"

set GXStar [pdbDelayDouble Gas_TEOS GX Cstar]
pdbSetString Gas_TEOS GX Equation_TEOS "-(GX_TEOS - $GXStar)"
term name = Reaction TEOS eqn = "GX"

set GKfd [pdbDelayDouble Silicon_TEOS GX Kfd]
pdbSetString Silicon_TEOS GX Equation_TEOS "-$GKfd*(Reaction_TEOS)"

set GKfg [pdbDelayDouble Silicon_TEOS GX Kfg]
pdbSetString Silicon_TEOS GX GrowthReaction "$GKfg*(Reaction_TEOS)"

```

a term called `Reaction` is created in `TEOS`. Note that the term also takes the `_TEOS` option to indicate that the value of `Reaction` will be taken from the `TEOS` side.

The velocities regarding the growth reaction flux are calculated internally as follows:

$$v_{Growth} = \frac{\text{Beta}}{\text{Expansion.Ratio} * \text{Density.Grow}} F_{Growth} \quad (817)$$

where  $F_{Growth}$  is the growth reaction flux defined using the `pdbSetString` command and `GrowthReaction` keyword as previously explained. `Beta` is the stoichiometry of the growing material, `Expansion.Ratio` is the conversion ratio from consumed material to the growing material, and `Density.Grow` is the density of the growing material. The default values for `Beta`, `Expansion.Ratio`, and `Density.Grow` are 1, 2.2, and  $2.2 \times 10^{22}$ , respectively. They can be changed by using the following commands:

```

pdbSetDouble <interface material> <ambient> Beta <n>
pdbSetDouble <interface material> <ambient> Expansion.Ratio <n>
pdbSetDouble <interface material> <ambient> Density.Grow <n>

```

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For example, for the above example, you can change these values with the following commands:

```
pdbSetDouble Silicon_TEOS GX Beta 1.1
pdbSetDouble Silicon_TEOS GX Expansion.Ratio 2.0
pdbSetDouble Silicon_TEOS GX Density.Grow 3e22
```

If `Expansion.Ratio` is set to 0, the material will dissolve but the new material will not form. (For example, silicon will dissolve but no TEOS will form. This is useful for silicidation.)

---

## Callback Procedures

Callbacks allow additional ‘intelligence’ to be built into the equations by allowing procedures to be called at run-time. These procedures build the equation strings according to user-specified options. By selecting model switches, the user can choose between different physical models to be represented in the equation strings. Having callback procedures that use a material name and a solution name as arguments, the same type of equation can be built for several materials, dopants, and defect species. In Sentaurus Process, all frequently used equations are built-in callback procedures.

There are six callback procedure–related keywords in Alagator: `InitProc`, `InitSolve`, `EquationInitProc`, `EquationProc`, `InitGrowth`, and `EquationGrowthProc`. `InitProc`, `EquationInitProc`, `InitSolve`, and `EquationProc` are used to define generic diffusion equations (see [Alagator for Diffusion on page 563](#)). In this section, the procedures specified by the keywords `InitGrowth` and `EquationGrowthProc` are explained:

- `InitGrowth` provides the Tcl callback procedure name that is usually used to reset or delete existing `pdb` equations or terms at the beginning of a diffusion simulation.
- `EquationGrowthProc` provides the Tcl callback procedure name that sets up equations for material growth.

The Tcl callback procedures are called at various stages during the execution of the `diffuse` command. In addition to the callback procedures, Sentaurus Process calls the `diffPreProcess` Tcl procedure before executing the `diffuse` command, and the `diffPostProcess` Tcl procedure after executing the `diffuse` command (see [Ion Implantation to Diffusion on page 340](#)).

[Figure 86 on page 589](#) shows the flowchart of the execution of a `diffuse` statement by Sentaurus Process, including generic material growth. The sections regarding diffusion are represented on a smaller scale and are shown in [Figure 84 on page 572](#).

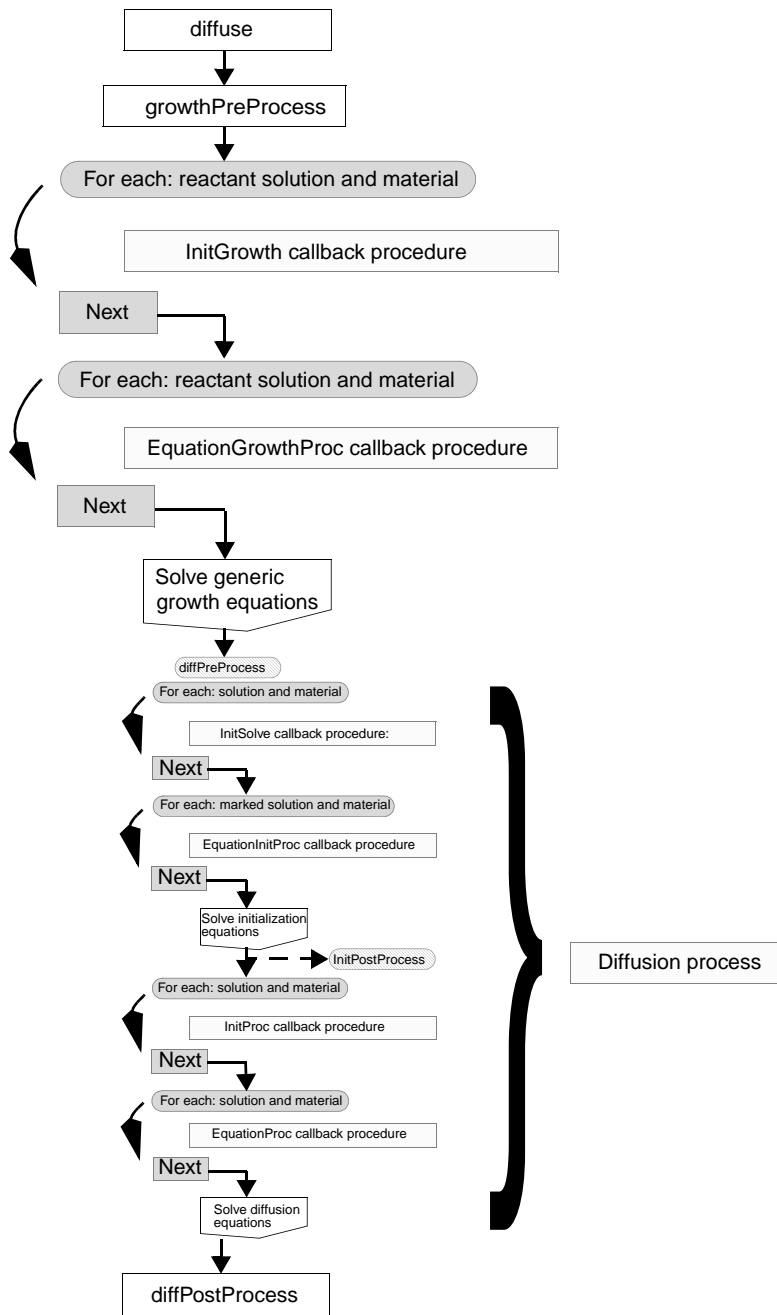


Figure 86 Flowchart with calls to the callback procedures during execution of diffuse command





```
    pdbUnSetString $Mat $Sol Equation
    LogFile "This callback procedure resets $Sol equation in $Mat."

    pdbUnSetString $Mat $Sol Equation_{$mater1}
    LogFile "This callback procedure resets $Sol equation in $Mat on $mater1 \
    side."

    pdbUnSetString $Mat $Sol Equation_{$mater2}
    LogFile "This callback procedure resets $Sol equation in $Mat on $mater2 \
    side."

    pdbUnSetString $Mat $Sol GrowthReaction
    LogFile "This callback procedure resets $Sol growth reaction equation in \
    $Mat."
}

pdbSetString Gas_TEOS      GX InitGrowth ResetInterfaceEquations
pdbSetString Silicon_TEOS GX InitGrowth ResetInterfaceEquations
```

The callback procedure, `ResetInterfaceEquations`, is similar to the `ResetEquations` procedure. The commands `FirstMat` and `SecondMat` used in the procedure return the names of the neighboring materials (for example, `Gas` and `TEOS` for `Gas_TEOS`). Then, the equations set for either side of the interface or the interface are unset including the generic growth reaction equation. This special procedure is called for `GX` at the `Gas_TEOS` and `Silicon_TEOS` interfaces. Sentaurus Process will print the following messages:

```
This callback procedure resets GX equation in TEOS.
This callback procedure resets GX equation in Gas_TEOS.
This callback procedure resets GX equation in Gas_TEOS on Gas side.
This callback procedure resets GX equation in Gas_TEOS on TEOS side.
This callback procedure resets GX growth reaction equation in Gas_TEOS.
This callback procedure resets GX equation in Silicon_TEOS.
This callback procedure resets GX equation in Silicon_TEOS on Silicon side.
This callback procedure resets GX equation in Silicon_TEOS on TEOS side.
This callback procedure resets GX growth reaction equation in Silicon_TEOS.
```

## Equation Procedure: EquationGrowthProc

The primary responsibility of the equation procedure is to construct the equation string for material growth reaction. It uses the keyword `EquationGrowthProc` in the parameter database. The keyword specifies the name of the callback procedure to be called by Sentaurus Process.



Here, the same callback procedure, `SetInterfaceEquations`, is used to set up the interface equations on both the `Gas_TEOS` and `Silicon_TEOS` interfaces. The commands `FirstMat` and `SecondMat` used in the procedure return the names of the neighboring materials (for example, `Gas` and `TEOS` for `Gas_TEOS`). The command `pdbIsAvailable` returns true (1) if the `Cstar` value is entered to the parameter database for the given solution name and material. In this example, it will return true for the `Gas_TEOS` interface and false for the `Silicon_TEOS` interface. Using this information and the 'if-else' statement, the equations can be set for the `Gas_TEOS` and `Silicon_TEOS` interfaces. Now, the diffusivities, reaction rates, and equilibrium values depend on the database entries.

## Epitaxy Growth Rate: GrowthRateProc

The `GrowthRateProc` callback procedure can be used to set the `GrowthReaction` `pdb` variable during epitaxial growth. The requirements are similar to `EquationGrowthProc`, except that there can be a different `GrowthRateProc` for each epitaxial ambient. For example:

```
proc mygrproc { Mat Amb } {
    pdbSetString $Mat $Amb GrowthReaction \
        "([simDelayDouble Diffuse EpiThick]- \
        [pdbDelayDouble $Mat $Amb NativeOffset])/ \
        [simDelayDouble Diffuse AnnealStepTime]"
}

pdbSet Gas_LTEOnOxide LTE GrowthRateProc mygrproc
```

This example demonstrates a number of simulation status values that are available to the `GrowthRateProc` implementer. The quantity `simDelayDouble Diffuse EpiThick` is the value of the `thick` parameter set in the `diffuse` or `temp_ramp` commands. The quantity `pdbDelayDouble $Mat $Amb NativeOffset` is set to the native layer thickness if a native layer was deposited; otherwise, it is 0. Finally, `simDelayDouble Diffuse AnnealStepTime` is the total time of the current `temp_ramp` segment or `diffuse` time.

If a new material is being deposited that is not a standard Sentaurus Process epi material, the following parameters should be set:

```
pdbSetDouble <mat.new>_Gas <ambient.name> Expansion.Ratio 1.0
pdbSetDouble <mat.new>_Gas <ambient.name> Density.Grow 1.0
```

where `<mat.new>` is the name of the new material being grown and `<ambient.name>` is the name of the ambient triggering the growth of `<mat.new>`.

## The growthPreProcess Procedure

The execution of every `diffuse` command starts with a call to the `growthPreProcess Tcl` procedure. The `growthPreProcess Tcl` procedure is used to initialize various reaction-related data fields or to preprocess the existing data fields.

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To enforce additional actions to be performed upon generic growth preprocessing, it is not necessary to overwrite the default implementation of the procedure `growthPreProcess`. Instead, to preserve the default initialization of data fields, it is recommended to redefine the procedure `UserGrowthPreProcess`. By default, `UserGrowthPreProcess` is an empty procedure and is called from the procedure `growthPreProcess` as one of the last commands.

---

## Generic Growth Summary: `pdb`, `TclLib`, `SPROCESS.models`

So far, it has been shown how to set up reaction equations and fluxes. The complete example can be divided into three major parts. The first part consists of `pdb` entries as follows:

```
pdbSetDouble TEOS GX Dstar "[Arrhenius 0.2 1.86]"
pdbSetDouble Gas_TEOS GX Cstar "1e17"
pdbSetDouble Silicon_TEOS GX Kfd "5e-2"
pdbSetDouble Silicon_TEOS GX Kfg "5e-2"
```

This part corresponds to the parameter database (see [Parameter Database on page 53](#)). All default Sentaurus Process model parameters are stored in the parameter database. The second part is the definition of reaction variable names, material names, and callback procedure names:

```
mater add name=TEOS
reaction name=TEOSreaction mat.l=Silicon mat.r=Gas mat.new=TEOS \
  new.like=oxide diffusing.species=GX ambient
pdbSetString TEOS GX InitGrowth ResetEquations
pdbSetString Gas_TEOS GX InitGrowth ResetInterfaceEquations
pdbSetString Silicon_TEOS GX InitGrowth ResetInterfaceEquations
pdbSetString Gas_TEOS GX EquationGrowthProc SetInterfaceEquations
pdbSetString Silicon_TEOS GX EquationGrowthProc SetInterfaceEquations
pdbSetString TEOS GX EquationGrowthProc SetEquations
```

The information for the default Sentaurus Process models is stored in the `TclLib` directory (see [Environment Variables on page 46](#)) in the `SPROCESS.models` file, which is read by Sentaurus Process as soon as the simulation starts. The file also contains information regarding solver types, implant directories, and material names.

The third part is the definition of diffusion/reaction models. The models are stored in the `TclLib` directory (see [Environment Variables on page 46](#)):

```
proc ResetEquations {Mat Sol} {
  LogFile "This callback procedure resets $Sol equation in $Mat."
  pdbUnSetString $Mat $Sol Equation
}
```

```

proc ResetInterfaceEquations { Mat Sol } {
  set mater1 [FirstMat $Mat]
  set mater2 [SecondMat $Mat]

  pdbUnSetString $Mat $Sol Equation
  LogFile "This callback procedure resets $Sol equation in $Mat."

  pdbUnSetString $Mat $Sol Equation_$mater1
  LogFile "This callback procedure resets $Sol equation in $Mat on $mater1 \
  side."

  pdbUnSetString $Mat $Sol Equation_$mater2
  LogFile "This callback procedure resets $Sol equation in $Mat on $mater2 \
  side."

  pdbUnSetString $Mat $Sol GrowthReaction
  LogFile "This callback procedure resets $Sol growth reaction equation in \
  $Mat."
}

proc SetEquations { Mat Sol } {
  LogFile "This callback procedure sets $Sol equation in $Mat."
  set diff [pdbDelayDouble $Mat $Sol Dstar]

  pdbSetString $Mat $Sol Equation "ddt($Sol) - $diff * grad($Sol)"
}

proc SetInterfaceEquations { Mat Sol } {
  set mater1 [FirstMat $Mat]
  set mater2 [SecondMat $Mat]

  if { [pdbIsAvailable $Mat $Sol Cstar] } {
    set GXStar [pdbDelayDouble $Mat GX Cstar]
    pdbSetString $Mat $Sol Equation_$mater2 "-({Sol}_$mater2 - $GXStar)"
    LogFile "This callback procedure sets $Sol equation in $Mat on $mater2 \
    side."
  } else {
    set GKfd [pdbDelayDouble $Mat $Sol Kfd]
    pdbSetString $Mat $Sol Equation_$mater2 "-$GKfd*({Sol}_$mater2)"
    LogFile "This callback procedure sets $Sol equation in $Mat on $mater2 \
    side."

    set GKfg [pdbDelayDouble $Mat $Sol Kfg]
    pdbSetString $Mat $Sol GrowthReaction "$GKfg*({Sol}_$mater2)"
    LogFile "This callback procedure sets $Sol growth reaction equation in \
    $Mat."
  }
}

```

---

## Modifying Diffusion Models

In Sentaurus Process, all equations of dopant diffusion models are constructed using callback procedures as previously explained. If you want to add a new expression to an existing equation or term, or to subtract a new expression from an existing equation or term, one of the following can be used:

- `UserAddEqnTerm`
- `UserSubEqnTerm`
- `UserAddToTerm`
- `UserSubFromTerm`
- `MultiplyTerm`

**NOTE** The `UserAddEqnTerm`, `UserSubEqnTerm`, `UserAddToTerm`, `UserSubFromTerm`, and `MultiplyTerm` commands should not be used within the callback procedures. They are designed to change diffusion equations without using the callback procedures.

**NOTE** The `UserAddEqnTerm`, `UserSubEqnTerm`, `UserAddToTerm`, `UserSubFromTerm`, and `MultiplyTerm` commands are not saved to the TDR files. If the input file is split, the commands must be included in the new input file.

---

## UserAddEqnTerm and UserSubEqnTerm

The commands `UserAddEqnTerm` and `UserSubEqnTerm` allow you to add a new expression to an existing solution variable equation or to subtract the new expression from an existing solution variable equation. The commands have the format:

```
UserAddEqnTerm <material> <solution> <expression> <side>  
UserSubEqnTerm <material> <solution> <expression> <side>
```

where:

- `<material>` is any valid material name.
- `<solution>` is any valid solution variable name.
- `<expression>` is the new expression to be added to or subtracted from the solution variable.
- `<side>` is the side of the interface material where the new expression will be added or subtracted.

For example, the command:

```
UserAddEqnTerm Silicon Vac "{2e-15*(Vac*Vac-1e-16*CX)}"
```

adds the expression " $\{2e-15*(Vac*Vac-1e-16*CX)\}$ " to the `Vac` equation in silicon during the PDE solve. Since the equations can be set in three different ways for interfaces, you have the option to specify the side to which the expression will be added or subtracted. For example, the commands:

```
UserAddEqnTerm Oxide_Silicon CX "(CX_Oxide - CX_Silicon)" Silicon  
UserSubEqnTerm Oxide_Silicon CX "(CX_Oxide - CX_Silicon)" Oxide
```

add the expression " $(CX\_Oxide - CX\_Silicon)$ " to the `Oxide_Silicon` interface equation for `CX` on the `Silicon` side, and subtract the same expression from the `Oxide_Silicon` interface equation for `CX` on the `Oxide` side, respectively. If no side information is given, the expression will be added to the `Oxide_Silicon` interface equation for `CX`.

---

## UserAddToTerm and UserSubFromTerm

The commands `UserAddToTerm` and `UserSubFromTerm` are used to add a new expression to an existing term or to subtract the new expression from an existing term. The commands have the format:

```
UserAddToTerm <material> <term> <expression>  
UserSubFromTerm <material> <term> <expression>
```

where:

- `<material>` is any valid material name.
- `<term>` is an existing term name.
- `<expression>` is the new expression to be added to or subtracted from the existing term.

For example the command:

```
UserAddToTerm Silicon VTotal "2*CX"
```

adds the expression " $2*CX$ " to the term `VTotal` in silicon.

In the same way, the command:

```
UserSubFromTerm Silicon VTotal "2*CX"
```

subtracts the expression " $2*CX$ " from the term `VTotal` in silicon.

## References

- [1] R. E. Bank *et al.*, “Transient Simulation of Silicon Devices and Circuits,” *IEEE Transactions on Electron Devices*, vol. ED-32, no. 10, pp. 1992–2007, 1985.



## CHAPTER 7    **Advanced Calibration**

---

*This chapter provides details about the use of Advanced Calibration in Sentaurus Process.*

---

### **Overview**

The Synopsys Consulting and Engineering group is working continually on improving the simulation models and optimizing the model parameters for the latest technology. This effort is based on long-standing experience of model calibration for customers and a comprehensive, growing database of state-of-the-art secondary ion mass spectrometry (SIMS) profiles.

With Advanced Calibration in Sentaurus Process, you have a set of models and parameters that have been calibrated to deep-submicron CMOS technology. With these parameters, you can obtain accurate results for many processes in device fabrication such as ion implantation, ultrashallow junction formation, surface dose loss, and channel and halo dopant diffusion.

The Advanced Calibration set of models and parameters is located in a single file. For the current Sentaurus Process, it has the file name `AdvCal_2013.03.fps` and is located in the directory `$STROOT/tcad/$STRELEASE/lib/sprocess/TclLib/AdvCal`.

The models and parameters of `AdvCal_2013.03.fps` are recommended for deep-submicron CMOS and SOI technology. Other technologies, such as power devices or SiGe devices, may require simpler or additional diffusion models, which are not yet included in the Advanced Calibration. The models have been tested extensively in 1D simulations and have proven to be accurate and robust.

Advanced Calibration also is available for Sentaurus Process Kinetic Monte Carlo (see [Advanced Calibration for Sentaurus Process KMC on page 553](#)).

## Using Advanced Calibration

To use Advanced Calibration in Sentaurus Process, at the beginning of the input file, insert the line:

```
AdvancedCalibration
```

or:

```
AdvancedCalibration 2013.03
```

This will source the file `$STROOT/tcad/$STRELEASE/lib/sprocess/TclLib/AdvCal/AdvCal_2013.03.fps`.

You have the option to use Advanced Calibration parameters and models from previous releases, for example:

```
AdvancedCalibration 2012.06
```

This will source the file `$STROOT/tcad/$STRELEASE/lib/sprocess/TclLib/AdvCal/AdvCal_2012.06.fps`.

---

## Additional Calibration by Users

Advanced Calibration is based on the assumption that all parameters that are not changed in the parameter files are the Sentaurus Process default parameters. To use the Advanced Calibration file `AdvCal_2013.03.fps`, it must be sourced before the real process description.

For deep-submicron process simulation, Advanced Calibration is usually a good starting point. You can further increase the accuracy of a certain technology by additional fine-tuning of a few physical parameters. This should only be performed by experienced users with a good understanding of the diffusion models and callback procedures of Sentaurus Process.

The best way to perform this is to put all additional calibration in a user calibration file, for example, `user_calibration.fps`. This file includes all project-specific changes of physical parameters or callback procedures with respect to Advanced Calibration.

In the process simulation file, at the beginning of the process simulation, insert the lines:

```
AdvancedCalibration 2013.03  
source ./user_calibration.fps
```

This method has two distinct advantages:

- There is a clear separation between the process flow, which is contained in the Sentaurus Process input file, and the selection of physical models and parameters. During calibration of Sentaurus Process for a specific technology, you can first set up the process flow in the input file of Sentaurus Process and then improve the accuracy of the process simulation by making changes only in their parameter file. Conversely, if you want to apply the same models and parameters to a different process, it is only necessary to change the file containing the process flow.
- The Advanced Calibration file is used as a starting point. The user calibration file (for example, `user_calibration.fps`) is usually very short and clear, in particular, for CMOS technology. You can see all parameter changes with respect to the original Advanced Calibration at a glance.

**NOTE** For detailed documentation of the contents and physical models included in Advanced Calibration as well as a discussion of its accuracy and limitations, refer to the *Advanced Calibration for Process Simulation User Guide*.

## **7: Advanced Calibration**

Additional Calibration by Users

## CHAPTER 8 Oxidation and Silicidation

---

*This chapter describes the oxidation models available in Sentaurus Process.*

---

### Oxidation

Sentaurus Process can simulate the thermal oxidation of silicon. Due to the conversion ratio from Si to SiO<sub>2</sub> being greater than one, new ‘volume’ is generated, which, in turn, leads to the motion of materials and mechanical stress in the structure. The oxidation process has three steps:

- Diffusion of oxidants (H<sub>2</sub>O, O<sub>2</sub>) from the gas–oxide interface through the existing oxide to the silicon–oxide interface.
- Reaction of the oxidant with silicon to form new oxide<sup>1</sup>.
- Motion of materials due to the volume expansion, which is caused by the reaction between silicon and oxide.

The oxidant diffusion equation is solved using the generic partial differential equation (PDE) solver of Sentaurus Process. For the simulation of thermal oxidation, there are two requirements:

- The silicon or polysilicon region is in contact with gas or an oxide region, which, in turn, is in contact with gas.
- The `diffuse` command specifies a reactive atmosphere.

If silicon or polysilicon is in contact with gas at the beginning of a thermal oxidation, an initial oxide layer is created automatically. The default thickness of this layer is 1.5 nm. The value of the initial oxide thickness is specified in the parameter database by:

```
pdbSet Grid NativeLayerThickness 1.5e-7
```

which controls the native layer thickness for oxidation and silicidation. There are several ways to specify a reactive atmosphere. Furthermore, temperature can vary during oxidation, and the ambient can contain contributions from different oxidants. The following sections describe how to handle these cases using Sentaurus Process.

It is important to note that oxidation occurs in conjunction with mechanics. The details of the mechanical equations, boundary conditions, and material models are given in the next chapter.

---

1. In this chapter, *oxide* refers to SiO<sub>2</sub>.

---

## Basic Oxidation

The `diffuse` command is used to specify two reactive ambients for oxidation, either H<sub>2</sub>O or O<sub>2</sub>. The oxidation temperature and time must be given. For example, a command for a simple oxidation using wet ambient temperature at 1000°C for 10 minutes is:

```
diffuse temperature=1000<C> time=10<min> H2O
```

A simple temperature ramp can be specified directly in the `diffuse` command by the keyword `ramprate`. This keyword sets the change in the temperature over time:

```
diffuse temperature=1000<C> time=10<min> O2 ramprate=10<C/min>
```

This example describes a dry oxidation of 10 minutes, starting at 1000°C and ending at 1100°C.

**NOTE** The value of `ramprate` can be negative if the temperature is required to decrease.

---

## Temperature Cycles

The second example given in [Basic Oxidation](#) also can be specified by using the `temp_ramp` command, for example:

```
temp_ramp name=MyTempRamp temperature=1000 time=10 O2 ramprate=10<C/min>
diffuse temp_ramp=MyTempRamp
```

The first line creates a temperature ramp with given conditions, and the second line specifies a diffusion referring to this temperature ramp.

To describe more complex temperature cycles within one `diffuse` command, multiple instances of the `temp_ramp` command can be used. A temperature ramp can consist of several segments and, for each segment, one `temp_ramp` command is required. In addition, segments can be grouped by using the same name for each segment. For example, a ramp-up, plateau, and ramp-down can be specified as:

```
temp_ramp name=MyCycle temperature=1000<C> time=5<min> H2O ramprate=20<C/min>
temp_ramp name=MyCycle temperature=1100<C> time=10<min> O2
temp_ramp name=MyCycle temperature=1100<C> time=10<min> ramprate=-10<C/min>
diffuse temp_ramp=MyCycle
```

If you want to set the minimum and maximum reaction/oxidation time steps in minutes globally, for all diffusion commands, the following commands can be used:

```
pdbSet Diffuse MinGrowthStep <n>
pdbSet Diffuse MaxGrowthStep <n>
```

See [Parameter Database on page 53](#) for other diffusion-related parameters.

---

## Ambients and Gas Flows

Sentaurus Process has a flexible scheme for dealing with gas flows. By default, several ambients are available, and you can also create additional ones for new reactions (see [reaction on page 1038](#)). [Table 63](#) lists the ambients that are available by default.

Table 63 Available ambients

Ambient name	Ambient type	Reactions
O2	react	Oxidation
H2O	react	Oxidation
HCl	inert	Gas reactions only
N2	inert	None
H2	inert	Gas reactions only
N2O	react	Oxynitridation
Epi	epi	Standard epitaxy
LTE	epi	Low-temperature epitaxy

The `react` and `inert` ambients can be specified in any combination using the `gas_flow` command. The `inert` ambients are inert in the sense that they do not switch on material reactions. However, `inert` ambients can be used in gas flows to change the partial pressure of react ambients through gas reactions or just taking part of the total pressure as is the case with  $N_2$ , for example. As the name implies, `react` ambients cause material reactions to occur, such as oxidation. The `epi`-type ambients trigger epitaxial growth and should not be used with any other ambient.

To specify an ambient is present and to set the partial pressure to  $1.0 * \text{total pressure}$ , use the shorthand parameter name `<ambient name>` in the `diffuse` or `gas_flow` command. The parameter `pressure` sets the total pressure and also is available on the `diffuse` or `gas_flow` command line. The default for total pressure is 1 atm. Only one ambient should be specified using the shorthand parameter `<ambient name>`. For epitaxy, specify the appropriate ambient by name.

## 8: Oxidation and Silicidation

### Oxidation

## Specifying Gas Flows

The `gas_flow` command is used to specify a mixed gas flow by specifying directly either the partial pressures of the gas components or the flow `<volume/time>`. When a `gas_flow` is specified, it can be referred to from the `temp_ramp` and `diffuse` commands.

The gases present during diffusion can either be specified as partial pressures or using gas flows. When using flow specifications, the partial pressure is computed from gas reactions, the presence of inert gases, and the total pressure. Alternatively, the partial pressure can be specified directly. The partial pressure can be set with either the `p<ambient name>` parameters or the `partial.pressure` parameter of the `gas_flow` command:

```
gas_flow name=MyGasFlow pH2O=0.5 pO2=0.5
```

or:

```
gas_flow name=MyGasFlow partial.pressure = {H2O=0.5 O2=0.5}
```

Specifying directly in the `diffuse` command is also possible, for example:

```
diffuse pH2O=0.5 pO2=0.5 temperature=1000 time=10<min>
```

Instead of specifying partial pressures directly, the gas components can be given in terms of flows using `flow<ambient name>` or the `flows` parameter, for example:

```
gas_flow name=MyGasFlow flowH2O=0.5 flowO2=0.5 flowH2=0.2 flowN2=1.0
```

or:

```
gas_flow name=MyGasFlow flows = {H2O=0.5 O2=0.5 H2=0.2 N2=1.0}
```

If flows are specified, Sentaurus Process calculates the partial pressures of the components assuming a complete reaction of the gases. Because the only effect of inert ambients in Sentaurus Process is to change the partial pressure of reacting ambients, inert ambients should only be set using flows in the `gas_flow` command.

To invoke the gas flow specification as given above, use:

```
temp_ramp name=MyTempRamp temperature=1000<C> time=10<min> gas_flow=MyGasFlow  
diffuse temp_ramp=MyTempRamp
```

or:

```
diffuse temperature=1000<C> time=10<min> gas_flow=MyGasFlow
```



## Computing Partial Pressures

Given a flow of O<sub>2</sub> in addition to a flow of H<sub>2</sub> or HCl for example, a chemical reaction between the components is taken into account: O<sub>2</sub> is reduced and H<sub>2</sub>O increases. A complete stoichiometric reaction is assumed. The final flows<sup>1</sup> after the reaction are computed in the AmbientReactions procedure as shown in Eq. 818.

If  $\text{flowO2}_{init} > 0.5 \cdot \text{flowH2}_{init}$ :

$$\begin{aligned}\text{flowO2}_{final} &= \text{flowO2}_{init} - 0.5 \cdot \text{flowH2}_{init} \\ \text{flowH2O}_{final} &= \text{flowH2O}_{init} + \text{flowH2}_{init} \\ \text{flowH2}_{final} &= 0\end{aligned}\tag{818}$$

else:

$$\begin{aligned}\text{flowO2}_{final} &= 0 \\ \text{flowH2O}_{final} &= \text{flowH2O}_{init} + 2 \cdot \text{flowO2}_{init} \\ \text{flowH2}_{final} &= \text{flowH2}_{init} - 2 \cdot \text{flowO2}_{init}\end{aligned}\tag{819}$$

In the case where not all of the H<sub>2</sub> is consumed by the reaction, a warning is displayed. If a contribution of HCl is given, the equations read as follows.

If  $\text{flowO2}_{init} > \text{flowHCl}_{init}$ :

$$\begin{aligned}\text{flowO2}_{final} &= \text{flowO2}_{init} - 0.5 \cdot \text{flowHCl}_{init} \\ \text{flowH2O}_{final} &= \text{flowH2O}_{init} + \text{flowHCl}_{init} \\ \text{flowH2}_{final} &= 0\end{aligned}\tag{820}$$

else:

$$\begin{aligned}\text{flowO2}_{final} &= 0 \\ \text{flowH2O}_{final} &= \text{flowH2O}_{init} + 2 \cdot \text{flowO2}_{init} \\ \text{flowHCl}_{final} &= \text{flowHCl}_{init} - \text{flowO2}_{init}\end{aligned}\tag{821}$$

---

1. The index *init* refers to the initial flows specified by users in the `gas_flow` command, and *final* describes the flow after the chemical reaction.

## 8: Oxidation and Silicidation

### Oxidation

The final flows are used internally to compute the partial pressure of each component. Partial pressures are the relevant quantity for the subsequent simulation. These are computed as:

$$P_{Comp} = \text{pressure} \cdot \frac{\text{flow}_{Comp_{final}}}{\sum_{Comp} \text{flow}_{Comp_{final}}} \quad (822)$$

where *Comp* holds for a certain component of the gas mixture and *pressure* is the total pressure.

### In Situ Steam-generated Oxidation

Switching on the *in situ* steam-generated (ISSG) Boolean parameter in the `gas_flow` command specifies that the gas flow condition is to be recognized for the ISSG oxidation (see [In Situ Steam-generated Oxidation on page 618](#)). For example:

```
gas_flow name=ISSGflow pressure=12<torr> flowH2=6 flowO2=12 ISSG
```

---

## Oxidant Diffusion and Reaction

For the rigorous simulation of the oxidation process, the dissolution of the oxidant species at the gas–oxide interface, the transport through the existing or already grown oxide, and the consumption at the oxide–silicon interface have to be simulated. The dissolution and consumption are modeled by boundary conditions; for the oxidant transport, a diffusion equation is solved in the oxide layer.

The oxidant species H<sub>2</sub>O, O<sub>2</sub>, and N<sub>2</sub>O are defined in the `SPROCESS.models` file (see [Default Simulator Settings: SPROCESS.models File on page 51](#)) using the `reaction` command (see [reaction on page 1038](#)):

```
reaction name=dryoxSi mat.l=Silicon mat.r=Gas mat.new=oxide \  
diffusing.species=O2 ambient.name=O2  
  
reaction name=wetoxSi mat.l=Silicon mat.r=Gas mat.new=oxide \  
diffusing.species=H2O ambient.name=H2O  
  
reaction name=n2ooxSi mat.l=Silicon mat.r=Gas mat.new=oxide \  
diffusing.species=N2O ambient.name=N2O
```

For mixed oxidant flows, for each species, one diffusion–reaction system is solved. For each oxidant, one dataset is allocated: H<sub>2</sub>O or O<sub>2</sub> or N<sub>2</sub>O [1/cm<sup>3</sup>].

Growth reaction fluxes at the reacting interfaces are defined using the Alagator scripting language (see [Alagator for Generic Growth on page 584](#)). These fluxes are divided internally by the particle density of oxide in order to obtain the growth velocities. Manipulation of these

fluxes is essential for the implementation of empirical growth models, such as the Massoud model, which is not yet covered by a diffusion equation.

In the case of a mixed gas flow, the contributions of both fluxes are summed. At the reaction front, the following reactions are assumed:



The conversion from Si to SiO<sub>2</sub> leads to a volume increase of 125%, which leads to motion and mechanical stresses in the compound.

The oxidant diffusion described by Fick's law leads to the diffusion equation:

$$\frac{\partial c}{\partial t} + \nabla j = 0, \quad \text{where } j = -D\nabla c \quad (824)$$

where  $D$  is the diffusivity of the oxidant and  $j$  is the particle flux. The flux of oxidants in the normal direction to the surface, going from the gas region to the oxide, is given by:

$$j = h \cdot (c^* - c) \quad (825)$$

where  $h$  is the mass transfer coefficient and  $c^*$  is the solid solubility of the oxidant. If  $h$  is sufficiently large, the concentration of oxidant at the gas-oxide interface is approximately equal to the solid solubility.

The coefficient  $h$  is defined in the parameter database as `MassTransfer` and can be set using the commands:

```
pdbSet Gas_Oxide O2 MassTransfer <n>
pdbSet Gas_Oxide H2O MassTransfer <n>
pdbSet Gas_Oxide N2O MassTransfer <n>
```

The solid solubility  $c^*$  is a function of the pressure:

$$c^* = p_{Comp} \cdot c_{ref}^* \quad (826)$$

where  $c_{ref}^* = c_{L0} e^{-\left(\frac{c_{L0}}{kT}\right)}$  is the reference solid solubility.

Its value can be set using the following commands:

```
pdbSet Oxide O2|H2O|N2O CL0 <n>
pdbSet Oxide O2|H2O|N2O CLW <n>
```

where the symbol `|` stands for the logical *or*.

## 8: Oxidation and Silicidation

### Oxidation

The flux caused by the chemical reaction at the oxidation front is described by:

$$j = \beta k c_{si} \quad (827)$$

The stoichiometry coefficient  $\beta$  is 1 for  $O_2$  and 2 for  $H_2O$ ,  $k$  is the chemical reaction rate, and  $c_{si}$  is the particle density at the oxide–silicon interface. The reaction rate and diffusivity are computed from the linear and parabolic rate constants used in the Deal–Grove model.

### Transition to Linear and Parabolic Rate Constants

Assuming the stationary state in Eq. 824, the growth rate in the 1D case can be described by the Deal–Grove model:

$$\frac{dx_{ox}}{dt} = \frac{B}{2x_{ox} + A} \quad (828)$$

where  $x_{ox}$  describes the thickness of the 1D oxide layer. This equation can be solved analytically. The parabolic rate constant is given by  $B$  and the linear rate constant is given by  $B/A$ . A deeper analysis reveals relations between the parabolic rate and diffusivity, and the linear rate and reaction rate. Assuming  $h \gg k$ :

$$D = \frac{\beta B c_{ox}}{2c^*} \quad (829)$$
$$k \approx \frac{c_{ox}(B)}{c^*(A)}$$

where  $C_{ox}$  is the equivalent oxygen concentration in oxide, for example, it is equal to the concentration of  $H_2O$  and one half (1/2) the concentration of  $O_2$ . Both the parabolic rate and linear rate are functions of pressure and temperature. For the temperature dependency, two Arrhenius functions, for a low-temperature and high-temperature regime, are available:

$$B(T) = \begin{cases} B0.h \cdot \exp\left(-\frac{BW.h}{k_B T}\right), & \text{if } T > BT.break \\ B0.l \cdot \exp\left(-\frac{BW.l}{k_B T}\right), & \text{else} \end{cases} \quad (830)$$

Taking pressure dependence into account,  $B$  reads:

$$B = B(p, T) = B(T) p_{Comp}^{Bp.dep/[bar]} \quad (831)$$

The parameters  $B0.h$ ,  $BW.h$ ,  $B0.l$ ,  $BW.l$ ,  $Bp.dep$ , and  $BT.break$  can be found in the parameter database in Oxide H2O | O2 | N2O.

An equivalent set of equations is solved for the linear rate  $B/A$ :

$$\frac{B}{A}(T) = \begin{cases} \text{BA0.h} \cdot \exp\left(-\frac{\text{BAW.h}}{k_B T}\right), & \text{if } T > \text{BAT.break} \\ \text{BA0.l} \cdot \exp\left(-\frac{\text{BAW.l}}{k_B T}\right), & \text{else} \end{cases} \quad (832)$$

with the corresponding set of parameters,  $\text{BA0.h}$ ,  $\text{BAW.h}$ ,  $\text{BA0.l}$ ,  $\text{BAW.l}$ ,  $\text{BAp.dep}$ , and  $\text{BAT.break}$ . These can be found in the parameter database:

```
Oxide_Silicon      H2O | O2 | N2O 100 | 110 | 100
Oxide_PolySilicon H2O | O2 | N2O 100 | 110 | 100
```

and can be set using the `pdbSet` command (for example, `pdbSet O2 110 BA0.h <n>` or `pdbSet H2O 100 BAT.break <n>`).

Parameters defining the diffusivity and parabolic rate constant are bulk properties and, therefore, are defined in oxide. Parameters defining the reaction rate and linear rate constants are interface properties and, therefore, are defined on interfaces. This data can also depend on the crystal orientation when crystalline materials are involved.

## Massoud Model

The Massoud model is an empirical model that describes an enhanced growth rate in the initial regime of the oxidation. The model can be seen as an extension of the Deal–Grove model and is in good agreement with measurement. Sentaurus Process uses a slightly different form of the originally suggested model:

$$\frac{dx_{ox}}{dt} = \frac{B}{2x_{ox} + A} + C \exp\left(-\frac{x_{ox}}{L}\right) \quad (833)$$

$x_{ox}$  is the one-dimensional unmasked oxide thickness. To account for the enhanced growth in the initial regime, the second term of [Eq. 833](#) contributes to the flux (compare with [Eq. 828](#)).

Both the parameters  $L$  and  $C$  depend on the crystal orientation and temperature:

$$C(T) = \begin{cases} \text{C0.h} \cdot \exp\left(-\frac{\text{CW.h}}{k_B T}\right), & \text{if } T > \text{MBAT.break} \\ \text{C0.l} \cdot \exp\left(-\frac{\text{CW.l}}{k_B T}\right), & \text{else} \end{cases} \quad (834)$$

## 8: Oxidation and Silicidation

### Oxidation

$$L(T) = \begin{cases} L0.h \cdot \exp\left(-\frac{LW.h}{k_B T}\right), & \text{if } T > \text{MBAT.break} \\ L0.l \cdot \exp\left(-\frac{LW.l}{k_B T}\right), & \text{else} \end{cases} \quad (835)$$

The parameters `L0.h`, `LW.h`, `L0.l`, `LW.l`, `C0.h`, `CW.h`, `C0.l`, `CW.l`, and `MBAT.break` can be found in the parameter database:

```
Oxide_Silicon O2 | H2O | N2O 100 | 110 | 111
Oxide_PolySilicon O2 | H2O | N2O 100 | 110 | 111
```

### Orientation-dependent Oxidation

For different crystal orientations, different reaction rates can be applied. Internally, Sentaurus Process computes the data fields `Ori100`, `Ori110`, and `Ori111`. If the normal vector on an interface coincides with a certain crystal orientation, the value for this orientation is one; if it is orthogonal, the value equals zero. Interpolation is used to compute the rates on orientations not coinciding with the crystallographic directions.

When saving results in TDR format, these data fields are not stored; however, they can be accessed by using the Alagator scripting language. The Tcl procedure `proc OxidantReaction` creates the terms `ReactionRateO2` and `ReactionRateH2O`:

$$k = k_{\langle 100 \rangle} \text{Ori100} + k_{\langle 110 \rangle} \text{Ori110} + k_{\langle 111 \rangle} \text{Ori111} \quad (836)$$

The reaction rates  $k_{\langle 100 \rangle}$ ,  $k_{\langle 110 \rangle}$ , and  $k_{\langle 111 \rangle}$  are computed from the linear rates  $B/A$  given for different orientations. The parameters `L0` and `C` used in the Massoud model depend on the crystal orientation as well.

For information about the TDR format, refer to the *Sentaurus Data Explorer User Guide*.

### Stress-dependent Oxidation

Stress-dependent oxidation (SDO) usually refers to the coupling of the oxidant diffusivity and reaction rate to the local stress field. To handle the stress-dependent oxidant diffusion and stress-dependent reaction rate, two data fields are created internally. The data field `Pressure` is stored by default, while `NStress` is not; however, both can be accessed by using the Alagator scripting language.

The data fields `Pressure` and `NStress` are defined as:

$$\text{Pressure} = -\frac{1}{3}(\sigma_{xx} + \sigma_{yy} + \sigma_{zz}) \quad (837)$$

and:

$$NStress = -\sum_j \sum_k \sigma_{jk} n_j n_k \quad (838)$$

The components of the stress tensor are given by  $\sigma_{jk}$  and the normal vector at the reaction front is given by  $n_j$ . The definition of `NStress` is only meaningful at an interface. If:

```
pdbSetBoolean Oxide Oxidant SDO 1
```

or:

```
pdbSet Oxide_PolySilicon H2O | O2 | N2O SDO 1
pdbSet Oxide_Silicon H2O | O2 | N2O SDO 1
```

is selected, the reaction rate and diffusivity are modified in the following way:

$$k(NStress, T) = k(T) \cdot \min \left\{ S_{max}, e^{\left( \frac{NStress \cdot V_k}{k_B T} \right)} \right\} \quad (839)$$

and:

$$D(Pressure, T) = D(T) \cdot \min \left\{ S_{max}, e^{\left( \frac{Pressure \cdot VD}{k_B T} \right)} \right\} \quad (840)$$

The activation volume `VD`, being a bulk property, is defined in `Oxide O2 | H2O | N2O`. The activation volume `Vk` controls the impact of the normal stress at the reaction front and, therefore, is defined on interfaces:

```
Oxide_Silicon | Oxide_PolySilicon O2 | H2O | N2O
```

For example:

```
pdbSet Oxide_Silicon O2 Vk <n>
```

To fully enable stress-dependent reaction rate, use the command:

```
pdbSet Diffuse SDReactionRate 1
```

$S_{max}$  is the maximum stress factor and is used to cap the exponential parts.  $S_{max}$  is defined in `Oxide O2 | H2O | N2O` as `MaxStressFactor`.

For example:

```
pdbSet Oxide O2 MaxStressFactor <n>
```

## 8: Oxidation and Silicidation

### Oxidation

For improved numerical stability, the exponential part can be approximated by a reciprocal function for a small exponent and a linear function for a large exponent. This option is switched off by default and can be switched on with the following command:

```
pdbSet Mechanics TS4CappedExp 1
```

and replaces the maximum stress factor used to cap the exponential part.

## Trap-dependent Oxidation

Impurities such as nitrogen and fluorine can be trapped at `Oxide_Silicon` interfaces during oxidation. This will reduce the number of oxidizing sites; therefore, the oxidation rate is reduced. To switch on the model, use the command:

```
pdbSet <interface material> O2 | H2O | N2O TrapDependent 1 | 0
```

The list of trapped impurities is given with the command:

```
pdbSet <interface material> O2 | H2O | N2O TrapList { Trapped impurity list }
```

For example, the following command switches on the trapping flux for nitrogen and fluorine:

```
pdbSet Oxide_Silicon O2 TrapList {Nitrogen Fluorine}
```

Two models are available for the trapping flux of impurities: `Trap` and `TrapGen`.

### Trap Model

The trapping flux of impurities is described with the interface `Trap` model by ignoring the detrapping flux. The total impurity flux at interfaces is the sum of the trapping flux into interfaces and the two-phase segregation. This can be achieved by setting the boundary condition to `Trap` (see [Boundary Conditions on page 344](#)). For example:

```
pdbSet Oxide_Silicon Nitrogen BoundaryCondition Trap
```

Since the surface reaction rate is proportional to the number of available oxidizing sites, the rate of oxidant consumption at the oxidizing interface is given by:

$$\vec{F} = k_s C_{oi} \left( 1 - \frac{\sigma_C}{\sigma_{TCMax}} \right) \vec{n}_i \quad (841)$$

where:

- $k_s$  is the surface recombination rate.
- $C_{oi}$  is the oxidant concentration at the interface.
- $\sigma_C$  and  $\sigma_{TCMax}$  are the impurity trapped density and the maximum trap density, respectively.



The maximum trap density is orientation dependent and can be specified using the following commands:

```

pdbSet <interface material> <trapped impurity> 100 CMax {<n>}
pdbSet <interface material> <trapped impurity> 110 CMax {<n>}
pdbSet <interface material> <trapped impurity> 111 CMax {<n>}

```

### TrapGen Model

The interface TrapGen model calculates not only the trapping flux, but also the generation flux of impurities. The generation flux by reaction due to the Gen.Ambient gas is added to the Gen.Material side. For example:

```

pdbSet Oxide_Silicon Nitrogen BoundaryCondition TrapGen
pdbSet Oxide_Silicon Nitrogen Gen.Ambient N2O
pdbSet Oxide_Silicon Nitrogen Gen.Material Oxide

```

The generation flux in the interface TrapGen model is calculated by:

$$\vec{F} = \rho v \left( \frac{v}{v_{norm}} \right)^{\alpha} \vec{n}_i \quad (842)$$

where:

- $\rho$  is the generation density.
- $v$  is the reaction velocity.
- $v_{norm}$  is the normalization velocity.
- $\alpha$  is the power of normalized velocity.

$\rho$ ,  $v_{norm}$ , and  $\alpha$  are specified with the parameters Gen.Density, Gen.Vnorm, and Gen.Power, respectively.

### Dopant-dependent Oxidation

A dopant-dependent oxidation rate is incorporated through the electron concentration dependence as:

$$k\left(T, \frac{n}{n_i}\right) = k(T) \cdot lc \quad (843)$$

where:

$$lc = 1 + \gamma_V (C_V - 1) \quad (844)$$

## 8: Oxidation and Silicidation

### Oxidation

$$\gamma_V = GAMMA0 \times \exp\left(\frac{-GAMMAW}{kT}\right) \quad (845)$$

and:

$$C_V = \frac{1 + C^+ \left(\frac{n_i}{n}\right) + C^- \left(\frac{n}{n_i}\right) + C^{\bar{=}} \left(\frac{n}{n_i}\right)^2}{1 + C^+ + C^- + C^{\bar{=}}} \quad (846)$$

The quantities in Eq. 846 are given by the following formulas:

$$C^+ = \exp\left(\frac{E^+ - E_i}{kT}\right) \quad (847)$$

$$C^- = \exp\left(\frac{E_i - E^-}{kT}\right) \quad (848)$$

$$C^{\bar{=}} = \exp\left(\frac{2E_i - E^- - E^{\bar{=}}}{kT}\right) \quad (849)$$

$$E^+ = 0.35eV \quad (850)$$

$$E^- = E_g - 0.57eV \quad (851)$$

$$E^{\bar{=}} = E_g - 0.12eV \quad (852)$$

$$E_i = \frac{E_g}{2} + 0.75 \ln(0.719)kT \quad (853)$$

$$E_g = 1.17 - \frac{(4.73 \times 10^{-4})T^2}{T + 636} eV \quad (854)$$

The dependence on carrier concentration is a function of the location along the oxidizing interface.

Dopant-dependent oxidation is off by default and can be switched on with the flag:

```
pdbSetBoolean Oxide_Silicon <O2|H2O> DopantDependentReaction 1
```

In [Eq. 845](#), the quantities `GAMMA0` and `GAMMAW` are set as follows:

```
pdbSetDouble Oxide_Silicon <O2|H2O> Gamma0 2360
pdbSetDouble Oxide_Silicon <O2|H2O> GammaW 1.1
```

The quantities  $E_g$  and  $E_i$  are defined as procedures called `DFactorEg` and `DFactorEi`, each taking a single argument, which is temperature. If you want to overwrite them, use:

```
proc DFactorEg { temp } {
    # enter the function here
}
```

Finally, [Eq. 846](#) is implemented using the expressions for  $C^+$ ,  $C^0$ ,  $C^-$ , and  $C^=$ , where  $C^0$  is identically equal to 1. To overwrite them, use:

```
pdbSetDoubleArray Oxide_Silicon <O2|H2O> \
    DopantReactFactor {1 <expr 1> 0 <expr 2> -1 <expr 3> -2 <expr4>}
```

## Diffusion Prefactors

The reactant diffusivities can be enhanced or retarded due to various new process conditions. If a new model does not exist to simulate the observed behavior, you may want to multiply the existing diffusivity with a prefactor. Sentaurus Process allows diffusivities to be multiplied by user-defined factors. For example, in the case of specified  $O_2$  and  $H_2O$ , these are given by:

```
term name=O2DiffFactor add Oxide eqn=1.0e18/(1.0*N2ox+1.0e18)
term name=H2ODiffFactor add Oxide eqn=1.0e18/(1.0*N2ox+1.0e18)
```

The effective diffusivity of  $O_2$  and  $H_2O$  will be multiplied by `O2DiffFactor` and `H2ODiffFactor`, respectively. In this example, the diffusivity of both reactants will be a function of the dataset `N2ox`. See [Chapter 6 on page 559](#) for the definition of terms.

---

## Oxidation with Dielectric on Top

Thermal oxidation of silicon with a dielectric on top can be simulated in Sentaurus Process using an Alagator generic growth script. Besides the three oxidation steps outlined at the beginning of this chapter, there are two additional ones:

- Diffusion of oxidants ( $H_2O$ ,  $O_2$ ) from the gas–dielectric interface through the dielectric to the dielectric–oxide interface;
- Diffusion of oxidants ( $H_2O$ ,  $O_2$ ) from the dielectric to oxide.

The first step involves the dissolution of the oxidant species at the gas–dielectric interface and the oxidant transport in the bulk dielectric. The second step is modeled by the boundary condition between the dielectric and oxide.

## 8: Oxidation and Silicidation

### Oxidation

This oxidation mode can be enabled or disabled with the commands [SetDielectricOxidationMode](#) on page 1058 and [UnsetDielectricOxidationMode](#) on page 1111.

---

## N<sub>2</sub>O Oxidation

In N<sub>2</sub>O oxidation or oxynitridation, nitrogen is trapped at Si–SiO<sub>2</sub> interfaces so that the number of oxidizing sites and, in turn, the oxidation rate are reduced. N<sub>2</sub>O oxidation is performed by specifying the N<sub>2</sub>O parameter in the `diffuse` statement. For the thick oxidation regime (in other words, the Deal–Grove model), the parameters for N<sub>2</sub>O oxidation are specified similar to O<sub>2</sub> or H<sub>2</sub>O. However, for thin oxidation, the Massoud model is modified by multiplying the nitrogen effect as follows:

$$r_{thin} = C \exp\left(-\frac{x_{ox}}{L}\right) \left(1 - \frac{\sigma_N}{\sigma_{max}}\right) \quad (855)$$

$\sigma_{max}$  can be defined for each of the three available silicon orientations and for polysilicon by specifying the `N.Thin.Max` values for the N<sub>2</sub>O ambient. For example:

```
pdbSet Oxide_Silicon N2O 100 N.Thin.Max {Double {[Arrhenius 1.55e14 0.0]}}
pdbSet Oxide_PolySilicon N2O 100 N.Thin.Max {Double {[Arrhenius 1.55e14 0.0]}}
```

---

## In Situ Steam-generated Oxidation

The low-pressure combustion of hydrogen–oxygen mixtures is effective in producing high-quality oxides. Combustion-like chemical reactions are initiated over the heated wafer, producing a high density of gas-phase radicals (O<sup>•</sup> and OH<sup>•</sup>) that react rapidly with silicon. The model for such ISSG empirically describes the oxidation by the radical O<sup>•</sup>, which dominates the typical ISSG oxidation. When the pressure is too low, which means the hydrogen–oxygen mixtures flow too fast, the reactant residence time is too short for chemical activity to occur. On the other hand, when the pressure increases over some extent, the oxygen-atom density is localized and falls off rapidly downstream of the flame so that the narrow reaction zone prevents oxygen atoms from reaching the wafer surface. The oxygen-atom concentration at the wafer surface is modeled by [1]:

$$C^* = C_{max}(p_{H_2}flow) \cdot BPD(\alpha, \beta, P_{max};P) \cdot RRZ(P_{lim};P) \quad (856)$$

$C_{max}(p_{H_2}flow)$  calculates the maximum oxygen-atom concentration depending on the partial pressure of hydrogen and the total flow of the hydrogen–oxygen mixtures:

$$flow = flow_{H_2} + flow_{O_2} \quad (857)$$

$$p_{H_2} = flow_{H_2} / flow \quad (858)$$

$$C_{max}(p_{H2}flow) = C_{max}(p_{H2}) \cdot (flow/1slm)^{C.FLOW.W} \quad (859)$$

$$C_{max}(p_{H2}) = C.H2.L.O \cdot \min(C.H2.Break, p_{H2})^{C.H2.L.W} + C.H2.H.S \cdot \max(p_{H2} - C.H2.Break, 0) \quad (860)$$

$BPD(\alpha, \beta, P_{max}; P)$  determines the profile of the oxygen-atom concentration with a given pressure. The dependence on the pressure is modeled by the beta prime distribution (BPD) as follows:

$$BPD(\alpha, \beta, P_{max}; P) = \frac{P_n^{\alpha-1} (1 + P_n)^{-\alpha-\beta}}{\left(\frac{\alpha-1}{\beta+1}\right)^{\alpha-1} \left(\frac{\alpha+\beta}{\beta+1}\right)^{-\alpha-\beta}} \quad (861)$$

$$P_n = \frac{\alpha-1}{\beta+1} \cdot \frac{P}{P_{max}} \quad (862)$$

where  $\alpha$  and  $\beta$  are specified by the parameters Alpha and Beta, respectively. The pressure at the peak oxygen-atom concentration,  $P_{max}$ , is modeled as follows:

$$P_{max} = P.Max.H2.O \cdot P_{H2}^{P.Max.H2.W} + P.Max.Flow.O \cdot (flow/1slm)^{P.Max.Flow.W} \quad (863)$$

$RRZ(P_{lim}; P)$  defines the rapid reaction zone where the oxygen atoms do not reach the silicon surface:

$$RRZ(P_{lim}; P) = \frac{1}{2} \operatorname{erfc}(P.Limit.Smooth \cdot (P - P_{lim})/1torr) \quad (864)$$

$$P_{lim} = P.Limit.O + \left( P.Limit.A + P.Limit.B \cdot e^{-P.Limit.W \cdot p_{H2}} \right) \cdot flow \quad (865)$$

The values of the parameters from [Eq. 859](#) through [Eq. 865](#) can be modified by:

```
pdbSet Oxide ISSG <parameter> <value>
```

The diffusivity and reaction rates of the oxygen atoms can be modified respectively by:

```
pdbSet Oxide ISSG D <value>
```

```
pdbSet Oxide_Silicon ISSG Ks <value>
```

The process conditions to invoke the ISSG oxidation are defined in the `diffuse` or `gas_flow` commands, for example:

```
diffuse temp=1000 time=1 pressure=12<torr> flowH2=6 flowO2=12 ISSG
```

---

## Silicide Models

Sentaurus Process allows you to define models for new materials and reactions. This ability has been used to define models for the growth of titanium, tungsten, cobalt, and nickel silicides. The following sections describe the kinetics of  $\text{TiSi}_2$  growth, the specification of the model and parameters, and suggestions for modeling other silicides.

---

### $\text{TiSi}_2$ Growth Kinetics

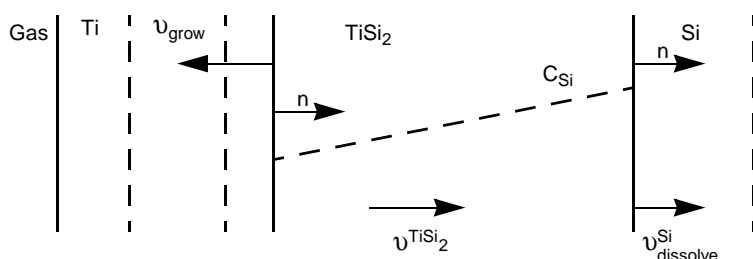


Figure 87 Velocities in 1D silicidation process

Titanium silicide is assumed to form when silicon atoms react in the silicide with titanium at the titanium silicide–titanium ( $\text{TiSi}_2$ –Ti) interface. The dissolution of silicon and the consumption of titanium lead to the deformation of the material layers in the structure.

**NOTE** While the discussion that follows describes the growth of  $\text{TiSi}_2$  on silicon, it also applies to growth of  $\text{TiSi}_2$  on polycrystalline silicon.

The silicidation process has three main steps:

- Dissolution of silicon and diffusion of silicon atoms from the  $\text{TiSi}_2$ –silicon interface through the existing  $\text{TiSi}_2$  to the Ti– $\text{TiSi}_2$  interface.
- Reaction of silicon with titanium to form new  $\text{TiSi}_2$ .
- Motion of materials due to the volume expansion, which is caused by the reaction between diffused silicon and titanium, and also by the dissolution of silicon at the  $\text{TiSi}_2$ –silicon interface.

**NOTE** The name of the silicide reactant field (which represents the concentration of silicon atoms in the silicide) is `iSilicon` to distinguish it from the dopant field `Silicon` in III–V materials.

If silicon or polysilicon is in contact with titanium at the beginning of a thermal silicidation, an initial TiSi<sub>2</sub> layer is created automatically as in the case of oxidation. The thickness of this layer is, by default, 1.5 nm.

The value of the initial TiSi<sub>2</sub> thickness is specified in the parameter database by:

```
pdbSet Grid NativeLayerThickness 1.5e-7
```

which also controls the native layer thickness for oxidation.

Sentaurus Process automatically recognizes the silicidizing interfaces and switches on the reaction equations.

---

## TiSi<sub>2</sub> Formation Reactions

At the TiSi<sub>2</sub>-silicon interface, there is the reaction:



where  $Si_{Si}$  is the silicon as a diffusing species on the silicon material side and  $Si_{TiSi_2}$  is the silicon as a diffusing species on the TiSi<sub>2</sub> material side. Therefore, silicon (on the Si side of the interface) reacts to form silicon atoms (on the TiSi<sub>2</sub> side of the interface). The reaction is reversible, allowing for the reformation of silicon (if silicon is released by nitridation of TiSi<sub>2</sub>, for example):

$$\begin{aligned} R_f &\equiv K_f(C_{Si} - C_{star}) \\ R_g &\equiv \text{Beta } R_f \end{aligned} \quad (867)$$

$R_f$  and  $R_g$  are the diffusion flux and growth reaction flux, respectively, at the TiSi<sub>2</sub>-silicon interface. The forward rate of this reaction depends only on temperature, while the reverse rate is also proportional to the concentration of diffusing silicon atoms in TiSi<sub>2</sub>.  $C_{Si}$  is the concentration of silicon in TiSi<sub>2</sub> and  $C_{star}$  is the equilibrium concentration of silicon at the TiSi<sub>2</sub>-silicon interface. Beta is the stoichiometry of the growing material whose default is 1.0.  $K_f$  is the mass transfer coefficient.

They can be changed using the following commands:

```
pdbSet Silicon_TiSilicide iSilicon Kf <n>
pdbSet Silicon_TiSilicide iSilicon Cstar <n>
pdbSet Silicon_TiSilicide iSilicon Beta <n>
```

## 8: Oxidation and Silicidation

### Silicide Models

For each silicon atom removed from the silicon side of the interface, the volume of silicon is reduced by:

$$\Delta V = \frac{\text{Beta}}{\text{Density.Grow}} \quad (868)$$

where `Density.Grow` is the density of the growing material whose default value is  $5 \times 10^{22}$ .

It can be changed by using the command:

```
pdbSet Silicon_TiSilicide iSilicon Density.Grow <n>
```

There is no new material formation at the  $\text{TiSi}_2$ -silicon interface. Silicon dissolves at this interface and is transported across the  $\text{TiSi}_2$  layer by simple diffusion:

$$\frac{\partial C_{Si}}{\partial t} = \nabla \cdot (D_{star} \nabla C_{Si}) \quad (869)$$

where  $C_{Si}$  is the concentration of silicon in  $\text{TiSi}_2$  and  $D_{star}$  is the diffusivity of silicon in  $\text{TiSi}_2$ . The following command changes the diffusivity:

```
pdbSet TiSilicide iSilicon Dstar {<n>}
```

At the  $\text{TiSi}_2$ -titanium interface, there is the reaction:



This reaction is assumed to be irreversible:

$$\begin{aligned} R_f &\equiv K_f(C_{Si} - C_{star}) \\ R_g &\equiv \text{Beta } R_f \end{aligned} \quad (871)$$

$R_f$  and  $R_g$  are the diffusion flux and growth reaction flux, respectively, at the  $\text{TiSi}_2$ -titanium interface. The reaction rate is proportional to the concentration of diffusing silicon at the  $\text{TiSi}_2$  side of the interface.  $C_{Si}$  is the concentration of silicon in  $\text{TiSi}_2$  and  $C_{star}$  is the equilibrium concentration of silicon at the titanium- $\text{TiSi}_2$  interface. `Beta` is the stoichiometry of the growing material whose default is 0.5.  $K_f$  is the mass transfer coefficient.

To change them, use:

```
pdbSet TiSilicide_Titanium iSilicon Kf <n>
pdbSet TiSilicide_Titanium iSilicon Cstar <n>
pdbSet TiSilicide_Titanium iSilicon Beta <n>
```



The volumes of titanium and  $\text{TiSi}_2$  change according to:

$$\Delta V = \frac{\text{Beta}}{\text{Expansion.Ratio} * \text{Density.Grow}} \quad (872)$$

where `Expansion.Ratio` is the conversion ratio from consumed material to the growing material, and `Density.Grow` is the density of the growing material. The default values for `Expansion.Ratio` and `Density.Grow` are 2.42 and  $2.34 \times 10^{22}$ , respectively. They can be changed by using the commands:

```
pdbSet TiSilicide_Titanium iSilicon Expansion.Ratio <n>
pdbSet TiSilicide_Titanium iSilicon Density.Grow <n>
```

---

## Tungsten-, Cobalt-, and Nickel-Silicide Models

The tungsten-, cobalt-, and nickel-silicide models are identical in form to the titanium-silicide model. The parameters of the models are different, however, reflecting the differences between the materials (see [2][3] for the tungsten-silicide model and [4][5] for the cobalt-silicide model). The names of the relevant materials are `Tungsten` and `TungstenSilicide` ( $\text{WSi}_2$ ), `Cobalt` and `CobaltSilicide` ( $\text{CoSi}_2$ ), and `Nickel` and `NickelSilicide` ( $\text{NiSi}$ ).

---

## Stress-dependent Silicidation

The stress-dependent silicidation model is experimental, and can become unstable and produce irregular shapes. Fundamental changes to the model are possible in future releases.

Similar to oxidation, the silicide reaction rate and the reactant diffusivity can be affected by local stress. For the silicide reaction, the speed of the reaction is assumed to be affected by the total stress energy, so that the stress effect is incorporated symmetrically with respect to tension versus compression.

To switch on stress-dependent diffusion, use the command:

```
StressDependentSilicidation <silicide>
```

For Version H-2013.03, `<silicide>` can be set only to `NickelSilicide`.

When the stress-dependent silicidation model is switched on, the reaction rate given in [Eq. 867](#) and [Eq. 871](#) (that is, at both metal–silicide and silicon–silicide interfaces) is suppressed by the normal stress:

$$K_f(\text{NStress}, T) = K_f(T) e^{-\left(\frac{\text{abs}(\text{NStress}) \cdot V_k}{k_B T}\right)} \quad (873)$$

Similarly, the diffusivity of the reactant `iSilicon` becomes pressure dependent:

$$D(\text{Pressure}, T) = D(T) e^{-\left(\frac{\text{abs}(\text{Pressure}) \cdot \text{VD}}{k_B T}\right)} \quad (874)$$

The activation volume `VD` is a bulk property and is defined in the silicide. The activation volume `Vk` controls the impact of the normal stress at the reaction front and is defined on interfaces:

```
Nickel_NickelSilicide | NickelSilicide_Silicon
```

For example:

```
pdbSet Nickel_NickelSilicide iSilicon Vk <n>
pdbSet NickelSilicide iSilicon VD <n>
```

In addition to switching on stress dependency of the silicide reaction, the command `StressDependentSilicidation` reduces the viscosity of the silicide to a point where viscous relaxation occurs at typical silicidation temperatures (see [StressDependentSilicidation on page 1084](#)). Similar mass relaxation effects have been proposed in the literature [6][7]. To modify the relaxation of the silicide, use one or both of the following commands:

```
pdbSet NickelSilicide Mechanics Viscosity0 <n>
pdbSet NickelSilicide Mechanics ViscosityW <n>
```

---

## Oxygen-retarded Silicidation

The silicidation process may be influenced by the presence of oxygen in the silicide. This oxygen is assumed to enter the silicide at interfaces with silicon dioxide and to diffuse in the silicide according to Fick's law. The oxygen retards the reaction of silicon atoms at the silicide–silicon and silicide–metal interfaces and the diffusion of silicon in the silicide; this is called oxygen-retarded silicidation (ORS). The retardation factor is assumed to be in the form of:

$$R_{factor} = 1 - \frac{ORS_{Oxygen}}{1 \times 10^{22}} \quad (875)$$

where `ORSOxygen` is the retardant solution name. The model can be switched on and off by using the command:

```
pdbSet TiSi2 Silicon ORS {0 | 1}
```

If the model is on,  $R_{factor}$  is multiplied by  $R_f$  of [Eq. 867, p. 621](#),  $D_{Star}$  of [Eq. 869, p. 622](#), and  $R_f$  of [Eq. 871](#). You can define the retardation factors using the `term` command, for example:

```
term name=SiliconReactFactor add TiSilicide /Titanium \
eqn = "((1-ORSOxygen_TiSilicide/1e22)>0)?(1-ORSOxygen_TiSilicide/1e22):(0.0)"
```

```
term name=SiliconDiffFactor add TiSilicide \  
  eqn = "(1-ORSoxygen/1e22)>0)?(1-ORSoxygen/1e22):(0.0)"  
  
term name=SiliconReactFactor add Silicon /TiSilicide \  
  eqn = "(1-ORSoxygen_TiSilicide/1e22)>0)?(1-ORSoxygen_TiSilicide/1e22):(0.0)"
```

**NOTE** The oxygen-retarded silicidation model can cause instabilities (such as a zigzag shape of the silicide boundary) because of a high concentration of silicon near the oxide. Solving the silicon diffusion equation in steady state reduces such instability. It can be switched on using the command:

```
pdbSet NickelSilicide Silicon Steady 1
```

---

## Triple-Point Control

During silicidation, triple points where more than two materials come together (such as oxide, silicon, silicide node) may move inadvertently due to material consumption around the node. To control the movement, a retardation factor around the triple point is applied to the velocities. The retardation factor is assumed to be:

$$R = \text{Factor} + \frac{2(1 - 2\text{Factor})}{\pi} \text{atan}\left(\frac{SDistance}{Distance}\right) \quad (876)$$

`Factor` is the suppression value at the triple point, and `Distance` is the rolloff length for silicidation triple-point suppression. The distance determines how far the suppression factor will be effective from the triple point. `SDistance` is the distance to the nearest node from the triple point and is calculated internally. The other parameters can be changed using the following commands:

```
pdbSet <mater> SilicidationTripleDistance {<n>}  
pdbSet <mater> SilicidationTripleFactor {<n>}
```

where `<mater>` is the interface material (for example, `Silicon_TiSilicide`). If you want to switch the triple-point control on or off, use the command:

```
pdbSet Mechanics SilicidationCorrection {1 | 0}
```

---

## Dopants and Defects in Oxides and Silicides

Dopants in oxides and silicides are modeled in the same way as in other nonsemiconductor materials. Transport within a silicide or an oxide is governed by simple diffusion (in other words, no electric field effects). For details on segregation at material interfaces, see [Boundary Conditions on page 344](#). Point defects can participate in reactions at interfaces with silicon.

While the current oxidation model specifies the generation of interstitials by the consumption of silicon, the current titanium silicide model specifies the generation of vacancies by the same mechanism.

---

## Numerics

During oxidation or silicidation, one material grows at the expense of another material. To handle the growth of materials, Sentaurus Process uses two different time loops – inner and outer – as shown in Figure 88 for the case of oxidation.

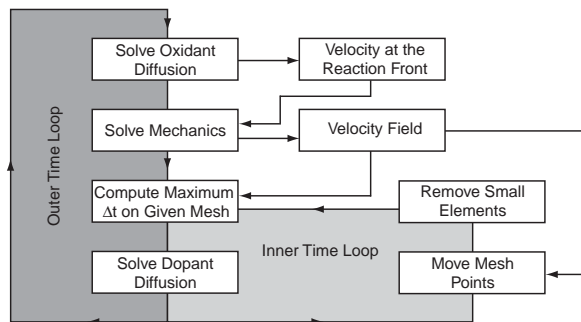


Figure 88 Flowchart for simulation of material growth

---

### Outer Time Loop

The diffusion equation for the oxidants is solved using the general PDE solver in Sentaurus Process. In addition, a predictor for the next time step (*oxidation time step*) is computed. When the concentrations of oxidants at the oxide–silicon interface are known, the corresponding growth velocities can be computed. These velocities serve as a boundary condition for the mechanics problem. After solving the mechanics problem, the velocity field in the entire structure is known. At this point, the program enters the inner time loop.

---

### Inner Time Loop

Given a mesh and the velocity field, a time step (*grid time step*) can be computed so that elements do not collapse when applying the velocities to the nodes of the mesh (moving mesh). In the next time step, the dopant diffusion is solved using the general PDE solver and a predictor for the next time step (*diffusion time step*) is computed. Then, mesh points are moved according to the velocity field and, subsequently, small mesh elements are removed.

After removing small elements, the next grid time step is computed. The smaller of the two time steps (grid time step and diffusion time step) is applied in the next time cycle. The inner

time loop runs as long as the time step of the outer loop (oxidation time step) is fulfilled. Then, the code goes into its second time step of the outer loop. An example of typical output during oxidation is:

```

...
Reaction Solve from 14.86min to 15.11min. Time step: 15.32s.
Mechanics Solve from 14.86min to 15.11min. Time step: 15.32s.
Diffusion Solve from 14.86min to 14.99min. Time step: 8.144s.
Diffusion Solve from 14.99min to 15.11min. Time step: 7.176s.
Reaction Solve from 15.11min to 15.37min. Time step: 15.4s.
Mechanics Solve from 15.11min to 15.37min. Time step: 15.4s.
Diffusion Solve from 15.11min to 15.25min. Time step: 8.361s.
Diffusion Solve from 15.25min to 15.29min. Time step: 2.077s.
Diffusion Solve from 15.29min to 15.37min. Time step: 4.967s.
...

```

This output reproduces the time-stepping scheme: `Reaction Solve` and `Mechanics Solve` occur in the outer time loop; whereas, `Diffusion Solve` occurs in the inner time loop.

As previously mentioned, after solving the mechanics problem, velocities are given on all mesh points. Mesh points are moved according to these velocities. This leads to a change in the geometry and, in some cases, also to a change in the topology of the structure at each time step. At a reactive interface, for example at the oxidation front, two velocities apply: one describes the growth of a material and one describes the consumption of another material.

The velocity describing the growth of the material is used to solve the mechanics problem, and the velocities describing the consumption of a material are used to update the structure or mesh. Therefore, mesh elements on the growing side of the oxidation front are *stretched*, and elements on the shrinking side are *compressed*. Edges on the growing side, which become too long with time, are split. Edges and elements on the shrinking side of the interface which become too small are removed. This is demonstrated in [Figure 89](#).

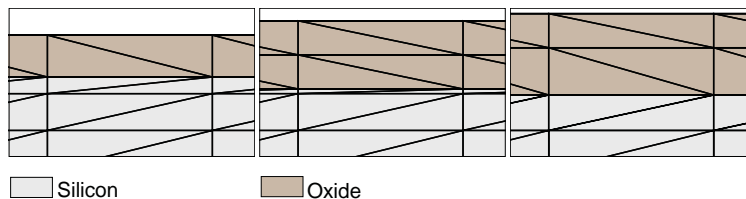


Figure 89 Meshing strategy during thermal oxidation

---

## References

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*This chapter discusses the computation of mechanical stress in Sentaurus Process.*

---

## Overview

Mechanical stress plays an important role in process modeling. It controls the structural integrity of the device, the yield from the process depends on stresses, the mobility of charged carriers is changed by stresses, and leakage currents also are a function of the stress in the system.

On a finer scale, stresses can affect dopant diffusion rates by modifying the band gap. They can affect oxidation rates and, therefore, can alter the shapes of thermally grown oxide layers.

In modern process flows, accurate computation of stress is important. However, there is a continual trend toward designing process flows that produce the right types of stress in the device. With appropriate stresses, device performance can be enhanced significantly.

Stress computation simulations are performed in four distinct steps:

- First, the equations for mechanics are defined. The equations used in Sentaurus Process define force equilibrium in the quasistatic regime.
- Second, the boundary conditions for these equations are defined. For the elliptic equations that arise from the equations of force equilibrium, boundary conditions are needed on all boundaries. Sentaurus Process allows Dirichlet or Neumann boundary conditions provided that certain minimum criteria are met. The minimum criterion is to constrain the structure sufficiently so that it has no rigid body modes.
- Third, material properties are defined. This is the part where the relationship between stresses and strains is defined. Some materials may hold stresses for a given strain without relaxing; these are *elastic materials*. Others may relax the stresses away; these are *viscous or viscoelastic materials*. Sentaurus Process provides a viscoelastic constitutive equation for the computation of mechanical stresses. By setting parameters appropriately, the border cases of a purely viscous and a purely elastic material can be simulated as well. The viscoelastic model used in Sentaurus Process uses a so-called Maxwell model for the deviatoric part and the dilatational part separately. The viscosity can depend on the local shear stresses, which make the viscosity a locally varying quantity and can lead to nonlinear mechanical behavior. In addition to elastic and viscoelastic materials, plastic materials may undergo irreversible deformation beyond the yield stress without fracture or

## 9: Computing Mechanical Stress

### Material Models

damage. Sentaurus Process provides a nonlinear material model with a von Mises yield criterion and a bilinear isotropic hardening law.

- Fourth, the mechanisms that drive the stresses are defined. In Sentaurus Process, this is performed through intrinsic stresses, thermal mismatch, material growth, lattice mismatch (silicon germanium), and densification. All these processes are additive in the linear elastic regime. In the nonlinear regime, they must be updated from the available stress history.

Stress is solved in all materials. However, during an inert diffusion, the stress computation can be switched off. Parameters describing material behavior, which will be introduced in this chapter, can be found in the parameter database:

```
<material> Mechanics
```

Some examples are `Viscosity0`, `ViscosityW`.

In the following sections, the constitutive equations are discussed in detail. These tensor equations can be split into two parts:

- The *dilatational part*, which corresponds to the trace of the tensor, describes the material behavior in the case of a pure volume change.
- The *deviatoric part* describes an arbitrary deformation but without changing the volume. For example, the strain tensor can be decomposed as follows:

$$\epsilon_{jk} = \underbrace{\epsilon'_{jk}}_{\text{deviatoric}} + \underbrace{\frac{1}{3} \left( \sum_l \epsilon_{ll} \right) \delta_{jk}}_{\text{dilatational}} \quad (877)$$

This decomposition will be used in subsequent equations to discuss the constitutive equation for the dilatational and deviatoric parts independently.

---

## Material Models

Sentaurus Process implements the viscous, viscoelastic, and elastic models in a general manner, where the viscous model and elastic model can be derived from the viscoelastic model. The viscous and viscoelastic models use shear stress–dependent viscosity. The elastic model also has the anisotropic elasticity where the elastic coefficients are dependent on the crystal orientation. The plasticity model describes the material behavior beyond yield, in other words, the transition from elastic behavior to plastic behavior.



## Viscoelastic Materials

The viscoelastic model for a Maxwell body is used to describe the stress–strain relationship. The equations are written in terms of dilatational and shear components. The equations for the volumetric part of the stress tensor<sup>1</sup> take the form:

$$\frac{\dot{\sigma}_v}{K} + \frac{\sigma_v}{\eta_v(T, \sigma_s)} = 3\dot{\epsilon}_v \quad (878)$$

and:

$$\sum_k \sigma_{kk} = -3p = 3\sigma_v \quad (879)$$

where  $\eta_v$  is the bulk viscosity. In addition, the relation of the stress and strain tensor to the hydrostatic pressure  $p$  is shown. The bulk modulus  $K$  can be computed from the Poisson ratio `PoissRatio` and Young's modulus `YoungsMod` as:

$$K = \frac{\text{YoungsMod}}{3(1 - 2 \cdot \text{PoissRatio})} \quad (880)$$

The deviatoric part of the stress tensor is described by:

$$\frac{\dot{\sigma}'_{jk}}{G} + \frac{\sigma'_{jk}}{\eta'(T, \sigma_s)} = 2\dot{\epsilon}'_{jk} \quad (881)$$

where  $\eta'$  is the shear viscosity. The shear modulus  $G$  can be computed from the Poisson ratio and Young's modulus as:

$$G = \frac{\text{YoungsMod}}{2(1 + \text{PoissRatio})} \quad (882)$$

By default, the viscoelastic response is applied to the deviatoric parts. The linear elastic model is used for the pressure-volume response, that is:

$$\sigma_v = K \sum_k \epsilon_{kk} \quad (883)$$

To apply the viscoelastic response to both the deviatoric parts and the volumetric part, use:

```
pdbSet Mechanics NoBulkRelax 0
```

---

1. The subscripts of vectors and tensors hold for the Cartesian coordinates  $x$ ,  $y$ , and  $z$ .

The shear viscosity  $\eta'$  is a function of the shear stress and the temperature  $T$ , where:

$$\eta'(T) = \text{viscosity0} \cdot \exp\left(-\frac{\text{viscosityW}}{k_B T}\right) \quad (884)$$

Usually, the value of `viscosityW` is negative and, therefore, the shear viscosity  $\eta'$  decreases with increasing temperature. The bulk viscosity has a similar Arrhenius expression defined by the parameters `viscosity0.K` and `viscosityW.K`. The dependency on the shear stress  $\sigma_s$  is discussed in [Shear Stress–dependent Viscosity on page 632](#).

---

## Purely Viscous Materials

Oxide and nitride, by default, are treated as viscoelastic materials. However, the viscosity is a function of the temperature (see [Eq. 884](#)). With increasing temperature, the viscosity decreases, that is, the material becomes increasingly more liquid. When the viscosity reaches a very low value, the first term in [Eq. 881](#) can be neglected:

$$\frac{\sigma'_{jk}}{\eta'(T, \sigma_s)} = 2\dot{\epsilon}'_{jk} \Leftrightarrow \sigma'_{jk} = 2\eta'\dot{\epsilon}'_{jk} \quad (885)$$

[Eq. 885](#) describes the deviatoric part of a purely viscous material. The relaxation time  $\tau = \eta'/G$  typically gives a good estimate of the behavior of a viscoelastic material. If  $\tau$  is much greater than the process time, the material is in the elastic regime. The material behaves viscoelastically if  $\tau$  is in the range of the process time. If  $\tau$  is very small, the material is in the viscous regime.

## Shear Stress–dependent Viscosity

For viscous and viscoelastic materials, the viscosity may depend on the temperature and the shear stress  $\sigma_s$ . The temperature dependency is described by [Eq. 884](#). The dependency on the shear stress is given by:

$$\eta(\sigma_s, T) = \eta(T) \cdot \frac{\sigma_s/\sigma_{\text{crit}}}{\sinh(\sigma_s/\sigma_{\text{crit}})} \quad (886)$$

The shear stress  $\sigma_s$  is computed from the local stress distribution based on the second invariant of the deviatoric part of the stress tensor:

$$\sigma_s = \sqrt{\frac{3}{2} \sum_j \sum_k \sigma'_{jk} \sigma'_{kj}} \quad (887)$$

The viscosity breakdown value  $\sigma_{\text{crit}}$  can be determined by:

$$\sigma_{\text{crit}} = \frac{2k_{\text{B}}T}{v_{\text{crit}}} \quad (888)$$

where:

$$v_{\text{crit}}(T) = v_{\text{crit}0} \cdot \exp\left(-\frac{v_{\text{crit}W}}{k_{\text{B}}T}\right) \quad (889)$$

By default, oxide and nitride are treated as viscoelastic materials with shear stress–dependent viscosity. The values for  $v_{\text{crit}0}$  and  $v_{\text{crit}W}$  also are set in the PDB:

```
<material> Mechanics
```

---

## Purely Elastic Materials

If the viscosity in [Eq. 881](#) is chosen high enough, the second term on the left can be neglected and the equation reads:

$$\frac{\dot{\sigma}'_{jk}}{G} = 2\dot{\epsilon}'_{jk} \Leftrightarrow \sigma'_{jk} = 2G\epsilon'_{jk} \quad (890)$$

This equation describes the deviatoric part of a purely elastic material. By default, silicon and polycrystalline silicon are treated as purely elastic materials. To achieve this, the viscosity of these materials is set to  $1 \times 10^{40}$  poise.

**NOTE**  $K$  and  $G$  are the primary parameters describing elastic materials, and not Young’s modulus and the Poisson ratio. When changing material properties with the `pdb` command, only a change of the primary parameters has an effect on the simulation. To obtain Young’s modulus and the Poisson ratio, use the following commands, respectively (see [KG2E on page 952](#) and [KG2nu on page 953](#)):

```
KG2E <BulkModulus> <ShearModulus>
KG2nu <BulkModulus> <ShearModulus>
```

**NOTE** When material data is given in terms of Young’s modulus and the Poisson ratio, use the following commands to convert them to the shear modulus and the bulk modulus, respectively (see [Enu2G on page 886](#) and [Enu2K on page 887](#)):

```
Enu2G <YoungsModulus> <PoissonRatio>
Enu2K <YoungsModulus> <PoissonRatio>
```

---

## Anisotropic Elastic Materials

The stress and strain relations for anisotropic elastic materials can be described using:

$$\sigma_i = C_{ij}\varepsilon_j \quad (891)$$

where  $\sigma_i$  and  $\varepsilon_j$  are the components of the engineering stress and strain, respectively, and  $C_{ij}$  is the component of the stiffness matrix. The engineering stress  $\sigma_i$  ( $i=1, \dots, 6$ ) corresponds to the stress-tensor components  $\sigma_{xx}$ ,  $\sigma_{yy}$ ,  $\sigma_{zz}$ ,  $\sigma_{xy}$ ,  $\sigma_{yz}$ ,  $\sigma_{xz}$ , and the engineering strain  $\varepsilon_j$  ( $j=1, \dots, 6$ ) corresponds to the strain-tensor components  $\varepsilon_{xx}$ ,  $\varepsilon_{yy}$ ,  $\varepsilon_{zz}$ ,  $2\varepsilon_{xy}$ ,  $2\varepsilon_{yz}$ ,  $2\varepsilon_{xz}$ .

**NOTE** The engineering shear-strain components differ from the shear-strain tensor components by a factor of 2.

### Cubic Crystal Anisotropy

The mechanical responses of a crystalline solid vary along various crystal orientations. For a cubic crystal, the axes of reference are chosen to be parallel to the crystal axes. In a coordinate system with axes aligned along the crystal axes, the symmetric stiffness matrix  $C$  has the following nonzero components:

$$\begin{aligned} C_{11} &= C_{22} = C_{33}, & C_{12} &= C_{23} = C_{13} \\ C_{44} &= C_{55} = C_{66} \end{aligned}$$

All other components are zeros. The anisotropic stress and strain relation is completely defined when three independent modulus parameters  $C_{11}$ ,  $C_{12}$ , and  $C_{44}$  are specified.

The degree of anisotropy for a given material can be measured by the departure from unity of the ratio  $A = 2 C_{44} / (C_{11} - C_{12})$ . The anisotropic model reduces to the isotropic model if the ratio  $A$  is equal to 1. When the simulation coordinate axes do not coincide with the crystal axes, the stiffness matrix  $C$  must be transformed accordingly. For this, note that  $C$  is actually a rank-4 tensor.

By default, the anisotropic elasticity model is switched off. The following command is required to switch on the model:

```
pdbSet Silicon Mechanics Anisotropic 1
```

The values of these three modulus parameters with respect to the cubic crystal axis can be defined using the following commands, which also show the default values for the crystalline silicon:

```
pdbSet Silicon Mechanics C11 16.57E11  
pdbSet Silicon Mechanics C12 6.39E11  
pdbSet Silicon Mechanics C44 7.96E11
```

The unit for these default values is dyn/cm<sup>2</sup>.

This model depends on the `wafer.orient` and `slice.angle` parameters specified in the `init` command.

## Orthotropic Model

Orthotropic materials have three planes of symmetry. In a coordinate system with axes aligned along the symmetry planes, the symmetric stiffness matrix  $C$  has the following nonzero components:

$$C_{11}, C_{22}, C_{33}, C_{44}=C_{55}=C_{66}, C_{12}=C_{21}, C_{13}=C_{31}, C_{23}=C_{32}$$

The symmetry planes of the model are specified in the wafer coordinate system (see [Wafer Coordinate System on page 64](#)) and depend on the `wafer.orient` and `flat.orient` parameters specified in the `init` command. The default symmetry plane directions are given by these two parameters. Therefore, the wafer in-plane symmetry plane directions are given by (the default) `flat.orient`={1 1 0}, that is, at a 45° angle to the xy plane of the wafer coordinate system. To align the symmetry planes with the wafer coordinate system, the `wafer.orient` parameter should be {0 0 1} (the default) and the `flat.orient` parameter should be set to {0 1 0}.

**NOTE** When the symmetry plane directions are specified, they remain the same for the entire structure and cannot be set regionwise.

Orthotropic material properties can be described by specifying nine independent parameters, namely, the Young's moduli in the symmetry planes ( $E_1, E_2, E_3$ ), the directional shear moduli ( $G_{12}, G_{23}, G_{13}$ ), and the directional Poisson ratios ( $\nu_{12}, \nu_{13}, \nu_{23}$ ). The other directional Poisson ratio are calculated from:

$$\frac{\nu_{ij}}{E_i} = \frac{\nu_{ji}}{E_j} \quad (892)$$

The stiffness matrix components are calculated from the specified material properties:

$$C_{kk} = E_k(1 - \nu_{ij}\nu_{ji}) \quad (893)$$

$$C_{ij} = E_i(\nu_{ji} + \nu_{jk}\nu_{ki}) \quad (894)$$

and  $i, j \neq k$ .

By default, the orthotropic model is switched off, and it is switched on using the command:

```
pdbSet <material> Mechanics Orthotropic 1
```

## 9: Computing Mechanical Stress

### Material Models

The material properties can be specified as:

```
pdbSetDouble <material> Mechanics <material parameter> <n>
```

specifically:

```
pdbSet Silicon Mechanics YoungsModulus1 162E10
pdbSet Silicon Mechanics YoungsModulus2 162E10
pdbSet Silicon Mechanics YoungsModulus3 162E10
pdbSet Silicon Mechanics PoissonRatio12 0.28
pdbSet Silicon Mechanics PoissonRatio13 0.28
pdbSet Silicon Mechanics PoissonRatio23 0.28
pdbSet Silicon Mechanics ShearModulus12 63.28E10
pdbSet Silicon Mechanics ShearModulus13 63.28E10
pdbSet Silicon Mechanics ShearModulus23 63.28E10
```

The values given also are the default values used. The units for the Young's modulus and shear modulus are dyn/cm<sup>2</sup>.

Orthotropic thermal expansion also is considered in this material model, and different coefficients of thermal expansion can be specified along the three symmetry planes:

```
pdbSet Silicon Mechanics ThExpCoeff1 3E-06
pdbSet Silicon Mechanics ThExpCoeff2 3E-06
pdbSet Silicon Mechanics ThExpCoeff3 3E-06
```

The specified values are the default values.

Temperature-dependent material properties can be specified for all the material parameters specified above. The variation of a property  $\xi$  can be specified as:

$$\xi(T) = \xi_{ref} + \xi'(T - T_{ref}) \quad (895)$$

where the reference value is the material parameter value specified in the input deck.

The values can be specified as:

```
pdbSet <material> Mechanics <material parameter>Rate <n>
```

for example:

```
pdbSet Silicon Mechanics ThExpCoeff1Rate 0
```

## Plastic Materials

Materials such as metals show linear elastic behavior at lower stresses but undergo permanent deformation at higher stresses. At low temperatures, permanent deformation in these materials is not sensitive to the rate of loading. Such material behavior is defined as plastic or elastic-plastic. Depending on the type of loading, plastic deformations may be computed using incremental plasticity or deformation plasticity.

To switch on the plastic material model, use the command:

```
pdbSet <material> Mechanics IsPlastic <n>
```

### Incremental Plasticity

Plastic material behavior under nonmonotonic loading is modeled using incremental formulation.

Incremental plasticity uses the von Mises yield criterion with associative flow and bilinear hardening. The von Mises yield criterion for isotropic solid materials takes the form:

$$F(\sigma'_{ij}, q_{ij}, \alpha) = \sqrt{(\sigma'_{ij} - q_{ij})(\sigma'_{ij} - q_{ij})} - Y(\alpha) = 0 \quad (896)$$

where  $q_{ij}$  is the back stress,  $\alpha$  is an isotropic hardening variable, and:

$$Y(\alpha) = \sqrt{\frac{2}{3}}(\sigma_y + H_{\text{iso}}\alpha) \quad (897)$$

is a function describing the change of yield surface with progressive yielding. The Einstein summation convention is used to define the tensor product in the above equation.  $\sigma_y$  is the yield stress in uniaxial tension.  $H_{\text{iso}}$  is the isotropic hardening modulus, which is constant for bilinear isotropic hardening. To set these two parameters, use the commands:

```
pdbSet <material> Mechanics FirstYield <n>
pdbSet <material> Mechanics Hardening.Modulus.Isotropic <n>
```

Under a small strain assumption, the strains (and strain rates) are decomposed additively:

$$\epsilon_{ij} = \epsilon_{ij}^e + \epsilon_{ij}^p \quad (898)$$

where  $\epsilon_{ij}^e$  are the elastic strains, and  $\epsilon_{ij}^p$  are the plastic strains.

For incremental plasticity, the plastic strains are determined by the plastic flow rule:

$$\dot{\epsilon}_{ij}^p = \dot{\gamma} \frac{\partial Q}{\partial \sigma_{ij}} \quad (899)$$

## 9: Computing Mechanical Stress

### Material Models

where  $\dot{\gamma} \geq 0$  is the slip rate, and  $Q$  is the plastic potential. Plastic flow is assumed to be volume preserving, so that plastic strain is purely deviatoric:

$$\varepsilon_{ij}^p \delta_{ij} = 0 \Rightarrow \varepsilon_{ij}^p = \varepsilon_{ij}^p \quad (900)$$

For associative plastic flow, the plastic potential  $Q$  is set equal to the yield function  $F$ . The evolution of the isotropic hardening variable and the back-stress variable are given by:

$$\dot{\alpha} = \dot{e}^p = \sqrt{\frac{2}{3}} \dot{\gamma} \quad (901)$$

and:

$$\dot{q}_{ij} = \frac{2}{3} \dot{\gamma} H_{kin} \frac{(\sigma'_{ij} - q_{ij})}{\sqrt{(\sigma'_{kl} - q_{kl})(\sigma'_{kl} - q_{kl})}} \quad (902)$$

where  $H_{kin}$  is the kinematic hardening modulus, and  $\dot{e}^p$  is the equivalent plastic strain rate. To set the kinematic hardening modulus, use the command:

```
pdbSet <material> Mechanics Hardening.Modulus.Kinematic <n>
```

For linear isotropic hardening, the hardening modulus is interpreted as the slope of the stress versus the plastic strain curve (as obtained from uniaxial tension test)  $H_{iso} = \frac{d\sigma}{d\varepsilon^p}$ . It differs from the elastic-plastic tangent modulus, which is defined as the slope of the stress versus total strain curve  $E^{ep} = \frac{d\sigma}{d\varepsilon}$ .

For combined isotropic and kinematic hardening, a common choice for hardening moduli is:

$$H_{kin} = (1 - \beta)\bar{H}; H_{iso} = \beta\bar{H}; \beta \in [0, 1] \quad (903)$$

where  $H$  is a constant.

The rate equations are discretized using backward Euler scheme and then solved using a radial return mapping algorithm (see [1] for more details).

The nonlinear nature of the plasticity model requires Newton iterations to achieve the equilibrium state for each loading step. At the end of each iteration, a check on the satisfaction of convergence criteria is made. More Newton iterations are performed until all the convergence criteria are satisfied within the specified tolerance or until the maximum number of iterations is reached. See [Time-Step Control for Mechanics on page 847](#) for details on convergence criteria and time-stepping for mechanics.



**NOTE** To define the plastic model, use nonzero values for the isotropic or the kinematic hardening modulus along with yield stress. In the absence of hardening, the numeric simulation of plastic deformation may become unstable.

## Deformation Plasticity

Plastic materials that do not have well-defined yield stress can be modeled using deformation plasticity. This model is based on the Ramberg–Osgood formula [2][3], which is only valid for monotonic loading. It is used mostly for plastic deformation around crack tips since it is well suited to the J-integral calculation.

For one dimension, an additive decomposition of strains under a small strain assumption is given as:

$$\varepsilon = \varepsilon^e + \varepsilon^p = \frac{\sigma}{E} + \alpha \left( \frac{\sigma_y}{E} \right) \left( \frac{\sigma}{\sigma_y} \right)^n \quad (904)$$

where  $\alpha$  and  $n$  are material parameters,  $\sigma$  is the stress in one dimension,  $\varepsilon$  is the total strain in one dimension, and  $E$  is Young's modulus.

Extending the formula to three dimensions, the strain components can be expressed as:

$$\varepsilon_{ij} = \varepsilon_{ij}^e + \varepsilon_{ij}^p = \overbrace{\frac{\sigma'_{ij}}{2G} + \frac{\sigma_{kk} \delta_{ij}}{9K}}^{\text{elastic}} + \overbrace{\frac{3}{2} \alpha \left( \frac{\sigma_y}{E} \right) \left( \frac{\sigma^{eq}}{\sigma_y} \right)^n \frac{\sigma'_{ij}}{\sigma^{eq}}}^{\text{plastic}} \quad (905)$$

where  $\sigma^{eq} = \sqrt{\frac{3}{2} \sigma'_{ij} \sigma'_{ij}}$  is the equivalent stress.

The plastic flow is assumed to be associative and is governed by the von Mises yield criterion.

Under monotonic loading, the total plastic strain can be written as:

$$\varepsilon_{ij}^p = \frac{3}{2} e^p \frac{\sigma'_{ij}}{\sigma^{eq}} \quad (906)$$

where  $e^p = \alpha \left( \frac{\sigma_y}{E} \right) \left( \frac{\sigma^{eq}}{\sigma_y} \right)^n$  is the total equivalent plastic strain.

Inverting the plastic strain expression gives:

$$\sigma^{eq} = \sigma_y \left( \frac{E}{\alpha \sigma_y} \right)^m (e^p)^m \quad (907)$$

with  $m = \frac{1}{n}$  defining the work hardening exponent.

The deformation plasticity equations do not require any integration due to total stresses and strains. However, the nonlinear expressions require Newton iterations to achieve the equilibrium state for each loading step. At the end of each iteration, a check on the satisfaction of convergence criteria is made. More Newton iterations are performed until all the convergence criteria are satisfied within the specified tolerance or until the maximum number of iterations is reached. See [Time-Step Control for Mechanics on page 847](#) for details on convergence criteria and time-stepping for mechanics.

**NOTE** Deformation plasticity must be used only with monotonic loading since the equations are not valid for unloading. This model must be used if the J-integral must be calculated around a crack tip with plastic strains.

---

## Viscoplastic Materials

Materials, such as metals at high temperatures, exhibit rate-dependent plasticity also known as viscoplasticity or creep. There are different ways to model such behavior:

- Anand model
- Power law creep

### Anand Model

The Anand model [4][5] is used for rate-dependent plasticity that combines creep and plastic deformation.

Assuming small strains, the strain rates and strains can be decomposed into elastic and viscoplastic parts in an additive manner:

$$\dot{\boldsymbol{\varepsilon}}_{ij} = \dot{\boldsymbol{\varepsilon}}_{ij}^e + \dot{\boldsymbol{\varepsilon}}_{ij}^{vp} \quad (908)$$

$$\boldsymbol{\varepsilon}_{ij} = \boldsymbol{\varepsilon}_{ij}^e + \boldsymbol{\varepsilon}_{ij}^{vp} \quad (909)$$

The elastic strains are evaluated using Hooke's law, while the Anand model is used to evaluate the viscoplastic part. The Anand model assumes that plastic deformation occurs at all values of strain, so instead of a yield function, a constitutive equation is used to relate stresses to viscoplastic strains. The flow rule for evolution of viscoplastic strains (volume preserving) is assumed to be of the familiar form:

$$\dot{\boldsymbol{\varepsilon}}_{ij}^{vp} = \sqrt{\frac{3}{2}} e^{-\alpha} \frac{\boldsymbol{\sigma}'_{ij}}{\|\boldsymbol{\sigma}'\|}; \|\boldsymbol{\sigma}'\| = \sqrt{\boldsymbol{\sigma}'_{ij} \boldsymbol{\sigma}'_{ij}} \quad (910)$$

The equivalent viscoplastic strain rate at constant temperature is given by a constitutive equation:

$$\dot{\epsilon}^{vp} = f(\|\sigma\|, s) = A \exp\left(-\frac{Q}{RT}\right) \left[ \sinh\left(\xi \frac{\|\sigma\|}{s}\right) \right]^{1/m} \quad (911)$$

where  $s$  is deformation resistance. It is defined in terms of an isotropic hardening function as:

$$\dot{s} = h(s) \dot{\epsilon}^{vp} = h_0 \left(1 - \frac{s}{s^*}\right)^a \operatorname{sgn}\left(1 - \frac{s}{s^*}\right) \dot{\epsilon}^{vp}; \quad a \geq 1 \quad (912)$$

The saturation value of deformation resistance at a given temperature and strain rate is expressed as:

$$s^* = \tilde{s} \left[ \frac{\dot{\epsilon}^{vp}}{A} \exp\left(\frac{Q}{RT}\right) \right]^n \quad (913)$$

In the above formulation:

- $A$  is a pre-exponential factor.
- $Q$  is the activation energy.
- $R$  is the universal gas constant.
- $T$  is absolute temperature in kelvin.
- $\xi$  is the stress multiplier.
- $m$  is the strain rate sensitivity.
- $h_0$  is the constant of athermal hardening or softening.
- $a$  is the exponent of athermal hardening or softening.
- $\tilde{s}$  is the coefficient for the saturation value of deformation resistance.
- $n$  is the exponent for the saturation value of deformation resistance.

Values for the material parameters  $A$ ,  $Q$ ,  $\xi$ ,  $m$ ,  $h_0$ ,  $a$ ,  $\tilde{s}$  and  $n$ , and the initial value for deformation resistance  $s_0$  are obtained by fitting experimental data for stress–strain (obtained from tension or compression tests conducted at various temperatures and strain rates) to the above equations. For details on how to obtain such data, refer to the literature [\[4\]\[6\]\[7\]\[8\]](#).

To set these parameters, use the commands:

```

pdbSetDouble <material> Mechanics Viscoplasticity.A <n>
pdbSetDouble <material> Mechanics Viscoplasticity.Q <n>
pdbSetDouble <material> Mechanics Viscoplasticity.Xi <n>
pdbSetDouble <material> Mechanics Viscoplasticity.m <n>
pdbSetDouble <material> Mechanics Viscoplasticity.h0 <n>
pdbSetDouble <material> Mechanics Viscoplasticity.a <n>
pdbSetDouble <material> Mechanics Viscoplasticity.stilde <n>

```

## 9: Computing Mechanical Stress

### Material Models

```
pdbSetDouble <material> Mechanics Viscoplasticity.n <n>  
pdbSetDouble <material> Mechanics Viscoplasticity.s0 <n>
```

**NOTE** For other materials, use the long form of the `pdb` commands to set parameter values.

A new material named `Solder` has been added to the PDB to model viscoplastic behavior. The default values for the above parameters for `Solder` material are based on 96.5Sn3.5Ag solder alloy as reported in [6].

To solve the above nonlinear equations, the rate terms are discretized using the backward Euler method, and the resulting algebraic equations are evaluated locally at every integration point using the Newton–Raphson iterative scheme.

To switch on the viscoplastic material model, use the command:

```
pdbSet <material> Mechanics IsViscoPlastic <n>
```

This flag must be switched on during the simulation if viscoplastic deformation exists. The nonlinear nature of the viscoplasticity model also requires Newton iterations to achieve equilibrium of mechanics equations at each loading step. At the end of each iteration, convergence criteria are checked. More iterations are performed until all the convergence criteria are satisfied within the specified tolerance or until the maximum number of iterations is reached. See [Time-Step Control for Mechanics on page 847](#) for details on convergence criteria and time-stepping for mechanics.

**NOTE** To avoid convergence problems, use small time steps at the beginning of the analysis. You can increase the number of time steps later, during the analysis, if it does not adversely affect the solution.

## Power Law Creep

The power law creep [9], also known as the Bailey–Norton creep, assumes creep strain to be of the following form:

$$\dot{\epsilon}^{cr} = A \exp\left(-\frac{Q}{RT}\right) \bar{\sigma}^n m t^{(m-1)} \quad (914)$$

where, for multiaxial loading:

- $\dot{\epsilon}^{cr} = \sqrt{\frac{2}{3} \dot{\epsilon}_{ij}^{cr} \dot{\epsilon}_{ij}^{cr}}$  is the equivalent creep strain rate.
- $A$  is a pre-exponential factor.
- $Q$  is the activation energy.

- $R$  is the universal gas constant.
- $T$  is the absolute temperature in kelvin.
- $\bar{\sigma} = \sqrt{\frac{3}{2} \sigma'_{ij} \sigma'_{ij}}$  is the equivalent stress or the von Mises stress.
- $\tilde{t}$  is the time (different from physical time).
- $n$  and  $m$  are exponents.

The above form is referred to as a time hardening form. A more commonly used form called the strain hardening form is obtained by eliminating the time variable:

$$\dot{\epsilon}^{cr} = m \left( A \exp\left(-\frac{Q}{RT}\right) \bar{\sigma}^n (\epsilon^{cr})^{(m-1)} \right)^{\frac{1}{m}} \quad (915)$$

Under a small strain assumption, strains (and strain rates) can be decomposed additively as:

$$\epsilon_{ij} = \epsilon_{ij}^e + \epsilon_{ij}^p + \epsilon_{ij}^{cr} \quad (916)$$

with creep strains being distinct from plastic strains.

Creep flow is assumed to be volume preserving ( $\epsilon_{ij}^{cr} \delta_{ij} = 0$ ) and is governed by:

$$\dot{\epsilon}_{ij}^{cr} = \frac{3}{2} \dot{\epsilon}^{cr} \left( \frac{\sigma'_{ij}}{\bar{\sigma}} \right) \quad (917)$$

When incremental plasticity is also active, the creep flow rule is modified to account for hardening:

$$\dot{\epsilon}_{ij}^{cr} = \frac{3}{2} \dot{\epsilon}^{cr} \left( \frac{\sigma'_{ij} - q_{ij}}{\bar{\sigma}} \right) \quad (918)$$

where:

- $\bar{\sigma} = \sqrt{\frac{3}{2} (\sigma'_{ij} - q_{ij})(\sigma'_{ij} - q_{ij})}$  is the equivalent stress.
- $q_{ij}$  is the back stress for kinematic hardening.
- Plastic flow equations are solved simultaneously with creep flow.

The material parameters  $A$ ,  $Q$ ,  $n$ , and  $m$  are obtained by fitting experimental data. To set these parameters, use the commands:

```

pdbSet <material> Mechanics Creep.A <n>
pdbSet <material> Mechanics Creep.Q <n>
pdbSet <material> Mechanics Creep.n <n>
pdbSet <material> Mechanics Creep.m <n>

```

**NOTE** For materials other than `Solder`, use the long form of these commands to set parameter values.

The default values for the above parameters have been added to the PDB to the `Solder` material based on the 96.5Sn3.5Ag solder alloy as reported in [10].

To solve the creep equations, the rate terms are discretized using the backward Euler method, and the resulting algebraic equations are evaluated locally at every integration point using the Newton–Raphson iterative scheme.

To switch on the creep material model, use the command:

```
pdbSet <material> Mechanics IsCreep <n>
```

This flag must be switched on during the simulation if creep deformation exists. The nonlinear nature of the creep model also requires global Newton iterations to achieve equilibrium of mechanics equations at each loading step. At the end of each iteration, convergence criteria are checked. More iterations are performed until all the convergence criteria are satisfied within the specified tolerance or until the maximum number of iterations is reached. See [Time-Step Control for Mechanics on page 847](#) for details on convergence criteria and time-stepping for mechanics.

**NOTE** To avoid convergence problems, use small time steps at the beginning of the analysis. You can increase the number of time steps later, during the analysis, if it does not adversely affect the solution.

---

## Swelling

Swelling refers to volumetric expansion of material. Swelling material behavior is defined by specifying strain rates at various temperatures that are interpolated linearly. To switch on the model, use the command:

```
pdbSetBoolean <material> Mechanics IsSwelling <n>
```

The swelling strain rate data is specified with a double array:

```
pdbSetArray <material> Mechanics SwellingStrainRate
  Temperature { <temp> {<SSR1> <SSR2> <SSR3>}
               <temp> {<SSR1> <SSR2> <SSR3>} ... }
```

where `<temp>` is the temperature in degree Celsius, and `<SSR1>`, `<SSR2>`, and `<SSR3>` are strain rates in the x-, y-, and z-direction, respectively, in  $s^{-1}$ .

Strain rates can be the same (isotropic) or different (anisotropic) in each of the three directions. For cyclic temperature loading, strain rate data must be given for loading (temperature increment) as well as unloading (temperature decrement). For example:

```

pdbSetDouble Mold Mechanics SwellingStrainRate Temperature {
  27 {0.0 0.0 0.0}
  77 {0.001 0.001 0.001}
  127 {0.002 0.002 0.002}
  80 {0.0012 0.0012 0.0012}
  25 {0.0 0.0 0.0}
}

```

If strain rate data is not given for unloading, loading data is used for increasing as well as decreasing temperatures.

Since strains are assumed to be small, swelling strain rates are added to other strain rates:

$$\dot{\epsilon}_{ij} = \dot{\epsilon}_{ij}^e + \dot{\epsilon}_{ij}^{sw} \quad (919)$$

and are integrated over time to give total strains:

$$\epsilon_{ij} = \epsilon_{ij}^e + \epsilon_{ij}^{sw} \quad (920)$$

where  $\epsilon_{ij}^{sw} = \dot{\epsilon}_{ij}^{sw} = 0$  for  $i \neq j$ .

For a given material, only one set of strain rate data can be specified for a solve step. If necessary, different strain rate data may be specified for the same material in a subsequent solve step.

---

## Mole Fraction–dependent Mechanical Properties

The mechanical properties of binary compounds change with the ratio of substance concentration. A mole fraction–dependent model for elastic moduli has been implemented for binary compounds such as SiGe. The elastic moduli are:

- Bulk modulus and shear modulus for isotropic materials
- C11, C12, and C44 for anisotropic elastic materials

and are computed by:

$$C_{AB} = C_A(1 - f(x)) + C_B f(x) \quad (921)$$

where:

- $C_{AB}$  denotes the elastic moduli of binary compound  $A_{1-x}B_x$ .

## 9: Computing Mechanical Stress

### Material Models

- $x$  is the mole fraction.
- $f$  is an interpolation function with  $f(0) = 0$  and  $f(1) = 1$ .

The mole fraction–dependent moduli for  $\text{Si}_{1-x}\text{Ge}_x$  are linear combinations of the elastic moduli of each material. The binary compound  $\text{Si}_{1-x}\text{Ge}_x$  is treated as silicon regions with germanium. The mole fraction–dependent model can be switched on for silicon with:

```
pdbSetBoolean Si IsCompound 1
```

Next, a list of binary compound materials with mole fraction–dependent elastic moduli is created by:

```
pdbSetString Mechanics BCompoundList {Silicon Germanium}
```

Finally, the interpolation function is defined as a double array, in other words,  $\{x_1 f_1 x_2 f_2 x_3 f_3 \dots\}$ . For example, a linear interpolation function can be specified with:

```
pdbSetDoubleArray SiliconGermanium CompoundInterp {0 0 1 1}
```

For nonlinear relations, a piecewise linear interpolation profile is used.

The mole fraction dependency can be applied to thermal expansion coefficients of materials using the command:

```
pdbSet Mechanics Compound.ThExpCoeff 1
```

when the binary compound model is switched on.

---

## Temperature-dependent Mechanical Properties

The mechanical properties of materials are different at high temperature from those at room temperature. The elastic modulus of typical materials decreases as temperature rises. Some materials show non-negligible changes of mechanical properties at different temperatures.

The temperature dependence of elastic moduli is assumed to be linear and included by a rate coefficient. For isotropic elasticity, this parameter is specified with:

```
pdbSet <material> Mechanics YoungsModulusRate <n>
```

For anisotropic elasticity, the coefficients are defined with:

```
pdbSet <material> Mechanics C11Rate <n>
```

```
pdbSet <material> Mechanics C12Rate <n>
```

```
pdbSet <material> Mechanics C44Rate <n>
```



A similar temperature-dependent effect is applied to the thermal expansion coefficient by using the command:

```
pdbSet <material> Mechanics ThExpCoeffRate <n>
```

to specify the rate coefficient. For the nonlinear temperature-dependent thermal expansion coefficient, a piecewise linear interpolation function is used. To switch on the model, use the command:

```
pdbSet Mechanics Interp.ThExpCoeff 1
```

The piecewise linear function is specified with:

```
pdbSet <material> Mechanics ThExpCoeff.Interp {<temp> <LCTE> <temp>  
<LCTE> ... }
```

For the first yield stress of plastic materials, an Arrhenius expression is used for the temperature-dependent effect. The prefactor and exponent of the Arrhenius expression are specified respectively with the following commands:

```
pdbSet <material> Mechanics FirstYield <n>  
pdbSet <material> Mechanics FirstYieldW <n>
```

---

## Plane Stress Analysis

In two-dimensional problems, the elastic models implemented above follow the plane strain formulation by default. Under the plane strain assumption:

$$\epsilon_{zz} = 0; \sigma_{zz} \neq 0 \quad (922)$$

While this is good for structures where the strain in the third direction is very small compared to the cross section, it would give inaccurate results for thin structures. Thin plate-like structures where one dimension is very small compared to the other two can be modeled under the plane stress assumption:

$$\epsilon_{zz} \neq 0; \sigma_{zz} = 0 \quad (923)$$

The strain  $\epsilon_{zz}$  is obtained as a function of other strains, for example, for purely elastic structures:

$$\epsilon_{zz} = -\nu(\epsilon_{xx} + \epsilon_{yy}) \quad (924)$$

The plane stress model can be switched on for a particular region using:

```
pdbSetBoolean <material> Mechanics PlaneStress 1
```

## 9: Computing Mechanical Stress

Equations: Global Equilibrium Condition

**NOTE** You can combine plane stress and plane strain formulations within a structure by switching on plane stress in only a few regions. However, such a simulation is *not* advisable.

If both plane stress and plane strain regions are present in a structure, the material thickness of regions can be specified by:

```
pdbSetDouble <material> Mechanics Thickness <d>
```

where <d> is specified in micrometers.

---

## Equations: Global Equilibrium Condition

The equations for mechanics in Sentaurus Process are the quasistatic equations of force equilibrium.

The strain rate tensor is related to the symmetric part of the velocity gradient and is given by:

$$\dot{\epsilon}_{jk} = \frac{1}{2} \left( \frac{\partial v_j}{\partial x_k} + \frac{\partial v_k}{\partial x_j} \right) \quad (925)$$

Strain is then related to stresses through any of the material models defined in [Material Models on page 630](#). For all models, the global equilibrium condition is given by:

$$\sum_k \frac{\partial \sigma_{jk}(\mathbf{v})}{\partial x_k} = 0 \quad (926)$$

The above equations are solved using the finite-element method. The solution is a vector representing the velocity components at each node. These velocities are used to compute the strain and stresses. The stresses and the boundary conditions determine the mechanical state of the system.

**NOTE** The stress and strain are derivatives of the velocity. They are, therefore, computed at one order of accuracy lower than the solution variable. This also means that they are discontinuous across the elements. When visualized, the stress values may appear badly converged even if the linear solver has converged.

In addition, the quasistatic mechanics equations are elliptic in nature and, therefore, are prone to high levels of shape dependence. This is most frequently seen at gate corners during polysilicon reoxidation steps or at the corners of the STI trench during liner oxidation. These equations also exhibit a high sensitivity to the mesh modification algorithms at these corners.

**NOTE** At sharp corners, the mechanics equations have a singularity. Therefore, it is not possible to discretize at a corner correctly using regular types of element.

---

## Boundary Conditions

Equations for stress equilibrium require boundary conditions to define the system completely.

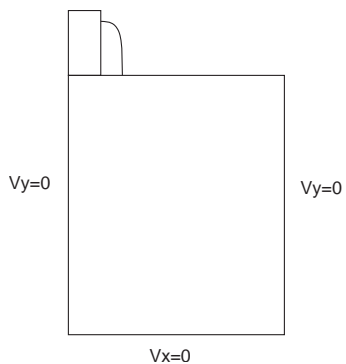


Figure 90 Default mechanics boundary conditions in Sentaurus Process axis orientation

In Sentaurus Process, various boundary conditions can be selected using:

```
pdbSet Mechanics <side> BoundaryCondition <model>
```

where:

- `<side>` is Left, Right, Front, or Back.
- `<model>` is HomNeumann or Dirichlet.

The default boundary conditions are zero velocities in the direction perpendicular to the boundary planes. Since velocities are set to fixed values along the boundaries, these boundary conditions are referred to as Dirichlet boundary conditions in directions perpendicular to boundary planes. The HomNeumann boundary condition is used when the plane must be free.

For example, if you want to set the ‘right’ plane to be free, use the command:

```
pdbSet Mechanics Right BoundaryCondition HomNeumann
```

## 9: Computing Mechanical Stress

### Boundary Conditions

The HomNeumann boundary condition implies a zero normal stress (shown in [Figure 91](#)).

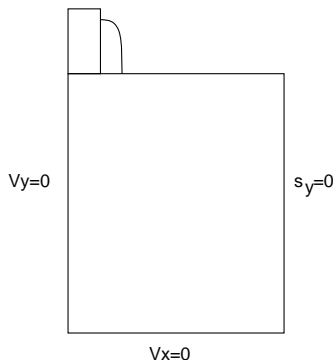


Figure 91 HomNeumann boundary condition on 'right' boundary plane

Dirichlet boundary conditions are imposed using the penalty method, by default. To adjust the penalty factor, use the command:

```
pdbSet Mechanics Boundary.Penalty.Factor {<n>}
```

The default penalty factor is  $1.0 \times 10^{12}$ . The larger this factor, the more accurate the enforcement of Dirichlet boundary conditions. However, using an extremely large penalty factor could lead to an ill-conditioned matrix and, therefore, could slow down the linear equation solver.

Alternatively, you can use the matrix reduction method to impose Dirichlet boundary conditions. To choose the penalty method or matrix reduction method, use the command:

```
pdbSet Mechanics Boundary.Method.Type {<model>}
```

where {<model>} is either Penalty or MatrixReduction.

**NOTE** To ensure the structure is bounded by a perfect rectangle, the displacements computed by these general boundary conditions are not applied to the structure. However, they evaluate the stresses correctly. This assumption is consistent with the small deformation assumption within each mechanics time step.

---

## Example: Applying Boundary Conditions

```
line x loc=-0.02 tag=e spacing=0.005
line x loc=0 tag=a spacing=0.005
line x loc=0.2 tag=b spacing=0.05

line y loc=0 tag=c spacing=0.05
line y loc=2 tag=d spacing=0.05

region silicon xlo=a xhi=b ylo=c yhi=d
```

```
region oxide xlo=e xhi=a ylo=c yhi=d  
init !DelayFullD  
pdbSetDouble Mechanics RefThExpCoeff 0  
pdbSet Mechanics Right BoundaryCondition HomNeumann  
pdbSet Oxide Mechanics Viscosity0 1e40  
pdbSet Oxide Mechanics ViscosityW 0  
temp_ramp name=trl temperature=600 ramprate=30<K/min> time=10<min>  
diffuse temp_ramp=trl  
struct tdr=rampup  
diffuse time=10 temp=900 wet  
struct tdr=postout
```

Sentaurus Process also provides a general way to specify boundary conditions for stress analysis through the `stressdata` command:

```
stressdata bc.location=<c> bc.value= { dx=<n> | dy=<n> | dz=<n> }
```

where:

- `bc.location` can be `Left|Right|Front|Back|Bottom`.
- `dx`, `dy`, and `dz` are used to specify displacement rates (default unit: cm/s).

The displacement rates are applied to the area defined through `bc.location`, where `Left|Right|Front|Back|Bottom` refer to the outer boundary surfaces of the simulation domain. At least at one node, the displacement along any coordinate system direction must be fixed to remove the rigid body motion.

---

## Pressure Boundary Condition

The pressure boundary condition is used to apply uniform pressure on the exterior boundary. The direction of the loading depends on the normal of the exterior surface. To apply the pressure boundary condition, use the `stressdata` command, for example:

```
stressdata bc.location = <c> bc.value = {pressure=<n>}
```

where `bc.location` can be `left`, `right`, `front`, `back`, `bottom`.

---

## Advanced Dirichlet Boundary Condition

A more advanced Dirichlet-type boundary condition also can be defined, which specifies both the translational and rotational velocities on the boundaries. It is defined using the command:

```
stressdata bc.location=<c> bc.rotation.axis= {xa=<c> | ya=<c> | za=<c>} \  
bc.value= {dx=<n> | dy=<n> | dz=<n> | rx=<n> | ry=<n> | rz=<n>}
```

where:

- `bc.location` can be `Left` | `Right` | `Front` | `Back` | `Bottom`.
- `dx`, `dy`, and `dz` specify displacement rates (default unit: cm/s).
- `rx`, `ry`, and `rz` specify rotational velocities (default unit: rad/s).
- `xa`, `ya`, and `za` specify the coordinates of the point around which the rotation occurs (default unit: cm).

---

## Periodic Boundary Condition

The periodic boundary condition is used for structures with a periodically repeating pattern. This condition is used on periodic structures with assigned master and slave boundaries. The slave boundary has the same deformation profile as the master boundary. In [Figure 92](#), the left and right boundaries are bound together by the periodic boundary condition.

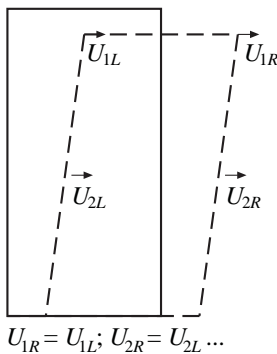


Figure 92 Periodic boundary condition

To apply the periodic boundary condition to the outer bounding surfaces, use the command:

```
pdbSet Mechanics <Left | Right | Front | Back> Periodic 1
```

If this command is specified on a sidewall, the opposite sidewall is defined automatically as a periodic boundary. Conflict of boundary condition definitions are checked on all sidewalls. For example, to apply a periodic boundary condition on the left and right sidewalls, use one of the following commands:

```
pdbSet Mechanics Left Periodic 1  
pdbSet Mechanics Right Periodic 1
```

Both the periodic and coupling boundary conditions are implemented using the penalty method. To adjust the penalty factor, use the command:

```
pdbSet Mechanics Constraint.Penalty.Factor <n>
```

The default penalty factor is  $1.0 \times 10^{13}$ . The larger this factor, the more accurately the periodic or coupling boundary conditions will be enforced. Using an extremely large penalty factor could lead to an ill-conditioned matrix and, therefore, slow down or even fail the linear equation solver.

**NOTE** If you choose to apply periodic boundary conditions, all other boundary conditions defined through the old `pdbSet` method will be ignored and must be redefined using the `stressdata` command.

---

## Time Step Control

It may be necessary to use time step control when viscous or viscoelastic materials are present in the structure. Usually, when dopants also are present, the time steps will be sufficiently limited by the diffusion solver. If dopants are not present, or for materials with a low viscosity, the time step control can be switched on with:

```
pdbSet Mechanics Visc.Step.Control 1
```

Time-stepping can be controlled with the displacement increment and with the relative relaxation time. To switch on these two options, use:

```
pdbSet Mechanics Visc.Step Limit.Disp 1
```

and:

```
pdbSet Mechanics Visc.Step Limit.ScaleT 1
```

respectively. For more control parameters, see “Mechanics Visc.Step” in the Parameter Database Browser.

---

## Stress-causing Mechanisms

Every mechanical system needs a set of stress-driving mechanisms to reach a stressed state. The stress-inducing mechanisms in Sentaurus Process are listed here.

---

### Stress Induced by Growth of Material

During the oxidation process, volume is *produced*. Consuming silicon of volume 1 during thermal oxidation produces oxide of volume 2.25. This process introduces velocities at a growing interface: a velocity vector pointing into the silicon describes the proceeding of the oxidation front, and a velocity vector pointing into the oxide accounts for the volume expansion as described above. The latter is responsible for the generation of mechanical stresses and, therefore, is used as a boundary condition for the mechanical problem.

---

### Densification-induced Stress

A typical densification process uses thermal heating to increase the density of a porous material. As the material density increases, its volume shrinks and the volume shrinkage generates stresses.

The densification-induced stress computation is switched on using the `density.increase` parameter in the `diffuse` command or the `temp_ramp` command, such as:

```
diffuse temperature=1000<C> time=30<min> \  
    density.increase= {[<regionName> = value] [<material> = value]}  
  
temp_ramp name=dens time=1 temp=1000 density.increase= { oxide=0.02 }  
diffuse temp_ramp=dens
```

The total amount of density increase can be specified per material or per region for a given `diffuse` (or `temp_ramp`) step as shown above. A proportional amount of density increase is applied during each time step of the densification process.

The densification operation can be performed for all existing materials, as well as new materials defined using the `mater` command:

```
mater add name=TEOS new.like=oxide  
diffuse time=1 temp=1000 density.increase = { TEOS = 0.03 }
```



For densification processes involving large amounts of volume shrinkage, the material boundaries and meshes can be updated using the following settings:

```
pdbSet Grid Inert.Modify.Mesh 1  
pdbSetDouble TEOS Grid MinimumVelocity 0
```

For a complete densification process that has distinguished density changes, multiple `diffuse` steps can be used with different density increases for each segment of the process.

## Selectively Switching Off Grid Movement

The parameter `MinimumVelocity` can be used to selectively switch off point or interface movement. This can be useful, for example, when a mechanics simulation computes a small amount of boundary movement that is either unwanted or could cause element quality to suffer in the vicinity, and the approximation of no movement is acceptable. In general, the command is:

```
pdbSet <material> Grid MinimumVelocity <speed>
```

If `<material>` is a bulk material (no underscore), the parameter applies to bulk points. If the speed of the bulk points is less than `<speed>` (in cm/s), Sentaurus Process truncates the speed to zero. On the other hand, if `<material>` is an interface material (having an underscore such as `PolySilicon_Silicon`), the parameter only applies to points on that interface.

**NOTE** The moving mesh operations can become unstable for values of `MinimumVelocity` that are neither very large nor zero. Very large values stop all motion, and 0 allows all motion.

---

## Stress Caused by Thermal Mismatch

Temperature changes during the process described by the `temp_ramp` command or the keyword `ramprate` in the `diffuse` command lead to stress in the structure caused by the different thermal expansion coefficients of the relevant materials. When necessary, the stress computation can be switched off by using the `stress.relax` flag:

```
diffuse temperature=1000<C> time=30<min> !stress.relax
```

**NOTE** If viscous or viscoelastic materials are present in the structure, the stress distribution may change even without a change in the temperature due to viscoelastic relaxation.

By default, stresses are computed during inert annealing for 2D simulations. To apply `!stress.relax` to all inert annealing steps, use the command:

```
pdbSet Compute NoStressRelax 1
```

## 9: Computing Mechanical Stress

### Stress-causing Mechanisms

The thermal expansion coefficient for certain materials can be found in the parameter database as follows:

```
<material> Mechanics ThExpCoeff
```

Thermal expansion only affects the dilatational part of the constitutive equation:

$$\sum_k \sigma_{kk} = 3K \left( \sum_k \varepsilon_{kk} - 3\alpha_{\text{rel}} \Delta T \right) \quad (927)$$

The change in the temperature is described by  $\Delta T$  and  $\alpha_{\text{rel}} = \alpha_{\text{mat}} - \alpha_{\text{subs}}$  is the relative thermal expansion coefficient of a certain material with respect to the thermal expansion coefficient of the substrate.

In certain examples, like bending, you may want to use absolute expansion coefficients instead of relative. This can be achieved by setting a parameter called `RefThExpCoeff` as follows:

```
pdbSetDouble Mechanics RefThExpCoeff 0.
```

All the thermal expansion coefficients are computed with respect to the substrate. This reference value is changed by setting a certain region as substrate and resetting the thermal expansion coefficient. A region can be tagged as the substrate in several ways:

- Use the `substrate` keyword when defining regions with the `region` command before the `init` command.
- If a saved structure is being loaded into Sentaurus Process, a region is tagged as the substrate with the command:

```
region name=<region_name> substrate
```

The reference thermal expansion coefficient can be directly set with:

```
pdbSetDouble Mechanics RefThExpCoeff <n>
```

This command overwrites the reference thermal expansion coefficient setting from the substrate.

Materials expand differently in different temperature ranges. The linear dependency of the thermal expansion coefficient on temperature can be specified by:

```
pdbSet Silicon Mechanics ThExpCoeffRate 4e-9
```

So the total thermal expansion coefficient at the elevated temperature  $T$  can be expressed as:

$$a = \text{ThExpCoeff} + \text{ThExpCoeffRate} \times (T - \text{RoomTemperature}) \quad (928)$$

where the room temperature is set to 300 K.

## Lattice Mismatch

The presence of impurities, such as germanium and carbon, can change the lattice parameters of crystalline silicon. This effect has been exploited in two ways technologically:

- Introducing an impurity during epitaxy to form a strained layer.
- Growing a substrate (typically, a very thick layer grown on a standard substrate) to produce a customized lattice constant.

However, most technological applications are based on the first use, for example, when SiGe source/drain pockets are grown on silicon substrates. For strained SiGe epitaxy, Sentaurus Process automatically computes and applies the strain, and no user input is necessary.

For customized lattice-spacing substrates or other material systems, more setup of the tool is required. This section explains the theory and implementation of this model and gives an example. [Figure 93](#) shows a simple SiGe wafer.

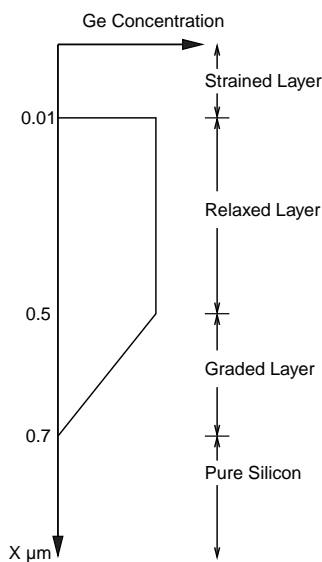


Figure 93 Simple SiGe wafer for customizing lattice-spacing

There are four main regions of the manufactured substrate. The silicon region has the graded buffer layer where the Ge concentration increases linearly from zero to the required concentration. The manufacturing process of this layer is designed such that all the dislocations are forced energetically to nucleate here, and the wafer is completely relaxed. The relaxed layer that is grown on top of the graded layer has no dislocations and no strain. The lattice-spacing of this layer is determined by the Ge mole fraction. The lattice-spacing of this layer controls the strains obtained in the top strained layer. The top strained layer is grown depending on the kind of strain required. If this layer is to be in a tensile state, the Ge concentration here must be less than that of the relaxed layer. In the case of a compressive state, the Ge concentration must

## 9: Computing Mechanical Stress

### Stress-causing Mechanisms

be greater than that of the relaxed layer. This layer has a thermodynamic limit on its thickness since the strain energy it contains should be less than the dislocation nucleation energy. The strain energy is directly proportional to the volume that is under the strain. The strain profile of germanium in silicon is given approximately by:

$$\varepsilon = 0.0425x \quad (929)$$

where  $x$  is the Ge mole fraction.

In the relaxed region, Sentaurus Process modifies the lattice-spacing. This results in no stresses due to the presence of germanium. In the strained region, the lattice-spacing is fixed by the lattice-spacing in the relaxed region. Now, using the Ge mole fraction in the strained region, the effective unstrained lattice-spacing is computed, and the stresses are based on the difference of the effective lattice-spacing and the lattice-spacing of the relaxed region.

For example, assume the strained layer has no Ge: The effective lattice-spacing is that of silicon given by  $L_{Si}$ . The lattice-spacing of the relaxed SiGe part is, for example,  $L_{SiGe}$ . The strain in the strained region is:

$$\varepsilon = (L_{SiGe} - L_{Si})/L_{Si} \quad (930)$$

The strain computed using [Eq. 930](#) is applied as a biaxial strain in the y- and z-directions.

## Using the Lattice Mismatch Model

For the most common case of SiGe layers grown on silicon substrates, the model is switched on by default, and strain is computed and updated as necessary. For simulating other material systems, a few settings are required to instruct Sentaurus Process how the strain should be computed.

If the substrate is not silicon or it is not the lowest most region in the substrate (that is, the largest x-coordinate), you must identify the substrate region in the wafer. Use the `region` command and include the keyword `substrate` for the appropriate region. If there is no substrate defined in the loaded structure, use the following command to tag a region as a substrate:

```
region name=<region_name> substrate
```

Regions isolated from the substrate by nonsubstrate materials must be tagged as substrate to account for the lattice mismatch effect.

For systems other than SiGe, Sentaurus Process must know the strain profile of the field in the substrate. The `strain_profile` command is used to specify this. The strain is specified as a piecewise linear function of the mole fraction. For Ge in silicon, it is:

```
strain_profile Silicon species=Germanium strain= {0 0.0425} ratio= {0 1}
```

or:

```
pdbSet Silicon Germanium Conc.Strain {0 0 1 0.0425}
```

The lattice mismatch model for SiGe is switched on by default. Next, for customized lattice-spacing substrates, the substrate must be given a strain profile. The strain profile can be specified with the `substrate_profile` command or the `profile` command as a piecewise linear function of the x-coordinate:

```
profile region=<region_name> name=Germanium \  
  concentration= {1e10 1e10 2e22 2e22 1e10 1e10} \  
  xcoord= {0 0.01 0.011 0.5 0.7 10} linear
```

The location of the top of the relaxed region must be specified in Sentaurus Process. Generally, this should not be at the top of the relaxed layer (see [Figure 93 on page 657](#)) because germanium diffusion during any anneal step can cause unrealistic stress values to appear in this area. The best location for the top of the relaxed region is approximately two-thirds of the relaxed layer thickness from the top of the relaxed layer. In this example, it is approximately 0.35  $\mu\text{m}$ . This reference position can be set with the command:

```
pdbSet Silicon Mechanics TopRelaxedNodeCoord 0.35e-4
```

**NOTE** In most cases, when the simulation does not require any SiGe substrate (for example, when SiGe source/drain pockets are grown on silicon substrates), this parameter is not needed. The reference lattice-spacing is the one of the substrate; Sentaurus Process detects automatically the adjacent silicon-like regions and applies to them the lattice mismatch model. For this reason, the value of this parameter defaults to the bottom coordinate of the structure.

Finally, for these concentrations to take effect and all mechanics computations to occur, you must add a short diffusion step if there is none.

The `update_substrate` command is deprecated. If used, the `update_substrate` command should be called only once for initialization assuming all strain profiles have not been accounted for lattice-mismatch strains.

During dopant redistribution, the lattice-spacing and lattice mismatch strains are updated, and the doping concentration at the top of the relaxed layer may change. To disable automatic updating of lattice-mismatch strains, use:

```
pdbSet Silicon Mechanics UpdateStrain 0
```

To switch off the lattice-spacing tracking at the top of the relaxed layer, use:

```
pdbSet Mechanics LatticeHistory 0
```

## Total Concentration Model

The total concentration model computes the total contribution of lattice mismatch stress with the current impurity concentration and the elastic moduli at the current temperature. For binary compound materials, the elastic moduli are computed with the current mole fraction. With this approach, the lattice mismatch stress is history independent and can change even with an unchanged doping profile.

This is the default lattice mismatch model. To switch off this model by computing the lattice mismatch stress increment with the elastic moduli during doping profile change, use the command:

```
pdbSet Mechanics Total.Concentration.Model 0
```

## Reference Concentration Model

The reference concentration model is a simplified lattice mismatch model, which does not distinguish the relaxed region and strained region by specifying the location of the top of the relaxed region. Only relative concentration accounts for the lattice-spacing and strain changes. For example, the strain in SiGe is:

$$\varepsilon = 0.0425 \cdot (C_{\text{Ge}} - C_{\text{ref}}) / C_{\text{Si}} \quad (931)$$

and the lattice-spacing is computed by  $L_{\text{SiGe}} = L_{\text{Si}} \cdot (1 + \varepsilon)$ , where  $C_{\text{Si}}$  is the lattice density of silicon and  $C_{\text{ref}}$  is the reference Ge concentration in SiGe defined by:

```
pdbSet Silicon Germanium Ref.Concentration 1e22
```

The lattice-spacing and strain from this model may not be physical in the relaxed region.

The reference concentration model is used when the structure is flipped for backside processing. To switch on this model, use the command:

```
pdbSet Mechanics Reference.Concentration.Model 1
```

---

## Strained Deposition

Impurity-induced stress can be introduced locally during deposition to account for a lattice-spacing change due to stress rebalancing. For example, the SiGe lattice-spacing during unconstrained growth gradually returns to the unconstrained SiGe lattice-spacing. The lattice mismatch effect should diminish during the SiGe growth.

The following steps are performed when strained deposition is enabled:

1. Deposit a new layer.
2. Apply a doping profile, and compute the lattice spacing of the newly deposited layer.
3. Set the lattice spacing of the deposited layer to that of the underlayer, and compute the mismatch strain.
4. Perform stress relaxation to establish stress equilibrium, and update the lattice spacing.
5. Merge layers if needed.

To correctly catch the relaxation effect, the thickness of the deposited layer must be chosen properly; a fine mesh is required. Multiple deposition can be particularly useful in such cases.

To switch on this model, use the command:

```
pdbSet Mechanics StrainedDeposition 1
```

and set the option `Strained.Lattice` in the `deposit` command.

The total concentration model is disabled during strained deposition. The reference concentration model should not be used with strained deposition.

---

## Edge Dislocation

The existence of crystal lattice defects, such as dislocation, affects the channel stress state. The impact of edge dislocation is included by superposing the dislocation-induced stress field from elasticity theory. Each edge dislocation can be defined with:

```
stressdata apply.dislocation dislocation.origin= {<n> <n> <n>}  
para.orient= {<n> <n> <n>} perp.orient= {<n> <n> <n>} region=<c> <material>
```

where:

- `dislocation.origin` is the location of the dislocation core.
- `para.orient` specifies the direction of the edge dislocation or the direction of the half plane.
- `perp.orient` is Burger's vector in the perpendicular direction to the half plane.

Here, the magnitude of `perp.orient` is the slip distance. You must supply either a region name or a material name. If `region` is specified, the stress field is superposed to this region. If `material` is specified, the stress field is applied to all regions of crystalline material.

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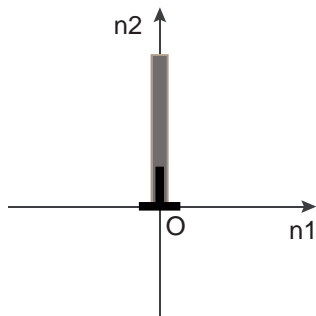


Figure 94 Edge dislocation located at the origin O; n1 is Burger's vector and n2 is the direction of the half plane

Singularity exists in the analytic solution at the dislocation core. Without using a nonlinear atomistic theory, the stresses in the core region within a few magnitudes of Burger's vector to the dislocation core are smoothed away. The factor for this core radius can be defined with:

```
pdbSet Mechanics Dislocation.Coresize.Factor 2.0
```

A prototype model for positioning the edge dislocations is available by minimizing the elastic strain energy [11]. The stress field from each edge dislocation is superposed. The elastic strain energy is determined after force equilibrium with edge dislocations at their initial locations. The initial location of edge dislocation serves as the initial guess and can be defined by:

```
stressdata !apply.dislocation dislocation.origin= {<n> <n> <n>} \  
para.orient= {<n> <n> <n>} perp.orient= {<n> <n> <n>} region=<c>
```

where `dislocation.origin` is the initial location of the edge dislocation, and `!apply.dislocation` is specified to delay applying the dislocation-induced stress field. Multiple edge dislocations with different Burger's vectors can be defined separately with this syntax.

When all the edge dislocations for minimizing the elastic strain energy are specified, you can start the optimization with the command:

```
stressdata origin.max= {<n> <n> <n>} origin.min= {<n> <n> <n>} \  
optimize.dislocation
```

where `origin.max` and `origin.min` define the range of dislocation positions in the specified region. Some additional parameters for optimization convergence control also can be defined in this command (see [stressdata on page 1081](#)).



The movement of edge dislocations depends on the gradient of the total elastic strain energy computed from a discrete integral over all elements. The target of the optimization is set to  $-5$  multiplied by the absolute value of the starting elastic strain energy. This factor can be changed with:

```
pdbSetDouble Mechanics Energy.Optimization.Factor <n>
```

The coordinates of the edge dislocations after optimization are returned in a Tcl list formatted as  $\langle x1 \rangle \langle y1 \rangle \langle x2 \rangle \langle y2 \rangle \dots$  for two dimensions, and  $\langle x1 \rangle \langle y1 \rangle \langle z1 \rangle \langle x2 \rangle \langle y2 \rangle \langle z2 \rangle \dots$  for three dimensions. The final stress state remains the same as before the edge dislocations are introduced. The edge dislocations may stop at the local minimum where the elastic strain energy has not reached the global minimum. In such a case, a new optimization step must be started with the initial guess of the edge dislocation positions adjusted based on the previous optimization result. It is also helpful to refine the mesh.

---

## Intrinsic Stress

Certain process steps require the deposition of materials with intrinsic stresses. Sentaurus Process can be used to model these process steps. The intrinsic stresses (`StressELXX`, `StressELYY`, `StressELZZ`, `StressELXY`, `StressELYZ`, `StressELZX`) can be prescribed in the `deposit` command (see [deposit on page 870](#)). After stress relaxation, the resulting stresses will be less than the prescribed ones by default. You can scale the prescribed stresses so that for a flat surface, the relaxed stress will be the same as the prescribed stress. To scale the stresses, use the command:

```
pdbSet Mechanics StressRelaxFactor 1
```

For deposition in 3D, you can specify stresses in specific layers using the `stressdata` command (see [stressdata on page 1081](#)). For example:

```
stressdata nitride syyi=1.4e10
```

sets the  $y$  component of the intrinsic stress in the nitride to  $1.4 \times 10^{10}$  dyn/cm<sup>2</sup>.

For interconnect simulations, intrinsic stresses in metal lines can be modeled as width dependent [12] with either a linear relation or a logarithmic relation, using the parameters defined through the `stressdata` command:

- If modeled as a linear relation, the total intrinsic stresses are given by:

$$\sigma_{xx} = \sigma_{xxi} + \sigma_{xx1} \frac{w_x}{w_b} \quad \sigma_{yy} = \sigma_{yyi} + \sigma_{yy1} \frac{w_y}{w_b} \quad \sigma_{zz} = \sigma_{zzi} + \sigma_{zz1} \frac{w_z}{w_b}$$

- If modeled as a natural logarithmic relation, the total intrinsic stresses are given by:

$$\sigma_{xx} = \sigma_{xxi} + \sigma_{xx2} \ln \frac{w_x}{w_b} \quad \sigma_{yy} = \sigma_{yyi} + \sigma_{yy2} \ln \frac{w_y}{w_b} \quad \sigma_{zz} = \sigma_{zzi} + \sigma_{zz2} \ln \frac{w_z}{w_b}$$

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where  $\sigma_{xxi}$ ,  $\sigma_{xx1}$ ,  $\sigma_{xx2}$ ,  $w_b$  are defined through the parameters `sxxi`, `sxx1`, `sxx2`, and `base` of the `stressdata` command. The other two components ( $yy$  and  $zz$ ) are defined in the same way, and  $w$  is calculated internally with respect to the region (not material) boundaries.

---

## Stress Rebalancing after Etching and Deposition

When materials are removed from or added to a given structure, physical stress distributions generally change with the corresponding geometry and boundary changes. In simulations, a stress-rebalancing step is required to re-establish the stress equilibrium in the structure and to conform the stress distributions to the new boundaries. By default, a stress-rebalancing operation is called after etching or deposition is performed. To omit the stress-rebalancing step, use:

```
pdbSet Mechanics EtchDepoRelax 0
```

## Automated Tracing of Stress History

Thermal residual stress in a given device structure is a function of its fabrication history, which consists of process steps at various temperatures and temperature ramps in between. To model stress evolution accurately, all temperature ramps should be traced. When the `pdb` parameter `StressHistory` is switched on, for example:

```
pdbSet Mechanics StressHistory 1
```

the temperature gaps between process steps such as diffusion, deposition, and etching are detected and filled with instant stress-rebalancing, solving for thermal mismatch strains and stresses.

---

## Saving Stress and Strain Components

By default, stress-tensor components are saved on both elements and nodes. The elastic portions of the strain-tensor components also are saved on both elements and nodes by default. The elastic strains are computed from stresses using isotropic elasticity by default. The anisotropic elasticity also can be used for a given crystalline material when the corresponding `pdb` parameter `Anisotropic` is set. The elastic strain-field computing and saving operation can be omitted by using the following command:

```
pdbSet Mechanics saveElasticStrain 0
```

The stress tensor can be decomposed and the resulting dilatational and deviatoric stress components can be saved on nodes when the following `pdb` parameter is switched on:

```
pdbSet Mechanics decomposeStress 1
```

---

## Description of Output Variables

The mechanics module in Sentaurus Process assumes that stresses and strains are defined on elements. However, not all tools can read or visualize element values. For this reason, Sentaurus Process performs an element-to-node interpolation of stresses as a postprocessing step and writes both forms of stresses to output.

The element stresses are prefixed by `StressEL` and the nodal stresses are prefixed by `Stress`. The tensor components are given by the post-fix (`XX`, `YY`, `ZZ`, `XY`, `YZ`, `ZX`).

In history-dependent materials, you cannot create a simple, closed-form relation between stresses and strains. It is useful, however, to compute the elastic part. The elastic component of the strain is an indicator of the stored strain energy in the system. In addition, the elastic component of the strain is the total strain in elastic materials such as silicon and polysilicon.

Pressure is one-third of the negative of the trace of the stress tensor:

$$P = -\frac{1}{3} \sum_i \sigma_{ii} \quad (932)$$

The field `LatticeSpacing` represents the lattice-spacing of the crystal at the location of the node. This is controlled by the presence of lattice-altering species such as germanium or carbon in the structure. In addition, the `strain_profile` command must be specified.

In Sentaurus Process, the `select` command is used to perform Tcl-level and Alagator-level operations. To access the stress components, use the `select` command.

The stresses and strains are represented as symmetric tensors. To access the `xx`, `yy`, and `zz` components of nodal stress values, the variable references for the `select` command are `Stress_xx`, `Stress_yy`, and `Stress_zz`, respectively. To access the `xy`, `yz`, and `zx` components, use `Stress_xy`, `Stress_yz`, and `Stress_zx`, respectively.

For element values, the Boolean keyword `element` of the `select` command must be set to `true`. To access the `xx`, `yy`, and `zz` components of the element stress values, the variable references for the `select` command are `StressEL_xx`, `StressEL_yy`, and `StressEL_zz`, respectively. To access the `xy`, `yz`, and `zx` components, use `StressEL_xy`, `StressEL_yz`, and `StressEL_zx`, respectively.

The old variable names for accessing the components of stress and strain tensors are supported as well. A comparison of the new names and the corresponding deprecated names is included in [Table 65 on page 668](#).

**9: Computing Mechanical Stress**  
 Saving Stress and Strain Components

Table 64 presents descriptions of the mechanics-related output data and whether the variables apply to elements or nodes.

Table 64 Variable names in Sentaurus Process output files

Variable name	Element/Node	Description	Unit
Displacement_x	Node	X component of displacement	cm
Displacement_y	Node	Y component of displacement	cm
Displacement_z	Node	Z component of displacement	cm
ElasticStrainXX	Node	XX component of elastic strain	Unitless
ElasticStrainXY	Node	XY component of elastic strain	Unitless
ElasticStrainYY	Node	YY component of elastic strain	Unitless
ElasticStrainYZ	Node	YZ component of elastic strain	Unitless
ElasticStrainZX	Node	ZX component of elastic strain	Unitless
ElasticStrainZZ	Node	ZZ component of elastic strain	Unitless
PlasticStrainXX	Node	XX component of plastic strain	Unitless
PlasticStrainXY	Node	XY component of plastic strain	Unitless
PlasticStrainYY	Node	YY component of plastic strain	Unitless
PlasticStrainYZ	Node	YZ component of plastic strain	Unitless
PlasticStrainZX	Node	ZX component of plastic strain	Unitless
PlasticStrainZZ	Node	ZZ component of plastic strain	Unitless
PlasticStrainEQV	Node	Equivalent plastic strain	Unitless
ViscoPlasticStrainXX	Node	XX component of viscoplastic strain	Unitless
ViscoPlasticStrainXY	Node	XY component of viscoplastic strain	Unitless
ViscoPlasticStrainYY	Node	YY component of viscoplastic strain	Unitless
ViscoPlasticStrainYZ	Node	YZ component of viscoplastic strain	Unitless
ViscoPlasticStrainZX	Node	ZX component of viscoplastic strain	Unitless
ViscoPlasticStrainZZ	Node	ZZ component of viscoplastic strain	Unitless
ViscoPlasticStrainEQV	Node	Equivalent viscoplastic strain	Unitless
CreepStrainELXX	Element	XX component of creep strain	Unitless
CreepStrainELXY	Element	XY component of creep strain	Unitless
CreepStrainELYY	Element	YY component of creep strain	Unitless
CreepStrainELYZ	Element	YZ component of creep strain	Unitless

Table 64 Variable names in Sentaurus Process output files

Variable name	Element/Node	Description	Unit
CreepStrainELZX	Element	ZX component of creep strain	Unitless
CreepStrainELZZ	Element	ZZ component of creep strain	Unitless
CreepStrainELEQV	Element	Equivalent creep strain	Unitless
SwellingStrainELXX	Element	XX component of swelling strain	Unitless
SwellingStrainELXY	Element	XY component of swelling strain	Unitless
SwellingStrainELYY	Element	YY component of swelling strain	Unitless
SwellingStrainELYZ	Element	YZ component of swelling strain	Unitless
SwellingStrainELZX	Element	ZX component of swelling strain	Unitless
SwellingStrainELZZ	Element	ZZ component of swelling strain	Unitless
LatticeSpacing	Node	Lattice-spacing	cm
Pressure	Node	Pressure	Pa
StressELXX	Element	XX component of element stress	Pa
StressELXY	Element	XY component of element stress	Pa
StressELYY	Element	YY component of element stress	Pa
StressELYZ	Element	YZ component of element stress	Pa
StressELZX	Element	ZX component of element stress	Pa
StressELZZ	Element	ZZ component of element stress	Pa
StressXX	Node	XX component of node stress	Pa
StressXY	Node	XY component of node stress	Pa
StressYY	Node	YY component of node stress	Pa
StressYZ	Node	YZ component of node stress	Pa
StressZX	Node	ZX component of node stress	Pa
StressZZ	Node	ZZ component of node stress	Pa
MisesStress	Node	von Mises stress	Pa
DeformationResistance	Node	Deformation resistance	Pa
ElasticEnergyDens	Node	Elastic strain energy density	J/m <sup>3</sup>
PlasticEnergyDens	Node	Plastic strain energy density	J/m <sup>3</sup>
ViscoPlasticEnergyDens	Node	Viscoplastic strain energy density	J/m <sup>3</sup>
CreepEnergyDensEL	Element	Creep strain energy density	J/m <sup>3</sup>

**9: Computing Mechanical Stress**  
Saving Stress and Strain Components

**NOTE** The stresses and strains in the output file are according to the UCS, unless you explicitly request to save in the DF-ISE coordinate system by using the math `coord.dfise` command. The UCS is the same as the Sentaurus internal coordinate system, but differs from the DF-ISE/TDR coordinates. Therefore, it is important to note the directions of the axes in 2D and 3D (see [Figure 95](#)).

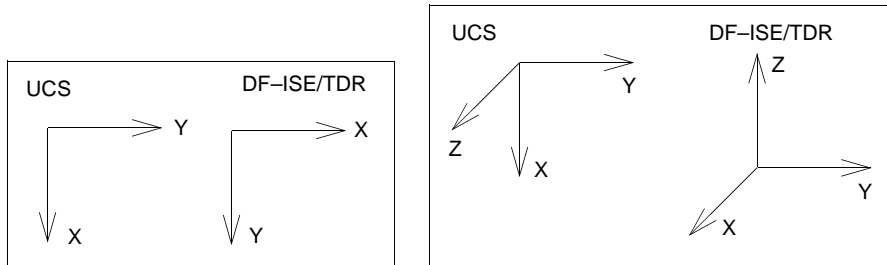


Figure 95 (Left) Axis orientation in 2D and (right) axis orientation in 3D

The axis directions in DF-ISE/TDR coordinates are different in 2D and 3D in the UCS. [Figure 95](#) shows the axis orientation in 2D and in 3D. Consequently, the values of the stress and strain components change.

For information about the TDR format, refer to the *Sentaurus Data Explorer User Guide*.

[Table 65](#) maps the fields from the `select` command to the fields in the output files of Sentaurus Process. The axis directions in Sentaurus Process are the same in 2D and 3D.

Table 65 Variable names in output files

Field name	Field name (deprecated)	2D	3D
StressEL_xx	StressELKK_x	StressEL-YY	StressEL-ZZ
StressEL_yy	StressELKK_y	StressEL-XX	StressEL-YY
StressEL_zz	StressELKK_z	StressEL-ZZ	StressEL-XX
StressEL_xy	StressELIJ_x	StressEL-XY	-StressEL-YZ
StressEL_yz	StressELIJ_y	Not applicable	StressEL-XY
StressEL_zx	StressELIJ_z	Not applicable	-StressEL-ZX
Stress_xx	StressKK_x	Stress-YY	Stress-ZZ
Stress_yy	StressKK_y	Stress-XX	Stress-YY
Stress_zz	StressKK_z	Stress-ZZ	Stress-XX
Stress_xy	StressIJ_x	Stress-XY	-Stress-YZ

Table 65 Variable names in output files

Field name	Field name (deprecated)	2D	3D
Stress_yz	StressIJ_y	Not applicable	Stress-XY
Stress_zx	StressIJ_z	Not applicable	-Stress-ZX
Pressure	Not applicable	Pressure	Pressure
MisesStress	Not applicable	MisesStress	MisesStress
PrincipalStress1	Not applicable	PrincipalStress1	PrincipalStress1
PrincipalStress2	Not applicable	PrincipalStress2	PrincipalStress2
PrincipalStress3	Not applicable	PrincipalStress3	PrincipalStress3
ElasticStrain_xx	ElasticStrainKK_x	ElasticStrain-YY	ElasticStrain-ZZ
ElasticStrain_yy	ElasticStrainKK_y	ElasticStrain-XX	ElasticStrain-YY
ElasticStrain_zz	ElasticStrainKK_z	ElasticStrain-ZZ	ElasticStrain-XX
ElasticStrain_xy	ElasticStrainIJ_x	ElasticStrain-XY	-ElasticStrain-YZ
ElasticStrain_yz	ElasticStrainIJ_y	Not applicable	ElasticStrain-XY
ElasticStrain_zx	ElasticStrainIJ_z	Not applicable	-ElasticStrain-ZX
PlasticStrain_xx	PlasticStrainKK_x	PlasticStrain-YY	PlasticStrain-ZZ
PlasticStrain_yy	PlasticStrainKK_y	PlasticStrain-XX	PlasticStrain-YY
PlasticStrain_zz	PlasticStrainKK_z	PlasticStrain-ZZ	PlasticStrain-XX
PlasticStrain_xy	PlasticStrainIJ_x	PlasticStrain-XY	-PlasticStrain-YZ
PlasticStrain_yz	PlasticStrainIJ_y	Not applicable	PlasticStrain-XY
PlasticStrain_zx	PlasticStrainIJ_z	Not applicable	-PlasticStrain-ZX
PlasticStrainEQV	Not applicable	PlasticStrainEQV	PlasticStrainEQV
ViscoPlasticStrain_xx	ViscoPlasticStrainKK_x	ViscoPlasticStrain-YY	ViscoPlasticStrain-ZZ
ViscoPlasticStrain_yy	ViscoPlasticStrainKK_y	ViscoPlasticStrain-XX	ViscoPlasticStrain-YY
ViscoPlasticStrain_zz	ViscoPlasticStrainKK_z	ViscoPlasticStrain-ZZ	ViscoPlasticStrain-XX
ViscoPlasticStrain_xy	ViscoPlasticStrainIJ_x	ViscoPlasticStrain-XY	-ViscoPlasticStrain-YZ
ViscoPlasticStrain_yz	ViscoPlasticStrainIJ_y	Not applicable	ViscoPlasticStrain-XY
ViscoPlasticStrain_zx	ViscoPlasticStrainIJ_z	Not applicable	-ViscoPlasticStrain-ZX
ViscoPlasticStrainEQV	Not applicable	ViscoPlasticStrainEQV	ViscoPlasticStrainEQV
Displacement_x	Not applicable	Displacement-Y	-Displacement-Z
Displacement_y	Not applicable	Displacement-X	Displacement-Y

## 9: Computing Mechanical Stress

### References

Table 65 Variable names in output files

Field name	Field name (deprecated)	2D	3D
Displacement_z	Not applicable	Not applicable	Displacement-X

The directionality is the same for other tensor fields such as `StressEL` and `ElasticStrain`.

---

## Tracking Maximum Stresses

During a typical process flow, the maximum stresses may be reached in a process step and, subsequently, the stresses may fall. If the material is prone to failure through delamination or nucleation of dislocations, the failure may occur when the maximum stress is reached. To always track the maximum stresses, set the following parameter:

```
pdbSet Mechanics SaveMaxStress 1
```

The `StressMaxEL` field is updated when the current stress is greater than the stored stress. In this way, the maximum is maintained throughout the process flow. The maximum element stresses and the von Mises stress are computed and stored.

By using the `stressdata` command (see [stressdata on page 1081](#)), a list of maximum stresses (hot spots) and their locations can be obtained. The hot spots can be evaluated by one of the six stress components (`sxx`, `syy`, `szz`, `sxy`, `syz`, and `szx`), the von Mises stress, the principal stress, or the hydrostatic stress (negative pressure value or the pressure). The command returns a list of maximum stress values (largest magnitude, largest tensile, largest compressive) and the corresponding location coordinates.

---

## References

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## 9: Computing Mechanical Stress

### References

*This chapter describes the mesh algorithms and meshing parameters available in Sentaurus Process.*

---

### Overview

Sentaurus Process automatically generates meshes as they are needed. The behavior of the automatic-meshing scheme is different in 3D than in 1D and 2D because of the time required to generate 3D meshes. In 1D and 2D, meshes are generated after every geometry operation such as `etch`, `deposit`, and `transform`. In 3D, meshes are only generated immediately before steps that require a bulk mesh, such as a `diffuse` or an `implant` command, and structure saving. This scheme can reduce the time spent when there are multiple geometry-changing steps without a `diffuse` or an `implant` command (or any other step requiring a mesh) in between.

Sentaurus Process uses Sentaurus Mesh as its mesh generation engine. Details of the meshing algorithms are provided, but for simplification, Sentaurus Mesh is used throughout.

The mesh generation process starts with a bisection algorithm, which places mesh points as instructed by the user. Afterwards, the mesh elements are created using a modified Delaunay-meshing algorithm. Refer to the [Mesh Generation Tools User Guide](#) for details about Sentaurus Mesh.

The meshes generated within Sentaurus Process can be refined adaptively, statically, or as a combination of adaptive and static refinements. The refinement can be specified using one of the major types of refinement box:

- Field based (adaptive meshing)
- Mask based
- Uniform (standard)
- Interface axis-aligned
- Interface offsetting (offset normal to the interface)

All these refinement types are user controllable. In addition, Sentaurus Mesh enforces mesh smoothing to limit the changes in element size from one element to the next. This smoothing is important for mechanics accuracy and convergence behavior (see [Mesh Refinement on page 674](#)).

## 10: Mesh Generation

### Mesh Refinement

One important algorithm affecting refinement behavior is the `UseLines` algorithm. This algorithm inserts lines created using the `line` command into the internal bisection algorithm before any other lines are introduced. Further mesh refinement proceeds by bisecting the boxes created by the `UseLines` lines. This has the effect of isolating static regions of a structure from regions where the boundaries are moving due to geometric operations. Geometry movement naturally causes perturbations to the mesh lines. The `UseLines` lines compartmentalize this mesh movement to minimize solution degradation from interpolation. For more information, see [UseLines: Keeping User-defined Mesh Lines on page 702](#).

**NOTE** Because this internal bisection algorithm in Sentaurus Process is different than the one used to create mesh refinement in the stand-alone Sentaurus Mesh tool, it is not possible to create meshes identical to those created with Sentaurus Mesh. However, element quality, stability, and the Delaunay properties should be qualitatively the same.

---

## Mesh Refinement

Mesh refinement is a two-step process:

- First, you define the refinement box.
- Second, the mesh is refined when the next remesh occurs either with an explicit `grid remesh` call or during standard geometry modifications such as etch, deposit, clip, or native layer formation.

The refinement boxes remain valid unless the list of refinement boxes is cleared with the `refinebox clear` command.

All refinement boxes have refinement criteria that add mesh and constraints that can be used to limit where the mesh refinement occurs. One type of refinement criteria is available for each type of box, and it essentially defines the box type. The refinement criteria and, therefore, the refinement box type can be either static or adaptive. All types of refinement box can be mixed as required. The refinement box constraints are specified along with the refinement criteria in the `refinebox` command and can be used in combination within one command.

The constraints available include:

- A material constraint using the `materials` parameter that takes a list of materials.
- Region constraints using the `regions` parameter that takes a list of region names.
- The `min` and `max` parameters that limit the size of the refinement box (which by default applies to all of the space).

Refinement information also can be extracted and written to a file readable by Sentaurus Mesh using the `mshcmd` flag in conjunction with the `smesh` parameter of the `struct` command (see [struct on page 1086](#)).

## Viewing Mesh Refinement

To aid in setting mesh refinement, you can store the current minimum edge length in each direction as a field using the command:

```
pdbSet Grid Set.Min.Edge 1
```

When specified, Sentaurus Process computes the smallest edge length in each direction and saves it in three fields:

- `MinXEdgeLength`
- `MinYEdgeLength` (for 2D or 3D structures)
- `MinZEdgeLength` (for 3D structures)

In addition, it prints the average edge length to the screen.

---

## Static Refinement

### Standard Refinement Boxes

The standard refinement box allows you to specify a smoothly varying mesh density inside the refinement box at three locations in the x-, y- and z-directions using the `xrefine` and `yrefine`, and `zrefine` parameter lists, respectively. If all three `xrefine`, `yrefine`, and `zrefine` values are specified, the mesh density varies quadratically in that direction. If two are specified, the variation is linear from top to bottom. If only one value is specified, a constant mesh density is assumed.

Refinement boxes also can be limited to refine only in one specific material or region using the `regions` or `materials` parameter.

### Examples

This is an example of specifying two refinement boxes and calling `remesh`:

```
refinebox min= {-0.25 0.4 0.0} max= {0.4 0.6 1.0} xrefine= {0.1 0.06 0.1} \  
  yrefine= {0.1 0.01 0.1} zrefine = {0.01} oxide  
refinebox min= {0.6 0.6} max= {0.8 0.8} xrefine= 0.1 silicon  
grid remesh
```

## 10: Mesh Generation

### Mesh Refinement

**NOTE** Calculating the linear or quadratic variation of the mesh density when two or three x-, y-, or z-direction values are given requires the specification of `min` and `max`. If `min` and `max` are not specified and at least one region is specified, the minimum and maximum values of the bounding box for that region serve as `min` and `max` for the calculation. If more than one region is specified, only the bounding box of the first region is used for the calculation, although all regions are used as constraints to the refinement.

## Interface Refinement Boxes

Refinement near interfaces can be specified using the `refinebox` command. So it is possible to have a large global default minimum interface mesh-spacing, for example, and a smaller localized value inside a box. The parameters affecting interface refinement are demonstrated in the following examples:

- Set the mesh criteria near the interface. This is the maximum size the first normal edge can be, and it is possible for the edge to be `0.5 min.normal.size`:

```
pdbSet Grid SnMesh min.normal.size <n>
```

- Set the growth rate of the edge size away from the interface:

```
pdbSet Grid SnMesh normal.growth.ratio.2d <n>
```

```
pdbSet Grid SnMesh normal.growth.ratio.3d <n>
```

- Set `min.normal.size` or `normal.growth.ratio` or both locally within a refinement box:

```
refinebox min.normal.size = <n> normal.growth.ratio = <n> \  
[interface.materials=<list> | interface.mat.pairs = <list of pairs>]
```

## Interface Offsetting Refinement Boxes

In addition, the Sentauros Mesh offsetting algorithm can be used to create offsetting layers at interfaces by giving the `offsetting` keyword, which also permits regionwise interface specification in addition to the materialwise possibility:

```
refinebox offsetting min.normal.size = <n> normal.growth.ratio = <n> \  
[interface.materials=<list> | interface.mat.pairs = <list of pairs>] \  
[interface.regions=<list> | interface.region.pairs = <list of pairs>]
```

For Sentauros Mesh offsetting, an additional keyword `offsetting.maxlevel` defines the number of layers to be generated at the interface.

The `offsetting.maxlevel` can be defined globally using the `mgoals` command, or on a materialwise or regionwise basis using the `refinebox` command as shown in the following three possibilities:

```
mgoals offsetting.maxlevel = <i>
refinebox offsetting.maxlevel = <i> interface.materials= { <string list> }
refinebox offsetting.maxlevel = <i> interface.regions= { <string list> }
```

**NOTE** For Sentaurus Mesh offsetting, `offsetting.maxlevel` can only be defined on a material or region basis with `interface.materials` or `interface.regions` or globally, not with `interface.mat.pairs` or `interface.region.pairs`.

**NOTE** For Sentaurus Mesh offsetting, `min.normal.size` and `normal.growth.ratio` can only be defined by material pair or region pair with `interface.mat.pairs` or `interface.region.pairs` or globally, not with `interface.materials` or `interface.regions`.

Offset-meshing parameters defined at interfaces using `interface.mat.pairs` or `interface.region.pairs` are interpreted in a symmetric way by default. This means that, given the specification of a material or region pair  $x_1/x_2$ , the parameters are defined for both  $x_1$  at the  $x_2$  interface and for  $x_2$  at the  $x_1$  interface. If the `!double.side` keyword is given, Sentaurus Mesh interprets  $x_1/x_2$  in a nonsymmetric way, that is, only for  $x_1$  at the  $x_2$  interface.

## Refinement Inside a Mask

Mask-based refinements are similar to standard refinements (see [Standard Refinement Boxes on page 675](#)), except that they have an additional constraint that is defined by a volume specified by a previously existing mask. This constraint is applied in addition to the normal box constraint defined by the `min` and `max` parameters. Mask-based refinements are a way to have layout driven refinements.

For example, if you specify `min` and `max`, the refinement area will be the intersection of the specified rectangle and the mask. If you specify a material name, the final refinement will be the intersection of the regions with such a material and the mask.

These constraints are specified using the `refinebox` command with the following options:

- A mask name (`mask`).
- Minimum and maximum coordinates in  $x$  where the refinement will be applied (`extrusion.min` and `extrusion.max`).
- An optional parameter to see if the refinement should extend some distance apart from the mask (`extend`).

## 10: Mesh Generation

### Mesh Refinement

Negative masks are also allowed. Mask boundaries are never interpreted as being infinite in any direction, even if they extend far from the simulation boundary. Consequently, *shrinking* a refinement by specifying a negative extension parameter might leave a region uncovered, even if the mask originally extended past the boundary. For example, if a mask from (-0.010 to 1) covers a domain from (0 to 2), applying an `extend` parameter of -0.02 will produce a refinement extending from (0.010 to 0.98), thereby leaving the region from 0 to 0.010 unrefined.

### Example

First, create a mask, and then a refinement box can be issued:

```
polygon name=pol segments= { -0.5 -0.5 -.25 -.5 -.25 -.05 .25 -.05 .25 -.5 \  
  .5 -.5 .5 0 -.5 0 }  
mask name = "Mask" polygons= { pol }  
#now that there is a mask it can be used to produce a refinement.  
refinebox name = "refi_mask" mask = "Mask" xrefine= { .075 .075 .075 } \  
  yrefine= { .075 .075 .075 } extrusion.min = 0 extrusion.max = 0.05 \  
  extend = -0.1
```

## Refinement Near Mask Edges

Refinement also can be constrained to be near mask edges. This mask edge-based refinement has three parameters available in the `refinebox` command:

- `mask.edge.refine.extent`
- `mask.edge.mns`
- `mask.edge.ngr`

The parameter `mask.edge.refine.extent` must be specified to switch on mask edge-based refinement and to set the lateral extent of the refinement from the mask edge. Vertically, the mask edge-based refinement can be controlled with the x-coordinate of the `min` and `max` parameters. The minimum mesh spacing near the mask edge is set with `mask.edge.mns` (the default is taken from the `pdb` parameter `Grid SnMesh min.normal.size`), and the growth of the edge length away from the mask edge is specified with `mask.edge.ngr` (default is 1.0, meaning the constant edges of lengths `mask.edge.mns` in the normal direction).

**NOTE** Similar to the `pdb` parameter `Grid SnMesh min.normal.size`, actual edge lengths may be up to two times smaller than `mask.edge.mns` at the mask edge because of the binary-tree refinement algorithm.

An example of using mask edge-based refinement is:

```
polygon name=p1 segments= { 1.0 1.0 1.0 5.0 3.0 5.0 3.0 2.5 2.0 2.5 2.0 1.0 }  
mask name=m1 polygons = p1
```



```
refinebox clear
# Prevent mesh propagation by defining regular coarse mesh
refinebox yrefine = 0.5 zrefine = 0.5
# Add edge-based refinement
refinebox mask = m1 mask.edge.mns = 0.08 mask.edge.refine.extent = 0.25

grid remesh
```

The resist layer was created later using the command;

```
photo mask = m1 thickness = 0.05
```

Figure 96 shows the result.

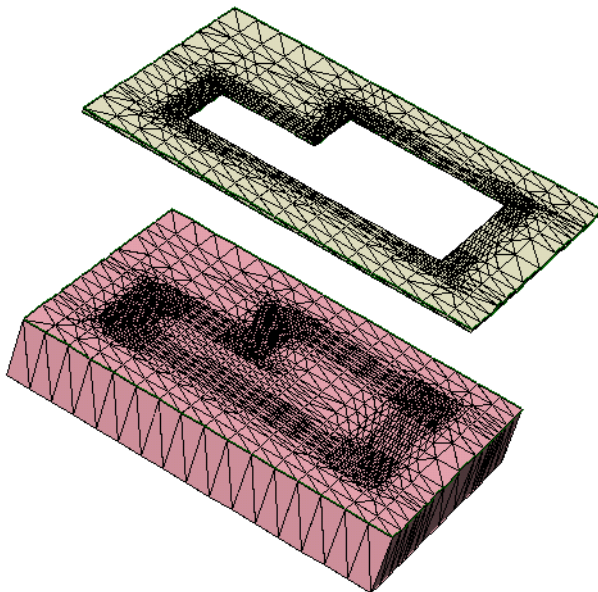


Figure 96 Mask edge-based refinement shown on the mask and in silicon

---

## Adaptive Refinement

Tailoring a mesh to a specific problem with static refinement boxes can be tedious and time-consuming. In addition, for some applications, dopant profiles evolve so much during the process that the areas where a finer mesh was needed at the beginning are very different from the areas where a finer mesh is needed at the end.

To accurately capture the entire evolution with a static mesh, it is necessary to put a fine mesh over large areas of the structure leading to long simulation times and large memory use. Adaptive meshing in Sentaurus Process addresses these issues.

## 10: Mesh Generation

### Mesh Refinement

The adaptive-meshing feature has a major component: field-based refinement.

For details, see [Tips for Adaptive Meshing on page 689](#).

The refinement parameters and criteria are the same for adaptive implantation as for field-based. When adaptive meshing is switched on, field-based refinement is performed during every remesh step and for any dimension (in 1D, 2D, or 3D). This happens for all etch, deposit, implant, native layer, regrid, and transform operations. In addition, during solve at a specified step interval, a check of the current mesh is made to determine whether a remesh is required; then the remesh is performed if necessary. For details, see [Adaptive Meshing during Diffusion on page 687](#). Finally, when adaptive meshing is used during implantation, in addition to adaptively refining the newly implanted species and damage, adaptive refinement (also based on existing fields) is applied simultaneously.

### Adaptive Refinement Criteria

Numerous refinement functions are available to deal with differing fields and situations. All functions involve some comparison between values on neighboring nodes and possible values between neighboring nodes. In some cases, the same refinement function is available in Sentaurus Mesh, and similar results to Sentaurus Mesh refinement will be obtained. The following refinement criteria are available:

- Relative difference (default)
- Absolute difference
- Logarithmic difference
- Inverse hyperbolic sine (asinh) difference
- Gradient
- Local dose error
- Interval refinement

These refinements can be applied globally (default) or they can be limited as follows:

- Boxwise
- Materialwise
- Regionwise

Detailed descriptions of the refinement types, their respective control parameters, and instructions for applying refinement constraints are given in subsequent sections. The default adaptive meshing parameters have been set to apply only relative difference criteria to the whole structure, and they typically produce a fairly coarse mesh. It is necessary to set one criterion or more to produce a mesh sufficiently fine to reach a required accuracy.

Adaptive meshing is switched off by default. To switch on adaptive meshing, use:

```
pdbSet Grid Adaptive 1
pdbSet Grid SnMesh UseLines 1 ;# Recommended with adaptive meshing
```

### Relative Difference Criteria

The relative difference between two neighboring nodes is computed as follows:

$$2 \frac{|C_1 - C_2|}{(C_1 + C_2 + \alpha)} \quad (933)$$

where  $C_i$  is the field value on node  $i$ , and  $\alpha$  is the field-specific refinement parameters set with:

```
pdbSet Grid <Field> Refine.Abs.Error <n>
```

or `def.abs.error` and `abs.error`, which are parameters of the `refinebox` command.

If the value of the expression in [Eq. 933](#) is greater than the maximum relative difference, the edge between node 1 and node 2 is split. To set the maximum relative difference, use:

```
pdbSet Grid <Field> Refine.Rel.Error <n>
```

or `def.rel.error` and `rel.error`, which are parameters of the `refinebox` command.

The quantity `<Field>` is the name of the field, and `<n>` is a unitless number for `Refine.Rel.Error` and `Refine.Abs.Error`; the units are the same as the units of the field. The default values for `Refine.Abs.Error` and `Refine.Rel.Error` are set from `<Field> = AdaptiveField`, except for the standard dopants, point defects, and `Damage` that have entries in the PDB.

The density of the mesh is sensitive to `Refine.Rel.Error` because it represents the target relative change of the field across an edge. For many standard situations, a number of the order of 1.25 gives a coarse mesh, and a number of approximately 0.5 often gives a fine mesh. The parameter  $\alpha$  sets a smooth cutoff such that values of the field below  $\alpha$  result in no refinement.

**NOTE** The relative difference criteria should only be used with fields that are always positive.

### Absolute Difference Criteria

The absolute difference between two neighboring nodes is computed simply:

$$|C_1 - C_2| \quad (934)$$

## 10: Mesh Generation

### Mesh Refinement

where  $C_i$  is the field value on node  $i$ . If the value of the expression in [Eq. 934](#) is greater than the maximum absolute difference, the edge between nodes 1 and 2 is split. The maximum allowable absolute difference can be set with:

```
pdbSet Grid <Field> Refine.Max.Difference <n>
```

### Logarithmic Difference Criteria

The logarithmic (base 10) difference between two neighboring nodes is computed as follows:

$$|\log(C_1 + \alpha) - \log(C_2 + \alpha)| \quad (935)$$

where  $C_i$  is the field value on node  $i$ , and  $\alpha$  is the low value cutoff that can be set with:

```
pdbSet Grid <Field> Refine.Abs.Error <n>
```

or `def.abs.error` and `abs.error`, which are parameters of the `refinebox` command.

If the value of the expression in [Eq. 935](#) is greater than the maximum logarithmic difference, the edge between nodes 1 and 2 is split. To set the maximum logarithmic difference, use:

```
pdbSet Grid <Field> Refine.Max.LogDiff <n>
```

or `def.max.logdiff` and `max.logdiff`, which are parameters of the `refinebox` command.

**NOTE** The logarithmic difference criteria should only be used with fields that are always positive. Use the `asinh` criteria for fields that can have negative values such as stresses.

### Inverse Hyperbolic Sine (asinh) Difference Criteria

The `asinh` difference between two neighboring nodes is computed as follows:

$$|\operatorname{asinh}(C_1) - \operatorname{asinh}(C_2)| \quad (936)$$

where  $C_i$  is the field value on node  $i$ . If the value of the expression in [Eq. 936](#) is greater than the maximum `asinh` difference, the edge between nodes 1 and 2 is split. To set the maximum `asinh` difference, use:

```
pdbSet Grid <Field> Refine.Max.AsinhDiff <n>
```

or `def.max.asinhdiff` and `max.asinhdiff`, which are parameters of the `refinebox` command.

## Gradient Criteria

The gradient between two neighboring nodes is computed as follows:

$$\frac{|C_1 - C_2|}{l_{12}} \quad (937)$$

where  $C_i$  is the field value on node  $i$ , and  $l_{ij}$  is the length of the edge between nodes  $i$  and  $j$ . If the value of the expression in Eq. 937 is greater than the maximum gradient, the edge between the two nodes is split. To set the maximum gradient, use:

```
pdbSet Grid <Field> Refine.Max.Gradient <n>
```

or `def.max.gradient` and `max.gradient`, which are parameters of the `refinebox` command.

## Local Dose Error Criteria

If an edge between two neighboring nodes is not split, the local dose error is computed as follows:

$$|0.5C_{12} - 0.25C_1 - 0.25C_2|l_{12}s_{12} \quad (938)$$

where:

- $C_i$  is the field value on node  $i$ .
- $C_{ij}$  is the concentration at the midpoint between nodes  $i$  and  $j$ .
- $l_{ij}$  is the length of the edge between nodes  $i$  and  $j$ .
- $s_{ij}$  is the box size perpendicular to the edge between nodes  $i$  and  $j$  (see Figure 97).

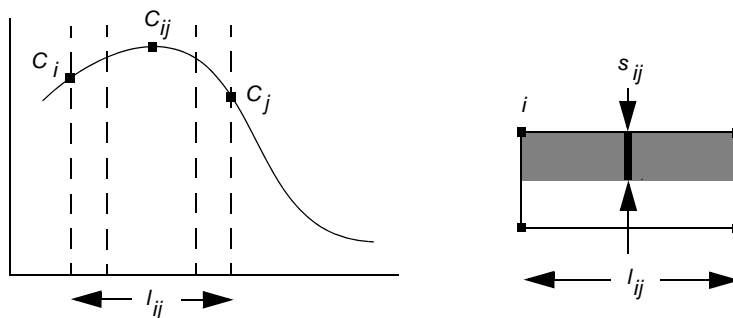


Figure 97 (Left) One-dimensional and (right) 2D representation of dose loss criteria

The function in Figure 97 (left) is taken from the previous mesh (or from an analytic implantation). The box with four points in Figure 97 (right) represents one cell of the mesh

## 10: Mesh Generation

### Mesh Refinement

refinement tree. The shaded area is the part of the 2D field under consideration. The dose in the shaded area is computed in two ways:

- As is
- If the edge between  $i$  and  $j$  is split

If the difference between these two ways is greater than `max.dose.error`, the edge is split.

The box size is 1.0 (unitless) in 1D; it is the box width (in cm) in 2D; and it is the box area ( $\text{cm}^{-2}$ ) perpendicular to the edge  $i-j$  in 3D. If the value of the expression in [Eq. 938](#) is greater than the normalized maximum local dose error, the edge between the two nodes is split. The local dose error can be set with:

```
pdbSet Grid <Field> Refine.Max.DoseError <n>
```

where `<n>` has units of  $\text{cm}^{-2}$ , or `def.max.dose.error` and `max.dose.error`, which are parameters of the `refinebox` command.

The local dose error is first multiplied by the simulation size before comparing it to the expression in [Eq. 938](#). The simulation size is 1.0 (unitless) in 1D, the simulation width (in cm) in 2D, and the simulation lateral area in 3D (in  $\text{cm}^{-2}$ ).

To estimate the total dose loss, you must estimate how many nodes carry a significant concentration of the field in question and then multiply that number by the local dose error to obtain approximately the maximum total dose error expected. (In practice, the dose error is often considerably less than this.) This quantity is relatively easy to understand and is less sensitive than some other parameters to process conditions.

### Interval Refinement

Interval refinement provides a way to refine the mesh such that field values within a certain interval are well resolved. Interval refinement produces mesh edges of a specified length wherever the field values are within a specified interval. Four parameters are required to define an interval refinement:

- A minimum and maximum value
- $C_{\min}$  and  $C_{\max}$
- A target length,  $lt$
- A target length scaling,  $s$

To preserve the anisotropy of the mesh, interval refinement examines each edge of a refinement cell and calculates an effective edge length  $l_{\text{eff}}$  defined by:

$$l_{\text{eff}} = \text{abs}((r_1 - r_2) \cdot \nabla C) \quad (939)$$

where  $r_1$  and  $r_2$  are the endpoints of the edge, and  $\nabla C$  is the average gradient of the field in the refinement cell. Edges that are nearly parallel to the contours of the field have effective edge lengths near zero. Edges that are nearly perpendicular to the contours have effective edge lengths near their actual edge length. Since edges are split only when they are longer than a given target length, edges that are parallel to the field contours are allowed to be longer than those that are perpendicular.

Interval refinement will split any edge whose effective edge length exceeds the effective target length. The effective target length is calculated differently depending on whether the field values on the edge overlap the interval specified by  $C_{\min}$  (`refinebox min.value`) and  $C_{\max}$  (`refinebox max.value`).

Let  $C_1$  and  $C_2$  be the values of the field on the endpoints of the edge. If the relation  $C_{\max} > C > C_{\min}$  is satisfied for any value of  $C$  between  $C_1$  and  $C_2$ , the edge overlaps the interval.

For edges that overlap the interval, the effective target length is exactly the target length that you specify (`refinebox target.length`), that is:

$$l_{\text{eff}} = l_t \tag{940}$$

For edges that do not overlap:

$$l_{\text{eff}} = l_t(1 + \log C_a - \log C_b)^2 s \tag{941}$$

where  $C_a$  is either  $C_{\min}$  or  $C_{\max}$ ,  $C_b$  is either  $C_1$  or  $C_2$ , and the values of  $C_a$  and  $C_b$  are chosen to minimize the difference.

The formula for  $l_{\text{eff}}$  outside the interval produces a graded mesh with an edge length that falls off parabolically with distance from the interval. Default values for the parameters of the interval refinements are defined in the PDB.

Table 66 lists `refinebox` parameters in the left column that can be used to specify boxwise refinement. The right column lists the corresponding PDB parameters that can be used to specify refinement criteria globally.

Table 66 Summary of refinement parameters

refinebox parameter	Corresponding entry in parameter database
<code>def.rel.error</code> , <code>rel.error</code>	Grid <Field> Refine.Rel.Error
<code>def.abs.error</code> , <code>abs.error</code>	Grid <Field> Refine.Abs.Error
<code>def.max.difference</code> , <code>max.difference</code>	Grid <Field> Refine.Max.Difference
<code>def.max.logdiff</code> , <code>max.logdiff</code>	Grid <Field> Refine.Max.LogDiff

## 10: Mesh Generation

### Mesh Refinement

Table 66 Summary of refinement parameters

refinebox parameter	Corresponding entry in parameter database
def.max.asinhdiff, max.asinhdiff	Grid <Field> Refine.Max.AsinhDiff
def.max.gradient, max.gradient	Grid <Field> Refine.Max.Gradient
def.max.dose.error, max.dose.error	Grid <Field> Refine.Max.DoseError
min.value	Grid <Field> Refine.Min.Value
max.value	Grid <Field> Refine.Max.Value
target.length	Grid <Field> Target.Length (um)
target.length.scaling	Grid <Field> Target.Length.Scaling

## Localizing Adaptive Meshing using refinebox Command

Adaptive meshing has been implemented through generalized refinement boxes. As such, adaptive refinement and the refinement parameters themselves can be set in a boxwise manner. The default adaptive refinement box covers the entire structure and relies on global parameters and field-based parameters for its default values. If you specify an adaptive refinement box, the default box is not created.

**NOTE** For field-based refinement, any adaptive `refinebox` that is manually created overrides the default adaptive `refinebox`. The default adaptive `refinebox` (that covers the entire structure) can be created explicitly with the command `refinebox adaptive`.

You can create one or more adaptive refinement boxes with different parameters. The most commonly used parameters control the size of the box (`min` and `max`), and the minimum and maximum edge lengths (`refine.min.edge` and `refine.max.edge`).

The default list of fields upon which to refine includes all dopants, point defects, and clusters in the structure. This list can be modified in several ways. For example, the following command overrides the default list:

```
pdbSet Grid <field> DoNotAdapt 1
```

The next example adds `Field1` and `Field2` to the default list for this particular box:

```
refinebox refine.add.fields = { Field1 Field2 ... }
```

The following command redefines the list of fields to be used as the basis for refinement; if set, this command overrides any add or subtract settings:

```
refinebox refine.fields = { Field1 Field2 ... }
```



## Examples

To switch on adaptive meshing, use:

```
pdbSet Grid Adaptive 1
```

To apply adaptive meshing only inside a box and to set the anisotropic edge minimum in the same box, use:

```
refinebox min= {0.0 0.0} max= {0.01 0.5} refine.min.edge= {0.001 0.25} adaptive
```

To refine only considering arsenic and boron, use:

```
refinebox refine.fields = {Arsenic Boron} adaptive
```

To create a default box and, in addition, to create a refinement box where  $r_F$  is modified locally for all species and  $\alpha_F$  is modified for only boron, use:

```
refinebox adaptive
refinebox min= {0.0 0.0} max= {0.01 0.5} def.rel.error= 0.9 \
abs.error= {Boron = 1.0e14} adaptive
```

## Adaptive Meshing during Diffusion

Adaptive meshing during diffusion is switched on by default when adaptive meshing is switched on (in other words, `pdbGet Grid Adaptive` returns 1). There is an additional control that allows for the prevention of adaptive meshing at low temperatures, which is specified like this:

```
pdbSet Grid Min.Adaptive.Temp <Temp C>
```

In any case, by default adaptive meshing is not performed during oxidation or silicidation. You can switch on adaptive meshing during these steps by setting:

```
pdbSet Diffuse Compute.Regrid.Steps 10 ;# during inert annealings
pdbSet Diffuse Growth.Regrid.Steps -1 ;# during oxidation and silicidation
pdbSet Diffuse Epi.Regrid.Steps -1 ;# during epitaxy
```

where <number> is the fixed interval of time steps. For the first parameter `Compute.Regrid.Steps`, the default is 10 steps and, for the other two, the default is -1, meaning it is off by default. After the specified number of steps is taken, the mesh is checked to see if the refinement criteria are satisfied (within some tolerance); a remesh is performed if necessary. Currently, the use of adaptive meshing during oxidation and epitaxy is possible.

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### Mesh Refinement

The refinement criteria check is performed as follows: Axis-aligned edges are checked to see if they satisfy:

$$\text{actual} < \text{Refine.Factor} * \text{error} / \text{maxerror} \quad (942)$$

where:

- `Refine.Factor` is a direction-dependent parameter of the PDB under `Grid`.
- `error` is the error functions given in [Eq. 933–Eq. 938](#).
- `maxerror` is the maximum error parameter associated with each refinement type.
- `actual` is the ‘actual’ edge length.

There is a cutoff percentage PDB parameter `Grid Refine.Percent` that limits the percent of edges that fail ([Eq. 942](#)) before a remesh is called. This check procedure is performed for every `Diffuse Compute.Regrid.Steps` whether a remesh is called or not. You can omit the refinement criteria check (which can be time-consuming for large meshes) and force a remesh by setting:

```
pdbSet Grid Refine.Check 0
```

[Table 67](#) summarizes the parameters available for adaptive meshing for diffusion.

Table 67 Adaptive meshing parameters

Parameter	Comment
<code>Compute Compute.Regrid.Steps</code>	Number of diffusion steps before refinement criteria are checked to decide if remeshing is required.
<code>Compute Pre.Regrid.Save</code>	To help with tailoring the mesh, files can be saved immediately before adaptive remeshing occurs during diffusion. The files are named <code>&lt;input_file_stub&gt;_preregrid_###_fps.tdr</code> where <code>&lt;input_file_stub&gt;</code> would be, for example <code>n1</code> , if the input file was <code>n1_fps.cmd</code> and <code>###</code> is an increasing index starting with 001.
<code>Grid Refine.Check</code>	If <code>Grid Refine.Check</code> is set to 1 (true), then refinement criteria are checked and remeshing occurs if necessary.  If it is set to 0 (false), remeshing occurs without a check.
<code>Grid Refine.Factor</code>	Tolerance factor for marking an edge too long.
<code>Grid Refine.Percent</code>	Allowed percentage of edges too long.

## Adaptive Meshing during Implantation

Adaptive meshing during implantation is active whenever adaptive meshing is switched on (in other words, `pdbGet Grid Adaptive` returns 1). It also may be enabled or disabled for each implant step using the `adaptive` parameter of the `implant` command.

Adaptive meshing during implantation differs from adaptive meshing for other process steps in one key respect: When performing an implantation step, the implanted concentrations are defined by analytic expressions instead of discretized field values. Therefore, the final values for the implanted fields are not known before the remeshing step begins so they must be computed as the mesh is refined.

By default, refinement on damage is handled differently from refinement on dopants. For the analysis of damage, the gradient is usually uninteresting, but the location of the crystal–amorphous interface is often critical. Therefore, refinement should be added to the mesh, not according to the damage gradient, but rather according to whether the damage is near the crystal–amorphous threshold. This is accomplished using an interval refinement (see [Interval Refinement on page 684](#)). By default, the minimum and maximum values of the interval are set to the value of the crystal–amorphous threshold ( $1.15 \times 10^{22} \text{ cm}^{-3}$ ). The target length is  $0.002 \text{ }\mu\text{m}$ , and the target length scaling is 1.0.

**NOTE** The default target-length setting of 2 nm can produce many mesh points for amorphizing implants in 3D. You should first try using a larger setting and then reduce it if necessary.

As the mesh is constructed, each cell of the refinement tree is evaluated to determine whether the refinement criteria are satisfied. The criteria for as-implanted fields are computed for each edge of the cell. If any criterion is not satisfied, the cell is split and the as-implanted concentrations are computed at the newly introduced points. This process continues until all refinement criteria are satisfied (or the minimum edge length is reached) for all cells on the refinement tree. Therefore, the constructed mesh satisfies the refinement criteria for all fields present in the structure, not solely the implanted fields.

For adaptive meshing during MC implantation, the analytic module is used to compute refinement, the mesh is formed, and afterwards, the implant profiles are computed with the MC module.

## Tips for Adaptive Meshing

The following list gives useful suggestions when using adaptive meshing:

- When setting boxwise meshing criteria, remember that any global criteria you have specified still apply inside the box. This means you cannot use boxwise meshing criteria to establish less stringent meshing criteria (such as a larger relative error) inside a box because the more stringent global criteria still apply. If you want to use different criteria for different parts of the structure, set the global criteria to the least stringent criteria and use boxes for more stringent criteria.
- To switch on adaptive meshing and use all the defaults, all that is needed is `pdbSet Grid Adaptive 1`. The main parameter for adjusting the amount of refinement is `pdbSet Grid AdaptiveField Refine.Rel.Error`, which defaults to 1.5. In many cases, this

## 10: Mesh Generation

### Mesh Refinement

does not refine sufficiently. Decreasing the value causes more refinement. The number of mesh points is sensitive to this value, and it is not generally recommended to use a value less than 0.25. This parameter generally meshes doping gradients well, but may leave the peaks too coarse. To refine the peaks, the best criterion to use is maximum dose error (`Grid AdaptiveField Max.Dose.Error`).

- To override the default refinement box used for field-based refinement (which covers the whole structure and applies to all solution variables), you need only to create an adaptive refinement box. To add criteria in addition to the default criteria, for example, to add finer criteria under the gate while preserving standard parameters elsewhere, you can create your own default refinement box. For example:

```
refinebox adaptive
refinebox min= {-0.01 -0.01} max= {0.15 0.05} adaptive def.rel.error=0.75
```

- The default refinement setting for implant damage can give too fine a mesh. Increase `Grid AdaptiveField Refine.Target.Length` from the default value of 0.002 to reduce refinement.

---

## Default Refinement

In two dimensions, by default, interface refinement is applied to any interface in which one of the neighboring bulk regions is of material `Silicon`, `Polysilicon`, or `Oxide`. In three dimensions, by default, interface refinement is applied only to interfaces where one of the neighboring bulk regions is `Silicon`. For other interfaces, the `min.normal.size` criterion is not applied. To view currently defined refinement boxes (including default refinement boxes), use:

```
refinebox print
```

Additional interface refinement can be specified with the command:

```
refinebox interface.materials= {<material1> <material2> ...}
```

This command specifies refinement at all interfaces to both `<material1>` and `<material2>`.

```
refinebox interface.mat.pairs= {<material1> <material2>}
```

This command specifies interface refinement at all interfaces where one side of the interface is `<material1>` and the other side is `<material2>`.

The interfaces that are refined are the union of `interface.materials` (all interfaces touching materials in the list) and `interface.mat.pairs` (only refined on material pairs found in the list first and second, third and fourth, and so on).

The default `min.normal.size` for all interface refinement boxes including the default ones is taken from the `pdb` parameter `Grid SnMesh min.normal.size`. Similarly, the default

value of `normal.growth.ratio` for all interface refinement boxes is taken from the `pdb` parameter `Grid SnMesh normal.growth.ratio.2d` in two dimensions and from `Grid SnMesh normal.growth.ratio.3d` in three dimensions.

To add an interface refinement, use the `refinebox` command.

To remove an existing interface refinement, first do `refinebox clear`, and then start again.

## Examples

The interfaces to be refined are defined as follows:

```
# Change the default min.normal.size (in micrometers)
pdbSet Grid SnMesh min.normal.size 2.0e-3

# Now modify which materials to apply interface refinement
# refine at all interfaces to silicon and poly (use the global min.normal.size
# and normal.growth.ratio)
refinebox clear
refinebox interface.materials= {silicon poly}
```

The next example shows refinement only at the silicon–oxide and polysilicon–oxide interfaces, and specifies a local value for interface refinement parameters:

```
refinebox clear
refinebox min.normal.size = 0.005 normal.growth.ratio = 3 \
  interface.mat.pairs= { Silicon Oxide PolySilicon Oxide }
```

---

## Refinement Box Manipulations: Using `transform.refinement`

Several transformation can be performed on refinement boxes using the `transform.refinement` command. This command works like the `transform` command (see [Stress Handling on page 734](#)), except for refinement boxes. This command accepts the following options:

- Transformation – either `translate`, `stretch`, `cut`, `rotate`, `flip`, or `reflect`.
- Transformation options – depend on the type of transformation. A displacement is required for `translate`, axis and angle for `rotate`, a box for `cut`, reflecting plane for `reflect`, the length and direction for `stretch`, and so on.
- `name` – applies the transformation to a particular refinement box if specified or to all of them otherwise.
- `name.new` – specifies the name of the transformed refinement.

## 10: Mesh Generation

### Mesh Settings

- `keep.original` – specifies whether to keep the original. Specifying `!keep.original` transforms the specified refinement box, while setting it to `keep.original` preserves the original refinement box and creates a new transformed one. This option is useful when you want to “copy and paste” refinements by, for example, translating them to a different position while keeping the original in place.

For example:

```
transform.refinement name="refbox" name.new="newRefBox" \  
  translate= { 0.1 0 0 } keep.original
```

creates a new refinement called `newRefBox` identical to `refbox` but displaced  $0.1 \mu\text{m}$  in x.

---

## Mesh Settings

The following tables list the parameters available for Sentaurus Mesh. To set the parameters in [Table 68](#), use:

```
pdbSet Grid SnMesh <Parameter name> <value>
```

Table 68 Parameters available for Sentaurus Mesh

Parameter	Default	Description
CoplanarityAngle	175 degrees	Any pair of faces with an angle of <code>CoplanarityAngle</code> or more will be considered coplanar.
CoplanarityDistance	1.0e-6 $\mu\text{m}$	Maximum deformation caused to the boundary when swapping the edge shared by a pair of adjacent faces.
DecimateBeforeImprint	true	Decimates the boundary before imprinting it with the axis-aligned mesh.
DelaunayTolerance	1.0e-4	Specifies how close the ridges and boundary faces conform to the Delaunay criterion.
DelaunayToleranceMat		Specifies an array pair of materials and tolerances to be used in those materials. For example: <pre>pdbSet Grid SnMesh DelaunayToleranceMat   {Silicon 0.01 Oxide 1.0}</pre>
DelaunayToleranceReg		Specifies an array pair of regions and tolerances to be used in those regions.
DelaunayType	constrained	Types of mesh generated by Sentaurus Mesh. Available types are box method, conformal, or constrained.
DelPsc	false	Indicates whether the Delaunay refinement for piecewise smooth complex (DelPSC) algorithm is applied to the boundary at the beginning of a mesh generation step.

Table 68 Parameters available for Sentaurus Mesh

Parameter	Default	Description
DelPscAccuracy	1e-4 $\mu\text{m}$	Specifies the accuracy used by the DelPSC algorithm when approximating high-curvature areas. This parameter is used during standard mesh generation (as opposed to using DelPSC during oxidation).
EdgeProximity	0.05	Specifies the minimum ratio of the edges generated when an edge is split.
FaceProximity	0.05	Specifies the minimum ratio of the faces generated when a face is split.
ImprintCoplanarFacesOnly	true	Imprints the binary tree on the coplanar sets of faces. This is useful to avoid over-refinement in curved areas.
ImprintCoplanarityAngle	179 degrees	Angle used to decide when two faces are coplanar. If two adjacent faces have an angle greater than this value, they will be added to the set of faces to be imprinted with the binary refinement tree cells.
max.box.angle.2d	120 degrees	Maximum angle in binary tree (2D only).
max.box.angle.3d	150 degrees	Maximum angle in binary tree (3D only).
MaxAspectRatio	1e6	Specifies the maximum-allowed aspect ratio of an element in the binary tree.
MaxBoundaryCutRatio.2d	0.01	Specifies the maximum-allowed ratio between the lengths of adjacent axis-aligned edges cutting material boundaries (2D only).
MaxBoundaryCutRatio.3d	0.01	Specifies the maximum-allowed ratio between the lengths of adjacent axis-aligned edges cutting material boundaries (3D only).
MaxConnectivity	1e37	Specifies the maximum number of elements connected to a point in the final mesh.
MaxNeighborRatio	3.0	Specifies the maximum-allowed ratio between the circumscribed spheres of neighboring elements.
MaxPoints	100000	Maximum number of points allowed by the Sentaurus Mesh delaunization module.
MaxSolidAngle	360 degrees	Specifies the maximum solid angle allowed in the elements of the mesh (3D only).
MaxTetQuality	1e37	Specifies the minimum <code>shortestEdge/circumradius</code> ratio allowed in the mesh (3D only).
MinAngle	0	Specifies the minimum angle allowed in the elements of the mesh (2D only).
minedge	1.0e-6 $\mu\text{m}$	Minimum edge length request.

## 10: Mesh Generation

### Controlling Mesh during Oxidation

Table 68 Parameters available for Sentaurus Mesh

Parameter	Default	Description
SliverAngle	175 degrees	Limits the maximum dihedral angle on one element when the delaunizer performs the sliver removal step.
SliverDistance	1e-2 $\mu\text{m}$	Limits the amount of “damage” done to the standard Voronoï diagram by the sliver removal algorithm. Note that the grid produced by the sliver removal algorithm is weighted Delaunay, so the standard Voronoï diagram is “damaged” unless the Voronoï weights are stored (see the <code>StoreDelaunayWeight</code> parameter). When the box method library reads those weights, it calculates the correct Voronoï diagram and coefficients to solve the PDEs.
StoreDelaunayWeight	0	When set to 1, stores the Delaunay–Voronoi weight ( <code>DelVorWeight</code> ) for the box method library.
UseLines	true	Specify 1 or 0. <code>UseLines</code> is specified in the <code>line</code> command in the mesh generated by Sentaurus Mesh.

---

## Controlling Mesh during Oxidation

Oxidation creates new regions and dramatically alters the shape of existing ones. Controlling the mesh is important. This section covers some mesh control methods.

---

### TS4 Mesh Library

The TSUPREM-4 moving-boundary meshing library is available from within Sentaurus Process (hereafter, referred to as the *TS4 mesh library*). By default, the TS4 mesh library performs the 2D mesh update.

The following statement switches off the TS4 mesh library and specifies the use of the old mesher:

```
pdbSet Grid UseTS4Mesh 0
```

`2D.MeshLib` is an alias of `UseTS4Mesh`.

The TS4 mesh library deposits the native oxide layer before oxidation by default. Since it removes all grids inside a gas region, the simulation performance is improved without any loss of accuracy. To use the MGOALS native layer in two dimensions, instead of the TS4 mesh library, use the command:

```
pdbSet Grid UseTS4Native 0
```



`2D.MeshLib.Native` is an alias of `UseTS4Native`.

For silicidation, a gas mesh is used by default. The following statement forces the use of the TS4-style gas mesh instead of the default gas mesh:

```
pdbSet Grid UseTS4GasMesh 1
```

## Control Parameters in TS4Mesh

The control parameters are specified with:

```
pdbSet Grid TS4Mesh <control parameter> <value>
```

The available control parameters are:

- `MergeSubAndAdd` <0|1> (default: 1)  
It optimizes the speed performance by merging the grid subtraction and addition procedures.
- `DoSubAfterStep` <0|1> (default: 0)  
Grid subtraction is performed after each diffusion step, while grid addition is performed after each mechanics step followed by the diffusion step. Switching on this flag forces only one diffusion step per each mechanics step. When this flag is switched on, `MergeSubAndAdd` is ignored.
- `SubTimeFactor` <double> (default: 1.5)  
The time step given by mechanics for grid removal is scaled by `SubTimeFactor`.  
**NOTE** Do not change the default.
- `MinSpaceOnInterface` <double> (default:  $2e-6$  [ $\mu\text{m}$ ])  
The nodes on an interface mesh must be rebuilt after meshing on the moving boundary since the bulk meshes along the interface can be added or removed. Instead of destroying and rebuilding the interface mesh, the TS4 mesh library tries to reuse the original node data on the interface mesh to minimize the interpolation error. The original nodes are detected when the location difference is less than `MinSpaceOnInterface`.  
**NOTE** Do not change the default.
- `ExactGridSpace` <0|1> (default: 1)  
On the growing material side of the interface, the triangular mesh elements expand. To maintain solution accuracy in the material (for example, calculating the diffusion of oxidant in the oxide), you must add nodes to the growing material. The addition of nodes

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### Controlling Mesh during Oxidation

to the growing material is controlled by `perp.add.distance`, `ExactGridSpace`, and `LocalGridSpace`.

**NOTE** `perp.add.distance` is the grid control parameter of each material, for example: `pdbSet Oxide Grid perp.add.distance 0.01e-4`

Precise grid spacing is obtained by adding new nodes in a growing layer at the distance specified by `perp.add.distance` from the existing node in the layer. Because only one node can be added at each point on an interface during a simulation time step, the size of the time step may need to be reduced to achieve the required spacing. This reduction in the time step can be disabled by specifying:

```
pdbSet Grid TS4Mesh ExactGridSpace 0
```

By default, `ExactGridSpace` is set to 1 to allow reducing the number of time steps to control the grid spacing. The algorithm does not allow grid points to be added at spacings less than 1 Å, and control of the spacing may not be precise for spacings less than 2 Å.

- `LocalGridSpace <0|1>` (default: 1)

The grid control algorithms and parameters apply to the entire structure. To avoid adding a very fine grid in field regions when growing gate oxides, an option allows the grid spacing to vary with the oxide growth rate. When `LocalGridSpace` is switched on, the grid spacing to be used at each point in the growing material is:

$$h = (v_{\max}/v) \text{ perp.add.distance}$$

where  $v$  is the growth rate at a point in the structure, and  $v_{\max}$  is the maximum growth rate at all interfaces of the same type in the structure. `LocalGridSpace` is switched on by default.

- `OrderFlatTri <0|1>` (default: 1)

When the area of a shrinking triangle becomes less than  $1e-15 \text{ (cm}^2\text{)}$  after a time step, the triangle is removed. When the shrinking triangle to be removed is located at a material interface and the removal of the triangle will result in a bad mesh, the material type of the shrinking triangle is replaced with the type of the growing neighbor material, instead of removing it. When those triangles are adjacent to each other, the reordering algorithm for the replacements smooths the interface shape after conversion.

- `MinAreaRemovalRatio <double>` (default: 10.0)

When a region has only one triangle surrounded by neighbors of different materials and its area is less than `MinAreaRemovalRatio` multiplied by  $1e-15 \text{ (cm}^2\text{)}$ , the material type of the triangle is replaced with the neighbor material that shares the longest edge with the triangle.

- `Min.Split.Distance <double>` (default:  $1e-8 \text{ [cm]}$ )

When multiple regions with the same material meet at one point, the point is split by inserting new elements. The parameter determines the minimum split distance.

---

## Moving Mesh and Mechanics Displacements

The displacements computed by the mechanics solution during oxidation are applied to the nodes after checking against the `MinimumVelocity` criterion defined for each region. Velocity is the computed solution variable and is multiplied by the time step to compute displacements. The nodes are moved by this amount.

The computed velocities are compared against `MinimumVelocity` and, if the computed velocity is greater than `MinimumVelocity`, the displacements are computed and applied. The `MinimumVelocity` is set with the command:

```
pdbSetDouble Silicon Grid MinimumVelocity <n>
```

---

## Grid Spacing

Grid spacing in the growing region is controlled by `perp.add.dist`. The value is in units of centimeter, and the edges in growing regions are checked to see whether they are nearly perpendicular to the interface.

If they are perpendicular, they are split if their length exceeds the `perp.add.dist` number. This value is set with the command:

```
pdbSet Oxide Grid perp.add.dist 2e-7 ;# unit is cm
```

---

## Grid Cleanup

During oxidation or silicidation, the growing region increases at the expense of a shrinking region. The shrinking regions then have a problem of small edges. Below a certain value, these edges must be removed entirely, and the mesh around them must be adjusted.

The short edge criterion is specified by the `Remove.Dist` parameter, which is specified in centimeters and is set as follows:

```
pdbSet Silicon Grid Remove.Dist 3e-8
```

**NOTE** Due to mesh quality constraints, this number must be kept above a value of  $2 \times 10^{-8}$  cm.

---

## Maximum-allowed Rate of Growth

For a minimal simulation time, it would be best if the entire thickness growth were simulated in one step. However, this is not possible. The reasons for this include:

- Nonconvergence of diffusion equations.
- Inability to track material interfaces if they grow more than one edge length of a triangle or a tetrahedron, and so on.

In the new growing region, new nodes are introduced and the data is interpolated from the nearby nodes; if growth is too fast, significant interpolation errors could occur.

The rate of growth can be controlled by the parameters `dThickness` and `IncreaseRatio`. The `dThickness` parameter (specified in micrometers) defines the maximum-allowed oxidation front displacement per time step and is set as follows:

```
pdbSet Diffuse dThickness 0.001
```

The `IncreaseRatio` parameter is the factor by which the time integration step is allowed to grow.

---

## Miscellaneous Tricks

Since Sentaurus Process oxidation does not allow the interface to traverse more than one element thickness at a time, speed can be achieved by having elements with longer edge lengths near the interface. This can be controlled by refinement boxes or the `pdb` parameter `Grid SnMesh min.normal.size`. Large structures, like those used in power devices, may need `min.normal.size` of 0.01  $\mu\text{m}$ , while submicron CMOS devices need 8  $\text{\AA}$ .

The mesh away from the interface is unrefined based on the `pdb` parameter `Grid SnMesh normal.growth.ratio.3d`. If the mesh is not unrefining fast enough, this number can be increased.

In large structures, the interface fidelity may not need to be as tight as that of 45-nm or 32-nm gate transistors. The `MGOALS accuracy` parameter can be increased to 1  $\text{\AA}$ , which will cause `MGOALS` to clean up interfaces of small (sub-1  $\text{\AA}$ ) features and ensure smooth long edges that speed up oxidation.

These are options available to the process engineer; however, care must be exercised in varying these parameters since they may affect the final structure significantly.

---

## Meshing for 3D Oxidation

Maintaining a conformal high-quality mesh during the simulation of 3D oxidation is very difficult because of the following requirements: moving boundaries, accurate dopant profiles, dose conservation, minimization of the number of mesh points, and maintaining high-quality mesh elements. In particular, handling the frequent collision of the oxidation front with points inside the silicon, polysilicon, or gas regions can cause intractable problems for the local mesh operations needed for maintaining dose conservation. These problems have not been completely solved in Sentaurus Process, so various global remeshing strategies have been implemented to try to recover when the local operations fail. Improvements in both the local and global meshing operations are in progress.

Before each diffusion time-step, the mesh is checked for the maximum possible time step until the first tetrahedron element collapses (becomes flat). If necessary, the time step is reduced. In the diffusion simulation, all mesh points are moved using the velocity and the time step. The mesh topology is not changed during the diffusion time step. At the end of the diffusion time step, a face-swapping algorithm is used to improve the mesh quality and to remove flat elements. After face-swapping, the mesh is checked for any remaining flat elements and any elements that have short edges, poor shapes, or small volumes. An attempt is made to remove these elements, followed by a face-flipping to improve the element quality allowing for the next time step to be sufficiently large.

This removal of local elements is a difficult task, which does not always succeed and frequently leads to bad elements surviving and enforcing small time steps. If this grid-limited time step becomes too small, a 3D Delaunay meshing algorithm is used in an attempt to construct a mesh for the given geometry and the set of bulk points that do not belong to any 'flat' elements.

**NOTE** If the delaunizer fails to construct a new mesh, a limited set of small time steps is allowed in an attempt to recover a reasonable size time step. If this does not succeed, the simulation is stopped with an error message.

---

## MovingMesh

This section describes an experimental feature that can be used for 3D oxidation. This feature called *MovingMesh* is activated with the following command before the `diffuse` command:

```
pdbSet Grid Use.MovingMesh 1      ;# switched on by default
```

Two important parameters control MovingMesh:

```
pdbSet Oxide Grid perp.add.dist 0.005e-4  ;# centimeter
```

```
pdbSet Grid Remove.Dist 0.001e-4         ;# centimeter
```

## 10: Mesh Generation

### Controlling Mesh during Oxidation

The `perp.add.dist` parameter specifies the distance that the oxide interface can move before new mesh points are inserted in the oxide. The unit is in centimeter.

The `Remove.Dist` parameter specifies the shortest distance the mesh vertices are allowed from the oxide interface. Shorter than this distance, the vertices will be removed. Do not specify a distance larger than the minimum oxide thickness. For a typical example with 1.5 nm native layer, `Remove.Dist` of 1.0 nm or less is appropriate. The unit is in centimeter.

The oxide interface can develop problematic geometric features like knife edges, noisy surfaces, or extremely thin gaps. You can enable geometry repair and surface remeshing by using:

```
pdbSet Grid MovingMesh Repair.Geometry 1      ;# switched on by default
```

The criteria to trigger geometry repair are based on the minimum dihedral angle and the maximum face angle:

```
pdbSet Grid MovingMesh Repair.Geometry.Min.Dihedral.Angle 5    ;# degree
pdbSet Grid MovingMesh Repair.Geometry.Max.Face.Angle 175      ;# degree
```

If the minimum dihedral angle between two triangles is below the threshold or the maximum face angle of a triangle is above the threshold, the geometry repair procedure starts.

The geometry repair procedure involves a multimaterial level-set (MLS) formulation. The resolution of the level-set cell size is controlled by:

```
pdbSet Grid MovingMesh Repair.Geometry.Resolution 0.001    ;# micrometer
```

The boundary representation (brep) of the new geometry must go through a meshing algorithm for curved surfaces called the Delaunay refinement for piecewise smooth complex (DelPSC) that improves the quality of triangles on brep surfaces. This algorithm is enabled by:

```
pdbSet Grid MovingMesh Apply.Brep.DelPSC 1      ;# switched on by default
```

DelPSC performs adaptive sampling on ridges (1D geometric feature) according to the refinement fields, the curvatures of the ridges, and the proximity among the ridges. On each surface patch (2D geometric feature), DelPSC performs adaptive sampling according to the refinement fields and the curvatures of the surface.

Ridge sampling also is controlled by:

```
pdbSet Grid MovingMesh Apply.Brep.DelPSC.Resolution 0.005    ;# micrometer
```

The above parameter ensures no ridge edge will be longer than the specification. It is useful, for example, when you have a straight line (no curvature) next to curved surfaces. You want the sampling points on the straight line to be fine enough to support the adjacent curved surfaces.

Note that you no longer require `Apply.Brep.DelPSC.Resolution` to be as small as the thin native layer thickness, because of the adaptive sampling based on proximity between nearby ridges.

To control accuracy in high curvature areas, you can specify the acceptable distance between the old and new curved surfaces by using:

```
pdbSet Grid MovingMesh Apply.Brep.DelPSC.Accuracy 0.0001    ;# micrometer
```

`MovingMesh` has facilities for troubleshooting run-time failures. A typical setting would be:

```
# Switch on level-1 diagnostics
pdbSetDouble debugLevel MovingMesh 1                ;# switched off by default

# Save intermediate result every 100 time steps
pdbSetDouble Grid MovingMesh Save.Interval 100      ;# switched off by default

# Save diagnostic files for Repair.Geometry and DelPSC
pdbSetDouble Grid MovingMesh Repair.Geometry.Monitor 1
                                                    ;# switched off by default
```

In level-1 diagnostics, the intermediate result will be saved after a certain number of time steps in the files:

```
<NodeName>_MovingMeshGridTimeStep<xxxx>.tdr
```

The frequency of saving is specified by the `Save.Interval` parameter. The files are written after mechanics and before diffusion to analyze the grid-limited time step.

In the event of failure in `Repair.Geometry`, the level-1 diagnostics will save files with names such as:

```
<NodeName>_remeshBrep{In,MLS,PSC,Out}.tdr
<NodeName>_applyBrepDelPSC{In,Out}.tdr
```

They are useful for checking whether the resolution parameters are adequate. The most likely cause of failure is a too coarse resolution to capture thin oxide layers and other small geometric features.

If the parameter `Repair.Geometry.Monitor` is set to 1, the intermediate files with names such as:

```
<NodeName>_remeshBrep_<xxxx>_{In,MLS,PSC,Out}.tdr
<NodeName>_applyBrepDelPSC_<xxxx>_{In,Out}.tdr
```

will be saved every time the repair geometry operation is triggered. These files are useful to monitor how the MLS and DelPSC algorithms perform at various points in a simulation.

---

## UseLines: Keeping User-defined Mesh Lines

During the `init` command, the line location and spacing specifications given by `line` commands are expanded into ticks and stored in the PDB and in TDR files. This is performed by default.

By carefully placing lines, you can isolate areas of the structure that changed (because of etching, deposition, and so on) from those that do not (such as bulk silicon). In this way, the mesh in areas that do not change will have the least amount of change, the least interpolation, and the most accurate results. Even the mesh in regions that do change will have a similar starting point and should also have minimal mesh-point movement coming from remeshing.

Lines for Sentaurus Process Kinetic Monte Carlo are stored separately from the lines used with continuum solvers (in other words, Sentaurus Mesh meshes). By default, line commands are applied to both KMC and continuum meshes. Use the parameter `!kmc` or `!mgoals` to not apply a particular `line` command. For example, for a `line` command to apply only to continuum, use `line !kmc`.

In the simplest case, all the `line` commands are specified before the `init` command, and they are saved and reused every time a remesh is performed. However, there are other cases described in the following sections that allow this feature to be more powerful.

All the `line` commands are specified before the `init` command, and they are saved and reused every time a remesh is performed. However, there are other cases described in the following sections that allow this feature to be more powerful.

---

### Using line Commands after init Command

The expansion of lines from `line` commands into ticks (in other words, all starting mesh line locations) is performed only at the point that the lines in that direction are needed. For example, x-lines are always expanded in the `init` command, but y-lines are only expanded when the first etch with a mask is given. Therefore, it is possible to load a 1D structure, give y-lines, and then expand to 2D, or give both y- and z-lines and expand to 3D.

After a particular direction or dimension is expanded, it is only possible to insert one tick at a time in that direction using the `line` command (in other words, the `spacing` parameter is thereafter ignored). For example, this could be because you identified the amorphous–crystalline interface in silicon.



This is handled by specifying one of the following:

- The `line` command in a dimension greater than the current dimension. For example, a y-line specification when the simulation is in 1D.
- The `line` command in a dimension at or less than the current dimension. For example, either an x-line or a y-line specified when the simulation is in 2D.

For more information about the operating dimension, see [Automatic Dimension Control on page 72](#).

## Dimension within Current Spatial Dimension

This is encountered if the user-specified x-lines and the current spatial dimension of analyses is 1D. Or, it could happen if you specify x- or y-lines in 2D, or x-, y-, or z- lines in 3D.

In this case, the `line` command ignores the `spacing` parameter and tries to insert only one tick as long as that tick (line) is not too close to an existing tick.

Inside the `init` command, the `line` commands are expanded into ticks using the `spacing` specifications for the dimension as they are needed. When additional `line` commands are given for dimensions where the ticks have already been expanded, the `spacing` parameter is ignored and one additional tick is added as long as it is not too close to an existing tick.

## Dimension Greater Than Current Spatial Dimension

This is encountered if you specified y- or z-lines, and the current spatial dimension of analyses is 1D. Or, it could happen if you specify z-lines and the current spatial dimension of analyses is 2D.

In this case, the `line` command is considered in its entirety, and the `spacing` parameter is used. All the intermediate lines are included in the list of ticks kept.

## Creating More Than One Structure

You can create more than one structure using `line`, `region` and `init` commands in one command file when using the `UseLines` feature. To ensure lines from the first structure are not inserted into subsequent structures, it is important to issue `line clear` before starting the definition of a new structure. For example:

```
#####  
line x loc=0 spacing=0.001  
line x loc=1 spacing=0.1  
line y loc=0  
line y loc=1
```

## 10: Mesh Generation

UseLines: Keeping User-defined Mesh Lines

```
region silicon
init !DelayFullD

# initial structure gives 96 nodes
LogFile [grid qual nodes]

grid remesh

# after remesh, 112 nodes
# because Sentaurus Process adds interface refinement
LogFile [grid qual nodes]

#####
# the lines from above are removed
# to start a new structure
line clear
line x loc=0
line x loc=1
line y loc=0
line y loc=1

region silicon
init !DelayFullD

# this tiny structure has only have 8 nodes
LogFile [grid qual nodes]

grid remesh
# grid remesh gives 44 nodes
LogFile [grid qual nodes]
```

---

## The UseLines and transform Commands

The ticks must be handled in a special manner with the `transform reflect`, `transform stretch`, `transform rotate`, `transform translate` and `transform cut` commands.

### The reflect Command

In the reflected region, the ticks are created after applying lateral inversion along the appropriate plane.

## The stretch Command

On applying `stretch` at a given coordinate in a given direction, the existing ticks in the stretched area are translated by the amount of the stretch. You must insert lines in the stretched area appropriately.

## The rotate Command

When applying `rotate`, the ticks also are rotated and properly transferred between x-ticks, y-ticks and z-ticks.

## The translate Command

The `translate` command shifts the ticks by the specified amount.

## The cut Command

The lines in the part of the structure that is cut are deleted.

---

## Examples

### Testing line Commands

Use the following example to test line commands:

```
line x loc=0 tag=a spacing=0.05
line x loc=0.1 spacing=0.05
line x loc=1 tag=b spacing=0.05
line y loc=0 tag=c spacing=0.01
line y loc=0.6 tag=d spacing=0.1

region silicon xlo=a xhi=b ylo=c yhi=d
init !DelayFullD

deposit oxide thickness=0.002 iso
grid remesh info=2

line y loc=0.026
line y loc=0.027
line y loc=0.028
line y loc=0.029
line y loc=0.025
line y loc=0.024
```

## 10: Mesh Generation

### Data Interpolation

```
line y loc=0.023

grid remesh

deposit poly thickness=0.18 iso
mask name=m1 left=-0.1 right=0.025
etch aniso thickness=0.2 poly mask=m1

struct tdr=linetest
```

## Showing Clearing Lines for a New Structure

Use the following example to show clearing lines and to prepare for another structure definition within the same command file:

```
line x loc=0 tag=a spa=0.125
line x loc=1 tag=b spa=0.125
line y loc=0 tag=c spa=0.125
line y loc=1 tag=d spa=0.125
region silicon xlo=a xhi=b ylo=c yhi=d
init

grid FullD

line clear

line x loc=0 tag=a spa=0.125
line x loc=1 tag=b spa=0.125
line y loc=0 tag=c spa=0.125
line y loc=1 tag=d spa=0.125
region silicon xlo=a xhi=b ylo=c yhi=d
init

line y loc=0.3 spa=0.01

grid FullD
```

---

## Data Interpolation

Sentaurus Process stores a copy of the mesh with all its data before performing any geometry-changing operation. This is the reference mesh used to interpolate data onto the new mesh. In 3D, a mesh is generated only when it is necessary, so you can have multiple `etch`, `deposit`, `photo`, and `strip` commands without the need to remesh in between. When a new mesh is required, data is interpolated from the stored mesh and data.

Data interpolation is performed material-wise. This is important because some nodal data can be discontinuous at material interfaces; for example, segregation causes a jump in concentration at the silicon–oxide interface. In addition, the precise location of an interface can

change slightly due to numeric noise in geometry-moving algorithms. Therefore, it is necessary to allow the data to be interpolated from points in the old mesh nearby, but only from the same material.

Data also can be interpolated from materials that are *Like* materials (that is, the material in the old mesh is *Like* the material in the new mesh, or the material in the new mesh is *Like* the material in the old mesh). When interpolating data at an interface, the preference is to use data from the same region, then data from the same material, and finally data from *Like* materials. If no match is found, then 0 is set for all data at that point.

For data defined on elements, the overlap of elements from the old mesh to the new mesh is used for weighting. Similar to nodal data, interpolation of elements near interfaces uses the region, material, and *Like* material preference order.

Multithreaded interpolation can be used to speed up interpolation in large 3D structures. Because of the memory-intensive nature of interpolation, typically, the performance benefit of multithreading saturates at two threads and can even decrease when using more than four threads. Therefore, for interpolation, the suggested maximum is to use two threads using the command:

```
math numThreadsInterp=2
```

---

## Troubleshooting

Sometimes, the mesh generation step fails and it is not clear what the problem may be. The following are recommendations of where to look when problems arise during meshing:

- Set `InfoDefault` to 2 or higher, for example:

```
pdbSet InfoDefault 2
```

- When Sentaurus Mesh prints the message:

```
"Short edge 1e-8 around points (x1, y1, z1) (x2, y2, z2)"
```

look at the input structure around the coordinates  $(x1, y1, z1)$  or  $(x2, y2, z2)$ , and check whether there is a singularity in that area (a crack, fold, surface overlap, and so on).

Sometimes, these singularities are the product of an etching or a deposition step, and action can be taken to improve the quality of the structure.

- Check the quality of the boundary printed for the steps preceding the mesh generation process. In particular, the following line provides an indication of quality (this is output if `InfoDefault` is 2 or higher):

```
minDihedralAngle: <angle> [near (x1, y1, z1),(x2, y2, z2)] at  
region=Nitride_1.
```

## 10: Mesh Generation

### Troubleshooting

If you see an angle of less than  $3^\circ$  in the geometry, this may indicate a problem in the structure at the given coordinates. The recommendation is then to look at the preceding process steps in Tecplot SV, and to see whether they can be modified to avoid creating the problem.

To visualize the problem area in Tecplot SV, you can create a rectangular zone that can be used as a marker to identify the problem. Select **Data > Create Zone > Rectangular**, and input a box where one of the corners is a coordinate reported by Sentaurus Mesh as problematic. The second corner of the box must be calculated manually to give a box large enough to be seen in the visualization window. Then, hide all materials except the box that you created. Magnify the rectangular zone, and display the material that was reported in the `minDihedralAngle` message. Now, you should see the artifact. Sometimes, you need to rotate the structure around the rectangular box to see what is happening to the geometry.

- In addition to this, you may need to add `!repair` to the `etch` or `deposit` command. This prevents the structure from being repaired and makes it easier to spot the problem in Tecplot SV.
- It is recommended to frequently save snapshots of the boundary file of the structure, especially before all mesh generation operations. This will help you to investigate possible problems in the input to the mesh generator. To accomplish this, use the command:

```
struct tdr.bnd=fileName
```

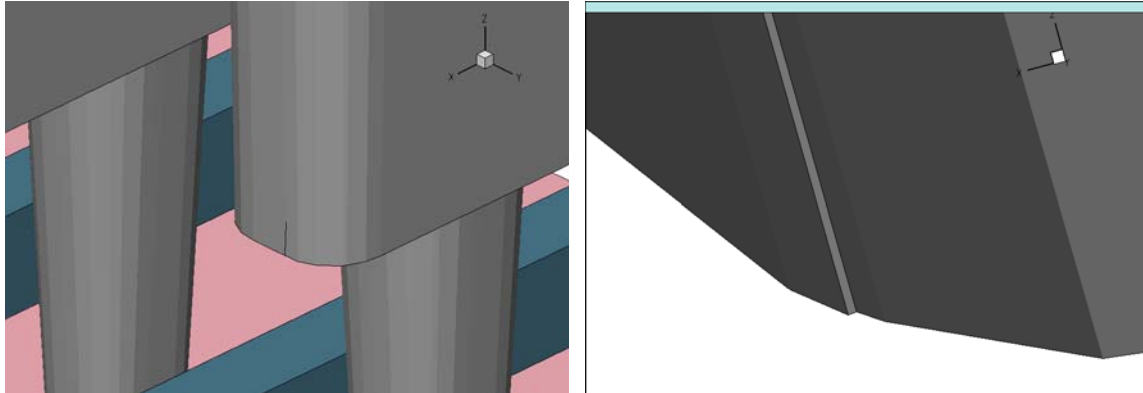


Figure 98 (Left) Example of artifact in geometry and (right) magnification of artifact

*This chapter describes the etching, deposition, and other geometry manipulations available in Sentaurus Process.*

---

## Overview

To perform etching and deposition using Sentaurus Process, seamless interfaces to the following modules have been created:

- MGOALS (1D, 2D, and 3D)
- Sentaurus Structure Editor (3D only)
- Sentaurus Topography and Sentaurus Topography 3D (limited availability)

By default, all operations are performed by the MGOALS library. This is the preferred method for performing geometric etching and deposition because of its robust and flexible algorithms. The etching and deposition operations are always simulated using geometric shapes or simple mathematical formulations; no physical processes are simulated. For a description of the MGOALS interface, see [MGOALS Interface on page 754](#).

Sentaurus Structure Editor is also available in 3D to perform basic and most common geometry-modeling process steps. For a description of the Sentaurus Structure Editor interface, see [Sentaurus Structure Editor Interface on page 767](#).

For physical etch and deposition, Sentaurus Process provides an interface to Sentaurus Topography and Sentaurus Topography 3D. For a description of the interfaces, see [Sentaurus Topography Interface on page 770](#).

---

## Functionality

Sentaurus Process provides a number of etching and deposition operations, in addition to purely geometric operations to help shape the geometry of the devices.

## Etching

The following types of etching are supported (see [Etching on page 711](#) for more details):

- Isotropic
- Anisotropic
- Directional
- Polygonal
- Trapezoidal
- Fourier
- Crystallographic
- Chemical-mechanical polishing (CMP)
- Piecewise linear

## Deposition

The following types of deposition are supported (see [Deposition on page 729](#) for more details):

- Isotropic
- Anisotropic
- Directional
- Polygonal
- Fill
- Fourier
- Crystallographic

## Masks and Photoresist

Masks offer an effect (similar to a masking layer) to limit the etch or deposition process to a certain window or to provide a convenient way to mimic lithographic patterning (see [The mask and photo Commands on page 741](#)).

## Geometry Creation and Transformations

You also can create and insert polygons and polyhedra, or read an existing 3D structure from a file (see [Inserting Polygons in Two Dimensions on page 762](#) and [Inserting Polyhedra in Three Dimensions on page 762](#)).

The shape library provides commands for generating some special shapes in Sentaurus Process (see [Shape Library on page 735](#)).

In addition, several geometric transformations are available including reflection, translation, rotation, flipping, cutting, and stretching (see [Geometry Transformations on page 748](#)).



---

## Etching and Deposition Types and Options

Three main specifications are required for all etching and deposition steps:

- Etch or deposit type
- Material or materials to be etched, or material to be deposited
- Amount of material to be removed or deposited

---

### Etching

The types of available etching are:

<code>type=angles.rates</code>	Etch according to a definition of a piecewise linear etch rate.
<code>type=anisotropic</code>	Etch in the vertical direction only.
<code>type=cmp</code>	Perform CMP. The coordinate of the new surface must be specified as <code>coord</code> .
<code>type=crystal</code>	Angle-dependent etching where etch rate is dependent on the crystallographic direction.
<code>type=directional</code>	Etch in one specific direction only.
<code>type=fourier</code>	Angle-dependent etching where etch rate is a cosine expansion of the etching angle.
<code>type=isotropic</code>	Etch rate is uniform in all directions.
<code>type=polygon</code>	Etch according to a user-supplied polygon (2D only).
<code>type=trapezoidal</code>	Etching allowing undercut and taper angle specifications (2D only), or taper and bottom angle specifications (3D).

**NOTE** To remove materials exposed to the top gas, use the `strip` command instead of the `etch` command. The `strip` command is used specifically for this purpose. It is more straightforward, less prone to user error, and more robust in delivering the expected results:

```
strip Photoresist
```

## 11: Structure Generation

### Etching and Deposition Types and Options

Each etch type requires the setting of parameters particular to that etch type. Many options are available and certain options are available only with certain etch types. [Table 69](#) summarizes the syntax options for each etch type.

Table 69 Options for etch and deposit command syntax (E=etching, D=deposition)

Area	Parameter name	isotropic	anisotropic	directional	cmp	polygon	fourier	crystal	trapezoidal	angles.rates
Rate	rate	ED	ED	ED					E	
	angles.rates									E
	coeffs						ED			
	mat.coeffs						E			
	crystal.rate							ED		
Stop criteria	time	ED	ED	ED			ED	ED	E	E
	thickness	ED	ED	ED					E	
	etchstop	E	E		E		E	E		E
	coord				E					
	etchstop.overetch	E	E		E		E	E		E
	isotropic.overetch		E	E						
Shape	polygon					ED				
	angle								E	
	undercut								E <sup>a</sup>	
	bottom.angle								E <sup>b</sup>	
	bottom.thickness								E <sup>b</sup>	
	direction			ED						
	ambient.rate								E <sup>c</sup>	
Beam	sources						ED			E
	shadowing		E <sup>c</sup> D	ED			ED			E
	shadowing.nonisotropic						ED			
Mesh	ast	ED	ED	ED	E	ED	ED	ED		E
	Adaptive	ED	ED	ED	E	ED	ED	ED		E
Mode	force.analytic	E	E	E						
	force.full.levelset	ED	E	ED			E <sup>d</sup> D <sup>d</sup>	E <sup>d</sup> D <sup>d</sup>	E	
	1D					ED				

- In 2D when not using `force.full.levelset`.
- In 3D when not using `force.full.levelset`.
- When used in conjunction with `force.full.levelset`.
- Full level-set is the default scheme for Fourier and crystallographic.

To specify the etch type, the parameter `type` is used. For some etch types, one of the following keywords can be used instead as a shorthand for specifying `type`: `isotropic`, `anisotropic`, `trapezoidal`, or `cmp`. The amount to be etched is specified as either thickness (by specifying `rate` and `time`) or an etchstop material with `etchstop`.

Etch types have been implemented in Sentaurus Process using three different methods (analytic, fast level-set, and general time-stepping level-set), which are described in [MGOALS Interface on page 754](#).

These methods may require different inputs to perform the steps and may take different effects into account. The method is selected depending on the specified parameters and the structure to be etched.

**NOTE** The simplest and fastest algorithm possible is chosen by default.

If simple isotropic, anisotropic, directional, or CMP etching of a single material is requested and for polygonal etching, an analytic algorithm is tried first. The analytic algorithm is the fastest and most accurate. However, in some cases, the resulting etching front might intersect itself. Because the analytic algorithm cannot handle this situation, the fast level-set method is used.

**NOTE** Although these methods are fast and can handle most simple etching tasks, they do not consider shadowing or visibility effects, and they cannot etch more than one material at a time.

The general time-stepping level-set method is chosen if you specify any rate versus angle-type etching (Fourier or crystallographic), or if you choose to etch different materials at different rates, or if the parameter `force.full.levelset` is specified. In addition, the general time-stepping level-set method can handle multiple etching beams and, optionally, shadowing.

The general time-stepping level-set scheme used in Sentaurus Process has the same limitations as all level-set methods:

- Sharp corners in the evolving front are rounded.
- Small front movement requires a fine level-set mesh, resulting in large memory use and long simulation times.
- The accuracy is limited by the size of the level-set mesh.

Besides the etching type, the materials to be etched and the amount of material to etch must be specified. The amount of material to be etched can be specified in three ways:

- Thickness
- Rate and time
- Using an etch stop

## 11: Structure Generation

### Etching and Deposition Types and Options

The etch rate may be specified using etch beams that are created in the `beam` command. Beams can be used only with the Fourier etch type. If an etch stop is specified, the etching stops as soon as the specified material is exposed to gas.

In addition, a mask specification can be given for all etch types, except CMP, trapezoidal, and polygonal to limit the areas where material is removed.

## Etching Tips

Some tips for etching are:

- If the total etch thickness is exactly the same thickness as the layer to be etched, numeric roundoff errors can cause thin pieces of the material to be retained. You should etch a little more (for example, 0.1%) than the thickness of the layer.
- Etching small thicknesses using a small `isotropic.overetch` or etching large structures can cause MGOALS to allocate a large amount of memory and increase simulation time to solve the level-set equation. The MGOALS parameter `resolution` can be increased for the simplified boundary movement mode, and the parameters `dx` and `dy` can be increased in the general boundary movement mode to reduce memory consumption. However, this may impact the accuracy.

## Etching Type: Isotropic

Isotropic etching removes material at the same rate in all directions. You can specify more than one material to be etched isotropically, in which case, the generalized level-set boundary movement module is invoked.

When isotropic etching uses the level-set method (either fast or general time-stepping), the final surface is obtained by solving a differential equation on a discrete mesh.

**NOTE** To control errors in the fast level-set method, use the `resolution` parameter in the `mgoals` command. For the general etch method, use either `resolution` or the `dx` and `dy` parameters of the `mgoals` command.

An example of a single-material isotropic etch is (see [Figure 99](#)):

```
etch silicon thickness = 0.05 type=isotropic
```

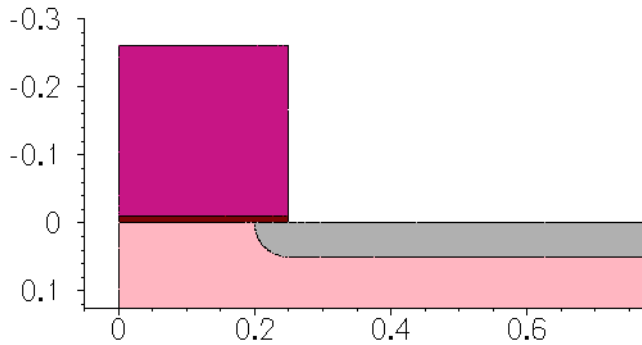


Figure 99 Single-material isotropic etch

An example of a multiple-material isotropic etch is (see [Figure 100](#)):

```
mgoals resolution=0.04  
etch material = {Silicon Oxide Poly} rate = {1.0 1.5 1.0} time = 0.05 \  
type=isotropic info=2
```

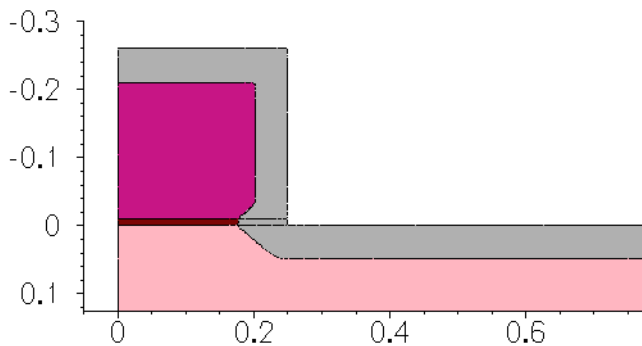


Figure 100 Multiple-material isotropic etch

## Etching Types: Anisotropic and Directional

Anisotropic etching is designed primarily to work with masks or masking layers. It also is frequently used to create spacers. Anisotropic etching etches material away in a direction that

## 11: Structure Generation

### Etching and Deposition Types and Options

is purely vertically downwards. It works well with structures such as those shown in [Figure 101](#).

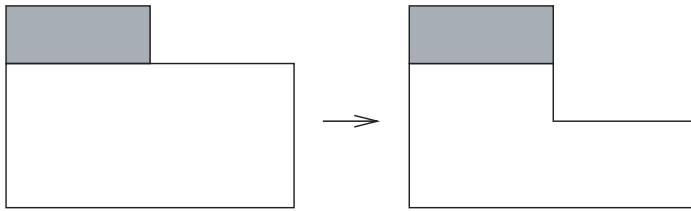


Figure 101 Anisotropic etching

Anisotropic etching can take more than one material if the same rate is specified for all etched materials. This can be useful to create multiple spacers since it does not produce small gaps which are hard to avoid when etching one spacer at a time. If you want to use different rates for each material then a better alternative can be Fourier etching.

If anisotropic etching is performed to etch the shaded region in the structure shown in [Figure 102](#), instabilities can arise. The resulting structure can be very different depending on the numeric roundoff errors.

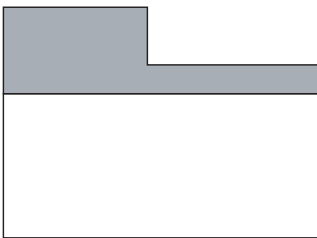


Figure 102 For this structure, anisotropic etching would not be stable

Anisotropic operations are sensitive to numeric noise at vertical or nearly vertical walls.

If the `etch` command is supposed to remove the entire layer, care must be taken to overetch by a small amount to prevent thin regions remaining due to numeric roundoff error.

**NOTE** It is more robust and better to use the `strip` command to remove all exposed layers of a certain material.

The directional etching method is similar to the anisotropic method. In this case, the specified etching rate is applied in the direction of the etching beam. Visibility effects are not considered. The etching window is determined from user-defined masks and from the exposed areas of the etched material (see [Figure 103 on page 717](#)).

For example:

```
etch silicon thickness = 0.05 type=anisotropic
```

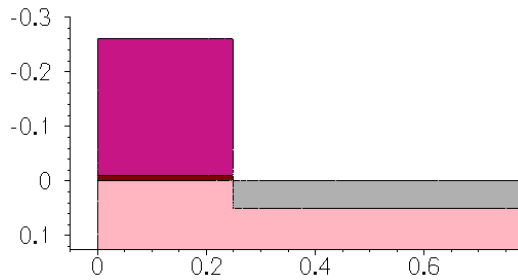


Figure 103 Anisotropic etching

In the next example, directional etching is demonstrated. The parameter `direction` sets the direction of the etching beam by setting values for  $\{x\ y\ z\}$ . This direction vector is normalized to 1.0 before being used by the etching module.

```
etch material=silicon rate = 0.05 time=1.0 type=directional direction = {1 1}
```

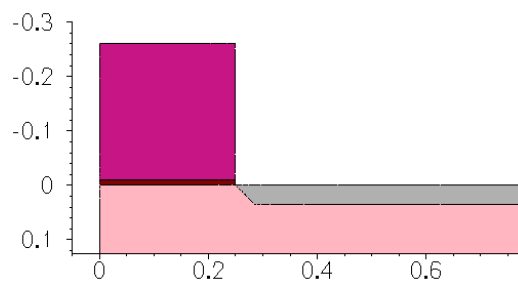


Figure 104 Directional etching (angled wall)

```
etch material=silicon rate = 0.05 time=1.0 type=directional direction = {1 -1}
```

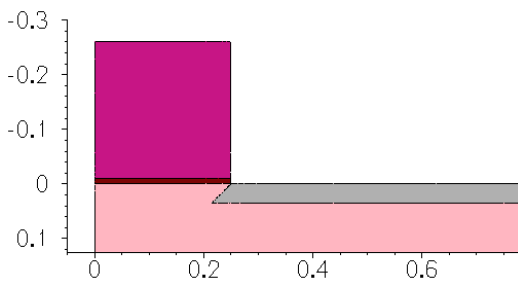


Figure 105 Directional etch undercutting

## 11: Structure Generation

### Etching and Deposition Types and Options

## Etching Types: Polygonal and CMP

Polygonal etching provides a way of modifying a region without having to define etching rates or the direction of the etch. The specified polygon is used to intersect the mesh elements. The elements inside the polygon are replaced by gas.

CMP is handled as a special case of polygonal etching. Mesh elements are intersected at the specified coordinate. All elements of the specified material above the coordinate are reassigned to gas.

```
etch type=cmp coord = 0.05 material=all
```

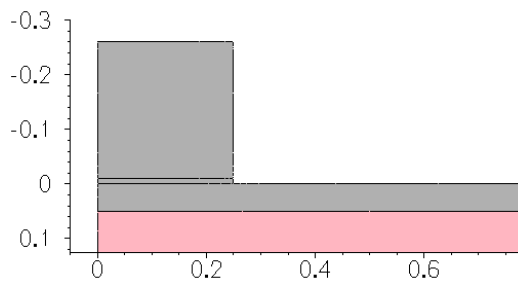


Figure 106 CMP

```
# Etch with polygon given as x1 y1 x2 y2 ... xn yn  
etch type=polygon material=silicon polygon= {-0.1 0.1 0.1 0.1 0.1 0.6 -0.1 0.6}
```

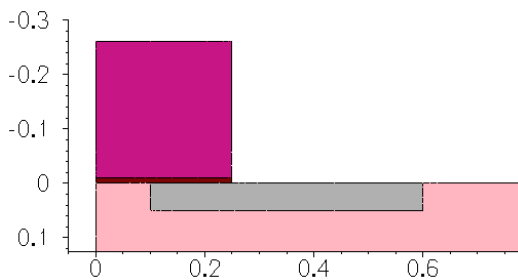


Figure 107 Polygonal etch



## Etching Type: Fourier

In Fourier etching, the etching rate is a function of the angle between the incident etching beam and the normal vector of the surface being etched. This allows for reasonably directional etching with control of the slope of sidewalls. The coefficients  $A_n$  are defined using `coeffs` (for a single-material etch) or `mat.coeffs` (for a multimaterial etch), and the etching rate is computed according to:

$$\text{etch rate} = \sum_{i=0}^m \text{factor}_i \sum_{j=0}^n A_j \cos^j \theta_i \quad (943)$$

where:

- $\theta_i$  is the angle between the incident beam  $i$  and the normal to the surface being etched.
- $\text{factor}_i$  is the `factor` given in the `beam` command for beam  $i$ .

Any number of coefficients  $A_j$  can be given for each material. If the parameters  $A_j$  are chosen such that negative etch rates would result in some slope angles, no etching will occur on the parts of the surface that have that slope. It is common to set the parameters  $A_j$  such that the etch rate for angles less than a certain angle are positive and drop below zero (resulting in no etching) above that angle. This produces a trench with a rounded bottom and a sidewall given by the angle where the etch rate drops to zero.

Fourier etching uses the full level-set model formulated after Lax–Friedrichs. This formulation shows good stability, leading to good accuracy of etching wall-angle control. The Lax–Friedrichs formulation results in slightly less corner sharpness.

### Etching Beams

The `beam` command is used to define the direction and relative strength of etching beams to be used with Fourier etching. The syntax is:

```
beam name=<beam_name> incidence=<angle> | direction= {<x> <y> <z>}
      factor=<relative_strength>
```

The angle of incidence of each beam is specified either by the `incidence` parameter in the `beam` command (`incidence=0` defines a vertical beam), or by a `direction` vector, which is normalized automatically to unit length. To be clear, the angle  $\theta_i$  in Eq. 943 is measured from the surface perpendicular to the angle of incidence for beam  $i$ . The relative strength `factor` is used to mix the strength of different beams. Each etching beam must be given a unique name.

Etching beams are assumed to be collimated, that is, a slight angular spread of beam direction is not considered.

## 11: Structure Generation

### Etching and Deposition Types and Options

The parameter `sources` of the `etch` command specifies the list of names of etching beams to be used in an etch operation.

A Fourier etching example follows (see [Figure 108](#)):

```
mgoals resolution=0.02
beam name=srcl direction = {1 0 0} factor=1
etch material=silicon type=fourier sources = srcl coeffs = {0 0 1.0} time=0.05
```

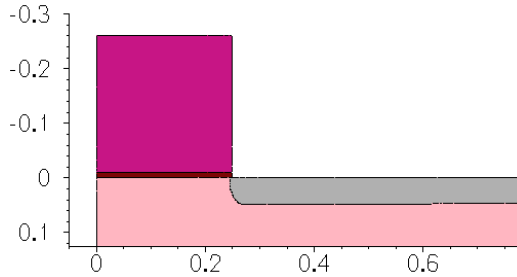


Figure 108 Fourier etching

Through the selection of Fourier coefficients, the angle of the etching wall can be controlled to a large degree. In particular, the first coefficient in the list,  $A_0$ , corresponds to the equivalent of the rate of isotropic etching. The second coefficient in the list,  $A_1$ , corresponds approximately to the equivalent of the rate of anisotropic or directional etching. The approximate formula for determining the etch wall angle is given as:

$$\varphi \approx \cos^{-1} \frac{-A_0}{A_1} \quad (944)$$

where  $\varphi$  is the angle of the etch wall measured from the horizontal plane. For example, the choice of  $A_0 = -0.5$  and  $A_1 = 0.7071$  results in an etch wall at an angle of approximately  $45^\circ$  from the horizontal as shown in [Figure 109 on page 721](#):

```
beam name=srcl direction= {0.1 0 0} factor=1
mgoals full.resolution= 0.05 resolution= 0.05
etch material= {silicon} type=fourier sources= {srcl} coeffs= {-0.5 0.7071} \
time=1.0.
```

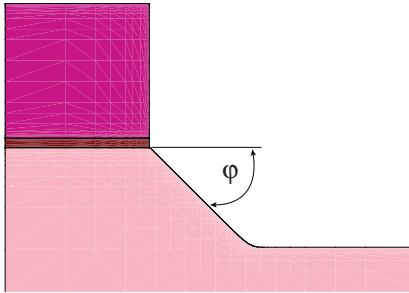


Figure 109 Example of Fourier etch

Another Fourier etching example shows the functionality in 3D and how multiple rates for multiple materials are specified using `mat.coeffs`. For 3D Fourier etching, also use the command `sde off`.

Etching coefficients chosen for this example are illustrative and may not be physically meaningful:

```
beam name=src1 direction= {1 0 0} factor=1
mgoals dx=0.1 dy=0.1 dz=0.1
sde off
etch info=10 sources= {src1} mat.coeffs= { Silicon= {-1 2} \
  Nitride= {-0.7 1.2} Oxide= {0.01} PolySilicon= {-0.05 0.2} } type=fourier \
  remesh=false time=1
```

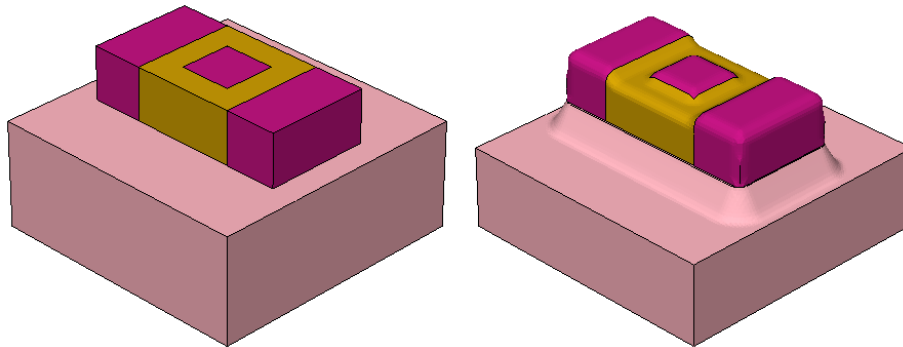


Figure 110 Three-dimensional multimaterial Fourier etching example before etching (*left*) before etching and (*right*) after etching

Currently, in 3D Fourier etching, shadowing is not implemented as it is in two dimensions.

## 11: Structure Generation

### Etching and Deposition Types and Options

#### Keywords shadowing and shadowing.nonisotropic

The keyword `shadowing.nonisotropic` is used instead of `shadowing` when you want to allow only the 0th-order Fourier coefficient to etch areas where the beam is shadowed. The keyword `shadowing` prevents all Fourier etching in areas shadowed from the beam; while the keyword `shadowing.nonisotropic` prevents only the Fourier coefficients of order one and higher from etching in areas where the beam is shadowed.

Be aware that even when this parameter is specified, the 0th-order Fourier coefficient  $A_0$  should continue to etch areas where the beam is shadowed. This permits a pseudo-isotropic etching that is independent of shadowing, while at the same time the full Fourier etching occurs only in areas where the beam is not shadowed.

#### Etching Type: Crystallographic

The parameter `crystal_rate` defines etching rates for different crystallographic orientations. These rates are used for `type=crystal`. For details on wafer orientation, see [Defining the Crystal Orientation on page 71](#). Crystallographic etching rates are specified in `crystal_rate` as a list of Miller indices and corresponding etching rates. The currently accepted indices are  $\langle 100 \rangle$ ,  $\langle 110 \rangle$ , and  $\langle 111 \rangle$ , as in the following example:

```
crystal_rate= {"<100>" =0.8 "<110>" =0.35 "<111>" =0.003}
```

Interpolation of the rate at a given point along the etch front is calculated as a linear combination of the  $\langle 100 \rangle$ ,  $\langle 110 \rangle$ , and  $\langle 111 \rangle$  rates weighted by the component of the etch front normal vector along the corresponding crystallographic direction.

**NOTE** You must add a space between the double quotation mark (") after the orientation and the equal sign.

A crystallographic etching example follows (see [Figure 111 on page 723](#)):

```
etch material=silicon type=crystal crystal_rate= {"<100>" =1.0 "<110>" =0.5 \  
"<111>" =0.001} time=0.25
```

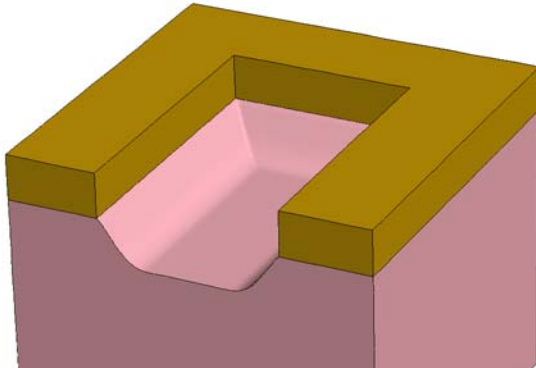


Figure 111 Crystallographic etching

## Etching Type: Trapezoidal

The trapezoidal etch model provides a simple but flexible approximation to a number of real etching processes. The location of the etch is determined by masking layers (that is, layers of nonetchable material that, if nonexistent, can be easily created with the `photo` command) and, therefore, does not require mask-dependent coordinates to be specified.

The trapezoidal model uses the following parameters to specify the shape of the region to be removed:

- `thickness` specifies the vertical depth (or a combination of rate and time).
- `angle` specifies the angle (in degrees) of the resulting sidewalls.
- `undercut` specifies the horizontal penetration of the etch under the edges of the masking layer. It only works in two dimensions.
- `bottom.angle` and `bottom.thickness` specify the angle and thickness of the sidewalls for a second etching after `thickness` and `angle` are already etched (3D only).

These parameters can be used to approximate a number of real etching processes including:

- Combinations of vertical and isotropic etches.
- V-groove etches.
- Etches that produce retrograde sidewall profiles.

**NOTE** Trapezoidal etching is not supported by Sentaurus Structure Editor. Consequently, the command `sde off` must be issued.

## 11: Structure Generation

### Etching and Deposition Types and Options

#### Trapezoidal 2D Etching

An etch with the trapezoidal model is performed in three steps:

1. A vertical etch to depth `thickness` is performed. This etch does not apply to portions of the surface that are masked by nonetchable materials or shadowed by etchable or nonetchable materials; nor is it used on segments of the surface that form an angle greater than `angle` to the horizontal.
2. A horizontal etch is performed. Surfaces that were exposed at the start of Step 1 are etched horizontally by the distance `undercut`. Surfaces that were exposed during Step 1 are etched by a distance proportional to the length of time between when they first became exposed and the end of Step 1. Therefore, a sidewall exposed three-fourths of the way into Step 1 is etched horizontally by one-fourth of `undercut`. (An exception is made when an `angle` greater than  $90^\circ$  is specified; this case is described below.)
3. Where overhangs of etchable material are present at the end of Step 2, a vertical upwards etch (that is, in the direction) is performed. On surfaces that were exposed at the start of Step 2, this etch is to a distance `undercut`. On surfaces that were first exposed during the course of Step 2, the distance of this etch is reduced in proportion to the time from the start of Step 2. This step approximates the undercutting of the mask due to the isotropic component of the etch.

When the `thickness`, `angle`, and `undercut` parameters satisfy the relationship:

$$\text{thickness} = \text{undercut} \cdot \tan(\text{angle}) \quad (945)$$

the etch approximates a vertical etch with an isotropic component. This is the case whenever two or fewer of the parameters `thickness`, `angle`, and `undercut` are specified with the option `Trapezoidal.Etch.Undercut` set to 1 (default is 0):

```
pdbSet Grid Trapezoidal.Etch.Undercut 1
etch material=silicon type=trapezoidal thickness=0.25 undercut=0.1
```

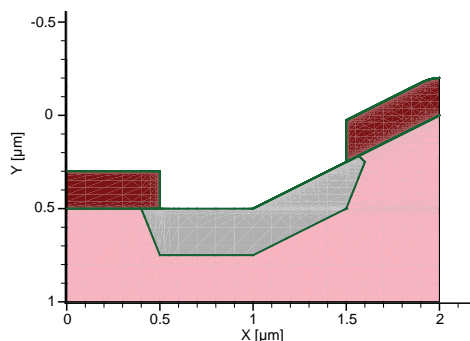


Figure 112 Trapezoidal etching example 1

The left half of [Figure 112 on page 724](#) shows the result when etching a planar substrate. The etch region is a trapezoid of depth `thickness`, extending a distance `undercut` beneath the mask edge, and with a sidewall slope of `angle` degrees. The right half of [Figure 112](#) shows the result when etching a nonplanar surface.

Step 1 of the sequence etches the exposed surface vertically to a depth of `thickness` micrometers. Step 2 etches the resulting sidewall in the horizontal direction, producing an undercutting of the mask and the sloped sidewall. In this case, Step 3 also has an effect, etching upwards from the undercut region. Therefore, the hook in the final silicon profile is the result of approximating the isotropic component of the etch. In every case, the intersection between the bottom of the etch region and the sidewall occurs directly under the edge of the mask.

[Figure 113](#) and [Figure 114](#) show what happens when [Eq. 945](#) is not satisfied.

```
etch material=silicon type=trapezoidal thickness=0.3 undercut=0.1 angle=45
```

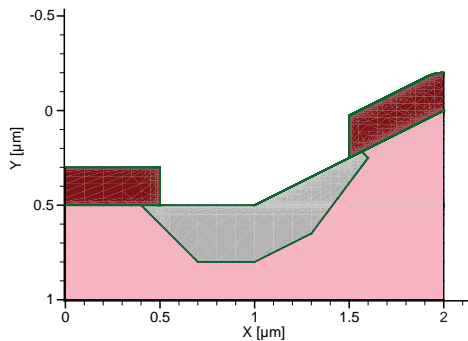


Figure 113 Trapezoidal etching example 2

```
etch material=silicon type=trapezoidal thickness=0.3 undercut=0.1 angle=135
```

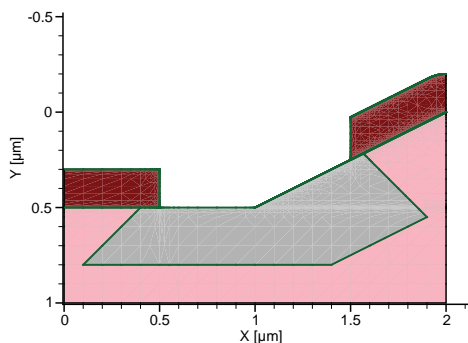


Figure 114 Trapezoidal etching example 3

In [Figure 113](#), you have  $\text{thickness}/\text{undercut} < \tan(\text{angle})$ . In this case, the sloped sidewall of the etch extends out under the opening in the mask. The intersection between the bottom of the etch region and the sidewall is no longer directly beneath the edge of the mask. If the mask opening is narrow enough, the bottom of the etch region disappears entirely, resulting in a V-groove etch. To produce this etch shape, Step 1 of the etch process is modified to reduce the

## 11: Structure Generation

### Etching and Deposition Types and Options

depth of the vertical etch near the edges of the mask opening. Note that, in this situation, even the smallest amount of nonetchable material can produce a triangular mound of unetched material in the final structure.

Figure 114 on page 725 shows the case with an angle greater than  $90^\circ$ . In this case, the bottom of the etched region is wider than the opening in the masking layer, producing overhanging sidewalls. This etch is accomplished by modifying Step 2 of the procedure to etch further horizontally at the bottom of the sidewalls formed by Step 1 than at the top. The apparent etch depth of  $0.5\ \mu\text{m}$  at the right side of the mask opening is the result of a  $0.3\ \mu\text{m}$  vertical etch of the original sloped surface (Step 1) followed by a  $0.4\ \mu\text{m}$  horizontal etch of the sloped “bottom wall” that results from Step 1.

### Trapezoidal 3D Etching

There are two possible cases for trapezoidal 3D etching:

- A thickness (or rate and time) and an angle (optional) are specified. If angle is not specified, it is considered to be  $90^\circ$  (vertical). In contrast with case 2, angle allows any value between  $0^\circ$  and  $180^\circ$ . Figure 115 contains examples for both cases.
- A thickness (or rate and time) and an angle (optional) plus bottom.thickness and bottom.angle (optional) are specified. If angle is not specified, it defaults to  $90^\circ$  (vertical). Here, a special condition applies: angle must be greater than or equal to  $90^\circ$ , while bottom.angle must be smaller than or equal to  $90^\circ$ . In other words, the *first etching* penetrates behind the mask, while the second one does the opposite. Figure 116 on page 727 shows an example of this type.

**NOTE** For 3D trapezoidal etching to succeed, the initial etching surface must be more or less flat.

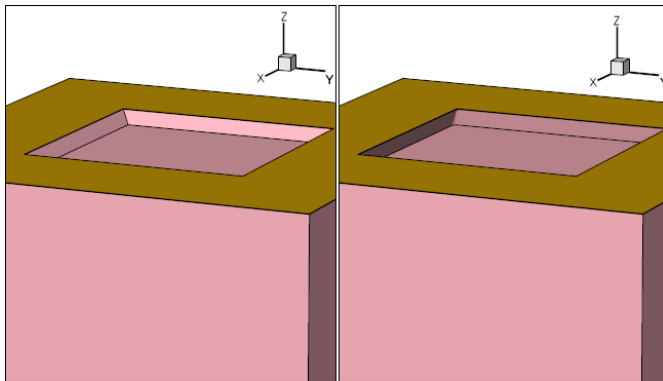


Figure 115 Trapezoidal 3D etching: (left) angle=45 thickness=0.3 and (right) angle = 110, thickness=0.44



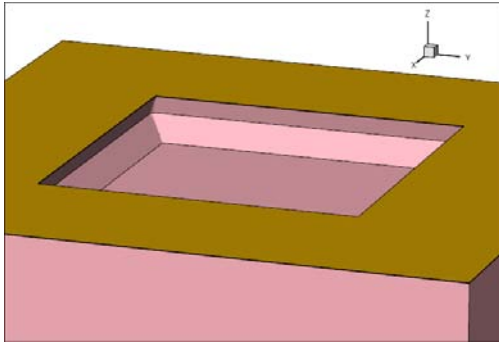


Figure 116 Trapezoidal 3D etching produced with the options `angle=110` `thickness=0.3` `bottom.angle=45` `bottom.thickness=0.400`

### Trapezoidal Etching Using `force.full.levelset`

When the keyword `force.full.levelset` is specified in conjunction with trapezoidal etching:

- Etch depth is controlled by rate and time, not by thickness.
- The parameter `ambient.rate` is used to approximate the underetch effect otherwise available in the non-`force.full.levelset` case controlled in 2D by `undercut`. If `undercut` is specified, `ambient.rate` will be approximated by `undercut/time`, and a warning message will be issued. The parameter `ambient.rate` also approximates underetching, controlled in three dimensions in the non-`force.full.levelset` case by the combination of `angle`, `bottom.angle`, and `bottom.thickness`.
- The parameters supported by the level-set solver such as `shadowing` become available.
- An additional parameter `roundness` (default value 1.0) can be used to increase the curvature of etching sidewalls.

### Etching Type: Piecewise Linear

In piecewise linear etching, the etch rate is a user-defined piecewise linear function of the angle between the incident etching beam and the normal vector of the surface being etched. You define the points of angle versus rate on a material-by-material basis, as per the following syntax:

```
angles.rates= { \  
  materialA = { angleA0 rateA0 angleA1 rateA1 ... angleAn rateAn } \  
  materialB = { angleB0 rateB0 angleB1 rateB1 ... angleBn rateBn } \  
  ...  
}
```

where  $\text{angle}_{n-1} \leq \text{angle}_n$ .

## 11: Structure Generation

### Etching and Deposition Types and Options

The rates and angles are interpreted as follows:

- Angles are given in degrees in the range  $[0^\circ, 180^\circ]$ .
- The rate for  $\text{angle} < \text{angle}_0$  will be  $\text{rate}_0$ , and the rate for  $\text{angle} > \text{angle}_n$  will be 0.
- The rate is calculated as the linear interpolation of the nearest two angle/rate pairs within which the angle lies.

While Fourier etching and trapezoidal etching also define the etch rate according to the angle between the beam direction and the surface normal, a piecewise linear function is a more general parameterization of etch rate versus angle that users control directly.

### Etching Beams

The `beam` command defines the direction and relative strength of etching beams to be used with piecewise linear etching (see [Etching Beams on page 719](#)).

The parameter `sources` of the `etch` command specifies the list of names of etching beams to be used in an etching operation.

### Example of Piecewise Linear Etching

This example is a piecewise linear etching (see [Figure 117](#)):

```
beam name=srcl direction= {1 0 0} factor=1
etch type=angles.rates sources=srcl time=0.2 \
  angles.rates= { Silicon= { 25 1.0 45 0.3 } }
```

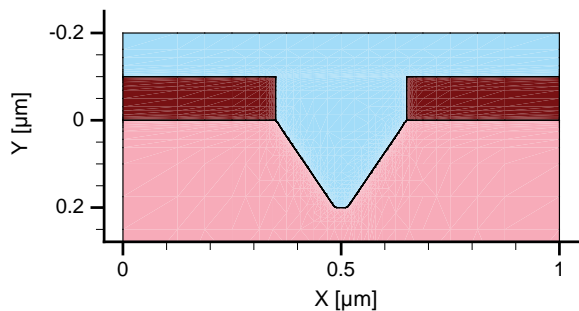


Figure 117 Piecewise linear etching

The piecewise linear function must be defined by users as smoothly as possible, avoiding discontinuous changes, to ensure well-defined level-set results.

---

## Deposition

To specify the deposition type, use either the parameter `type` or one of the parameters `anisotropic`, `isotropic`, `fill`, or `fourier`. To specify the thickness of the deposited layer for isotropic and anisotropic deposition, use either the parameter `thickness`, or the `rate` and `time` parameters. Besides the deposition type and thickness, you must specify the material to be deposited (only one material is allowed per `deposit` command). To do this, specify the material name in the command or the parameter `material=<material_name>`.

The following deposition types are supported:

<code>type=anisotropic</code>	Performs anisotropic deposition.
<code>type=isotropic</code>	Performs isotropic deposition.
<code>type=fill</code>	Performs a fill of the structure with the specified <code>material</code> up to the coordinate specified with the parameter <code>coord</code> .
<code>type=fourier</code>	Performs Fourier deposition.
<code>type=polygon</code>	Performs a polygonal deposition which requires the <code>polygon</code> argument. The specified polygon is used to intersect all mesh elements of material gas. Then, elements inside the polygon are assigned to the specified material. (Not available in MGOALS3D.)
<code>anisotropic</code>	Equivalent to <code>type=anisotropic</code> .
<code>isotropic</code>	Equivalent to <code>type=isotropic</code> .
<code>fill</code>	Equivalent to <code>type=fill</code> .
<code>fourier</code>	Equivalent to <code>type=fourier</code> .

The number of steps for a deposition is specified as `steps=<n>`. The specified `time` or `thickness` is subdivided accordingly. Subdividing a deposition into several steps might be useful if stresses are initialized in the deposited layer. A stressed film of a given thickness can be deposited at the same time or in several steps. Sentaurus Process simulates stress rebalancing after each deposition step. Multistep deposition is known to generate more realistic stress profiles compared to depositing the entire layer and then performing one stress rebalancing calculation.

By default, the material is deposited on the surface exposed to the upper gas region. If the structure has buried gas bubbles, they will be left untouched. To deposit inside those gas bubbles specify the `fill.buried` parameter in the `deposit` command.

## 11: Structure Generation

### Etching and Deposition Types and Options

## Mask Naming

The name of a mask also can be specified in the `deposit` command. In this case, the material is deposited outside the specified mask. Deposition inside a mask requires the mask to be inverted by specifying the parameter `negative` in the `mask` command defining the mask (see [Photoresist Masks on page 744](#)).

For deposition, the analytic method, the fast level-set method, and the full level-set method are available. In 2D, the analytic method is the preferred method for performing deposition, and the level-set method is used when the analytic method is not possible because a front collision is detected. In 3D, the analytic method is used for anisotropic deposition, the fast level-set method is used for isotropic deposition, and the full level-set method is used for Fourier deposition.

In the newly deposited region, constant field values can be initialized. For isotropic deposition, you can define piecewise linear solution fields as a function of the distance from the original surface.

## Deposition Type: Isotropic

For simple conforming deposition, the boundary is offset an equal distance in all directions.

An isotropic deposition example follows (see [Figure 118](#)):

```
deposit nitride thickness = 0.05 type=isotropic
```

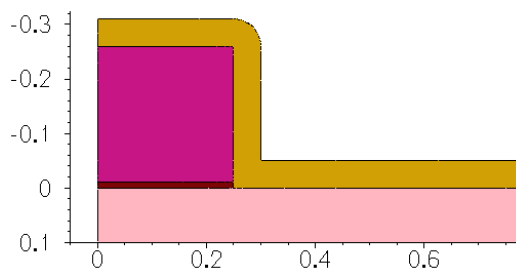


Figure 118 Isotropic deposition

## Deposition Types: Fill and Polygonal

Fill is a special case of polygonal deposition. The mesh elements of material gas are intersected at the specified coordinate. Gas elements below the coordinate are reassigned to the specified material.

**NOTE** Polygon deposition is not available in MGOALS3D.

Figure 119 is a polygonal deposition example:

```
deposit type=polygon material=nitride polygon= {0.1 0.1 0.1 0.6 -0.31 \
0.6 -0.31 0.1}
```

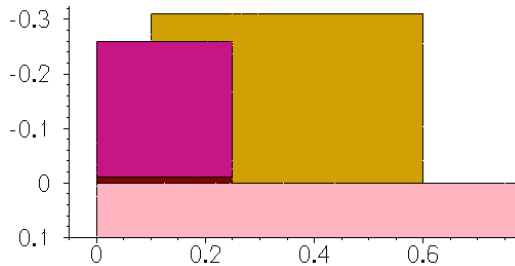


Figure 119 Polygonal deposition

Figure 120 shows a fill example:

```
deposit material=nitride type=fill coord= -0.31
```

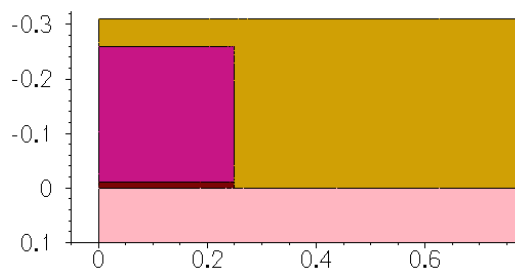


Figure 120 Fill example

## Deposition Type: Crystallographic

Crystallographic deposition takes advantage of the full level-set method to grow single materials whose rate of growth is determined by the crystallographic directions. The crystal is assumed to be cubic regardless of the material being deposited. Deposition rates can be set for the  $\langle 100 \rangle$ ,  $\langle 110 \rangle$ , and  $\langle 111 \rangle$  directions. These rates will be applied to their respective equivalent directions based on cubic symmetry, for example, the  $\langle 100 \rangle$  rate will apply to the  $\langle 010 \rangle$ ,  $\langle 001 \rangle$ ,  $\langle -100 \rangle$ ,  $\langle 0-10 \rangle$ , and  $\langle 00-1 \rangle$  directions.

Figure 121 on page 732 is a crystallographic deposition example:

```
deposit type=crystal material=nitride time = 0.05 \
crystal.rate = { <100> = 1.0 <110> = 0.1 <111> = 0.05 }
```

## 11: Structure Generation

### Etching and Deposition Types and Options

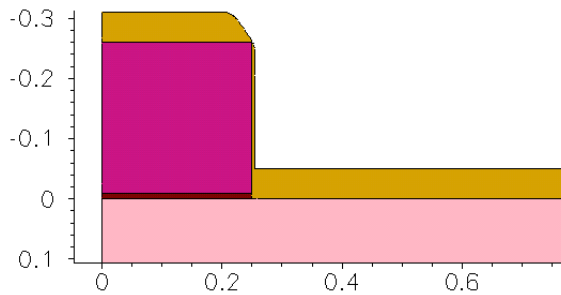


Figure 121 Crystallographic deposition (vertical direction is  $\langle 100 \rangle$ , lateral direction is  $\langle 011 \rangle$ )

Crystallographic deposition also can be simulated using an atomistic technique (see [Epitaxial Deposition on page 507](#)).

### Deposition Type: Fourier

Fourier deposition takes advantage of the full level-set method to grow single materials whose rate of growth is defined by a function of the angle between the surface normal of the material boundary and the deposit beams. The definition and calculation of the deposit shape are exactly analogous to the case of Fourier etching as described in [Etching Type: Fourier on page 719](#).

For Fourier deposition, first, define the deposition beam in the same way as in Fourier etching:

```
beam name=<beam_name> incidence=<angle> | direction= {<x> <y> <z>}
factor=<relative_strength>
```

Use the `sources` and `coeffs` parameters in the same way as in Fourier etching, shown in the following Fourier deposition example:

```
beam name=srcl direction= {1 0 0} factor=1
deposit nitride time=0.2 fourier sources= {srcl} coeffs= { -0.3 0.7 }
```

The `coeffs` parameter has units of  $\mu\text{m}/\text{minute}$  and, by default, `time` is given in units of minutes. To use Fourier deposition in 3D, additionally use the following command to override the default Sentaurus Structure Editor deposit method:

```
sde off
```

**NOTE** The relationship between the `A0` and `A1` parameters in Fourier deposition can be used to create a good reproduction of the TSUPREM-4 deposit parameter `ANISOTRO` by using the formula  $A1/A0 = ANISOTRO - 1$ .

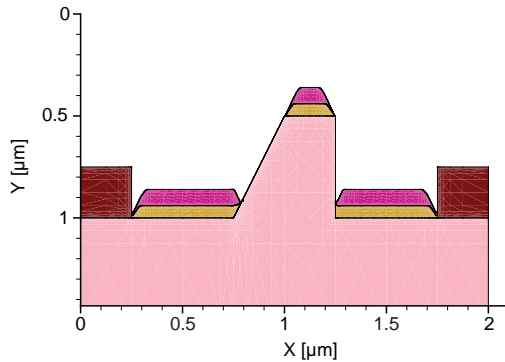


Figure 122 Two-dimensional Fourier deposition: for purposes of illustration, nitride is deposited selectively on silicon using Fourier deposition and, then, an additional Fourier deposition step adding polysilicon is performed using nitride as the selective deposit material

## Selective Deposition

Selective deposition is optionally available. Using the `selective.materials` parameter, you can select one or more materials to seed growth of the overlayer. When using 2D or 3D MGOALS, multiple `selective.materials` can be specified. In 3D SDE mode, only one material can be specified in the `selective.materials` list. Selective deposition can be used with isotropic, anisotropic, or Fourier deposition types.

## Fields in Deposited Layers

For isotropic deposition, piecewise linear fields can be specified in the deposited layer. A `doping` command must be used for each field; each `doping` command must assign a unique name. A list of names of the doping is then specified in the parameter `doping` of the `deposit` command as a string array:

```
doping name=strainGe field=Germanium depths= {0 0.1} values= {1e22 1e22}
deposit material= oxide doping= {strainGe} type= isotropic \
thickness=0.1
```

These commands create a linear germanium field in the newly deposited oxide layer. Depth 0 corresponds to the initial surface (the bottom of the new layer).

Constant field values can be defined for all types of deposition as follows:

```
deposit material= oxide type= isotropic thickness=0.1 \
fields.values= {Vacancy=1e10 Germanium=2e22}
```

## 11: Structure Generation

### Etching and Deposition Types and Options

**NOTE** To create layers with intrinsic stress, use the field names `StressELXX`, `StressELXY`, `StressELYY`, `StressELZZ`, `StressELYZ`, and `StressELXZ`. It is not necessary to specify all components of stress. Those that are not specified are assumed to be initially at zero. If stresses are added in this way, they will be rebalanced after the deposition is completed. The actual value of the stress may differ from the value that was deposited.

Constant concentrations can be defined for known solution fields (known solution fields must have been defined before the `deposit` command, either in the `SPROCESS.models` file or the command file of the user) as:

```
deposit material= {oxide} type= isotropic thickness= 0.1 Vacancy \  
concentration=1e10
```

---

## Stress Handling

In addition to optionally including an automatic ramp-up or ramp-down before etching and deposition, by default, Sentaurus Process automatically rebalances the stresses after etching and deposition. This updates the stress fields at the temperature of the etch or deposit step based on the new geometry.

For the best stress results, it is necessary to control the temperature history. This includes thermal ramp-up to process temperature, back to room temperature, and similarly ramp-up and ramp-down for etch, and also for deposition. However, as a minimum, the elastic stress rebalancing can be handled automatically by switching on the stress history (see [Chapter 9 on page 629](#) and [Automated Tracing of Stress History on page 664](#)).

It is sometimes useful to switch off this stress rebalancing step in 3D because the rebalance triggers a new mesh to be created and, in 3D, meshing is delayed until it is needed. Therefore, if you are more concerned about simulation time than stress accuracy, you should specify:

```
pdbSet Mechanics EtchDepoRelax 0
```

to allow multiple etch and deposit steps to be performed without a mesh being generated in between.



---

## Shape Library

The shape library provides commands for generating some special-shaped polyhedra in Sentaurus Process. These shapes are created using Sentaurus Structure Editor. The shape library is an interface to use those shapes in Sentaurus Process.

There are two ways to use the shapes from the shape library: MGOALS mode or SDE mode. In MGOALS mode, polyhedra are created using Sentaurus Structure Editor. The generated polyhedra then can be inserted into a Sentaurus Process structure using the `insert` command. The MGOALS mode is activated with the command `sde off`.

In SDE mode, polyhedra are not created directly. Instead, the Sentaurus Structure Editor structure itself is modified by inserting the shapes (replacing other materials). To activate the SDE mode, use the command `sde on`.

In both modes, the correct coordinate transformation for the UCS (specified using `math coord.ucs`) and for the DF-ISE coordinate system (default, or specified using `math coord.dfise`) is applied.

The commands available in the shape library are:

- `PolyHedronSTI` creates a shallow trench isolation (STI)-shaped polyhedron.
- `PolyHedronSTIacc` creates an STI concave active corner-shaped polyhedron.
- `PolyHedronSTIaccv` creates an STI convex active corner-shaped polyhedron.
- `PolyHedronCylinder` creates a cylinder-shaped polyhedron.
- `PolygonWaferMask` creates a wafer mask polygon.
- `PolyHedronEpiDiamond` creates an epitaxial diamond-shaped polyhedron.

Additional commands that create parameterized custom shapes can be defined by users using the scripting capabilities of Sentaurus Process and Sentaurus Structure Editor.

### PolyHedronSTI

The syntax of the `PolyHedronSTI` command is:

```
PolyHedronSTI name direction X0 Y0 Depth Zmin Zmax Tsti Asti Hsti Rd Rb Ru  
[material]
```

where:

- The `name` parameter is set to the name for the polyhedron.
- The `direction` parameter can be set to `left`, `right`, `front`, or `back`, which tells the facing direction of the STI polyhedron.

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- The optional `material` parameter is used to specify the material of the inserted shape in the SDE mode. In the MGOALS mode, the material of the inserted shape can be specified in the `insert` command.
- For other parameters, see [Figure 123](#).

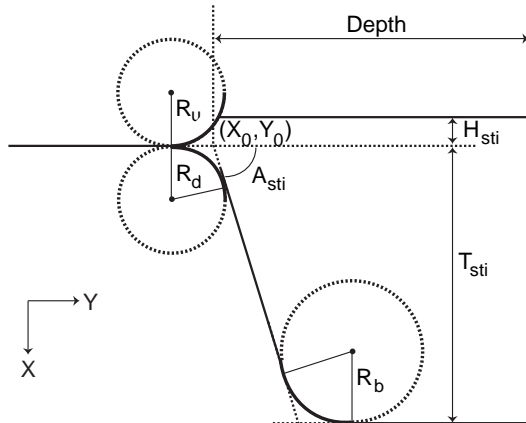


Figure 123 Parameters for generating STI-shaped polyhedron

[Figure 124](#) shows some generated STI shapes in different directions. [Figure 125 on page 737](#) shows STI shapes with different  $T_{sti}$  and  $R_b$  values.

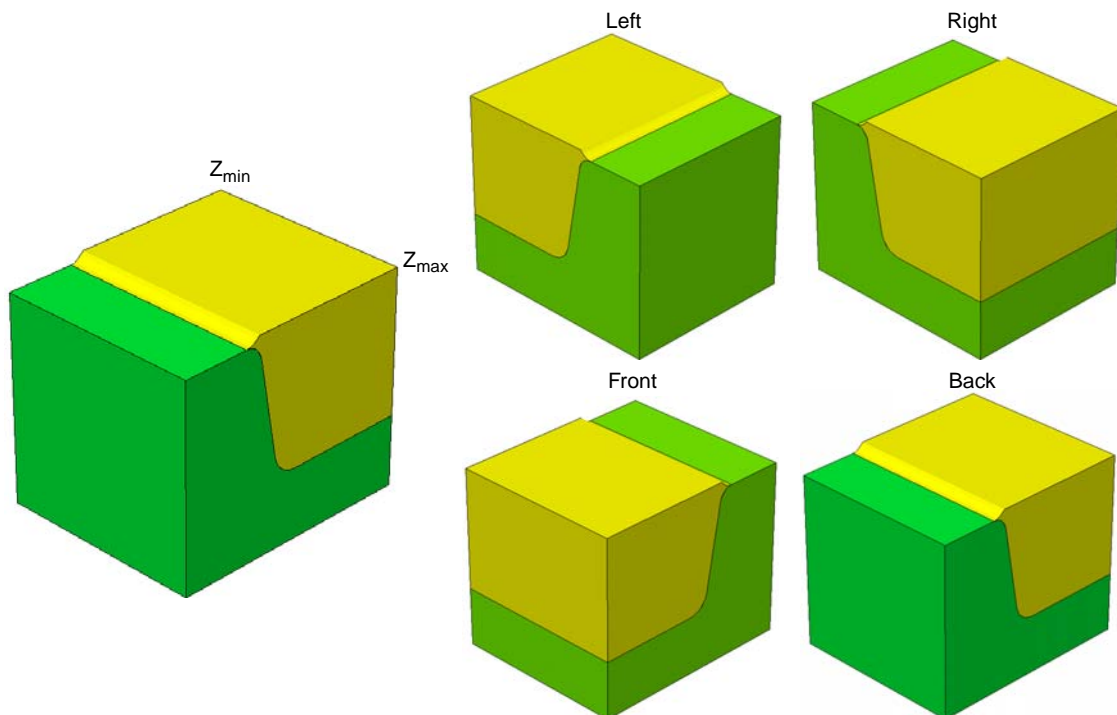


Figure 124 STI-shaped polyhedra in different directions

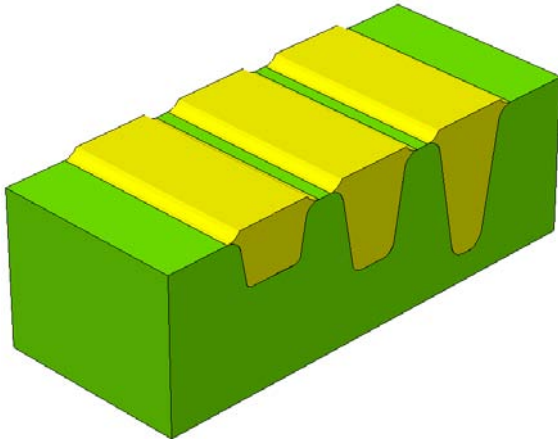


Figure 125 STI-shaped polyhedra with different Tsti and Rb

## PolyHedronSTIaccc

The syntax of the PolyHedronSTIaccc command is:

```
PolyHedronSTIaccc name direction X0 Y0 Z0 Tsti Asti Hsti Rd Rb Ru Rac  
[material]
```

where:

- The name parameter is set to the name for the polyhedron.
- The direction parameter can be set to rb (right back), lb (left back), lf (left front), or rf (right front).
- The Rac parameter is the radius of the STI concave corner.
- For other parameters, see [Figure 123 on page 736](#).

[Figure 126](#) shows STI concave corner-shaped polyhedra in different directions.

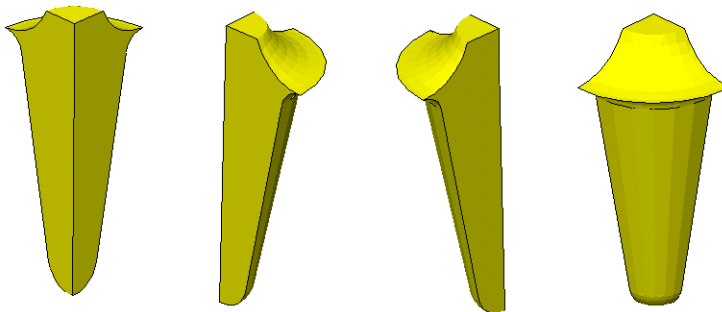


Figure 126 STI concave corner-shaped polyhedra in different directions: (from left to right) left back, right back, left front, and right front

## PolyHedronSTIaccv

The syntax of the PolyHedronSTIaccv command is:

```
PolyHedronSTIaccv name direction X0 Y0 Z0 Depth Tsti Asti Hsti Rd Rb Ru Rac  
[material]
```

where:

- The name parameter is set to the name for the polyhedron.
- Same as the PolyHedronSTIacc command, the direction parameter can be set to rb, lb, lf, or rf.
- The Rac parameter is the radius of the convex corner.
- For other parameters, see [Figure 123 on page 736](#).

[Figure 127](#) shows a generated STI convex corner-shaped polyhedron.

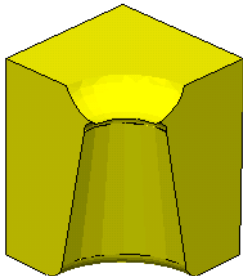


Figure 127 STI convex corner-shaped polyhedron

[Figure 128 \(left\)](#) shows a structure generated by combining the above three STI commands. [Figure 128 \(right\)](#) illustrates the directions of the STI shapes.

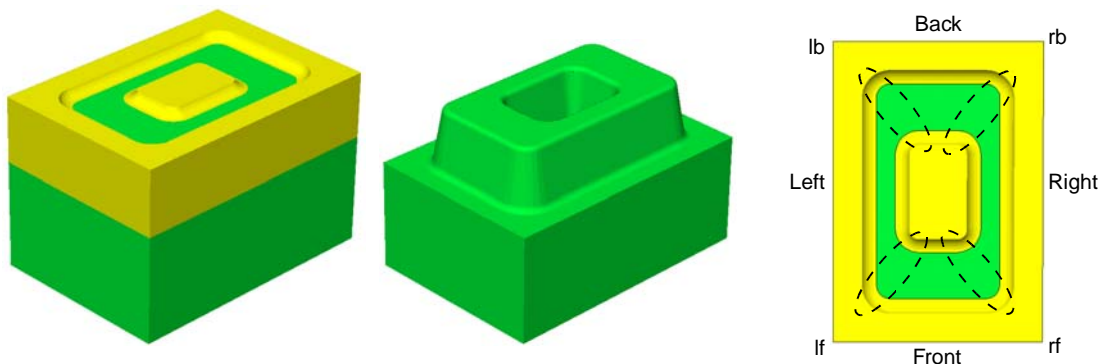


Figure 128 (Left) STI structures and (right) polyhedron directions

## PolyHedronCylinder

The syntax of the `PolyHedronCylinder` command is:

```
PolyHedronCylinder name X0 Y0 Z0 Rc Hc [material]
```

where:

- The name parameter is set to the name for the polyhedron.
- Other parameters give the center coordination, the radius, and the height for the cylinder (see [Figure 129](#)).

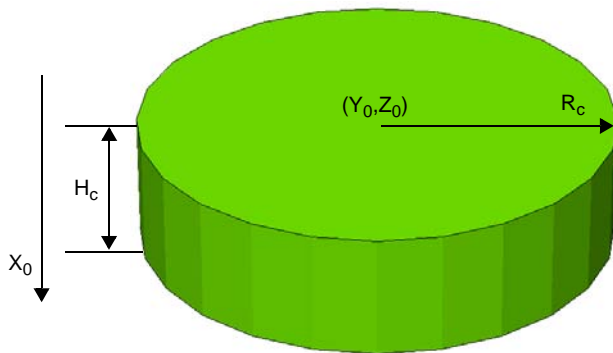


Figure 129 Cylinder-shaped polyhedron

## PolygonWaferMask

The syntax of the `PolygonWaferMask` command is:

```
PolygonWaferMask name Y0 Z0 Rw Lf
```

where:

- The name parameter is set to the name for the polyhedron.
- Other parameters give the location and size for the mask (see [Figure 130 on page 740](#)).

**NOTE** This command only works in MGOALS mode.

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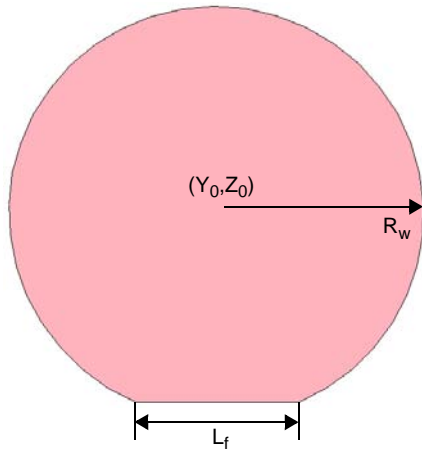


Figure 130 Wafer mask-shaped polygon

## PolyHedronEpiDiamond

The syntax of the PolyHedronEpiDiamond command is:

```
PolyHedronEpiDiamond name X0 Y0 Z0 Wepi Lepi Hup Hdown Drecess [material]
```

where:

- The name parameter is set to the name for the polyhedron.
- For other parameters, see [Figure 131](#).

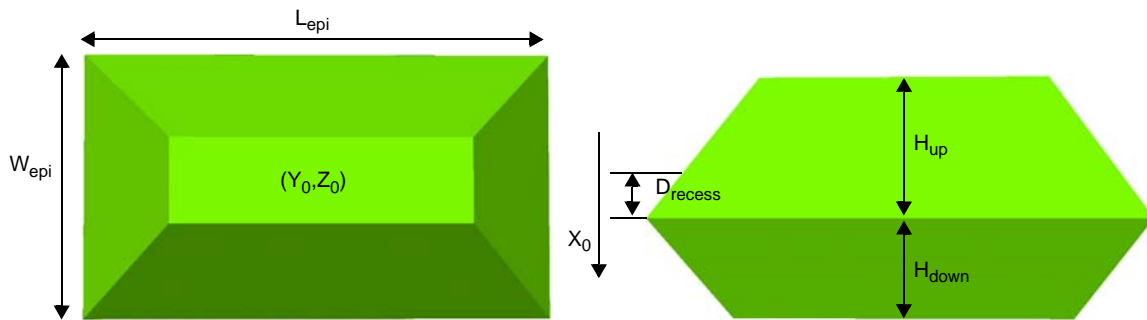


Figure 131 Epitaxial diamond-shaped polyhedron

---

## The mask and photo Commands

A quick way to mimic lithographic patterning is using the `photo` command. The `photo` command takes a mask and effectively does a resist spin-on step followed by an exposure bake and etch. The resist layer produced has vertical walls and is by default a negative of the mask, but the positive sense can optionally be created as well.

In addition to the `photo` command, the `etch` and `deposit` commands allow you to specify a mask directly. The parameter `mask` in the `etch`, `deposit`, and `photo` commands specifies the name of one mask that has been previously defined using a `mask` command or by reading in masks from a layout using the IC WorkBench EV Plus interface (see [Chapter 12 on page 795](#)).

The mask will have an effect similar to a masking layer; it limits the etch or deposition process to a certain window. By default etching is not performed for points inside the mask, unless the parameter `negative` is used in the mask definition. Similarly, deposition of a new layer in the `deposit` command and of the photoresist layer in the `photo` command is performed outside the mask unless the `negative` parameter is specified in the mask command in which case deposition happens inside the mask only.

**NOTE** Always specify the masks and the simulation domain such that masks do not end exactly on the boundary of the simulation domain, but end inside or extend safely beyond the boundary of the simulation domain.

The `mask` command creates a mask. You can define the geometry of the mask directly in the command file or can read masks from a layout file. Masks defined in the command file must be given a name; otherwise, the names are read from the layout file.

If the parameter `list` is specified in a `mask` command, information about the existing masks is printed. If `name` is specified as well, information about the specified mask is printed.

If the parameter `clear` is specified in a `mask` command, all previous mask definitions are removed. If a `name` is specified as well, only the specified mask is removed.

A mask can be defined directly in the command file by using three different types of geometry object:

- Segments
- Rectangles
- Polygons

Each mask may be composed of an arbitrary number of such objects.

## 11: Structure Generation

### The mask and photo Commands

Segments are defined as:

```
mask name= pmask segments= { -0.1 0.6 0.7 1.1 }
```

Pairs of subsequent values define the y-coordinates of the beginning and end of one mask segment. Therefore, an even number of coordinates must be specified in the `segments` parameter. The pairs may be defined in arbitrary order, and the segments defined by pairs of coordinates may touch or overlap each other. In 3D, masks defined by segments are extended over the entire range of z-coordinates.

A rectangular mask is defined as:

```
mask name=nimask left=0.2 right=1 front=0.2 back=1 negative
```

The `left` and `right` parameters define the minimum and maximum extensions of the mask along the y-axis; the `front` and `back` parameters define the minimum and maximum extensions of the mask along the z-axis.

**NOTE** Only one rectangle can be specified per mask command. The `front` and `back` parameters may be omitted; in this case, the mask is equivalent to a mask with one segment. Additional mask commands with the same name can be used to add rectangles. The rectangles defined for a mask may arbitrarily intersect or touch each other.

Masks also can be defined by a list of names of polygons. These named polygons must have been defined before the mask command using one `polygon` command for each named polygon:

```
polygon name=LShape2 segments= {0.0 -1.5 0.0 -0.5 0.5 -0.5 0.5 1.5 1.5 \  
1.5 1.5 -1.5}  
mask name=Mask2 polygons= {LShape2} negative
```

**NOTE** The segments in the `polygon` command are defined as a sequence of y- and z-coordinates. The polygon is closed implicitly by connecting the last point to the first. Each polygon for a mask must not touch or intersect itself. The polygon may be specified with arbitrary orientation (clockwise or counterclockwise in the yz plane). It does not matter if different polygons for a mask touch or intersect each other.

Masks also can be defined by a combination of all three types of geometry object: segments, rectangles, and polygons. Different objects may touch or overlap each other.

In 1D, the entire simulation domain is masked if the coordinate origin is masked. Any point along the y-axis in a 2D simulation and any point of the yz rectangle of the simulation domain in a 3D simulation are inside the mask if they are contained in any one of the geometry objects



defined for the mask. Specifying the parameter `negative` inverts the mask. In other words, any point outside all the geometry objects defined for the mask is *masked*.

These commands can be used to invert a mask at any time after it has been defined:

```
mask name=aaa negative
mask name=aaa !negative
```

**NOTE** In the `etch` command, the masked area is not etched. While in the `photo` and `deposit` commands, the photoresist or the specified material is deposited in the unmasked area.

Masks can also be combined using a set of Boolean operations. The operations are specified using the `bool` parameter (see [Boolean Masks on page 744](#)).

Layouts which have been defined in the GDSII format can be read into Sentaurus Process using the ICWBEV Plus interface, see [Chapter 12 on page 795](#). Alternatively, masks can also be read from a layout file in DF-ISE format (default file extension `.lyt`). The TCAD layout tool Ligament Layout Editor can save DF-ISE layout files as well as read in simple GDSII files. In order to read the layout directly into Sentaurus Process, the name of the layout file must be specified as `layoutfile=aaa.lyt` in a `mask` command.

All mask rectangles and polygons read from a `.lyt` file are converted into named polygons. These polygons then are collected into masks according to the names contained in the `.lyt` file.

When using a layout file, the relation between the layout coordinate system and the Sentaurus Process coordinate system may need to be defined. By default, the layout-x axis (the horizontal direction in Ligament Layout Editor) corresponds to the Sentaurus Process z-axis. The layout-y axis (the vertical axis in Ligament Layout Editor) corresponds to the Sentaurus Process y-axis. This definition matches the default definition of the parameter `slice.angle` in the `init` command and the coordinate x- and y-axes when displaying the Sentaurus Process simulation results.

The coordinate transformation between the Sentaurus Process coordinate system and the layout coordinate system can be defined in two ways:

- In the `mask` command that specifies the layout file, the name of one mask may be specified. If a mask with the specified name is contained in the layout file, it is used to position and orientate the simulation domain in the layout.
- Otherwise, a mask with the specified name must have been defined before using a `mask` command. The specified mask is defined in layout coordinates. It may be defined as a rectangle or a polygon, containing at least two points.

In the case of a rectangle (either defined by a SIM3D mask in Ligament Layout Editor or defined in a `mask` command), the point with the minimum layout-x and layout-y coordinate is used as the origin of the Sentaurus Process coordinate system. The direction from

## 11: Structure Generation

The mask and photo Commands

(`min.layout-x`, `min.layout-y`) to (`min.layout-x`, `max.layout-y`) is used as the Sentaurus Process y-axis.

If a polygon of at least two points is used (defined either as a SIM2D line segment in Ligament Layout Editor or a mask defined as a polygon), the first point defined is used to place the origin of the Sentaurus Process coordinate system. The direction from the first to the second point of the mask is used as the orientation of the Sentaurus Process y-axis.

The local coordinates of the specified mask with respect to the selected Sentaurus Process y-axis and origin are used as default extensions of the simulation domain. If a polygon mask with only two points is used, the default extension in the z-direction is 0. The default extension in the y-direction is defined by the distance between the two points. The default extensions in the y- and z-directions as defined by the mask are reported. If no extensions have been defined using the `line y` command or the `line z` command or both commands, the default extensions are defined for the simulation when the layout file is read.

If a layout file is loaded, but no mask name is specified, the `Cutline2D` command that may have been specified in the `init` command to define the parameter `slice.angle` will be used to orientate the coordinate systems. The first point specified in the `Cutline2D` command is used as the origin of the Sentaurus Process coordinate system. The direction from the first to the second point is chosen as the direction of the Sentaurus Process y-axis. If `Cutline2D` is used, no default extensions of the simulation domain are defined.

---

## Photoresist Masks

To define photoresist layers, use the `photo` command and specify a mask. Sentaurus Process defines photoresist layers by specifying the minimum thickness of the resist and selecting the name of a mask that has been defined by the `mask` command. By default, the photoresist will be deposited outside the specified mask and will have a flat top similar to spin-on resist. If the parameter `negative` has been specified when defining the mask, a photoresist is created inside the mask.

---

## Boolean Masks

Two masks can be combined using the `bool` parameter of the `mask` command. The Boolean operations include: `+`, `^`, `*` and `-`. In addition, masks can be transformed using the following operations: `rotate`, `scale`, `mirror`, `array`, `bias`, `over_under`, `under_over`, and `offset`.

The `bool` option only accepts simple expressions as described in the examples in [Table 70](#). Complex nested expressions (for example, `bool= "(M1 + M2) - bias(-50, M3 + M4)"`)

are not possible in this implementation and, therefore, must be reduced to simple operations. In addition, the `bool` option cannot be used together with the `layoutfile`, `polygon`, and `negative` options.

Table 70 Boolean operations

Operation	Example	Description
+	<code>bool= "mask1+mask2"</code>	Unites (merges) <code>mask1</code> and <code>mask2</code> .
-	<code>bool= "mask1-mask2"</code>	Subtracts <code>mask2</code> from <code>mask1</code> .
*	<code>bool= "mask1*mask2"</code>	Produces the intersection of <code>mask1</code> and <code>mask2</code> .
^	<code>bool= "mask1^mask2"</code>	Produces a mask that contains the nonoverlapping portions of <code>mask1</code> and <code>mask2</code> (XOR operation).
-	<code>bool= "-mask"</code>	Produces a mask that is the complement of the input mask.
rotate	<code>bool= "rotate(direction,mask) "</code>	Produces a mask that is rotated with respect to the input mask. The <code>direction</code> parameter can be either <code>left-90</code> or <code>right-90</code> .
scale	<code>bool= "scale(factor,mask) "</code>	Produces a mask that is scaled with respect to the input mask using the floating-point value of <code>factor</code> .
mirror	<code>bool= "mirror(axis,mask) "</code>	Mirrors a mask with respect to a local axis specified by <code>x</code> or <code>y</code> .
array	<code>bool= "array(nx, ny, dx, dy, mask) "</code>	Produces an array of $n_x \times n_y$ masks separated by a distance specified with <code>dx</code> and <code>dy</code> .
bias	<code>bool= "bias(delta,mask) "</code>	All mask edges on the input mask are offset in the normal direction by the specified amount. A positive <code>delta</code> value expands the mask, while a negative <code>delta</code> shrinks it. Zero or negative area sections of the mask are eliminated from the output mask. Overlapping sections of the mask are merged.
over_under	<code>bool= "over_under(delta, mask) "</code>	Expands and then shrinks the input mask by <code>delta</code> . This effectively merges areas in close proximity and is equivalent to <code>bias(delta, bias(-delta, mask))</code> .
under_over	<code>bool= "under_over(delta, mask) "</code>	Shrinks and then expands the input mask by <code>delta</code> . This eliminates small areas and is equivalent to <code>bias(delta, bias(-delta, mask))</code> .
offset	<code>bool= "offset(dy, dz) "</code>	Translates the mask by the specified amount. The <code>dz</code> parameter is ignored in 3D.

---

## Line Edge Roughness Effect

Line edge roughness (LER) is the deviation of feature edges from ideal straight lines due to statistical fluctuations in photolithographic processes. Sentaurus Process uses the `line_edge_roughness` command to apply randomized deviations to straight mask edges, for example:

```
line_edge_roughness normal= "z" masks= {mask1} correlation.length= 25.00<nm> \
  standard.deviation= 5.00<nm> max.segment.length=5.00<nm>
```

The random noise function  $f_{\text{random}}$  applied to mask edges by the `line_edge_roughness` command is generated from the power spectrum of a Gaussian autocorrelation function. The Gaussian autocorrelation shape is characterized by the standard deviation distance  $\Delta$  specified by the `standard.deviation` parameter and the correlation length  $\Lambda$ , specified by the `correlation.length` parameter:

$$\text{Autocorrelation}(f_{\text{random}}) = \Delta^2 \sqrt{\pi} \Lambda e^{-(x^2/\Lambda^2)} \quad (946)$$

$f_{\text{random}}$  is obtained by Fourier synthesis, applying the inverse Fourier transform to [Eq. 946](#), after adding random phases. In this way, random deviations of the mask edges can be obtained from run to run, which correspond to LER profiles having the same standard deviation  $\Delta$  and correlation length  $\Lambda$ .

These random deviations are added in discrete form to the mask edges in question. First, the mask edge is subdivided into discrete segments complying with the user parameter `max.segment.length`. Second, the deviation at each segment endpoint is added in the direction normal to the initial mask edge orientation.

LER is applied by default to all edges of the mask. You can limit which edges in a named mask are to receive LER by the parameter `normal`, which specifies either the y-axis (Y) or the z-axis (Z). If `normal` is specified, only those edges in the named masks normal to the given axis are chosen for LER to be applied. LER is applied only once per mask. Mask segments along the device bounding box do not receive LER.

The parameter `!random.reseed` bypasses the reseeding of the random number generator before the random phases are added. By using this parameter, the shape of the noise function and, therefore, the LER result, can be reproduced from one run to the next if needed for comparison.

The parameter `random.seed` can reproduce specific LER calculations from one run to the next by setting the same random seed in both runs. When stored in a TDR file in split simulations, the parameter `random.seed` is included when saving `line_edge_roughness` to the TDR file, even if it is not specified by users, to ensure proper reproduction of the same LER in a subsequent reload of the TDR file.

**NOTE** The structure is extruded automatically to three dimensions if it is less than three dimensions and the `line_edge_roughness` command is used.

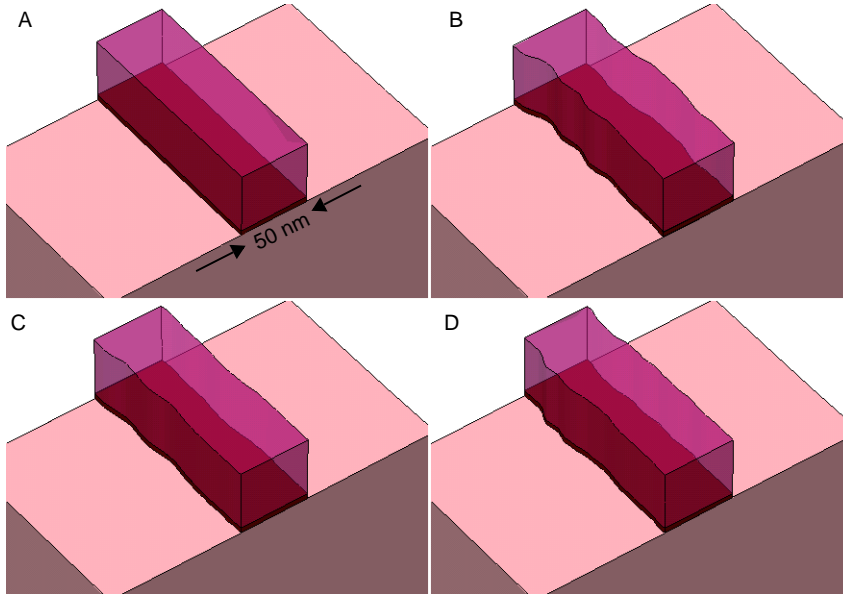


Figure 132 Example of 3D structure with LER applied using different values of standard deviation  $\Delta$  and correlation length  $\Lambda$  : (A) no LER applied, (B) LER applied with  $\Delta = 4$  nm and  $\Lambda = 20$  nm, (C) LER applied with  $\Delta = 2$  nm and  $\Lambda = 20$  nm, and (D) LER applied with  $\Delta = 2$  nm and  $\Lambda = 12$  nm

The following strategy is used to address the problem of nearly collinear LER mask points that may trigger removal by decimation during meshing. Avoiding the decimation of nearly collinear LER mask points is desirable because removing such points may perturb the power spectrum of the Gaussian autocorrelation function represented by the mask shape and may also result in meshing difficulties.

If the parameter `max.tries` is set to a nonzero value, LER masks are checked for nearly collinear points, which would result in decimation by the mesher:

```
line_edge_roughness max.tries=30
```

If any points in the LER mask are decimated by the mesher, based on the current `mgoals accuracy` setting, the LER mask is rejected and the LER generation process is restarted. After each restart, the detection and restart process is repeated until an acceptable LER mask is generated or until the number of attempts exceeds `max.tries`.

When `max.tries` is exceeded, Sentaurus Process stops with an error message that suggests using a smaller value of `mgoals accuracy` or a larger value of `max.segment.length` in the `line_edge_roughness` command.

The default value of `max.tries` is 0, meaning no decimation check is performed, no retries are attempted, and the initial mask LER is accepted as it is, even with nearly collinear points.

---

## Geometry Transformations

Transformations supported in Sentaurus Process are reflection, stretch, cut, rotation, translation, and flip:

- The transform `reflect` command is used with `left`, `right`, `front`, or `back` to perform the reflection centered on the outer boundary of the simulation domain. At the reflection side, regions are not merged immediately to allow a clean transform `cut` afterward if required. The grid can be merged with `grid merge` command manually, but if not, the structure will naturally be merged for any geometry changing operation later (except `transform reflect`). It is also possible to discard the original structure when reflecting by specifying the optional parameter `!keep.original`.
- The transform `stretch` command is used to indicate a mesh cutting at the position given by the `location` parameter. The two pieces of mesh defined by the cut plane are translated perpendicular to the cut plane, and new elements are inserted with a size given by the `length` parameter.
- The transform `cut` command is used to crop the structure. If used with `left`, `right`, `front`, or `back`, the default will cut the structure in half at the midpoint along the given direction. The `location` parameter is used to modify the cut to a position not in the middle. For a more general crop operation, the `cut` parameter can be used with the `min` and `max` parameters that specify the cropping box.
- The transform `rotate` command is used to rotate a structure. An axis and angle should be specified. Only  $90^\circ$ ,  $180^\circ$ , and  $270^\circ$  angles are allowed for the x-axis, and  $180^\circ$  for the y- and z-axis. In the case of 2D simulations, rotations will produce an extruded 3D simulation.
- The transform `translate` command shifts the structure the specified quantity. Since it is a pure translation, it will not change the aspect of the structure.

In 2D, all transformations are performed by MGOALS. In 3D, if the SDE mode is on, the appropriate Scheme commands are dispatched to Sentaurus Structure Editor to transform the structure. If the SDE mode is off, MGOALS performs the `reflect`, `rotate`, `translate`, `stretch` and `cut` operation.

All these transformations also will be applied to the existing refinements, which will be cut, stretched, rotated, translated, and reflected. To disable this feature, set `Grid Transform.Updates.Refinement` to `false`.

The transformations `stretch` and `flip` are not supported by Sentaurus Process KMC.

## Refinement Handling during Transformation

All these transformations also apply to the existing refinements created with either the `refinebox` or the `line` command. Detailed descriptions of refinement handling are provided with each operation here.

To disable this feature, set `Grid Transform.Updates.Refinement` to `false`.

## Contact Handling during Transformation

The only special contact handling occurs during `transform reflect`. In this case, contacts that straddle or touch the reflecting plane are enlarged to the reflected area (only one contact remains). The remainder of the contacts are duplicated and are renamed by appending a suffix as follows:

- For right or left reflection, the contact on the left after reflection will be named `<original contact name>.1` (where `<original contact name>` was the name of the contact before the reflection operation), and the contact on the right after reflection will be named `<original contact name>.2`.
- Similarly, for front or back reflection, the front contact (which has a larger z-coordinate) will be named `<original contact name>.2`, and the back contact will be named `<original contact name>.1`.
- For up or down reflection, the upper contact will be named `<original contact name>.1`, and the lower contact will be named `<original contact name>.2`.

You can rename contacts after the `reflect` command, or at any time, using the command:

```
contact name= <old contact name> new.name= <new contact name>
```

For example, after reflection, you can use the command:

```
contact name= SourceDrainContact.1 new.name= Source
```

where the original contact name before reflection was `SourceDrainContact`.

**NOTE** It is recommended to specify all contacts *after* all transform operations other than `transform reflect` to avoid problems during contact creation.

## The transform reflect Command

The `transform reflect` command is used to reflect the structure about the left, right, front, or back boundary (at minimum y, maximum y, maximum z, or minimum z). If any remeshing or other mesh modification operations are performed after a `transform reflect` command, the symmetry will be lost. An extra `!keep.original` parameter discards the original structure leaving only the reflected one.

Examples:

```
transform reflect left
transform reflect ymin
transform reflect front
transform reflect left !keep.original
```

**NOTE** The option `remesh` is disabled in `reflect` because it may disrupt the symmetry of the reflected structure. However, the command `grid merge` can be used afterward to remove same-material interfaces at the reflecting plane.

## Refinement Handling during Reflection

In the case of `!keep.original`, lines coming from both the `line` command and refinement boxes are reflected along with the structure. However, when the original structure is kept, some special handling is required.

Typically, during any geometry operation, lines created with the `line` command that have been defined outside the bounding box will be removed. Therefore, there is no danger of the reflected lines conflicting with the original lines.

For refinements created with refinement boxes, if the refinement box is constrained spatially (that is, the `min` or `max` parameter has been used in the definition), then the box will be duplicated, and the name of the new box will be `reflected_<name>` where `<name>` is the name of the original refinement box. If the original and reflected refinement boxes overlap, there is no problem since the refinement criteria are the same.

---

## The transform stretch Command

The `transform stretch` command stretches the structure in the left, right, down, up, front, or back directions at a given coordinate location by offsetting one side of the structure by the specified length. If there is no vertical line of edges at the specified location, MGOALS creates



such a line and then stretches the structure. The data at the two ends of the stretched region is exactly the same as that of the unstretched mesh.

Examples:

```
transform stretch location=0.001 length=5 right
transform stretch down loc=0.5 length=200 info=2
```

**NOTE** Do not use together with the atomistic mode (KMC).

## Refinement Handling during Stretch

During the stretch operation, mesh lines that were created with the `line` command in the part of the structure being stretched are translated with the structure. No new lines are introduced into the expanded region. The refinement boxes that straddle the stretch location are increased in size by the stretch distance to follow the structure.

---

## The transform cut Command

The `transform cut` command cuts at or near the requested coordinate location. The location defines a line in 2D or a plane in 3D that divides the structure into the left and right, or front and back, or up and down parts. You can select the left/right, or front/back, or up/down region to be removed. If a line of element edges in 2D or a plane of element faces in 3D can be identified by MGOALS, the operation eliminates only the elements in the removed region. This works well if a structure had been reflected and needs to be cut back to the original (unreflected) structure. If a line of element edges in 2D or a plane of element faces in 3D cannot be found, a mesh-cutting operation is performed. By default, MGOALS tries to find a mesh line or plane near the specified coordinate. Then, MGOALS removes entire mesh elements rather than cutting mesh elements to avoid arbitrarily small edges and poor element quality. To disable the search feature and perform the operation exactly where specified, use the `!mesh.align` option of the `transform` command, which will invoke a remesh unless `!remesh` also is specified.

Examples:

```
transform cut location=0.5 right
transform cut left loc = 0.0
```

You also can use the `cut` command to crop the mesh by specifying a rectangle/brick defined by the upper-left-front and lower-right-back corners, specified with the `min` and `max` parameters. The cut operation retains the region enclosed by the rectangle/brick. By default, MGOALS tries to find a mesh line or plane near the specified coordinate and removes the whole mesh elements instead of cutting the mesh (which could lead to arbitrarily small edges and poor element quality). To suppress searching of a nearby mesh line or plane and to perform

the operation exactly at the specified location, specify `!mesh.align`. This automatically invokes a remeshing unless `!remesh` is specified.

Examples:

```
transform cut min= {-2 -1} max= {11 0}  
transform cut min= {-10 1.35 0.15} max= {10 1.65 0.4}
```

## Refinement Handling during Cut

During the cut operation, lines created with the `line` command that are outside of the simulation domain after the cut are removed and, similarly, any refinement box that lies completely outside the simulation domain after the cut is removed as well.

---

## The transform flip Command and Backside Processing

The `transform flip` command was introduced specifically to allow a convenient way to perform process steps on the back of a wafer. During the `transform flip` command, the structure is rotated 180° about a line by default in the center of the structure parallel to the y-axis. Therefore, the structure is upside down after the flip and in the same location. Because most operations in Sentaurus Process require a `Gas` region on top, a gas region is added automatically. In addition, many meshing operations require a solid material at the bottom of the structure, so the `Gas` region that was previously on top of the structure is converted to an auxiliary material called `BackMat`. If the structure is flipped again, the reverse happens, namely, `BackMat` is converted to `Gas`, and `Gas` is converted to `BackMat`. Any operation is allowed on a structure that has been flipped one or more times; however, the current bottom of the structure is never an active surface for any operation such as oxidation, epi, etching, and deposition.

There is great flexibility in the handling of the auxiliary material at the back of the structure. The material itself defaults to `BackMat` as mentioned, but you can choose another material using the command `pdbSet Grid Back.Material <material>`.

The material `BackMat` inherits its parameters from (is Like) `Gas` so that it behaves like gas for dopant diffusion simulation. For implantation, the material is converted to `Photoresist` so no implant tables are required for this material. Similarly, for mechanics, the only way to obtain `Gas`-like mechanics boundary conditions at interfaces to the back material is to use an actual `Gas` region. Therefore, the back material is converted automatically to `Gas` before each mechanics call and is converted back directly afterwards. Finally, when a region of material `BackMat` is saved in a structure, it is first converted to `Gas`, so that other tools reading the structure will have the proper material. However, it is also given a Sentaurus Process-specific tag, so that Sentaurus Process knows the region should actually be `BackMat`.

Another important point regarding mechanics simulations on flipped structures is that only a modified version of the lattice mismatch model is available. With this model, the command `substrate top.relaxed.coord` is no longer available for modification. Instead, the lattice-mismatch strain is added using the reference concentration model. This model uses a reference concentration and bases all strains directly on the difference between the strain field and that reference (see [Reference Concentration Model on page 660](#)).

**NOTE** To avoid switching from the standard lattice mismatch model to the reference concentration lattice mismatch model after `transform flip` is used, switch on the reference concentration model. This should be performed before initial structure creation using:

```
pdbSet Mechanics Reference.Concentration.Model 1
```

for those simulations using `transform flip`.

**NOTE** When performing laser annealing on a structure that has been flipped, the following settings are recommended (see also [Flash or Laser Anneal Model on page 220](#)):

```
pdbSet Grid Zero.Back.Material 0
mater add name= MyBackMat new.like=Silicon add
pdbSet Grid Back.Material MyBackMat
pdbSet ImplantData Back.Material MyBackMat
```

**NOTE** Do not use together with the atomistic mode (KMC).

## Refinement Handling during Flip

Refinements during a flip operation are handled in the same way as refinements during reflection in the case of `!keep.original`. Lines coming from both the `line` command and refinement boxes are reflected along with the structure.

---

## The transform rotate Command

The `transform rotate` command rotates the structure the specified angle in the specified axis using (0,0,0) as the rotation center. It accepts two parameters `axis` and `angle` to specify the rotation axis and angle, respectively. For Y and Z, 180 degrees can be specified. For X, 90, 180, and 270 degrees are allowed.

It might happen that during the rotation the existing initial gas has to be moved to a side or the bottom of the structure instead of being at the top. In these cases, new gas will be added to the top.

The `transform rotate` command applies to 3D and 2D simulations. For 2D simulations, a rotation in the z-axis will produce another 2D simulation, but rotations in the x-axis and y-axis will produce a structure equivalent to extruding the z-axis and then performing the rotation.

## Refinement Handling during Rotation

During a rotation operation, lines coming from both the `line` command and refinement boxes are rotated along with the structure.

---

## The transform translate Command

The `transform translate` command does not change the aspect of the structure. It only adds the coordinate specified in the `translate` parameter to all the nodes, that is, it displaces the structure or shifts it in space. It is equivalent to changing the origin of coordinates by a fixed quantity.

Similarly, mesh lines created with the `line` command and the bounding box of refinement boxes (which are specified with the `min` and `max` parameters of the `refinebox` command) are translated with the structure.

---

## MGOALS Interface

By default, etching and deposition operations are performed using the MGOALS library in 1D, 2D, and 3D. The MGOALS library operates as follows:

- The starting structure is analyzed for the interfaces that will change during the operation.
- The geometry-changing operations are performed.
- In 2D, the entire structure is remeshed. During remeshing, nodes in the silicon region are retained as much as possible in their original locations. In most cases, a high percentage of the nodes are retained after remeshing. This minimizes interpolation errors. In 3D, the structure is remeshed only if the next step requires an up-to-date mesh.

---

## MGOALS Boundary-moving Algorithms

MGOALS uses either an analytic method or a fast level-set method to perform boundary-modifying operations. In general, the analytic method is faster, less memory intensive, and more accurate. However, it cannot handle deposition in concave regions or etching of convex areas when there are boundary collisions and self-intersections.

The analytic method is fast, accurate, and uses a simplified string algorithm. Due to speed and accuracy advantages, MGOALS always tries to perform an analytic operation. If self-intersections are detected in the new boundary, MGOALS automatically switches from the analytic method to the fast level-set method. Both the analytic and the fast level-set methods can handle simple etch and deposition processes.

Besides the analytic method and the fast level-set method, a general time-stepping level-set method is available to handle more complex etch types such as Fourier, crystallographic, and multimaterial etching, and to include shadowing effects.

Both level-set methods use an approach similar to that described in [1]:

- First, the level-set method identifies the interface or the part of an interface to be moved. This computation is based on nonetched overlayers, masks, and if necessary, visibility due to directional constraints specified by the user.
- Second, evolution of the moving interface is performed using either the fast-marching scheme, which solves the time-independent boundary-value formulation of the Hamilton–Jacobi equation (or Eikonal equation), or “full levelset,” a time-dependent, initial-value formulation of the same equation. The fast-marching scheme computes the new boundary location for all times in a single step. The nature of the equation is such that it captures and handles collisions. However, the equation cannot identify when the collision actually occurred. The “full levelset” formulation which is a time-dependent, initial-value formulation is used for multimaterial, Fourier, and crystallographic etching, and for handling shadowing effects. Its time-stepping algorithm allows for recalculating the front velocity at every time step.

In MGOALS, the fast-marching and level-set equations are solved on a separate Cartesian mesh that is independent of the simulation grid. For a description of the parameters that control the Cartesian mesh, see [MGOALS Boundary-moving Parameters on page 756](#).

After solving the level-set equations, the newly created boundary is extracted from the level-set function on the Cartesian mesh and then incorporated into the simulation mesh. The exact replication of the extracted boundary in the mesh can be expensive and can transfer unwanted noise from the level-set solution into the structure. To resolve these issues, MGOALS allows a certain smoothing to be performed on the extracted boundary.

In 2D, to incorporate the new boundary into the simulation grid, a simplified meshing step is performed. A simple mesh is created for the modified regions and connected to the mesh in unchanged regions. Since this mesh is not suitable for process simulation, by default, a full remesh is performed after each etching and deposition step.

In 3D, almost all boundary-modification operations performed by MGOALS use the analytic method. The only exceptions are isotropic deposition and etching, which are performed using the fast level-set method. The new material boundary is integrated into the structure using a set of polyhedral Boolean operations.

## MGOALS Boundary-moving Parameters

Parameters to specify the resolution of the Cartesian mesh and the interface/boundary fidelity are defined in an `mgoals` command before the `etch` or `deposit` command. These parameters are applied to the entire structure. The interface quality and resolution are controlled by `accuracy`, `resolution`, and `full.resolution`. The actual size and placement of the Cartesian mesh bounding box is calculated starting with the initial interface being etched, extended based on the time and rates given by the user, or in the case of `etchstop` materials, extended based on the distance from the initial front to the `etchstop` materials.

### The accuracy Parameter

The `accuracy` parameter is used to control the noise and features at an interface. A small value of `accuracy` allows only small deviations between the boundary extracted from the level-set function and the piecewise linear segments incorporated into the simulation mesh. As a result, a large number of small segments may be created. In addition, a value of `accuracy` that is too small may *interpret* numeric noise as surface features, which MGOALS requires to reproduce in the simulation mesh. The default value for `accuracy` is  $1.0 \times 10^{-5} \mu\text{m}$ .

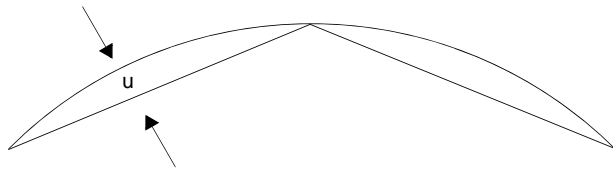


Figure 133 The curved surface represents the extracted new boundary and the piecewise linear segments represent the simplified boundary incorporated into the simulation mesh. The `accuracy` parameter ensures that  $u \leq \text{accuracy}$ .

### The resolution Parameter

The value of the `resolution` parameter controls the element size in the Cartesian mesh used to perform level-set based etching and deposition. Since the thickness of the layer to be deposited or etched is user specified, the grid size is defined as a fraction of the thickness of the modified layer. The size of each grid element of the level-set mesh is given by the product of the value of the `resolution` and the etch or deposit thickness.

The `resolution` is specified in the `mgoals` command and the etch or deposit thickness is specified in the `etch` or `deposit` command, respectively. This scheme usually provides a good approximation of the required level-set resolution and is computationally efficient. The default value for `resolution` is 0.1.

**NOTE** Providing a small `resolution` parameter for thin layers may lead to excessive time and memory consumption. For example, if an isotropic deposit of 1 nm thickness is performed with `resolution=0.1`, a level-set grid size of 1 Å will result.

**NOTE** For a thick etching or deposition, it may be necessary to reduce the resolution. For example, a 1  $\mu\text{m}$  deposition with `resolution=0.1` leads to a level-set grid size of 100 nm that may lead to a poor approximation of sharp corners and rounded areas in the new boundary.

### General Time-Stepping Level-Set Parameters

The general time-stepping level-set method has a few additional parameters to control and balance accuracy, simulation time, and memory use. Usually, the full time-stepping level-set method is used in situations where more intricate boundaries will be generated. The full time-stepping level-set method is needed for Fourier, crystallographic, and multimaterial etching types, and for etching with shadowing on. It is also used if the `force.full.levelset` parameter is given.

The `full.resolution` parameter can be used for the time-stepping level-set algorithm in the same way `resolution` is used for the fast level-set algorithm. You also can specify the actual spacing of the Cartesian mesh in the x-direction or y-direction or both directions, with the `dx` and `dy` parameters (and the z-direction in 3D with `dz`). Reducing the mesh size causes the time-stepping method to allocate more memory, to take smaller time steps, and to increase the solve time for each time step, thereby increasing the overall simulation time.

**NOTE** In previous releases, the *Upwind* formulation of the time-stepping level-set method provided users with the `mgoals` parameters `reinitfrequency` and `reinititerations` to control the frequency and quality of level-set reinitialization. The currently implemented Lax–Friedrichs formulation does not provide these parameters to users, since reinitialization is performed at every time step.

### Level-Set Cartesian Mesh and Resolution: Internal Calculations

The Cartesian mesh extent or bounding box, the `resolution` and `full.resolution` criteria, and the grid spacing criteria `dx`, `dy`, and `dz` interplay in the following ways.

The Cartesian mesh encompasses the initial interface between the Gas and all the materials the user has defined to be etched. It also encompasses the entire movement of the etching front expected throughout the entire etch process. In the case of time-based etching with the `time` keyword, an etching distance is computed based on the requested etch time multiplied by the maximum expected etch rate. The `resolution` or `full.resolution` keyword is then used as the approximate mesh spacing unless overridden by `dx`, `dy`, or `dz`. The number of resulting Cartesian mesh lines follows as required to achieve the desired mesh spacing within the Cartesian mesh bounding box.

In the case of material `etchstop`, the bounding box of the Cartesian mesh is calculated based on the initial Gas/etch-material interface, and its extent is determined by the position of `etchstop`.

materials in the simulation domain—the estimated maximum etching distance. The target mesh spacing in 2D is the `resolution` or `full.resolution` multiplied by the estimated maximum etching distance. In 3D, the target mesh spacing is set to the `min.levelset.size`, as the estimated maximum etching distance is not calculated in 3D for this purpose. From the Cartesian mesh bounding box size and the target mesh spacing, possibly overridden by `dx`, `dy`, and `dz`, the number of Cartesian mesh lines is determined.

### Limitations of Level Set

As a general approach, while level set is especially useful for shadowing, multimaterial, sophisticated etch velocity functions (for example, surface normal dependent or crystal direction dependent), and complex evolution of etch surfaces (that is, complicated structures), it is generally not a good choice when sharp or exact corners, and straight or exact etch walls, are required, such as in anisotropic etching.

This limitation is due to the implicit representation of the structure as a rectilinear grid of distance functions used to calculate the evolution of the moving surfaces.

---

## MGOALS 3D Boundary-moving Algorithms

MGOALS can perform 3D geometric etching and deposition operations, hereafter referred to as the *MGOALS3D mode*. Since interfacing with Sentaurus Structure Editor is the default method for 3D geometric operations, MGOALS must be activated using the command:

```
sde off
```

In MGOALS3D mode, a combination of level-set, fast marching, and analytic techniques are used to perform geometric operations similar to 2D. Unlike Sentaurus Structure Editor, MGOALS3D can reliably handle complicated boundaries (that is, those represented by polyhedra instead of geometric primitives). Such boundaries are created by 3D MGOALS `etch`, `deposit`, and `transform` commands.

**NOTE** After any one of these three process steps is performed in 3D, all subsequent geometry operations should be performed using MGOALS3D.

The use of the level-set method for thin etches or deposits can be prohibitively CPU and memory intensive, especially for large structures or for very thin etch or deposit steps. To address this issue, etches and deposits less than 1 nm use the analytic method by default. The thickness of this cutoff can be modified using the `analytic.thickness` parameter of the `mgoals` command.

To produce meshes with the highest quality elements and the fewest points, you should reduce the number of interfaces in the structure. This is especially true for 3D. However, because



region-merging is inconsistent with the paint-by-numbers mode, the default behavior in 3D is not to merge regions. When the MGOALS mode is switched on, it is assumed that you are not running the paint-by-numbers mode, so region-merging is switched on.

**NOTE** When the command `sde off` is specified, region-merging is switched on regardless of the previous setting.

---

## Summary of MGOALS Etching and Deposition Algorithms

[Table 71 on page 760](#) summarizes the algorithms used internally to implement etching and deposition:

- Level set (LF) – General time-stepping level-set algorithm with Lax–Friedrichs (LF) formulation.

This is the most general algorithm. All level-set algorithms have the disadvantage of a certain amount of rounding at corners and edges. The LF formulation has added stability, which can result in slightly more rounding at corners and edges.

- Level set (UW) – General time-stepping level-set algorithm with Upwind (UW) formulation.

The UW formulation is less stable and less reliable. This algorithm is used only for 2D isotropic single-material etching with shadowing or for 2D isotropic multimaterial etching.

- Fastmarch (fast level-set method) – This is used in simple 1D or 2D directional and anisotropic etching.
- Geometric – Three-dimensional etching algorithm creates a shaped boundary representation *tool*, which is applied through Boolean operations to the existing structure “blank” to obtain the final etching shape.
- Analytic – One-dimensional or 2D etching algorithm calculates and inserts an analytically calculated etching shape into the device structure.

**11: Structure Generation**  
MGOALS Interface

Table 71 Summary of etching algorithms used for different etching input parameters

Material	Shadowing	Etching type	Structure dimension	Etchstop mechanism		
				Time and rate	Material Etchstop	Thickness
Single material	No shadowing	Isotropic	1D/2D	Analytic	Level set (UW)	Analytic
			3D	Geometric	Level set (LF)	Geometric
		Fourier	1D/2D/3D	Level set (LF)	Level set (LF)	Not supported
		Directional	1D/2D	Fastmarch	Fastmarch	Fastmarch
			3D	Geometric	Level set (LF)	Geometric
		Anisotropic	1D/2D	Fastmarch	Fastmarch	Fastmarch
			3D	Geometric	Level set (LF)	Geometric
			Shadowing	Isotropic	2D	Level set (UW)
3D	Level set (LF)				Level set (LF)	Level set (LF)
Fourier	2D/3D			Level set (LF)	Level set (LF)	Not supported
Directional	2D/3D			Level set (LF)	Level set (LF)	Level set (LF)
Anisotropic	2D/3D			Level set (LF)	Level set (LF)	Level set (LF)
	2D/3D			Level set (LF)	Level set (LF)	Level set (LF)
Multimaterial	No shadowing	Isotropic	2D	Level set (UW)	Level set (UW)	Level set (UW)
			3D	Level set (LF)	Level set (LF)	Geometric
		Fourier	2D/3D	Level set (LF)	Level set (LF)	Not supported
		Directional	2D	Level set (LF)	Level set (LF)	Level set (LF)
			3D	Level set (LF)	Level set (LF)	Geometric
		Anisotropic	2D	Level set (LF)	Level set (LF)	Level set (LF)
			3D	Level set (LF)	Level set (LF)	Geometric
		Shadowing	Isotropic	2D	Level set (UW)	Level set (UW)
	3D			Level set (LF)	Level set (LF)	Geometric
	Fourier		2D/3D	Level set (LF)	Level set (LF)	Not supported
	Directional		2D	Level set (LF)	Level set (LF)	Level set (LF)
			3D	Level set (LF)	Level set (LF)	Geometric
	Anisotropic		2D	Level set (LF)	Level set (LF)	Level set (LF)
			3D	Level set (LF)	Level set (LF)	Geometric

## MGOALS Backward Compatibility

Default parameters and algorithm settings used by the MGOALS library may change from release to release in the pursuit of more accurate, more realistic, and more stable structure generation results. To use default parameters and settings from a previous release, enter the required release as a string parameter in the `mgoals` command, for example:

```
mgoals "G-2012.06"
```

Partial support for this backward compatibility is available starting with Version D-2010.03 with more complete support starting with Version E-2010.12.

## Boundary Repair Algorithm

Anisotropic or directional operations can produce residual material when the walls of the etched material are not perfectly vertical or aligned to the etching beam. These residual materials usually cause problems to the mesh generator since they contain sharp angles and small features that cannot be meshed. To correct this problem, MGOALS has implemented a repair algorithm that analyzes the structure and eliminates small, unwanted features.

The repair algorithm can be used with the `etch`, `deposit`, and `photo` commands. Those commands include a Boolean parameter named `repair` that controls the repair algorithm. The repair algorithm is enabled by default in 3D and disabled in 2D. To activate or deactivate the repair algorithm, include `repair` or `!repair` in the command specification. For example:

```
etch material= {Silicon} type=anisotropic rate = 0.001 time=1.0 !repair
```

---

## Inserting Segments in One Dimension

The `insert` command defines and inserts regions defined by segments in one dimension. You can choose which materials or regions are replaced, and the name and material of the new region.

Multiple regions can be inserted in one step. However, to insert multiple regions, the name cannot be specified. If multiple regions are inserted, machine-generated names are used. For more information, see [insert on page 942](#).

---

## Inserting Polygons in Two Dimensions

Two-dimensional regions defined by polygons can be created and inserted directly into a 2D simulation.

Polygons are created with the `polygon` command. This command accepts several options to specify how to create the polygon:

- `points` is followed by a list of points defining the polygon.
- `rectangle`, with `min` and `max`, specifies the rectangle limits.
- `segments` is followed by pairs of numbers specifying the coordinate where each segment starts and the previous one finishes.
- `xy` specifies the polygon will be created in the `xy` plane.

Since the standard use of the `polygon` command (see [The mask and photo Commands on page 741](#) and [Using Polygon and Rectangle Mask in 2D Simulation on page 773](#)) is to create masks for etch, deposit and photo, the default coordinates are `y` and `z` for the `segments` and `min` and `max` options. Consequently, the option `xy` must be specified in order for the polygon to be created in the `xy` plane instead of the `yz` plane.

- `tdr` is followed by the name of a TDR file to import the polygon from, and the parameter `materials` instructs the reader which polygon to read if there are many.

For examples of polygon creation, see [Polygon Creation and Insertion in MGOALS2D on page 786](#).

The `insert` command takes a mandatory `polygon` parameter containing the name of the polygon and inserts it into the structure. It allows specifying the parameters `replace.materials`, `new.material`, `replace.regions`, and `new.region` in a very similar way to the insertion in 3D (see [Inserting Polyhedra on page 765](#)).

For an example of polygon insertion, see [Polygon Creation and Insertion in MGOALS2D on page 786](#).

---

## Inserting Polyhedra in Three Dimensions

Regions defined by polyhedra can be inserted into an existing structure in three dimensions. The `polyhedron` command creates a polyhedron `<phname>` and adds it to the internal polyhedron list:

```
polyhedron name=<phname>  
  (tdr=<filename> [!rotate] [materials = {mat1 mat2}] [regions = { r1 r2 }])||  
  (brick = { <minx> <miny> <minz> <maxx> <maxy> <maxz> } )||
```

```
(polygons = { <polname> } min=<value> max=<value> })|  
(polygons = { <polname_1> ... <polname_n> })
```

You can build a polyhedron in four different ways; however, only one of them can be used at a time in one `polyhedron` command:

- Reading it from a TDR boundary file.
- Creating a rectangular prism (brick) polyhedron.
- Extruding a 2D `<polname>` polygon in the x-dimension.
- Creating a polyhedron from the beginning using its constituent polygonal faces `<polname_1>` to `<polname_n>`.

## Reading Polyhedra from a TDR Boundary File

The `polyhedron` option:

```
tdr=<filename> [!rotate] [materials = {mat1 mat2}] [regions = { r1 r2 }]
```

reads all the polyhedra included in a TDR boundary file called `<filename>`.

The parameter `materials` is optional and is used to choose which materials are included. In addition to explicit material names, the keyword `bulk.materials` is available to specify all nongaseous materials.

The parameter `regions` is optional and is used to choose which regions of the boundary are included.

If neither `regions` nor `materials` is specified, all regions are assumed to be included. If both `regions` and `materials` are specified, the union of the two is assumed.

The extra option `!rotate` is used to avoid the automatic rotation that Sentaurus Process performs when reading polyhedra to transfer them from the TDR boundary file (assumed to be in DF-ISE coordinates) to the Sentaurus Process structure in Sentaurus Process coordinates.

Several polyhedra can be included in the TDR file. Any valid TDR boundary file is allowed, regardless of the tool used to create it.

For an example, see [Reading a TDR file on page 789](#).

## Creating a Rectangular Prism

The `polyhedron` option:

```
brick = { <minx> <miny> <minz> <maxx> <maxy> <maxz> }
```

creates a rectangular prism given its two corners in Sentaurus Process coordinates.

For an example, see [Defining a Brick on page 792](#).

## Extruding a 2D Polygon

The `polyhedron` option:

```
polygons = { <polname> } min=<value> max=<value> }
```

takes an existing 2D polygon (created with the `polygon` command) and extrudes it in the x-direction from `min` to `max` to build a 3D polyhedron. The command expects the polygon to be planar. Only one polygon name is expected in the `polygons` list.

For an example, see [Extruding a 2D Polygon on page 790](#).

## Creating a Polyhedron from Its Constituent Polygonal Faces

The `polyhedron` option:

```
polygons = { <polname_1> ... <polname_n> }
```

builds a polyhedron given its definition as a set of polygons. The polygons are `<polname_1>` to `<polname_n>`. Obviously, the command expects the polygon list to form a valid polyhedron, that is, a compact, enclosed, nonintersecting 3D space. The polygons can be created with the `polygon` command.

For an example, see [Creating a Polyhedron using Polygons on page 791](#).

## Sentaurus Structure Editor Interface: External Mode

This mode differs from the standard `sde` mode in that a structure can be created inside Sentaurus Structure Editor independent of the existing Sentaurus Process structure. The minimum syntax needed for creating an external structure is:

```
sde external { <sde commands> }
```

Where `<sde commands>` are scheme commands sent directly to Sentaurus Structure Editor. As an option, a polyhedron can be specified to initialize the structure, and after `sde`

external, further geometric commands such as `etch`, `deposit`, and `transform` operate on the external structure until the command `sde off` is specified. For more options for the `sde` command, see [sde on page 1050](#). To create a polyhedron from the external structure, the parameter `external.sde` of the polyhedron command must be given. In the following example, an aluminum sphere is inserted into the Sentaurus Process structure:

```
math coord.ucs
sde external {
  (sdegeo:create-sphere (position 0.4 0.0 0.0) 0.9 "Aluminum" "Aluminum_1")
}
polyhedron name= sphere external.sde
sde off
insert polyhedron= sphere
```

**NOTE** Commands sent directly to Sentaurus Structure Editor through the `sde` command need to consider the Sentaurus Process coordinate system. In the previous example, the UCS coordinate system (same as Sentaurus Process coordinate system) is used, so the x coordinate is vertical ( $-x$  is up), and y and z are lateral directions. If `math coord.ucs` is not specified, the z-axis is vertical ( $+z$  is up) and x and y are lateral.

## Inserting Polyhedra

The `insert` command is:

```
insert polyhedron=<phname> [replace.materials= { mat1 mat2 }]
  [replace.regions= {r1 r2 }] [new.material=<matname>] [new.region=<regname>]
```

**NOTE** The parameter `polyhedron` is mandatory and specifies the name of the polyhedron with which to operate. This polyhedron must be previously defined with the `polyhedron` command (see [Inserting Polyhedra in Three Dimensions on page 762](#)).

The parameter `replace.materials` is optional and specifies a list that indicates the materials to be replaced by the polyhedron. In addition to explicit material names, the keyword `bulk.materials` is allowed. If `bulk.materials` is specified, it means that all materials in the structure, except gas, will be replaced.

The parameter `replace.regions` is optional and specifies a list that indicates the regions to be replaced by the polyhedron. If neither `replace.regions` nor `replace.materials` is specified, it means that all materials are replaced. If both `replace.regions` and `replace.materials` are specified, the union of the two is assumed.

The parameter `new.material` is optional. If set, all the regions in the polyhedron will change to the specified material. This option does not change the polyhedron information except

## 11: Structure Generation

### MGOALS Interface

temporarily during the duration of the `insert` command. The material name in the inserted polyhedron is inserted, but not in the original polyhedron.

The parameter `new.region` is optional and valid only when there is one region. When set, the region name is set to the specified one after insertion. The region name in the inserted polyhedron is affected, but not the original polyhedron.

The `insert` command can be used to perform *polyhedron etch* and *polyhedron deposit* as well as the more general polyhedron insert functionality. Polyhedron etch is performed by specifying `new.material=gas` in the `insert` command or by creating a gas polyhedron. Polyhedron deposit is performed by specifying `replace.materials=gas` in the `insert` command as well as choosing one or more bulk regions or materials in the `polyhedron` command, such as `materials=bulk.materials` or `new.material=Silicon`.

**NOTE** The boundaries of the polyhedra to be inserted must not overlap any interfaces or outer boundaries of the structure. Otherwise, it is likely the operation will fail.

For examples of polyhedron insertions, see [Reading a TDR file on page 789](#), [Extruding a 2D Polygon on page 790](#), [Creating a Polyhedron using Polygons on page 791](#), and [Defining a Brick on page 792](#).

---

## 3D Structure Assembly in MGOALS3D Mode

MGOALS3D can read an existing 3D structure from a file and paste it into the current 3D simulation. To activate MGOALS, use the command:

```
sde off
```

The command used to perform structure assembly is:

```
paste direction = [back | front | left | right] tdr= <filename>
```

where:

- `direction` can be `back`, `front`, `left`, or `right`.
- `filename` is the file to paste, in TDR format, which must be specified.

Sentaurus Process automatically shifts the structure read from the file to the appropriate quantity in `x`, `y`, and `z` to fit to the current structure. Nevertheless, Sentaurus Process will not automatically stretch the incoming structure. Consequently, for the operation to succeed, the sizes of the pasting planes of the incoming structure and the existing one must be the same.

The values of the fields are conserved for each structure and are interpolated at the interface between the structures.



---

## Multithreading

Some of the more sophisticated etching and deposition types require the use of the level-set method (such as multimaterial etching, crystal etching and deposition, Fourier etching and deposition, use of etch stops or shadowing). This can be time-consuming, especially for 3D summations. To minimize simulation time, the MGOALS library allows for a multithreaded solution of the level-set equations.

The multithreaded operation can be invoked using:

```
math numThreads = <n>
```

or:

```
math numThreadsMGoals = <n>
```

where <n> is an integer. It is suggested to keep <n> at or below 4 to obtain reliable speed improvement.

---

## Sentaurus Structure Editor Interface

By default, etching and deposition operations are performed using the MGOALS library in 1D, 2D and 3D. However, the Sentaurus Structure Editor can also be used to perform 3D etch, deposit, and geometry transformation operations.

Sentaurus Structure Editor is a 3D geometry editor that uses the ACIS solid geometry modeling kernel and the Scheme scripting language. Structures are created using CAD operations and process emulation operations. All 3D `etch`, `deposit`, `strip`, `photo`, `mask`, and `transform` commands are translated into appropriate Scheme commands that are then dispatched to Sentaurus Structure Editor.

Sentaurus Structure Editor is integrated as a library in Sentaurus Process. The command controlling Sentaurus Structure Editor from within Sentaurus Process is the `sde` command.

Sentaurus Structure Editor also can be used as a stand-alone tool to build the final structure by using both its GUI and scripting capability. Then, the final structure can be used in Sentaurus Process either as a boundary file or after remeshing the structure with one of the available stand-alone mesh generation tools. The mesh or the boundary for the final structure is loaded and before each implant or diffuse step, the material of all regions, not yet present in the structure for the process step, is changed to gas.

Finally, there is an external mode. The Sentaurus Structure Editor external mode allows independent (in other words, external) structures built in Sentaurus Structure Editor to be

## 11: Structure Generation

### Sentaurus Structure Editor Interface

inserted into structures created with MGOALS. This mode was designed to take advantage of the best of MGOALS (advanced geometry-moving algorithms) and Sentaurus Structure Editor (solid modeling capabilities). For more information on this mode, see [Sentaurus Structure Editor Interface: External Mode on page 764](#).

Hereafter, standard Sentaurus Structure Editor interface mode (`sde on`) will be referred to as the *SDE mode*.

As usual, simulations may start in one or two dimensions. If a 3D mask is encountered and if `z`-lines have been defined, the structure will be extruded to three dimensions, and if the SDE mode is switched on, the Sentaurus Structure Editor interface will be initialized. All subsequent structure-modifying steps in the `etch`, `deposit`, `strip`, `photo`, and `transform` commands are dispatched to Sentaurus Structure Editor.

**NOTE** Reading a discretized 3D structure in Sentaurus Structure Editor can be unstable; most isotropic operations (`deposit` or `etch`) will fail if this method to initialize Sentaurus Structure Editor had been used. Therefore, when initializing a 3D simulation, you should store and load `.sat` files, rather than simply loading a 3D TDR boundary or grid file.

When the 3D structure has been initialized in Sentaurus Structure Editor, structure generation commands (`mask`, `etch`, `deposit`, `photo`, `strip`, and `transform`) are translated by Sentaurus Process into appropriate Scheme commands and then dispatched to Sentaurus Structure Editor.

**NOTE** Currently, a few options of the `etch` command cannot be translated into appropriate Scheme constructs: Fourier etching, trapezoidal etching, crystallographic etching, and shadowing effects are not supported in 3D. The parameter `etchstop` only works with `cmp` but not with other `etch` types.

The modified structure will be retrieved from Sentaurus Structure Editor and remeshed when a command that requires the geometry and the mesh to be synchronized (for example, `implant`, `diffuse`, and `struct` commands that write the mesh to a file) is found in the Sentaurus Process command file.

This ‘lazy’ remeshing (only when needed) minimizes the number of 3D remeshing operations and, therefore, increases both the robustness and speed of the 3D structure generation and remeshing.

There is a separate command to configure and control the interface to Sentaurus Structure Editor and to specify Scheme commands directly. The syntax of this Sentaurus Structure Editor command is:

```
sde {<scheme command>} [on] [off] [remesh] [logfile=<c>] [SdeCheck]
```

The command:

```
sde on
```

must be specified in each 3D simulation so that the simulation is performed using the Sentaurus Structure Editor interface.

To change to MGOALS3D, use:

```
sde off
```

The parameter `logfile` provides a file name to record all Scheme commands that are dispatched to Sentaurus Structure Editor. At the end of the simulation, a complete Scheme script is generated that can be used in a stand-alone run, for example:

```
sde -l logfile.scm
```

for debugging, testing different algorithms, or fine-tuning a few command parameters for Sentaurus Structure Editor without rerunning the Sentaurus Process simulation. These modified parameters and algorithm selections can later be incorporated into the `etch`, `deposit`, and other commands by specifying the parameter `sde` in these commands:

```
deposit oxide thickness=5<nm> isotropic sde= {"algorithm" "lop" "adaptive" \  
#t "radius" 0.075}  
etch silicon thickness=0.2<um> isotropic sde= {"algorithm" "lop" "radius" \  
0.07 "vexity" "convex" "blend-global" "steps" 1 "overetch" 0.2}  
deposit oxide thickness=5<nm> isotropic sde= {"algorithm" "lop" }
```

**NOTE** The Scheme language is incompatible with the Tcl used by Sentaurus Process. Therefore, all Scheme commands and parameter settings must be enclosed by a pair of braces. The opening brace must be on the same line as the `sde` parameter.

In the `sde` command (not the parameter), the braces may contain any number of Scheme commands, each of which starts on a new line.

Since the braces protect the Scheme commands and parameter settings from being parsed by Tcl, they must not contain any calls to Tcl procedures in Tcl expressions. The Scheme language provides its own set of expressions, parameter definitions, and other language constructs.

## 11: Structure Generation

### Sentaurus Topography Interface

You should increase the default verbosity level when working with the `sde` command:

```
pdbSet InfoDefault 1
```

The Sentaurus Structure Editor library does not provide any error-processing facility for errors that have occurred during the solid modeling operations. This can become time consuming if a structure generation step fails and a long `diffuse` or `implant` simulation is performed for an incorrect structure. To avoid this, use a few runs with the `-f` command-line option to adjust the commands and to verify that the proper structure is created. In addition, by default, all boundary files that are written in `struct` commands in the fast mode and before remeshing are read and checked for any geometric inconsistencies. If any defects are observed, the simulation is stopped with an error. To prevent this checking, specify the parameter `!SdeCheck`.

**NOTE** By default, Sentaurus Process performs stress relaxation at the end of each etching and deposition step. This requires that a boundary-fitted mesh be constructed at the end of each step. If you do not want to track the stress through all the process steps, use the `pdbSet Mechanics EtchDepoRelax 0` command before starting 3D structure generation.

**NOTE** To prevent adjacent regions of the same material (for example gas regions) from merging, switch off region-merging using the command `pdbSet Grid No3DMerge 1`. During the process, as more regions need to be considered (for example, nitride spacer), appropriate materials must be reverted from gas to the required materials.

Finally, the option `Grid Auto3DMergeAndSeparate` (off by default) adds the following commands at the end of `photo` and `depo` when switched on:

```
(sdegeo:bool-unite (find-material-id 'depositedMaterial'))  
(sde:separate-lumps)
```

Only the last one is added after etching.

---

## Sentaurus Topography Interface

Sentaurus Process provides an interface to both Sentaurus Topography, the 2D physical etch and deposit simulator, and Sentaurus Topography 3D, the 3D physical etch and deposit simulator.

---

## Sentaurus Topography

Each `sptopo` command first transfers the current 2D geometry from Sentaurus Process to Sentaurus Topography. Then, it dispatches the command to Sentaurus Topography. Finally, it retrieves the modified 2D geometry from Sentaurus Topography and remeshes it using the MGOALS mesher in 2D.

Sending a new geometry from Sentaurus Process to Sentaurus Topography has been restricted to cases where the geometry has actually been modified in Sentaurus Process after last retrieving the structure from Sentaurus Topography, for example, when using Sentaurus Process `etch` or `deposit` command. Provisions also are made to detect whether Sentaurus Topography has actually modified the structure or simply a definition of it; for example, a new machine has been added to Sentaurus Topography. Remeshing is restricted to the commands that actually have changed the structure.

During the syntax check, Sentaurus Topography commands are dispatched to Sentaurus Topography and checked for syntactical correctness. The supported syntax of the `sptopo` command is:

```
sptopo <sptopo command>
```

or:

```
sptopo {  
    <sptopo command>  
    <sptopo command>  
    ...  
}
```

The first form of the `sptopo` command allows use of all the usual Sentaurus Process Tcl constructions in the parameter specifications of `<sptopo_command>`. This form of the command is parsed through the Tcl interpreter. Otherwise, the syntax used for the `<sptopo_command>` is the same as in each of the commands for a stand-alone Sentaurus Topography run. In Sentaurus Process command files, each `sptopo` command must start with the `sptopo` string.

The pair of braces in the second form of the command prevents this `sptopo` command from being parsed by the Tcl interpreter. No Tcl expressions must be used in the second form of the `sptopo` command. On the other hand, any number of Sentaurus Topography commands can be provided in the second form of the command, each on a separate command line. If necessary, the structure will be sent from Sentaurus Process to Sentaurus Topography once at the beginning, and retrieved and remeshed once at the end of the entire command sequence.

## 11: Structure Generation

### Sentaurus Topography Interface

Examples:

```
sptopo {
  deposit material=Oxide thickness = 0.005
  deposit material=PolySilicon thickness = 0.180
}
```

Two planar deposition steps are performed in Sentaurus Topography:

- The first fills the structure with oxide up to 5 nm above the top material position.
- The second adds a planar layer of 180 nm polysilicon.

The structure is sent to Sentaurus Topography once, retrieved, and remeshed once at the end of both deposition steps.

If masks are required in a Sentaurus Topography simulation, segments can be specified in the `sptopo` command as shown below. Alternatively, the Sentaurus Process `photo` command can be used with a mask to define a photoresist layer that will protect certain areas from being etched in a `sptopo etch` command.

The Sentaurus Process `strip` command or the command:

```
sptopo etch material=Photoresist complete
```

can be used later to remove the entire photoresist layer.

```
sptopo {
  mask name=m1 s0=-1.1 e0=-0.3 s1=0.3 e1=1.1
  etch material=PolySilicon depth=0.185 mask=m1

  machetch name=oxe1 material=Oxide anisotropy=1 rate=1
  etch machname=oxe1 time = 0.02 dx=0.03 dy=0.03 mask=m1
}
```

The preceding example defines a mask in Sentaurus Topography including:

- Geometric etching of polysilicon which is strictly vertical and restricted to the outside of the specified mask segments
- An anisotropic etching machine
- Execution of an anisotropic oxide etching in Sentaurus Topography

To increase the default verbosity level when working with the `sptopo` command, use:

```
pdbSet InfoDefault 1
```

For a complete list of commands, parameters, and syntax rules of the Sentaurus Topography simulator, refer to the *Sentaurus Topography User Guide*.

---

## Sentaurus Topography 3D

Sentaurus Process provides an interface to Sentaurus Topography 3D. This interface makes advanced etching and deposition models of Sentaurus Topography 3D available from within Sentaurus Process.

The subset of 3D commands that are needed for etching and deposition is available through the interface. One single command, `topo`, in Sentaurus Process enables all the interface functionality. The `topo` command is followed by the respective Sentaurus Topography 3D commands:

```
topo <Sentaurus Topography 3D command>
```

For a list of the supported Sentaurus Topography 3D commands, refer to the *Sentaurus Topography 3D User Guide*.

---

## Examples

---

### Using Polygon and Rectangle Mask in 2D Simulation

```
line x loc=-0.3 tag=ox
line x loc=-0.2 tag=top
line x loc=1.1 tag=bot
line y loc=-0.1
line y loc=1.1
region silicon xlo=top xhi=bot
init
polygon name=LShape2 segments= {-0.1 -1.5 -0.1 -0.5 0.5 -0.5 0.5 1.5 1.5 \
    1.5 1.5 -1.5}
mask name=Mask2 polygons= {LShape2} negative left=0.2 right=0.3 front=-0.1 \
    back=0.2
etch silicon anisotropic thickness=0.5 mask=Mask2
struct tdr=final
```

## 11: Structure Generation

### Examples

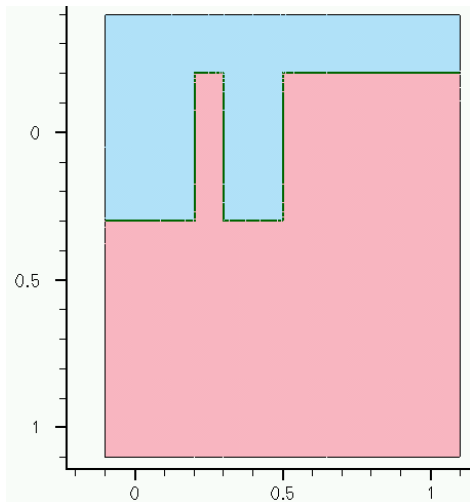


Figure 134 Final result of 2D anisotropic etching with rectangle and polygon mask

---

## 3D Etching after 2D LOCOS Simulation (Sentaurus Structure Editor Interface)

A 2D simulation result is loaded (LOCOS with nitride layer), modified in 2D, extruded to 3D, and in 3D the polysilicon and oxide are etched.

```
# load a 2D locos structure
init tdr=initial

mgoals min.normal.size=0.02 accuracy=1e-4 max.box.angle=165 \
  normal.growth.ratio=4
refinebox min= {-10 -10 -10} max= {10 10 10} xrefine=0.4 yrefine=0.4 \
  zrefine=0.4
# --- allow expanding structure to 3D ---
line z loc=-0.6 spacing=0.1
line z loc=0.5 spacing=0.1

# still in 2D
strip nitride

deposit PolySilicon thickness=100<nm> isotropic
struct tdr=locos1
sde logfile=2d3d.scm on
pdbSet InfoDefault 1
polygon name=LShape2 segments= {-0.1 -0.4 0.6 -0.4 0.6 0.2 1.1 0.2 \
  1.1 0.4 0.4 0.4 0.4 -0.2 -0.1 -0.2}
mask name=Mask2 polygons= {LShape2}
```



```
etch PolySilicon anisotropic mask=Mask2 thickness=0.41  
etch Oxide thickness=30<nm> anisotropic  
struct tdr=locos2
```

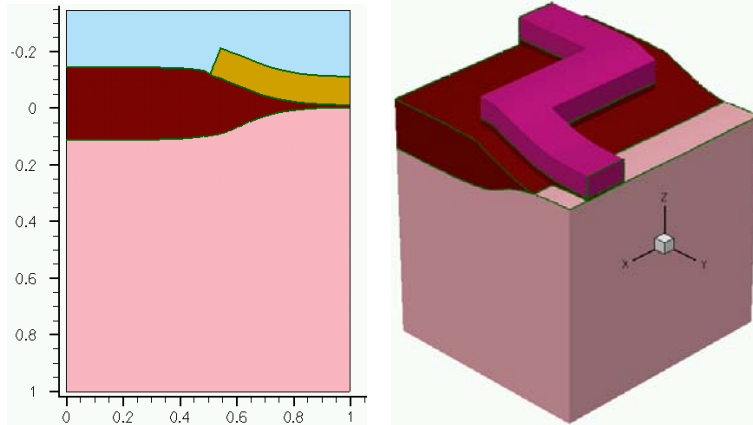


Figure 135 (*Left*) Initial 2D structure after LOCOS formation and (*right*) final result after extruding to 3D and etching of poly and oxide

## Using Layout File for 3D Etching (Sentaurus Structure Editor Interface)

This series of examples demonstrates how to use the layout file `simple.lyt` to define masks for 3D etching.

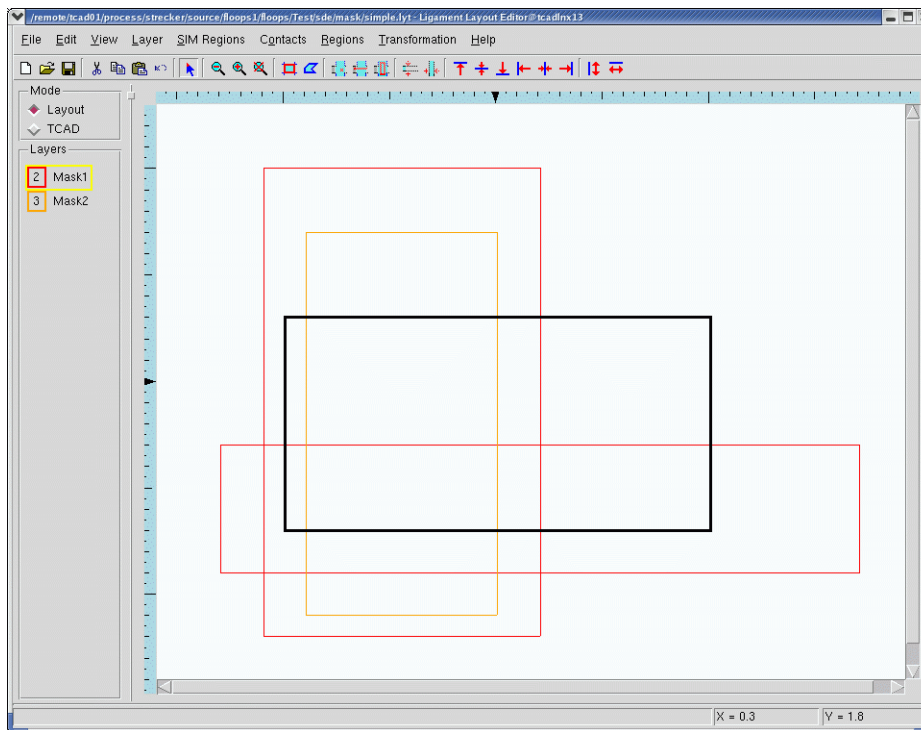


Figure 136 View of simple.lyt file in Ligament Layout Editor

Input file `mask0_fps.cmd`: The origin of the Sentaurus Process coordinate system coincides with the origin in `simple.lyt`; the y-axis of Sentaurus Process is aligned to the vertical axis in `simple.lyt`:

```
line x loc=-0.25 tag=gastop spac=0.05
line x loc=0.0 tag=substop spac=0.01
line x loc=1.5 tag=subsbottom spac=0.2
line y loc=1.65 spac=0.1
line y loc=1.95 spac=0.1
line z loc=0.15 spac=0.1
line z loc=0.6 spac=0.1

region silicon xlo=substop xhi=subsbottom

mgoals min.normal.size=0.02 accuracy=1e-4 max.box.angle=165 \
normal.growth.ratio=4
```

```
refinebox min= {-10 -10 -10} max= {10 10 10} xrefine=0.2 yrefine=0.2 \  
    zrefine=0.2  
refinebox interface.materials = {Silicon Oxide}  
init  
deposit oxide thickness=100<nm> isotropic  
sde logfile=mask0.scm on  
pdbSet InfoDefault 1  
  
mask layoutfile=simple.lyt  
  
# deposition with masks deposits where there is no mask  
# so invert the mask used for deposition  
mask name=Mask2 negative  
  
deposit nitride thickness=0.25<um> anisotropic info=1 mask=Mask2  
  
struct bndfile=mask0_0.bnd  
etch oxide thickness=120<nm> type=anisotropic mask=Mask1  
  
struct bndfile=mask0_1.bnd  
  
struct tdr=mask0
```

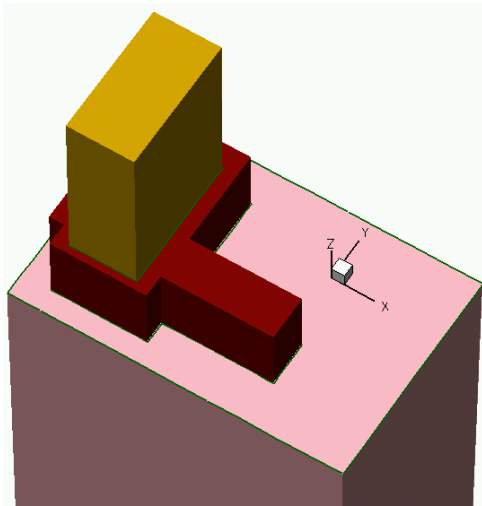


Figure 137 Final structure after simulation of mask0\_fps.cmd

## 11: Structure Generation

### Examples

Input file `mask1_fps.cmd`: A `CutLine2D` is used to place the simulation domain in the layout file. The extensions of the 3D simulation domain in the y- and z-directions must be specified using line commands. The cutline is defined as the diagonal through the structure used in `mask1_fps.cmd`, such that the Sentaurus Process origin is shifted and the coordinate system is rotated compared to `mask0_fps.cmd`:

```
line x loc=-0.25 tag=gastop spac=0.05
line x loc=0.0 tag=substop spac=0.01
line x loc=1.5 tag=subsbottom spac=0.2

line y loc=0. spac=0.1
line y loc=0.4 spac=0.1

line z loc=-0.2 spac=0.1
line z loc=0.15 spac=0.1

region silicon xlo=substop xhi=subsbottom

mgoals min.normal.size=0.02 accuracy=1e-4 max.box.angle=165 \
  normal.growth.ratio=4
refinebox min= {-10 -10 -10} max= {10 10 10} xrefine=0.2 yrefine=0.2 \
  zrefine=0.2
refinebox interface.materials = {Silicon Oxide}

# define a coordinate transformation for a placement and rotation
# of a layout file
init slice.angle=[CutLine2D 1.65 0.15 1.95 0.6]

deposit oxide thickness=100<nm> isotropic
sde logfile=mask1.scm on
pdbSet InfoDefault 1

# do not specify any name ==> use the outline from the init command
# to place the Sentaurus Process coordinate system in the layout.
# the first specified point becomes the origin of the Sentaurus Process
# coordinate system and the direction of the outline becomes the direction
# of the Sentaurus Process z-axis.
mask layoutfile=simple.lyt

# deposition with masks deposits where there is no mask
# so invert the mask used for deposition
mask name=Mask2 negative

deposit nitride thickness=0.25<um> anisotropic info=1 mask=Mask2
```

```

struct bndfile=mask1_0.bnd
etch oxide thickness=120<nm> type=anisotropic mask=Mask1
struct bndfile=mask1_1.bnd
struct tdr=mask1

```

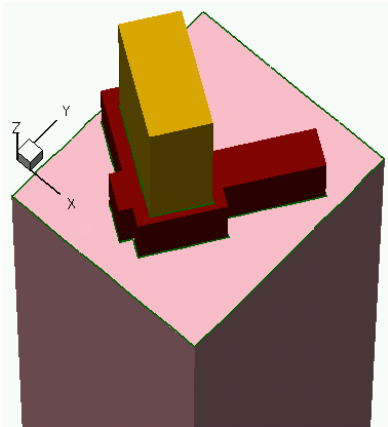


Figure 138 Final result of mask1\_fps.cmd

Input file mask2\_fps.cmd: A SIM3D mask is used, defined in the layout file:

```

# Use a layout file and place it according to the mask SIM3D, defined in the
# layout file itself.

# SIM3D defines an axis aligned rectangle in the layout plane. The point
# with the smallest layoutX and layoutY coordinates defines the
# origin of the Sentaurus Process coordinate system. The direction of the
# layoutX axis is used for the Sentaurus Process z-axis
# and the direction of the layoutY axis is used for the Sentaurus Process
# y-axis.

# The width of the rectangle (max(layoutX)-min(layoutX)) defines the
# default extension in Sentaurus Process z-direction.
# The height of the rectangle (max(layoutY)-min(layoutY)) defines the
# default extension in Sentaurus Process y-direction.
# If you specify line y and/or line z, your definitions are used.
# Otherwise the default extensions are used to define line y and line z
# when reading the layout file.

line x loc=-0.25 tag=gastop spac=0.05
line x loc=0.0 tag=substop spac=0.01
line x loc=1.5 tag=subsbottom spac=0.2

region silicon xlo=substop xhi=subsbottom

mgoals min.normal.size=0.02 accuracy=1e-4 max.box.angle=165 \
normal.growth.ratio=4

```

## 11: Structure Generation

### Examples

```
refinebox min= {-10 -10 -10} max= {10 10 10} xrefine=0.2 yrefine=0.2 \  
  zrefine=0.2  
refinebox interface.materials = {Silicon Oxide}  
init  
deposit oxide thickness=100<nm> isotropic  
sde logfile=mask2.scm on  
pdbSet InfoDefault 1  
mask layoutfile=simple.lyt name=SIM3D  
  
# In Sentaurus Process, deposition with masks deposits where  
# there is no mask so invert the mask used for deposition  
mask name=Mask2 negative  
  
deposit nitride thickness=0.25<um> anisotropic info=1 mask=Mask2  
struct bndfile=mask2_0.bnd  
etch oxide thickness=120<nm> type=anisotropic mask=Mask1  
struct bndfile=mask2_1.bnd  
struct tdr=mask2
```

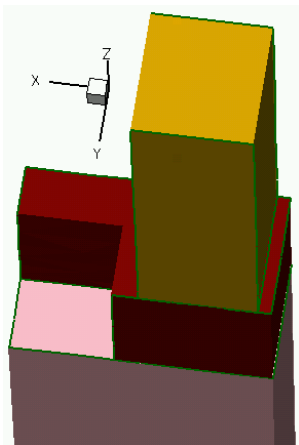


Figure 139 Final simulation result for mask2\_fps.cmd; the y- and z-extensions are not specified in the command file but are taken from the SIM3D mask in simple.lyt (black line in [Figure 136 on page 776](#))

---

## 3D Trench Etching, Sloped Sidewall with Predefined Angle (Sentaurus Structure Editor Interface)

```
line x loc=-0.25 tag=gastop spac=0.05  
line x loc=0.0 tag=substop spac=0.01  
line x loc=0.5 tag=subsbottom spac=0.2  
  
line y loc=0.0 spac=0.1  
line y loc=0.4 spac=0.1
```

```

line z loc=0 spac=0.1
line z loc=0.6 spac=0.1
region silicon xlo=substop xhi=subsbottom

mgoals min.normal.size=0.02 accuracy=1e-4 max.box.angle=165 \
  normal.growth.ratio=4
refinebox min= {-10 -10 -10} max= {10 10 10} xrefine=0.2 yrefine=0.2 \
  zrefine=0.2
refinebox interface.materials = {Silicon Oxide}

init concentration=1.4e+15<cm-3> field=boron wafer.orient=100
deposit oxide thickness=0.01 type=isotropic
fset NitrideThick 0.1
deposit nitride thickness=0.1 type=isotropic

mask name=STI left=-1 right=0.2 front=-1 back=0.4
deposit Photoresist isotropic thickness=0.5

sde logfile=sti3d.scm on
pdbSet InfoDefault 1

etch Photoresist anisotropic thickness=0.5*1.5 mask=STI
struct bndfile=photol.bnd
fproc etchAngle { Angle Material Depth } {

  set alpha [expr ${Angle}*atan(1.0)/45.0] ; #Degree to radiant conv.
  set x1     [expr sin($alpha)] ; #x-component of etch directional vector
  set x2     [expr cos($alpha)] ; #y-component of etch directional vector
  set x3     [expr cos($alpha)] ; #z-component of etch directional vector
  set etchRate [expr 1.0/sin($alpha)]
  etch material=$Material time=$Depth type=directional \
    direction= { $x1 $x2 $x3 } rate=$etchRate
}

fset NitrideAngle 89.0
etchAngle $NitrideAngle Nitride $NitrideThick*1.5

etch Oxide anisotropic thickness=0.02
strip Photoresist
fset TrenchAngle 84.0
fset TrenchDepth 0.2
etchAngle $TrenchAngle Silicon $TrenchDepth

struct bndfile=final.bnd
struct tdr=final

```

## 11: Structure Generation

### Examples

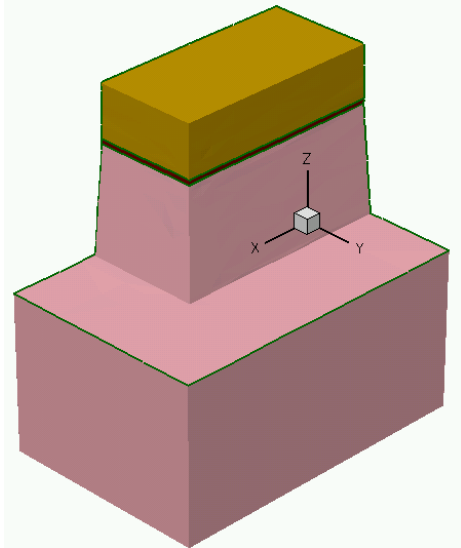


Figure 140 Final result of simulation of STI etching with predefined sidewall angles

---

## 3D Etching after 2D LOCOS Simulation using MGOALS3D

An example, similar to [3D Etching after 2D LOCOS Simulation \(Sentaurus Structure Editor Interface\) on page 774](#), but with some extra processing steps, can be performed using MGOALS3D. The script is as follows:

```
# Switch off stress relaxation after depo/etch
pdbSet Mechanics EtchDepoRelax 0

# Load a 2D locos structure
init tdr=initial

mgoals resolution=0.2 min.normal.size=0.02 accuracy=1e-4 max.box.angle=165 \
  norm
refinebox min= {-10 -10 -10} max= {10 10 10} xrefine=0.4 yrefine=0.4 zrefine=0.

# --- allow expanding structure to 3D ---
line z loc=-0.6 spacing=0.1
line z loc=0.5 spacing=0.1

# Still in 2D
strip nitride

deposit PolySilicon thickness=100<nm> isotropic
struct tdr=locos1
#sde logfile=2d3d.scm on
```



```

sde off
pdbSet InfoDefault 2
pdbSet Grid sMesh 1

polygon name=LShape2 segments= {-0.1 -0.4 0.6 -0.4 0.6 0.2 1.1 0.2 1.1 0.4}
mask name=Mask2 polygons= {LShape2}

etch PolySilicon anisotropic mask=Mask2 thickness=0.41
struct tdr=locos2

etch Oxide thickness=30<nm> anisotropic
struct tdr=locos3

mgoals resolution=0.3
deposit oxide thickness=10<nm> isotropic
struct tdr=locos4

mgoals resolution=0.2
deposit nitride thickness=100<nm> isotropic
struct tdr=locos5

etch nitride thickness=120<nm> anisotropic
struct tdr=locos6 bnd

```

The initial 2D LOCOS structure (`initial.tdr`) is the left one represented in [Figure 135 on page 775](#). The `sde off` command is used to overwrite the standard setting and MGOALS is used.

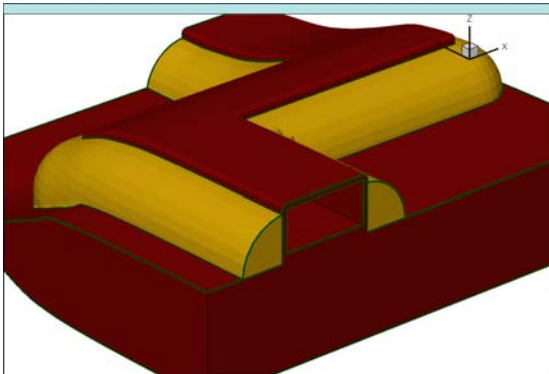


Figure 141 Script result simulated with MGOALS3D; polysilicon and silicon are not shown to better reveal the structure features

---

## Structure Assembly in MGOALS3D

The following scripts creates a tdr file to be “pasted”

```

set gate 30e-3
set sti 55e-3
set sti_thick 100e-3
set gas_top 86e-3
set silicon_depth 300e-3
set zsize 640e-3
set SiO2gate 1.5e-3
set spacer 30e-3
set spacer_thick 30e-3
set extra 60e-3
set poly 80e-3
set factor 1.1

sde off
line x loc=0.0 tag=xtop
line x loc=$silicon_depth tag=xbottom
line y loc=0.0 tag=yleft
line y loc=[expr 2*$extra + 2*$spacer + 2*$sti + $gate] tag=yright spacing =
0.002
line z loc=0
line z loc=0.05
line z loc=0.1
region silicon xlo=xtop xhi=xbottom

init
#STI
set ll1 [expr 0]
set rr1 [expr $sti]
set ll2 [expr $sti + 2*$extra + 2*$spacer + $gate]
set rr2 [expr $ll2 + $sti]
mask negative name=sti_mask left=$ll1<um> right=$rr1<um>
mask negative name=sti_mask left=$ll2<um> right=$rr2<um>
etch silicon thickness=$sti_thick mask=sti_mask anisotropic
deposit oxide fill coord=[expr -$SiO2gate]
#poly gate
deposit polysilicon thickness=$poly isotropic
set ll3 [expr $sti + $extra+$spacer]
set rr3 [expr $ll3 + $gate]
mask name=gate_mask left=$ll3 right=$rr3
etch polysilicon mask=gate_mask anisotropic thickness=$poly
#spacer
deposit nitride thickness=$spacer_thick isotropic
etch nitride thickness=[expr $spacer_thick * $factor] anisotropic

```

```
#rotate and transform into a 3D structure
transform rotate angle=90 axis = {X}
struct tdr=rotateX
```

Figure 142 on page 786 (*upper right*) shows the created structure.

Now, a simple structure is created with the same dimensions in the plane to be pasted and the structures are put together:

```
set xsize 0.3
set ysize 0.1
set zsize 0.32

line x loc=0.0      tag=xleft
line x loc=$xsize/2 tag=xmed
line x loc=$xsize   tag=xright
line y loc=0.0      tag=ybottom
line y loc=$ysize/2 tag=ymed
line y loc=$ysize   tag=ytop
line z loc=0        tag=zinit
line z loc=$zsize/2 tag=zmed
line z loc=$zsize   tag=zend
region oxide  xlo=xleft xhi=xmed ylo=ymed yhi=ytop zlo=zinit zhi=zmed
region silicon xlo=xleft xhi=xmed ylo=ymed yhi=ytop zlo=zmed zhi=zend
region silicon xlo=xleft xhi=xmed ylo=ybottom yhi=ymed zlo=zinit zhi=zend
region silicon xlo=xmed xhi=xright ylo=ybottom yhi=ytop zlo=zinit zhi=zend

init
sde off
struct tdr = orig
paste direction = "right" tdr = "rotateX"
struct tdr = pasted_right
```

Figure 142 (*upper left*) shows the structure created before the `paste` operation, and the final result is shown in the lower-left figure.

## 11: Structure Generation

### Examples

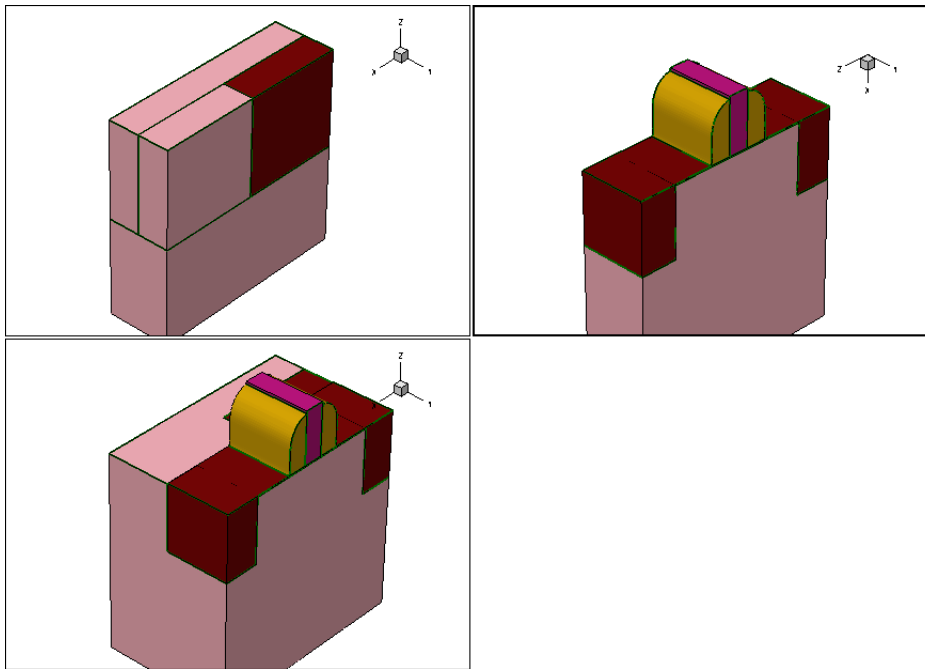


Figure 142 (Upper left) The initial structure, (upper right) the structure read from the file, and (lower left) the final structure after paste command

---

## Polygon Creation and Insertion in MGOALS2D

The following script creates a 2D structure and saves it into a file:

```
set gate 30e-3
set sti 55e-3
set sti_thick 100e-3
set gas_top 86e-3
set silicon_depth 300e-3
set zsize 640e-3
set SiO2gate 1.5e-3
set spacer 30e-3
set spacer_thick 30e-3
set extra 60e-3
set poly 80e-3
set factor 1.1
refinebox min = { 0 0 } max = { 0.1 2 } xrefine = { 0.0012 0.0015 0.0015 }
line x loc=0.0 tag=xtop
line x loc=$silicon_depth tag=xbottom
line y loc=0.0 tag=yleft
line y loc=[expr 2*$extra + 2*$spacer + 2*$sti + $gate] tag=yright spacing =
```

```

0.002
region silicon xlo=xtop xhi=xbottom

init
#STI
set ll1 [expr 0]
set rr1 [expr $sti]
set ll2 [expr $sti + 2*$extra + 2*$spacer + $gate]
set rr2 [expr $ll2 + $sti]
mask negative name=sti_mask left=$ll1<um> right=$rr1<um>
mask negative name=sti_mask left=$ll2<um> right=$rr2<um>
etch silicon thickness=$sti_thick mask=sti_mask anisotropic
deposit oxide fill coord=[expr -$SiO2gate]
#poly gate
deposit polysilicon thickness=$poly isotropic
set ll3 [expr $sti + $extra+$spacer]
set rr3 [expr $ll3 + $gate]
mask name=gate_mask left=$ll3 right=$rr3
etch polysilicon mask=gate_mask anisotropic thickness=$poly
#spacer
deposit nitride thickness=$spacer_thick isotropic
etch nitride thickness=[expr $spacer_thick * $factor] anisotropic
struct tdr=orig

```

Now, a triangular polygon is created in the xy plane and is called box:

```

point name=p1 coord = { -0.2 0.2 }
point name=p2 coord = { 0.2 0.25 }
point name=p3 coord = { 0.1 0.1 }
polygon name=box xy points = { p1 p2 p3 }

```

Finally, the triangular polygon is inserted into the original structure as Aluminum, but only in the nitride and silicon materials:

```

insert polygon = "box" replace.materials = { "Silicon" "Nitride" } \
    new.material = "Aluminum"
struct tdr=points

```

[Figure 143 on page 788](#) (*upper left*) shows the initial structure, and the lower-left figure shows the results after the insertion.

You also can read the polygon from a TDR file and insert it later. The following script reuses the files from the previous example by doing that. It reads the Aluminum material as a polygon, and inserts it in the original script as oxide in silicon material only:

```

init tdr=orig
polygon name=box xy tdr = "points_bnd.tdr" materials = "Aluminum"
insert polygon = "box" replace.materials = "Silicon" new.material = "Oxide" \

```

## 11: Structure Generation

### Examples

```
info=4  
struct tdr=tdr
```

Figure 143 (lower left) shows the results after the insertion.

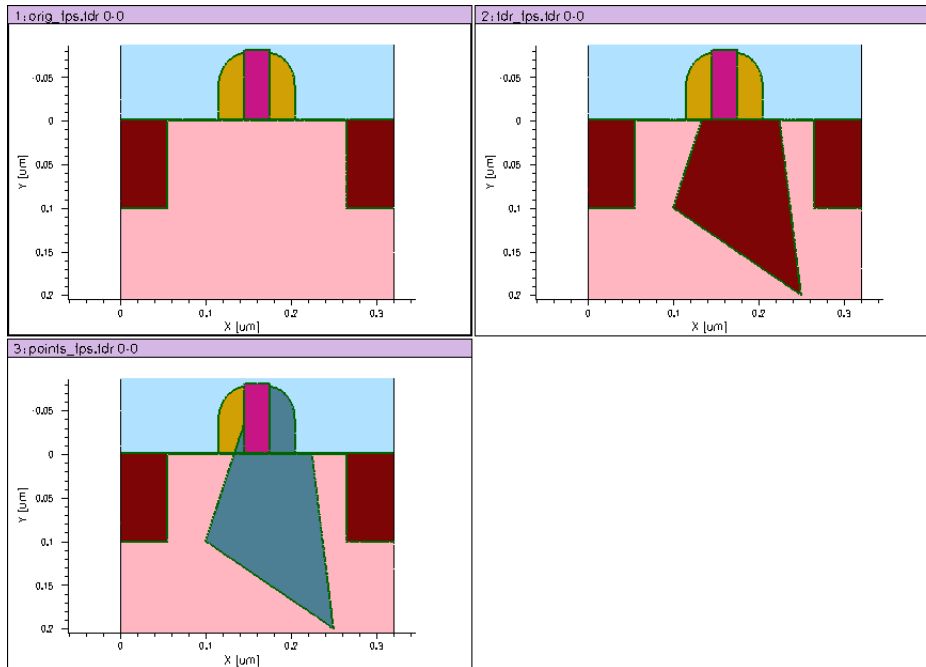


Figure 143 Use of insert command in a 2D simulation: (upper left) initial 2D structure, (lower left) triangular polygon being inserted in the initial structure for silicon and nitride only, and (upper right) the results of reading the triangle of the lower-left figure and inserting it as oxide in the silicon of the initial structure

---

## Polyhedron Creation and Insertion in MGOALS3D

All the following examples use the structure in [Figure 144](#) as a starting point to be modified by polyhedron creation and insertion.

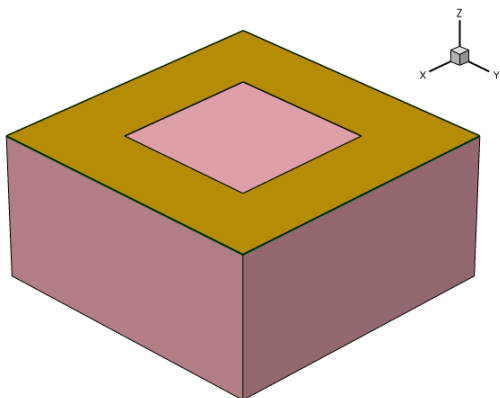


Figure 144 Initial 3D structure used for polyhedron creation and insertion examples

### Reading a TDR file

This example uses two spheres created with Sentaurus Structure Editor using the following script:

```
(sde:clear)

(sdegeo:create-sphere (position 3.0 3.0 4.7) 0.9 "Silicon" "Silicon_1")
(sdegeo:create-sphere (position 0.7 0.7 4.7) 0.9 "Gas" "Gas_2")

(sdeio:save-tdr-bnd "all" "sphere.tdr")
```

The spheres are inserted into Sentaurus Process. The gas sphere etches the material, while the silicon one is deposited:

```
init tdr=initial

refinebox clear
sde off

polyhedron name=sphere tdr=sphere.tdr materials = { Silicon Gas }
insert polyhedron=sphere

struct bndfile=result
```

## 11: Structure Generation

### Examples

Figure 145 shows the result of the above script.

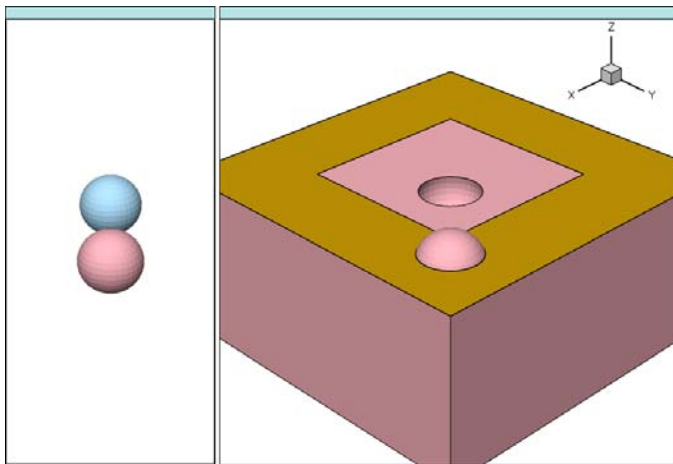


Figure 145 (Left) Polyhedra included in a TDR boundary file and (right) effect of inserting them in initial structure

## Extruding a 2D Polygon

This example creates a simple 2D polygon – a triangle:

```
init tdr=initial
math coord.ucs
refinebox clear
sde off
```

```
polygon name=triangle segments = { -4.2 -3.0 3.2 0.5 -4.7 4.2 }
```

The polyhedron command uses the triangle to extrude in the x-direction:

```
polyhedron name=prism polygons = { triangle } min=-6 max=2
```

Finally, to insert it, specify new.material as gas to etch the extruded polygon:

```
insert polyhedron=prism new.material=Gas

struct bndfile=result
```



Figure 146 shows the result.

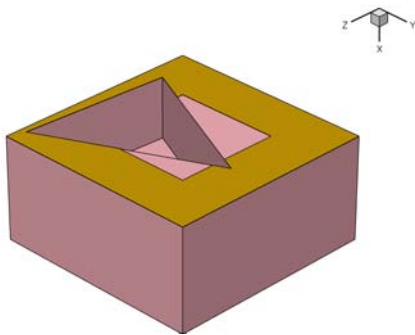


Figure 146 Etching an extruded polygon

## Creating a Polyhedron using Polygons

This example defines the polyhedra from the beginning using polygons:

```

init tdr=initial
refinebox clear
sde off

point name=p1 coord = { -6.5 2.0 2.0 }
point name=p2 coord = { -2.0 4.0 1.5 }
point name=p3 coord = { -2.0 2.0 3.0 }
point name=p4 coord = { -2.0 1.5 1.0 }

polygon name=face1 points = { p1 p2 p3 }
polygon name=face2 points = { p1 p3 p4 }
polygon name=face3 points = { p1 p2 p4 }
polygon name=face4 points = { p2 p3 p4 }

polyhedron name=tetrahedron polygons = { face1 face2 face3 face4 }

```

Now, the initial structure is etched using the new polyhedron:

```

insert polyhedron=tetrahedron new.material=Gas
struct bndfile=result

```

## 11: Structure Generation

### Examples

Figure 147 shows the simulation results.

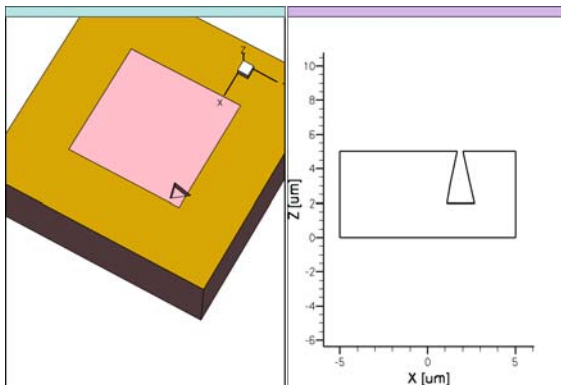


Figure 147 Etching of a polyhedron defined by using polygons: (*left*) 3D general view and (*right*) y-plane cut view

## Defining a Brick

The `brick` option provides a convenient way to define a rectangular prism by defining the lower and upper corners. The script is as follows:

```
init tdr=initial
refinebox clear
sde off

polyhedron name=smallCube brick = { -6 -4 -2 -1 4.5 1 }
```

Now, you can use the polyhedron to insert an oxide brick into the simulation:

```
insert polyhedron=smallCube new.material=Oxide
struct bndfile=result
```

Figure 148 shows the result.

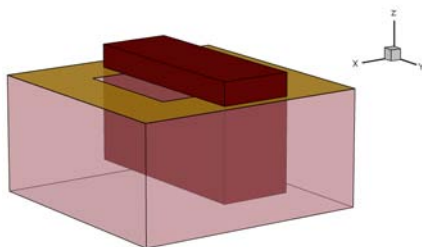


Figure 148 Oxide brick inserted in initial structure

## References

- [1] J. A. Sethian, *Level Set Methods and Fast Marching Methods: Evolving interfaces in computational geometry, fluid mechanics, computer vision, and materials science*, Cambridge: Cambridge University Press, 1999.

## 11: Structure Generation

References

## CHAPTER 12 ICWBEV Plus Interface for Layout-driven Simulations

---

*This chapter presents strategies for using the IC WorkBench EV Plus–TCAD Sentaurus interface.*

---

### Overview

The IC WorkBench EV Plus (ICWBEV Plus)–TCAD Sentaurus interface drives the TCAD simulations from the GDSII or OASIS layout file provided by designers, which could be at any level of integration in the hierarchy: full chip, test chip, or a single cell.

The TCAD simulation domain can be conveniently chosen using specific markups in the layout file. A single process flow can be defined for all devices in the layout and can be applied easily with minimal adjustments for 1D, 2D, and 3D simulation domains. For meshing, it provides the unique feature of layout-driven meshing. Electrical contacts can be defined easily using auxiliary masks.

This chapter includes the following sections:

- [ICWBEV Plus Introduction for TCAD Users on page 796](#) provides basic ICWBEV Plus training, especially with relevance to TCAD.
- [Files Relevant to ICWBEV Plus–TCAD Sentaurus on page 806](#) introduces the relevant files and file formats used in the ICWBEV Plus–TCAD Sentaurus interface. Specifically, the Sentaurus markup file (\*\_mkp.mcr) and TCAD layout file (\*\_lyt.mcr).
- [ICWBEV Plus Batch Mode and Macros on page 811](#) introduces working with macros and running ICWBEV Plus in batch mode.
- [TCAD Layout Reader of Sentaurus Process on page 812](#) presents the TCAD layout reader of Sentaurus Process that provides a file-based interface between ICWBEV Plus and Sentaurus Process.

---

## ICWBEV Plus Introduction for TCAD Users

Before discussing the ICWBEV Plus–TCAD Sentaurus interface, it is important to have an understanding of ICWBEV Plus itself.

The general ICWBEV Plus training is a good starting point. Here, the focus is mainly on ICWBEV Plus operations that are most relevant to TCAD Sentaurus users.

For details, refer to the ICWBEV Plus tutorials and manuals, which are accessed through the main window of ICWBEV Plus (**Help > Topics**). The homepage of the online documentation is displayed (see [Figure 149](#)).

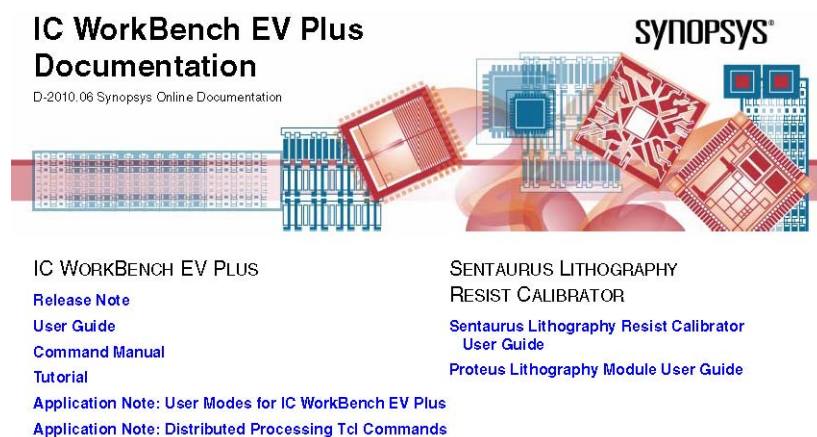


Figure 149 Homepage of ICWBEV Plus online documentation

The first step consists of opening a layout file, which is typically in GDSII format.

---

## Opening GDSII Layout Files

To open a GDSII or an OASIS layout file:

1. Set the environment variable `ICWBEV_USER` to activate the ICWBEV Plus Sentaurus User Mode:

```
setenv ICWBEV_USER SENTAURUS
```

2. Launch ICWBEV Plus by typing:

```
icwbev
```

3. Select the file to be opened: **File > Open > Browse for GDSII > Select GDSII > Open.**

**NOTE** Use ICWBEV Plus Version B-2008.12 or later.

## Graphical User Interface of ICWBEV Plus

Figure 150 shows the graphical user interface (GUI) of ICWBEV Plus and illustrates the typical layout of work, panes, and toolbars. The panes can be moved and reconfigured as needed.

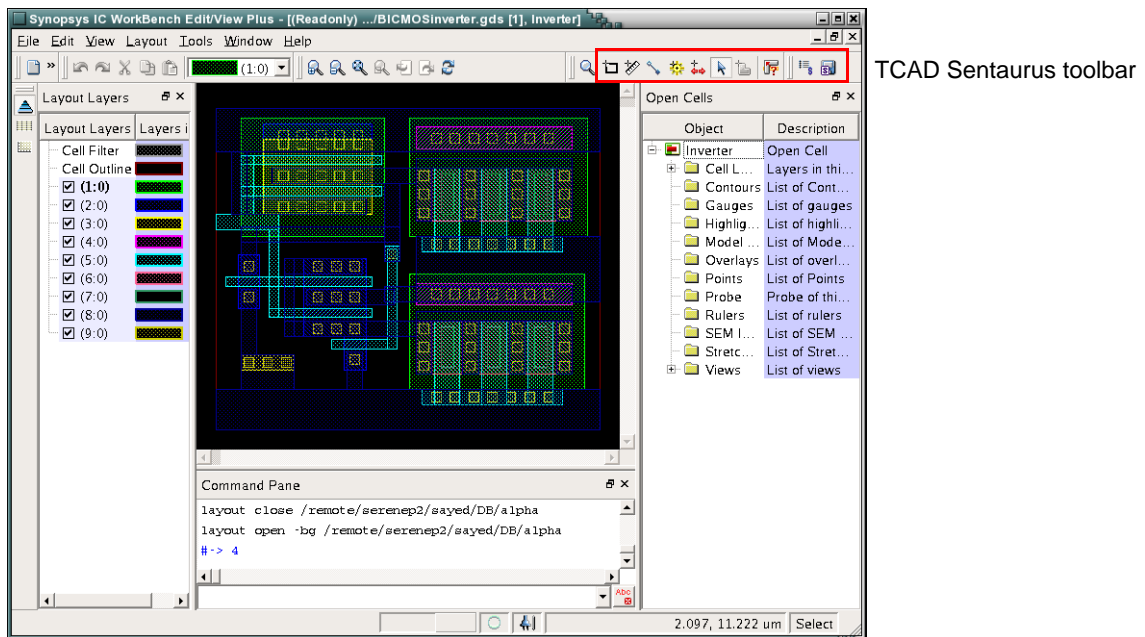


Figure 150 ICWBEV Plus main window, with TCAD Sentaurus-specific buttons (red box)

Figure 150 includes the following TCAD-relevant items in the GUI:







- The Layout Layers pane shows the list of layers.
- The Command Pane shows commands after GUI operations. Commands also can be entered directly in this pane.
- The Open Cells pane contains details about layers and markups including the TCAD-relevant markups.

## 12: ICWBEV Plus Interface for Layout-driven Simulations

### ICWBEV Plus Introduction for TCAD Users

The TCAD Sentaurus toolbar is located in the upper-right corner of the main window. [Table 72](#) describes the relevant toolbar buttons.

Table 72 TCAD Sentaurus-specific toolbar buttons

Button	Description	Button	Description
	3D simulation domain (highlight)		Stretch utility
	2D simulation domain (gauge)		Save TCAD layout
	1D simulation domain (point)		Save markups

## Sentaurus Markups

Sentaurus markups are used to add the simulation domain in 1D, 2D, and 3D domains as needed. The Command Pane in [Figure 151](#) shows the commands after adding Sentaurus markups in the layout using GUI actions.

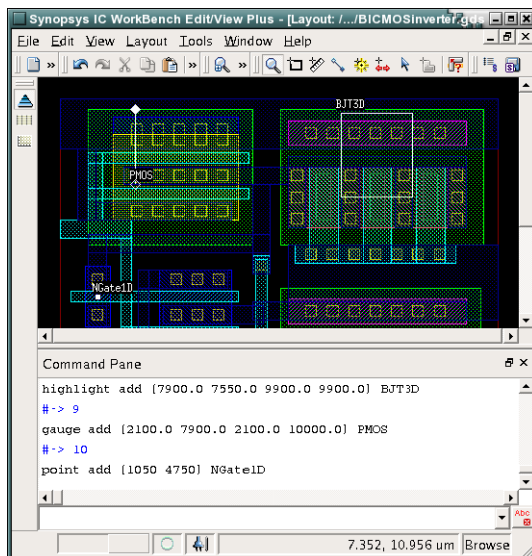


Figure 151 Adding Sentaurus markups to a layout

To add a 3D simulation domain (highlight), a 2D simulation domain (gauge), or a 1D simulation domain (point), click the respective toolbar button and draw a rectangle, a line, or a point on the layout, respectively.



**NOTE** A 2D simulation domain (gauge) has a direction. The starting point is given as an open diamond, and the endpoint is given as a filled diamond. A gauge that runs parallel to an edge of a layer must have a finite orthogonal distance to that edge. If a gauge is collinear with the edges of a layer, this edge might not be included in the 2D mask.

The default naming convention is:

- For highlights, SIM3D<n>.
- For gauges, SIM2D<n>.
- For a point, SIM1D<n>.

where <n> is an automatically incremented number.

For 2D TCAD simulations, it can be useful to work with composite simulation domains, for example, when the different contacts in a device layout cannot be connected by a single straight line. In this case, it is not possible to perform a 2D device simulation after a 2D process step using a single 2D simulation domain. However, a 2D TCAD simulation using a composite 2D simulation domain is feasible. In this case, the various 2D cuts in the layout are *daisy-chained* to form a composite 2D simulation domain.

An example of a composite simulation domain is shown in [Figure 152](#), which shows a close-up of the layout of a bipolar transistor with two 2D TCAD simulation domains. The simulation domain labeled BJTBE cuts through two base–contact fingers and one emitter finger. The simulation domain labeled BJTC cuts through the collector contact.

**NOTE** The two simulation domains are orthogonal and not contiguous.

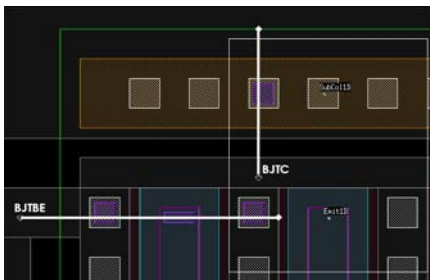


Figure 152 Layout of a bipolar transistor with two 2D simulation domains: BJTBE cuts through two base–contact fingers and one emitter finger, and BJTC cuts through the collector contact

[Figure 153 on page 800](#) shows the 2D TCAD simulation results obtained with a composite simulation domain consisting of both the BJTBE and BJTC domains. Using a composite simulation domain allows simulating a functional bipolar junction transistor (BJT) even for a 2D TCAD simulation.

## 12: ICWBEV Plus Interface for Layout-driven Simulations

### ICWBEV Plus Introduction for TCAD Users

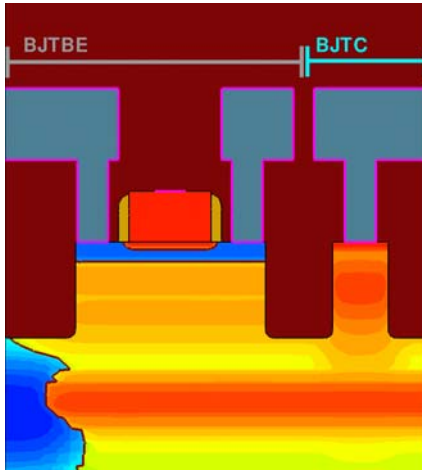


Figure 153 Two-dimensional TCAD simulation results using composite simulation domain consisting of the 2D domains BJTBE and BJTC

---

## Stretch Utility

The stretch utility provides a convenient way to parameterize a layout by inserting a uniformly stretched segment into the layout. For example, this feature can be used to generate a set of transistors that have different gate lengths but are otherwise identical.

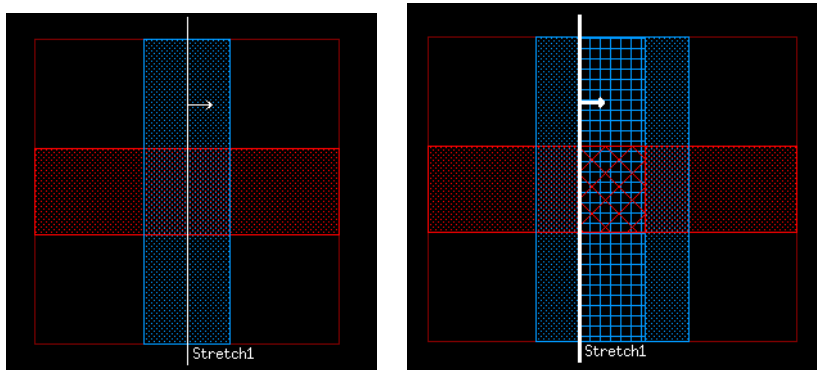


Figure 154 (Left) Snapshot of sample ICWBEV Plus layout with stretch utility line and (right) effective layout seen by Sentaurus Process when the layout is loaded with a positive stretch amount

A stretch line must be defined in ICWBEV Plus first. The stretch amount is set after loading the TCAD layout with the Sentaurus Process command:

```
icwb stretch name= "<stretch-name>" value= <stretch-amount>
```

This feature can be used for simple parameterization of layouts for quantities such as threshold rolloff. [Figure 155](#) shows a close-up of the layout containing an NMOS transistor. In addition, two stretch lines are shown. The stretch line labeled `NMOS_W` is used to vary gate width, and the one labeled `NMOS_L` is used to vary the gate length in an NMOS.

To add a stretch line:

- Click the stretch utility toolbar button, and draw a line across the required region in the layout.

**NOTE** The stretch line must cross the entire simulation domain to which it should be applied. Stretch lines can be used for 2D and 3D simulation domains.

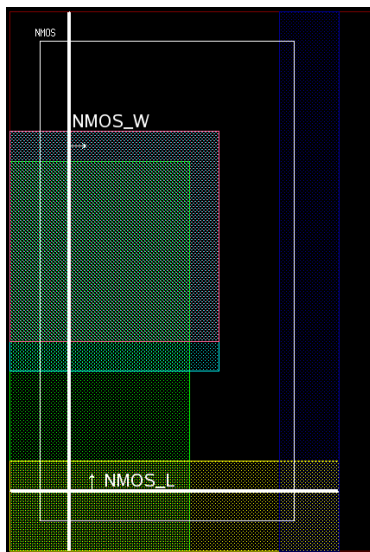


Figure 155 Adding stretch lines in a layout to vary gate width and gate length

[Figure 156 on page 802](#) shows the resulting changes in the NMOS gate width and gate length. The default naming scheme for a stretch line is `Stretch<n>`.

For example, to apply a stretch at run-time in Sentaurus Process, use a command such as:

```
icwb stretch name= "NMOS_W" value=@Stretch@
```

where `NMOS_W` is the name of the stretch variable. Here, the amount of stretching is defined using the Sentaurus Workbench variable `@Stretch@`. A positive stretch value is used for expansion; a negative value leads to shrinkage.

## 12: ICWBEV Plus Interface for Layout-driven Simulations

### ICWBEV Plus Introduction for TCAD Users

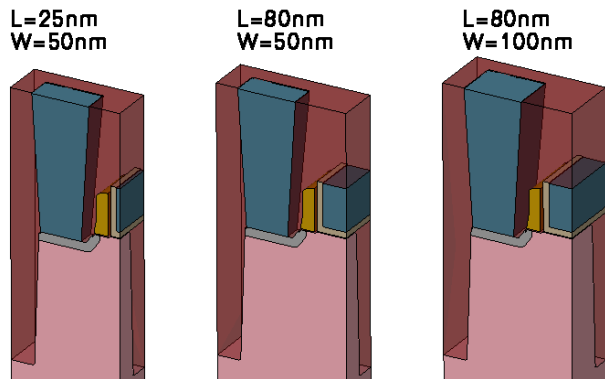


Figure 156 Effect of stretch utility on 3D NMOS structure showing variation in width and length

---

## Renaming Markups

Markups can be renamed and edited.

To rename markups:

1. **View > Views > Open Cells.**
2. Expand the markup type, for example, **Highlights**.
3. Click the respective Sentaurus Process markup to edit the name.
4. Click the coordinates to edit the coordinate values.

Figure 157 shows the Open Cells pane, displaying the list of Sentaurus Process markups and their coordinates that can be edited as required.

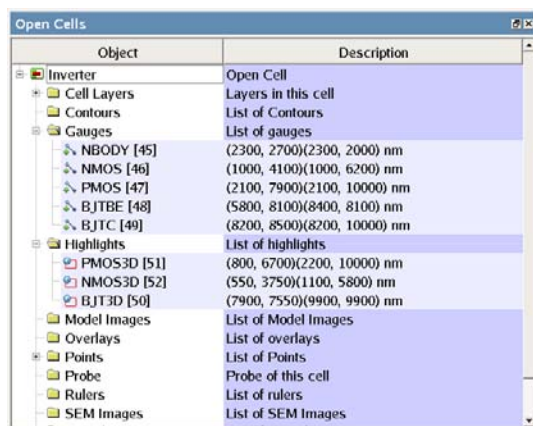


Figure 157 Open Cells pane showing list of objects with descriptions

---

## Auxiliary Layers

Auxiliary layers are used, for example, to denote the position of electrical contacts in a layout. To add auxiliary layers, first a layer must be declared and attributes must be defined. [Figure 158](#) illustrates how to define a layer and its attributes.

To add auxiliary layers, draw a polygon defining the region of the layer:

1. Open the layout for editing: **Edit > Cell Edit**.
2. Select the active layer.
3. Select the shape tool.
4. Draw a polygon.

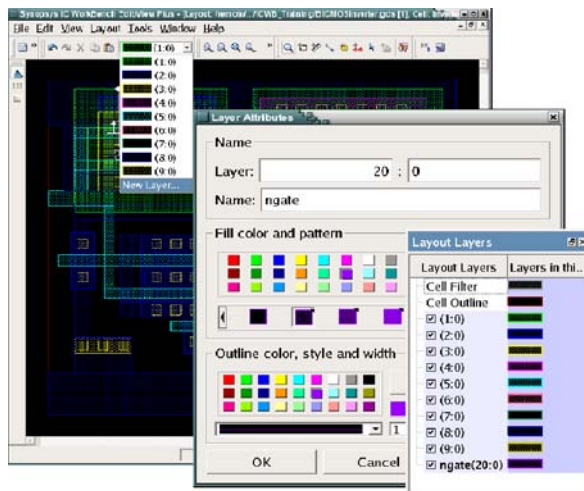


Figure 158 Defining a layer and its attributes

---

## Editing Polygons

If required, polygons can be edited. You can edit polygons by either:

- Resizing a rectangle.
- Converting a rectangle to a polygon.

## Resizing a Rectangle

To resize a rectangle:

1. If not already open, open the layout for editing: **Edit > Cell Edit**.
2. Activate the selector tool.
3. Click the polygon edge to select it.
4. Move the edge as needed.

Figure 159 shows a rectangle highlighted for editing.

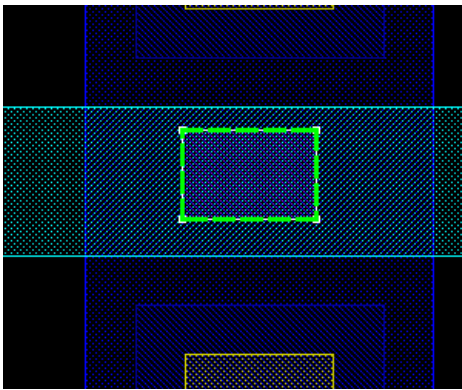


Figure 159 Moving the edge of a rectangle: select the rectangle and drag an edge

## Converting a Rectangle to a Polygon

To convert a rectangle to a polygon:

1. Click the polygon edge to select it.
2. Right-click and select **Split Edge**.
3. Move the edge as needed.

Figure 160 illustrates the procedure.

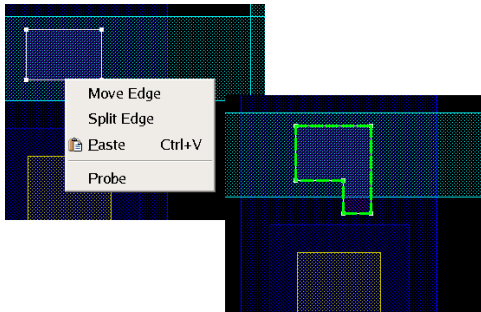


Figure 160 Converting a rectangle to a polygon

---

## Nonaxis-aligned Simulation Domains

The ICWBEV Plus–TCAD Sentaurus interface supports nonaxis-aligned domains. To realize nonaxis-aligned simulation domains, the GDSII layout is rotated by a given angle, and the TCAD simulation domain is added as discussed in [Sentaurus Markups on page 798](#).

To rotate a GDSII layout:

1. **Layout > Transform.**
2. In the Cell Transformation dialog box, enter the values of the fields as required.

Figure 161 shows the transformation of a GDSII layout and the transformation parameters.

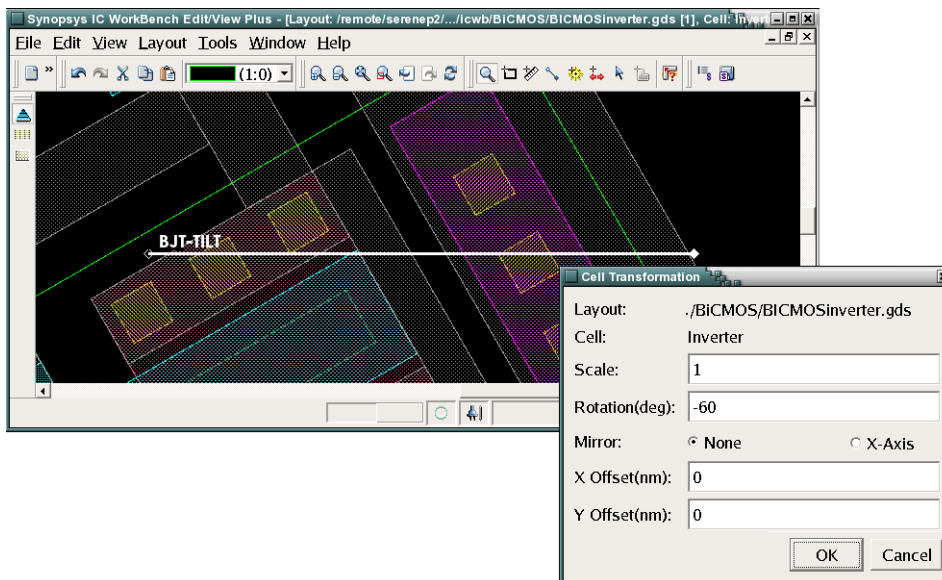


Figure 161 Rotation of layout with transformation parameters

---

# Files Relevant to ICWBEV Plus–TCAD Sentaurus

After adding Sentaurus Process markups in ICWBEV Plus, the markup information is saved in two different files:

- *Sentaurus markup file*: This file format is based on the standard ICWBEV Plus macro language. It can be used to reload and re-edit Sentaurus Process markup. It also contains a reference to the original, potentially large, GDSII file.
- *TCAD layout file*: This file format is used as an internal file format for the exchange of layout information between ICWBEV Plus and TCAD Sentaurus. It is based on the standard ICWBEV Plus macro language. This file is flat and does not contain a reference to the GDSII file. It is a small file because it contains only the parts of the layout needed for TCAD Sentaurus.

After performing the necessary operations on the layout file, save the resulting Sentaurus markup file.

---

## Saving the Sentaurus Markup File

To save a Sentaurus markup file:

1. Click the Save markups button (see [Table 72 on page 798](#)).  
The Save Sentaurus Markup File dialog box is displayed (see [Figure 162 on page 807](#)).
2. Select the option **Include New Layers in Markup File** to save auxiliary layers.  
  
**NOTE** Including new layers in the markup file keeps the original GDSII file intact.
3. Select the layout file corresponding to the markup file using one of the three options shown in [Figure 162](#):
  - a) **Active Layout**: Select this option when using a centrally located GDSII layout. This option is particularly useful when working with a very large full-chip layout.
  - b) **Choose File**: Select this option when working with an edited or a local version of the GDSII layout.
  - c) **Markups Only**: Select this option to manage the layout pointer and marker pointer separately. This option suppresses storing of the layout file pointer.
4. Type the file name in the **Save File as** field.
5. Click **OK**.

The recommended extension for saving the file is `_mkp.mac`, for example, `BiCMOS_mkp.mac`.



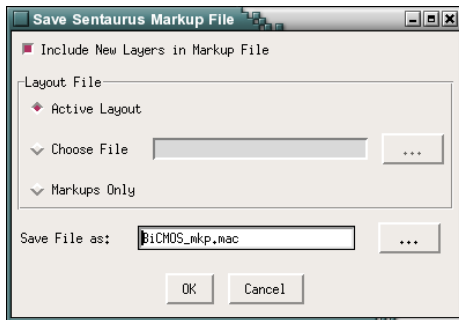


Figure 162 Saving Sentaurus Markup File dialog box

---

## Contents of Sentaurus Markup File

This section describes a typical markup file with a brief explanation. For a description of keywords, refer to the *IC WorkBench EV Plus User Guide*.

Version information:

```
# Sentaurus markup information - Fri Jan 11 17:15:39 PDT 2013  
# version - D-2010.06-14 (Production)
```

Setting for treating self-intersection: By default, all layers are ORed. This convention is expected by all subsequent tools and, therefore, this setting should not be altered.

```
default winding 1
```

Pointer to layout file:

```
layout open [<path>]/BICMOSinverter.gds Inverter
```

Global transformations:

```
cell transform 1.0 0.0 0 0.0 0.0
```

Layer declarations and display settings:

```
layer add 1:0  
layer configure 1:0 -name NWELL -fill #00ff00 -outline #00ff00  
-lineStyle solid -lineWidth 1 ...
```

Open cell for editing (here, for adding new polygons):

```
cell edit_state 1
```

## 12: ICWBEV Plus Interface for Layout-driven Simulations

Files Relevant to ICWBEV Plus–TCAD Sentaurus

Auxiliary layers:

```
polygon -layer 20:0 {950 5150 950 5350 1150 5350 1150 5150}  
...
```

Simulation domains:

```
point add {8900 8100} Emit1D  
gauge add {2100.0 7900.0 2100.0 10000.0} PMOS  
highlight add {7900.0 7550.0 9900.0 9900.0} BJT3D  
...
```

File end:

```
select clear  
catch {view default}
```

---

## Reloading the Markup File

To edit a markup file, you must reload it.

To reload a markup file:

1. **File > Open.**

The Open File dialog box is displayed (see [Figure 163](#)).

2. In the **Files of type** field, select **Flag Files (\*.mac)** or **Macro Files (\*.mac)**.

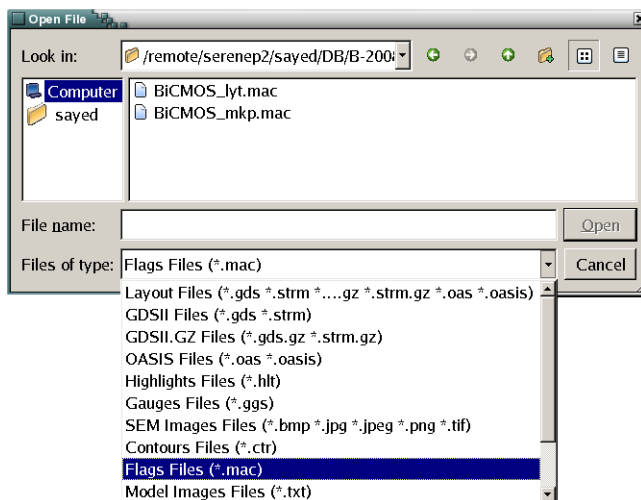


Figure 163 Open File dialog box for reloading the markup file

---

## Saving the TCAD Layout File

To save the TCAD layout file:

1. Click the Save TCAD layout button (see [Table 72 on page 798](#)).  
The Save Layout Information for Sentaurus dialog box is displayed (see [Figure 164](#)).
2. Save the file.  
The recommended extension for the TCAD layout file is `_lyt.mac`, for example, `BiCMOS_lyt.mac`.

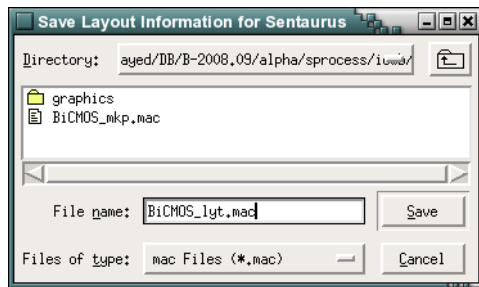


Figure 164 Saving the TCAD layout file

---

## Contents of TCAD Layout File

This section describes the contents of the TCAD layout file and the differences between the contents of the Sentaurus markup file and TCAD layout file.

Version information: Same as [Contents of Sentaurus Markup File on page 807](#).

Setting for treating self-intersection: Same as [Contents of Sentaurus Markup File](#).

Pointer to layout file: Commented out.

Global transformations: Commented out.

Initialization of this self-contained layout:

```
layout new <cell name> -dbu 1e-09
```

Layer declarations and display settings: Same as [Contents of Sentaurus Markup File](#).

File end: same as [Contents of Sentaurus Markup File](#).

## 12: ICWBEV Plus Interface for Layout-driven Simulations

Files Relevant to ICWBEV Plus–TCAD Sentaurus

Simulation domains in a layout file are described below. Point, gauge, and highlight coordinates are mentioned first, and all polygons associated with the given simulation domains are listed:

- 1D simulation domains:

```
point add {8900 8100} Emit1D
polygon -layer 1:0 {8890 8090 8910 8090 8910 8110 8890 8110}
...
```

- 2D simulation domains:

```
gauge add {2100.0 7900.0 2100.0 10000.0} PMOS
rectangle -layer 1:0 {2090 10010 2110 7890}
...
```

- 3D simulation domains:

```
highlight add {7900.0 7550.0 9900.0 9900.0} BJT3D
polygon -layer 1:0 {7890 7540 9910 7540 9910 9910 7890 9910}
...
```

In the TCAD layout file, layers are clipped to simulation domains. In addition, these layers are repeated for each simulation domain. For better viewing, layers are padded 10 units (nm).

To change the padding value, use:

```
set sentaurus::min_buffer <new_number>
```

---

## Reloading the TCAD Layout File

For debugging purposes, reload the TCAD layout file.

To reload the file:

- **File > Open > Macro File (\*.mac).**

**NOTE** Do not extract a TCAD layout from a reloaded TCAD layout. TCAD layout files should always be extracted from the Sentaurus markup file.

---

## ICWBEV Plus Batch Mode and Macros

---

### Starting ICWBEV Plus in Batch Mode

To extract the TCAD layout file in batch mode, add the following command to the end of the markup file:

```
sentaurus::get_sentaurus sentaurus <name>_lyt.mac  
exit
```

To start ICWBEV Plus in batch mode run the following command from the shell prompt:

```
> icwbev -nodisplay -run <name>_mkp.mac
```

---

### ICWBEV Plus Macros

ICWBEV Plus macros can be used to create simple layouts. An example of a macro is:

```
default winding 1  
layout new a -dbu 1e-09  
cell transform 1.0 0.0 0 0.0 0.0  
layer add 0:0  
layer configure 0:0 -name {} -fill #ff0000  
layer add 1:0  
layer configure 1:0 -name {} -fill #ff0000  
cell edit_state 1  
polygon -layer 0:0 {0 0 0 100 50 100 50 0}  
polygon -layer 1:0 {-25 25 75 25 75 75 -25 75}  
select clear  
catch {view default}
```

---

### Tcl-based Macros for Layout Parameterization

The macro language of ICWBEV Plus is Tcl based. [Figure 165 on page 812](#) shows a rectangle that has been replicated four times. The following Tcl command performs the replication:

```
layout new a -dbu 1e-09  
layer add 0:0  
layer configure 0:0 -name {}  
cell edit_state 1  
set SHIFTS [list 0 100 200 300 400]  
foreach SHIFT $SHIFTS {
```

## 12: ICWBEV Plus Interface for Layout-driven Simulations

### TCAD Layout Reader of Sentaurus Process

```
eval rectangle -layer 0:0 { $SHIFT 0 [expr 50+$SHIFT] 50 }  
}
```

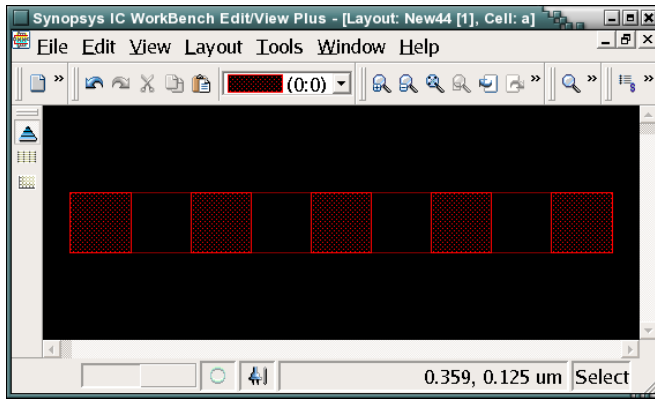


Figure 165 Shift operation using macros

---

## TCAD Layout Reader of Sentaurus Process

The TCAD layout reader of Sentaurus Process provides a file-based interface between ICWBEV Plus and Sentaurus Process. Some of its key features include:

- Loading the TCAD layout (optional rescaling)
- Layout query functions
- Selecting a simulation domain
- Applying stretches
- Creating masks
- Mask-driven meshing
- Mask-driven contact assignment

The following sections discuss these features in detail.

---

### Loading the TCAD Layout

To load a TCAD layout: in Sentaurus Process use the following command:

```
icwb filename= "<filename.mac>" [scale=<scale>]
```

Coordinates found in the TCAD layout file are multiplied by the value of the optional parameter `scale` as the file is read.

For example, to load the TCAD layout file `BiCMOS_lyt.mac` and apply a rescaling factor of  $1/1000$  to convert the ICWBEV Plus default unit of nanometer to the Sentaurus Process default unit of micrometer:

```
icwb filename= "BiCMOS_lyt.mac" scale=1e-3
```

---

## Finding Simulation Domains

To generate a list of the simulation domains:

```
icwb list domains
```

For example:

```
set Domains [icwb list domains]
-> icwb: Domains -> Emit1D NBODY NMOS BJT3D PMOS3D
```

---

## Finding Layer Names and Layer IDs

Each layer in the TCAD layout file has a unique ID of the form `<int>:<int>`, for example `3:0`. A layer also can have an optional explicit layer name such as `NWELL`. If no explicit layer name has been set in ICWBEV Plus, the TCAD layout reader uses the layer ID as the default layer name. The TCAD layout reader refers to layers always by the layer name.

To find the layer names:

```
icwb list layerNames
```

For example:

```
set LNames [icwb list layerNames]
-> icwb: LNames -> NWELL NPDIFF POLY EMIT METAL CONT ndrain ngate nsource base
emitter collect
```

To find the layer IDs:

```
icwb list layerIDs
```

For example:

```
set LIDs [icwb list layerIDs]
-> icwb: LIDs -> 1:0 2:0 3:0 4:0 5:0 6:0 7:0 8:0
```

## Selecting the Simulation Domain

To select a single or a composite simulation domain:

```
icwb domain = <domain-name> | <list-of-2d-domain-names>
```

For example, to select a single simulation domain (which can be 1D, 2D, or 3D):

```
icwb domain = { PMOS }
```

To define a composite simulation in 2D:

```
icwb domain = { NBODY NMOS PMOS BJTBE BJTC }
```

---

## Finding Domain Dimensions

To find the domain dimensions:

```
icwb dimension
```

This command returns 3 for 3D simulation domains (highlight), 2 for 2D simulation domains (gauge), and 1 for 1D simulation domains (point).

For example:

```
set DIM [icwb dimension]  
-> icwb: dimension -> 3
```

---

## Finding Bounding Box of Domain

To find the coordinates of the bounding box of the simulation domain in the global layout coordinates:

```
icwb bbox xmin | xmax | ymin | ymax
```

For example:

```
set LXmin [icwb bbox xmin] ; set LXmax [icwb bbox xmax]  
set LYmin [icwb bbox ymin] ; set LYmax [icwb bbox ymax]  
-> icwb: Layout Bounding Box -> 7.9 9.9 7.55 9.9
```

To find the coordinates of the bounding box that automatically recenters the simulation domain to start at the origin:

```
icwb bbox left | right | back | front
```



For example:

```
set Ymin [icwb bbox left] ; set Ymax [icwb bbox right]
set Zmin [icwb bbox back] ; set Zmax [icwb bbox front]
-> icwb: Centered Bounding Box -> 0 2.35 0 2
```

**NOTE** Sentaurus Process works with the centered coordinates.

---

## Interface with line Commands

After storing the bounding box of the simulation domain in the Tcl variables such as Ymin, Ymax, Zmin, and Zmax, these variables can be used in line commands to define the initial substrate and mesh in Sentaurus Process. For example:

```
if { $DIM == 3 } {
    line y location= $Ymin spacing=100.0 tag=left
    line y location= $Ymax spacing=100.0 tag=right
    line z location= $Zmin spacing=100.0 tag=back
    line z location= $Zmax spacing=100.0 tag=front
    set Ydim "ylo=left yhi=right"
    set Zdim "zlo=back zhi=front"
} elseif { $DIM == 2 } {
    line y location= $Ymin spacing=100.0 tag=left
    line y location= $Ymax spacing=100.0 tag=right
    set Ydim "ylo=left yhi=right"
    set Zdim ""
} else {
    line y location=-0.5 spacing=100.0 tag=left
    line y location= 0.5 spacing=100.0 tag=right
    set Ydim "ylo=left yhi=right"
    set Zdim ""
}
eval region silicon xlo=top xhi=bot $Ydim $Zdim
```

---

## Creating Masks

To create a mask from a layer:

```
icwb.create.mask layer.name= (<string>|<string list>)
    [name= <string>] [polarity= (positive|negative)] [info=<n>]
    [shift= {dy dz}] [stretchypos= {yo dy}] [stretchyneg= {yo dy}]
    [stretchzpos= {zo dz}] [stretchzneg= {zo dz}]
```

## 12: ICWBEV Plus Interface for Layout-driven Simulations

### TCAD Layout Reader of Sentaurus Process

Masks can be created in the following ways:

- Mask name defaults to the layer name:

```
icwb.create.mask layer.name= POLY
```

- Give an explicit name to the mask. For example, to distinguish between the positive mask and negative counterparts:

```
icwb.create.mask layer.name= NWELL name= NWELL    polarity= positive
icwb.create.mask layer.name= NWELL name= NOTNWELL polarity= negative
```

Several layers can be *OR*ed to create a single mask. The following command illustrates the OR procedure:

```
icwb.create.mask layer.name= "NPDIFF PPDIFF NPLUG PBASE" name= STI info=1
```

The `info` flag directs more detailed information about the mask creation process to the log file.

To automatically create mask layers with both polarities, use the following macro:

```
icwb.create.all.masks
```

The resulting mask names are `<layername>_p` for the positive version and `<layername>_n` for the negative version.

The optional keywords `shift`, `stretchypos`, `stretchyneg`, `stretchzpos`, and `stretchzneg` allow you to modify individual layers during the mask generation with `icwb.create.mask`. For example, to generate a mask that corresponds to layer `1:0` shifted by  $0.25\ \mu\text{m}$  along the *y*-direction and by  $-0.1\ \mu\text{m}$  along the *z*-direction, use:

```
icwb.create.mask layer.name= 1:0 shift= {0.25 -0.1}
```

For 2D simulation domains, the *z*-shift can be omitted.

The keywords starting with the word `stretch` allow you to stretch individual layers in a manner similar to the `icwb stretch` command. (The latter, however, is applied to all layers and takes the location of the stretch from the TCAD layout file.) The remaining part of the keyword determines if the stretch is applied along the *y*- or *z*-direction, and if the layer is stretched to the positive or negative side of the stretch position. For example, to move the vertices of layer `1:0`, which have a *y*-coordinate less than 1.2 by  $-0.25\ \mu\text{m}$ , use:

```
icwb.create.mask layer.name= 1:0 stretchyneg= {1.2 -0.25}
```

This command operates on layer vertex coordinates and does not check if the resulting polygon is valid. When using these commands to shrink layers, you must ensure that the resulting polygons are still well defined, for example, not self intersecting.

More than one `shift` and `stretch` keyword can be used in an `icwb.create.mask` command. As these operations may not be commutative, you must note the order in which these operations are applied if more than one is used. First, the `shift` is applied, and then `stretchypos`, `stretchyneg`, `stretchzpos`, and finally `stretchzneg` are applied.

**NOTE** This order is hard coded and not influenced by the order the keywords appear on the command line.

**NOTE** If you have a large layout with masks containing many polygons, it can take some time until the Tcl function `icwb.create.all.masks` parses and creates the masks. In this situation, you can use the command `icwb create.all.masks` to create all the masks (see [icwb on page 916](#)). This command works like the Tcl version but creates the masks much faster.

---

## Layout-driven Meshing

To create a refinement box that is tied to layers in the ICWB TCAD layout file:

```
icwb.refine.mask layer.name= (<string> | <string list>) [name= <string>]
    [oversize=<n>] xtop=<n> xbot=<n> <other options> [info=<n>]
```

Layout-driven meshing can be particularly useful when meshing in critical regions, such as the channel and emitter areas of BiCMOS devices. The following example illustrates the use of the `POLY` layer for meshing placement:

```
icwb.refine.mask name= UnderPoly layer.name= POLY oversize= 0.1 \
    xtop= -1.51 xbot= -1.35 info= xrefine= 0.02 yrefine= 0.02
icwb.refine.mask name= SiOxPo layer.name= POLY oversize= 0.1 \
    xtop= -1.51 xbot= -1.35 min.normal.size= 0.005 \
    interface.mat.pairs= {Silicon Oxide Silicon Polysilicon}
```

The `oversize` parameter gives the option to mesh in areas wider than the layer. [Figure 166](#) and [Figure 167 on page 818](#) demonstrate the use of the `oversize` parameter in the emitter region of a BJT and the channel region of an NMOS, respectively.

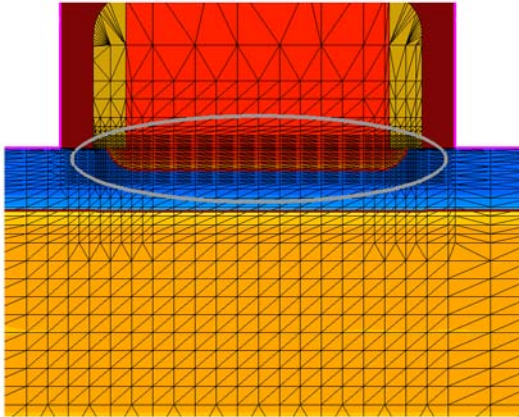


Figure 166 Meshing in emitter region of BJT; the oversize parameter is set to 0.1  $\mu\text{m}$

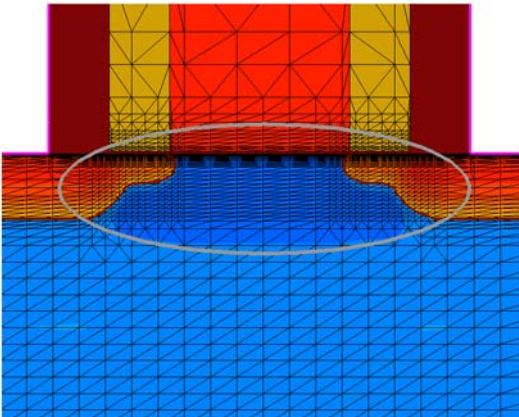


Figure 167 Meshing in channel region of NMOS; the oversize parameter is set to 0.1  $\mu\text{m}$

The utility command `icwb.refine.mask` interfaces with the standard `refinebox` command by providing information about the refinement extent (minimum and maximum) based on the selected layer.

- NOTE** The extent of the refinement box in the primary direction must be given explicitly with the keywords `xtop` and `xbot`. Any other commands are passed on.
- Layout-driven mesh refinements are applied under the layer itself. They cannot be applied under the inverse of a layer. Consider defining auxiliary layers in ICWBEV Plus to facilitate layout-driven meshing in areas that do not coincide with an existing layer.
- This feature supports only layers with axis-aligned edges. Slanted edges may result in a large number of refinement boxes, which may not appropriately represent the original shape.

---

## Layout-driven Contact Assignment

The `icwb.contact.mask` command creates contacts for subsequent device simulations that are tied to a layer in the TCAD layout file. The command serves as an interface between the TCAD layout and the Sentaurus Process `contact` command by automatically obtaining the lateral placement of the contact from the specified layout layer, taking the vertical placement from the argument list and passing all other options directly to the `contact` command. The syntax of the command is:

```
icwb.contact.mask layer.name= (<string> | <string list>)  
[name=<string>] <other options> [info=<n>]
```

The command supports both box and point contact types:

- A box-type contact consists of elements at the surface of one region or material inside the box. The lateral extent of the box is determined automatically from the layer segment (2D) or the polygon bounding box (3D), while the vertical extent is taken from the `contact` command keywords `xlo` and `xhi`.
- A point-type contact contains all the boundary elements of one region. The lateral position of the point is determined automatically as the midpoint of the layer segment (2D) or the polygon bounding box (3D), while the vertical position is taken from the `contact` command keyword `x`.

Often, there is no layer in the layout provided by designers that can be used readily for the creation of contacts. In this case, add auxiliary layers in ICWBEV Plus to be used as markups for device contacts.

The following example demonstrates the assignment of gate and drain contacts using layout-driven contact assignment:

```
icwb.contact.mask layer.name= ndrain name= drain point aluminum \  
  replace x= -2.0  
icwb.contact.mask layer.name= ngate name= gate box polysilicon \  
  adjacent.material=oxide xlo= -2.05 xhi= -1.95
```

The location in the primary direction must be given explicitly with either the keyword `x` for a point-type contact, or with the keywords `xlo` and `xhi` for a box-type contact. Any other command is passed on to the `contact` command. The keyword `name` is optional. If no name is given, the name of the layer is used as the contact name.

[Figure 168 on page 820](#) shows a layout on which auxiliary layers have been added for layout-driven contact assignment. [Figure 169 on page 820](#) shows the 2D boundary after the process simulation with Sentaurus Process depicting the gate, drain, and source contacts.

## 12: ICWBEV Plus Interface for Layout-driven Simulations

### TCAD Layout Reader of Sentaurus Process

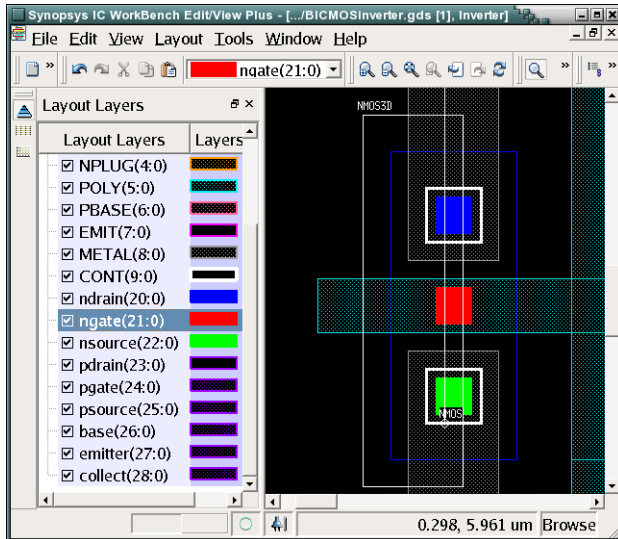


Figure 168 Auxiliary layers added for gate, source, and drain contacts are represented by rectangles of solid color in the layout

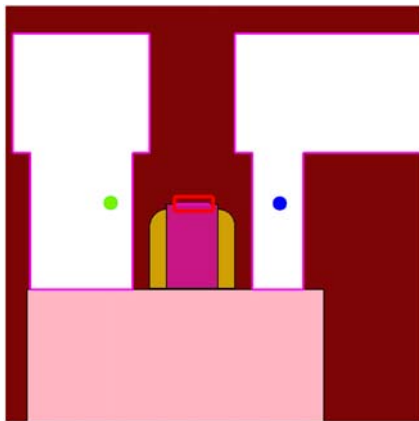


Figure 169 Final boundary after TCAD simulation showing gate (red), drain (blue), and source (green)

---

## Aligning Wafer and Simulation Domain

To correctly support tilted process steps for 2D and 3D simulation domains, the alignment between the wafer and the simulation domain must be declared using the `slice.angle` keyword in the `init` command.

The TCAD layout reader command `icwb slice.angle.offset` returns the relative angle of the active simulation domain so that the slice angle can be adjusted as needed.

Table 73 lists the returned `slice.angle.offset` values for:

- A 3D simulation domain (SIM3D1).
- A 2D domain along the layout x-axis extending from left to right (SIM2DXLR), right to left (SIM2DXRL), along the layout y-axis from top to bottom (SIM2DYTD) and bottom to top (SIM2DYDT).

The following commands realize a tilted process:

```
set SliceAngle -90
set SliceOffset [icwb slice.angle.offset]
init silicon field=Boron concentration=1e13 \
    slice.angle= [expr $SliceAngle+$SliceOffset]
implant phosphorus dose=4e12<cm-2> energy=100<keV> tilt=30 rot=0
```

Table 73 Slice angle offset values for different domains

Domain	SliceOffset value
SIM3D1	90
SIM2DXLR	0
SIM2DXRL	180
SIM2DYDT	90
SIM2DYTD	-90

Figure 170 shows a sample layout with a 3D simulation domain and the four 2D simulation domains previously discussed. Figure 171 on page 822 and Figure 172 on page 822 show the dopant profiles after the tilted implants for the different simulation domains.

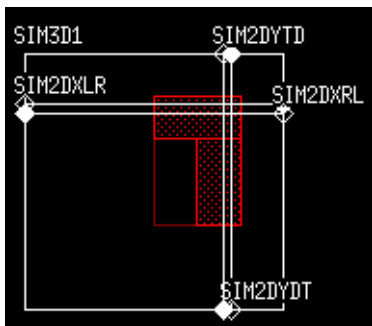


Figure 170 Structure layout where implant is performed at highlighted L-shaped red region

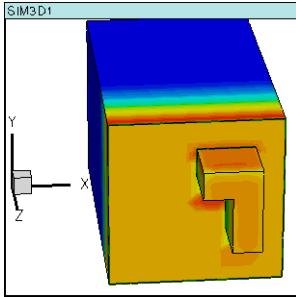


Figure 171 Three-dimensional implanted profile

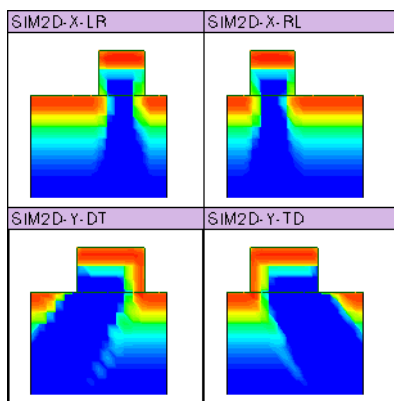


Figure 172 Two-dimensional implanted profile for selected slice angles as mentioned in [Table 73 on page 821](#)

---

## Additional Query Functions

The TCAD layout reader of Sentaurus Process provides additional layout query functions. For example, the following command returns a list of segments in the given layer for a 2D simulation domain:

```
set Segments [icwb list.segments layer.name= "<layer-name>"]
```

For a 3D simulation domain, the following command returns a list containing the bounding boxes for all polygons in the given layer (this command also can be used for 2D):

```
set PolyBBoxes [icwb list.polygon.bounding.bboxes layer.name= "<layer-name>"]
```

For a 3D simulation domain, the following command returns a list containing a tessellated representation of polygons in the given layer (this command also can be used for 2D):

```
set PolyTessel [icwb list.polygon.tessellations layer.name= "<layer-name>"]
```



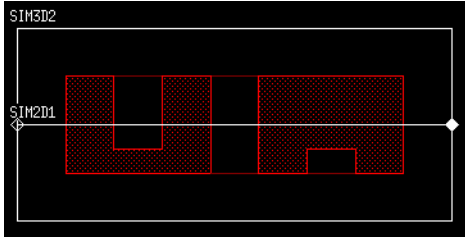


Figure 173 Sample layout containing two polygons

For example, [Figure 173](#) shows a simple layout containing two polygons in layer 0:0. The following commands:

- Load the TCAD layout file (here, called `ORG_lyt.mac`).
- Select the 2D simulation domain `SIM2D1`.
- Query the segment, the bounding boxes, and the tessellations:

```
icwb filename= "ORG_lyt.mac"
icwb domain= "SIM2D1"

set Segments [icwb list.segments layer.name= "0:0"]
LogFile "Segments: $Segments"
# -> Segments 100 200 300 400 500 800

set BBoxes [icwb list polygon.bounding.bboxes layer.name= "0:0"]
LogFile "BBoxes: $BBoxes"
# -> BBoxes: {100 0 200 0} {300 0 400 0} {500 0 800 0}

set Tessellations [icwb list polygon.tessellations layer.name= "0:0"]
LogFile "Tessellations: $Tessellations"
# -> Tessellations: {100 0 200 0} {300 0 400 0} {500 0 800 0}
```

**NOTE** The bounding box and tessellation queries are supported for 2D, and they return flat rectangles. The returned y-values are the same as for the segment query; however, zeros are padded for the z-direction.

When loading the 3D simulation domain `SIM3D2`, the set of rectangles returned by the `polygon.bounding.bboxes` query and the `polygon.tessellations` query are different:

```
icwb filename= "ORG_lyt.mac"
icwb domain= "SIM3D2"

set BBoxes [icwb list polygon.bounding.bboxes layer.name= "0:0"]
LogFile "BBoxes: $BBoxes"
# -> BBoxes: {100 100 300 400} {100 500 300 800}

set Tessellations [icwb list polygon.tessellations layer.name= "0:0"]
```

## 12: ICWBEV Plus Interface for Layout-driven Simulations

TCAD Layout Reader of Sentaurus Process

```
LogFile "Tessellations: $Tessellations"  
# -> Tessellations: {100 100 150 200} {100 200 150 300} {100 300 150 400}  
# {100 500 150 600} {100 700 150 800} {150 100 300 200} {150 300 300 400}  
# {150 500 300 600} {150 600 300 700} {150 700 300 800}
```

The `polygon.bounding_boxes` query returns the bounding box rectangle for each polygon in the layer, while the `polygon.tessellations` query breaks each polygon into a set of rectangles and then returns these rectangles. The set of rectangles covers the same area as the original polygon, while the bounding box rectangles may cover a larger area.

Figure 174 shows the rectangles returned by the two query functions as an ‘effective/equivalent’ layout for better comparison with the original layout shown in Figure 173 on page 823.

**NOTE** The tessellation procedure supports only polygons with axis-aligned edges.

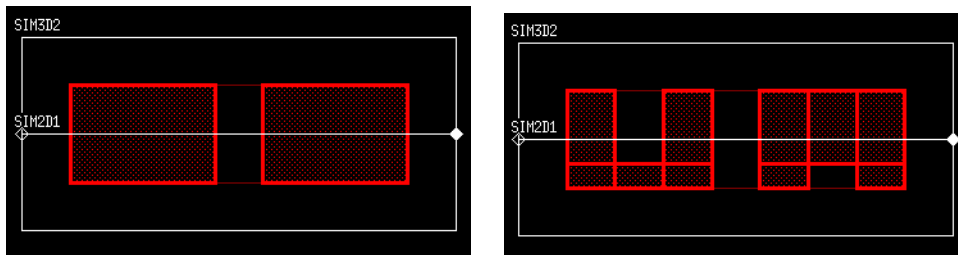


Figure 174 Set of rectangles returned by (*left*) `polygon.bounding_boxes` query and (*right*) `polygon.tessellations` query for polygons shown in Figure 173

## CHAPTER 13 Extracting Results

---

*This chapter presents strategies for analyzing simulation results.*

---

### Overview

This chapter covers basic tasks such as obtaining a list of materials currently in the structure, and obtaining 1D dopant profiles from 2D or 3D structures to more complex ones, such as looping through all materials and extracting Pearson parameters for each material. The following commands perform these tasks: `select`, `slice`, `layers`, `interface`, `interpolate`, `print.ld`, `FitPearson`, `mater`, `FitPearsonFloor`, `FitArrhenius`, and `FitLine`.

All these Sentaurus Process commands are built-in procedures designed to work with the tool command language (Tcl). These commands allow you to take full advantage of the programmability of the Sentaurus Process input language and provide a powerful framework for performing complex customized tasks.

These commands return or accept a Tcl list to perform their respective functions. The Tcl list can be viewed and processed by the user, passed to another function, written to a file, or read from a file. For example, the `slice` command returns a Tcl list of  $xy$  pairs where the  $x$  value gives the depth [ $\mu\text{m}$ ] and the  $y$  value gives the value chosen with the `select` command. This list can be viewed with the Tcl `puts` command, written to a file with the Tcl `open` and `puts` commands, or processed with another command such as fitting a Pearson function to the profile with the `FitPearson` command.

An understanding of basic Tcl commands and Tcl lists is helpful to utilize fully the flexibility of these commands. For convenience, some basic aspects of Tcl are described to enable you to work efficiently with these commands, and examples of basic results analysis are provided.

---

### Saving Data Fields

Sentaurus Process automatically saves all solutions, active dopant concentrations, total dopant concentrations, electrostatic potential, net active concentrations, point-defect concentrations, and total point-defect concentrations along with mechanical stress results in a TDR file. The total and active concentrations of dopants and the total concentration of defects are created only after a diffusion step. Therefore, if there is no diffusion, some of these fields may be missing

### 13: Extracting Results

#### Selecting Fields for Viewing or Analysis

in the TDR file. You can control the fields that will be saved in the TDR file using the `SetDFISEList` command (see [SetDFISEList on page 1057](#)).

Since the active and total dopant concentrations are defined as terms in Sentaurus Process, they are converted automatically to data fields with the same name when saved to TDR files. Because the conversion is handled internally, the data fields are not kept in the memory.

You can create new data fields and store them in a TDR file. For example:

```
sel z= "BActive/BTotal" name=BActiveRatio store
```

will divide the active boron concentration by the total boron concentration, and will save the results in a data field called `BActiveRatio`. The parameter `store` ensures that the newly created field will be saved in a TDR file. To see whether a field will be saved in a TDR file, the `select` command with the option `permanent` can be used (see [select on page 1053](#)), for example:

```
sel name= Boron permanent
```

will return 1 if the field will be saved in a TDR file. Otherwise, it will return 0.

---

## Selecting Fields for Viewing or Analysis

Most analytic tasks begin with the `select` command, which is used to select a data field to be viewed or operated on (see [select on page 1053](#)). A data field in Sentaurus Process is a quantity that varies over the simulation domain, such as dopant concentration or electrostatic potential distribution. The value of the data field is defined with an Alagator expression and is set with `z` parameter of the `select` command.

The expression can be simply the name of a solution variable (such as `Boron`, `H2O`, or `Stress_x`) or it can be a complex expression depending on what is required. If the expression is the simple name of an existing data field, the `select` command selects this data field.

If it is more complex expression, the `select` command creates a corresponding data field and then selects it, for example:

```
select z= BTotal                ;# Select the total boron concentration
                                # term
select z= "Arsenic+Phosphorus-Boron" ;# Create and select a data field using
                                # solution variables
select z= log10(BActive)        ;# Create and select a data field from
                                # the active boron concentration
```

The list of available data fields can be retrieved by using `select list`. The name that can appear in the expression of the `z` parameter can be either a data field or a term.

A term is defined with the `term` command and is also an expression containing solution variables, data fields, constants, and so on (see [term on page 1099](#)). Numerous terms are created automatically in the `diffuse` command (see [diffuse on page 875](#)) and any of these terms can be selected.

When a data field is selected (or created and selected) with the `select` command, the data field can be viewed or operated on. The following commands can operate on the selected field: `slice`, `layers`, `interpolate`, `print.data`, `print.1d`, and `plot.1d`.

---

## Obtaining 1D Data Cuts

After a `select` command has been issued, you can obtain 1D cuts through the data along one of the principal axes using the `slice` or `print.1d` command. The `slice` command returns a list of coordinate data pairs. To make a cut perpendicular to  $x$ , specify the `x` parameter, similarly for  $y$  and  $z$ .

The `print.1d` command returns a list of data-point lists. Each data-point list contains the coordinate, data value, and the material name at that coordinate. Again, a cut perpendicular to  $x$  is made by specifying the `x` parameter and, similarly, for the  $y$  and  $z$  cuts.

The `plot.1d` command can be used to view profiles with a temporary X11 graphics tool.

---

## Examples

Sentaurus Process can run in interactive mode if there is no command file given on the command line. In this case, you are prompted with the `sprocess>` prompt for commands. If a command file is given, commands are read from this file. In interactive mode, the return value of the commands is always displayed. You can set variables to the return value of a command by using the syntax:

```
set var [command]
```

In this case, `command` is executed and a Tcl variable `var` is created if it does not already exist, and the value of `var` is set to the return value of `command`. In addition, the return value of `command` is displayed. It is also possible to write the return value to a user-defined file. The following examples demonstrate the differences and functionality of the `slice` and `print.1d` commands:

```
sprocess> select z= Vacancy
sprocess> slice y=0.6
{-1.000000e-02 4.804720e+16
-9.340278e-03 5.869015e+16
```

## 13: Extracting Results

### Examples

```
...
0.000000e+00 5.969905e+17
0.000000e+00 7.075867e+17
7.421875e-04 7.618894e+17
...
sprocess> print.ld y=0.6
{ Distance      Value      Material }
{ -1.00000e-02  4.80472e+16  Oxide   }
{ -9.34028e-03  5.86902e+16  Oxide   }
...
{ 0.00000e+00   5.96991e+17  Oxide   }
{ 0.00000e+00   7.07587e+17  Silicon }
{ 7.42188e-04   7.61889e+17  Silicon }
...
```

Here, the `slice` command returns raw coordinate data pairs, whereas `print.ld` returns a header and coordinate data-material triplets. In both cases, the coordinates are given in micrometers and the concentration is in  $\text{cm}^{-3}$ .

To illustrate how data from these functions can be manipulated with Tcl, suppose you require a 1D profile of vacancy, which starts with 0.0 as the first coordinate, and the vacancy concentration to be in  $\mu\text{m}^{-3}$ .

First, create a Tcl list from the data returned by the `slice`, and convert data in that list to a new list, such as:

```
set vacList[lindex [slice y=0.6] 0]      ;# Create a new list from slice
                                         ;# command called vacList
set offset [lindex vacList 0]            ;# Grab the offset, that is, the
                                         ;# first coordinate
list modList                             ;# Create new Tcl list where modified
                                         ;# data will reside
foreach { coord data } $vacList {\
    lappend modList [expr $coord-$offset] ;#Convert coordinate by subtracting
                                         ;# the offset and append to modlist
    lappend modList [expr $data*1.0e-12] ;# Convert data to um^-3 units and
                                         ;# append to modlist
}
```

The above example uses the following Tcl commands;

- `lindex` retrieves a given element of a list.
- `list` creates a list.
- `lappend` appends an element to the end of a list.
- `expr` evaluates a math expression.
- `foreach` is used for looping.

For example, to write modList to a file called xy.dat:

```
set fileID [open xy.dat w]                ;# Use the Tcl open command
                                           ;# to open a file for writing
foreach { x y } $modList { puts $fileID "$x $y" } ;# Write modList line by line
close $fileID
```

---

## Determining the Dose: Layers

The `layers` command (see [layers on page 967](#)) computes the dose of the selected data field along one of the principal axes. The syntax to specify the cut is the same as the `slice` command (see [slice on page 1073](#)). As with the other commands, the information is returned as a list of lists:

```
sprocess> sel z=Vacancy
sprocess> set layerInfo [layers y=0.5]; # For a 2d structure,
                                         either x or y must be specified
{      Top      Bottom      Integral      Material}
{-2.06000e-01  -6.00000e-03    9.98843e+14  Silicon}
{-6.00000e-03   0.00000e+00    3.97970e+09e  Oxide}
{ 0.00000e+00   1.00000e+00    2.81858e+05  PolySilicon}
```

The top and bottom coordinates are in micrometers. To obtain the total integrated dose along  $y=0.5$ , use:

```
sprocess> set total 0
0
# Loop over layerInfo list of lists skipping header list,
# and retrieve the 3rd element of each list (first element has 0 index)
# which corresponds to the Integral for that layer.
sprocess> for { set i 1 } { $i < [llength $layerInfo] } { incr i } {
> set total [expr $total + [lindex [lindex $layerInfo $i] 2]]
> }
sprocess> puts $total
9.991288377e+14
sprocess>
```

In addition to the Tcl commands used in the previous section, this example uses the following:

- `llength` returns the size of a given list.
- `incr` increases an integer by 1.

For more information about the `layers` command, see [layers on page 967](#).

## 13: Extracting Results

Extracting Values and Level Crossings: interpolate

---

# Extracting Values and Level Crossings: interpolate

The `interpolate` command has two purposes: to obtain the position at which a profile crosses a particular value and to retrieve a value at a particular location in space. Interpolation is used to accomplish both tasks.

The four main parameters of this command are `x`, `y`, `z`, and `val`. The command operates on a selected data field. In 1D, you must supply either `x` or `val`. If `x` is supplied, Sentaurus Process returns the value at `x`. If `val` is supplied, Sentaurus Process returns the locations at which the selected profile crosses `val`.

In 2D, two of the four parameters must be given (not `z`) and, in 3D, three of the four parameters must be given. For example, in 2D, if `x` and `val` are given, the locations along `x` where `val` is crossed are returned. If `x` and `y` are given, the value at this location is returned. For more information, see [interpolate on page 950](#).

---

# Extracting Values during diffuse Step: extract

The `extract` command is used to extract historical data during `diffuse` steps. This command allows you to define the data extraction script with the `command` parameter. The extraction script is composed typically of the `select` command for choosing the data field for extraction and the `interpolate` command for retrieving the value at a specified location. Only values returned by the `interpolate` command, at each time step, are stored in the historical data values.

For example, to extract the boron concentration at position 0.04  $\mu\text{m}$  in the silicon and the YY component of the element stress at position  $-0.001 \mu\text{m}$  in the oxide for each `diffuse` substep:

```
extract name=etest command= {
  sel z=Boron
  interpolate Silicon x=0.04
  sel z=StressEL_yy element
  interpolate Oxide x=-0.001
}
```

This command must be defined before the `diffuse` step. After the `diffuse` steps of interest, the following command retrieves the extracted data values for the defined extraction `etest`:

```
extract name=etest print
```



The values are returned as a Tcl list with the format:

```
<time1> <Boron1> <Syy1> <time2> <Boron2> <Syy2> ...
```

The following script demonstrates how to manipulate this list for more formatted output:

```
set extdata [extract name=etest print]
foreach { time bval sval } $extdata {
  puts "$time $bval $sval"
}
```

Output from the above script is:

```
0.000000e+00 4.738727e+15 6.000000e+09
1.000000e-04 4.738727e+15 4.793201e+09
2.503231e-04 4.738727e+15 4.793201e+09
5.509694e-04 4.738727e+15 4.793201e+09
1.152262e-03 4.738727e+15 4.793201e+09
...
```

For more information, see [extract on page 895](#).

---

## Fitting Routines: FitLine, FitArrhenius, FitPearson, and FitPearsonFloor

The following commands provide fitting capabilities in Setaurus Process:

- The `FitLine` command is used to find the best offset and slope for a given set of data, for example:

```
sprocess> foreach temp { 700 800 900 1000 } {
> lappend dat $temp
> lappend dat [expr 110 + 10*$temp]
> }
sprocess> FitLine $dat ;# Get the slope, offset, and correlation factor
10.0 110.0 1.0
```

- The `FitArrhenius` command is used to find the best prefactor and energy for an Arrhenius fit of a given profile, for example:

```
sprocess> list dat ;# This is the list to be passed to FitArrhenius
sprocess> foreach temp { 700 800 900 1000 } {
> SetTemp $temp
> lappend dat $temp ;# dat will contain "temp" - "Arrhenius val" pairs
> lappend dat [Arrhenius 0.1 1.0]; ;# Arrhenius takes prefactor and
;# activation energy
> }
sprocess> FitArrhenius $dat ;# Send the list to FitArrhenius
```

## 13: Extracting Results

### Resistivity

```
0.0999999308634 1.00030363776 -0.999999999866 ;# Return prefactor, energy
                                         # and corr factor
sprocess>
```

The `FitArrhenius` command takes a list of temperature–function pairs. The unit of temperature is degree Celsius. The return value is a list where the first member is the prefactor, the second member is the activation energy [eV], and the third member is the correlation factor. Absolute values of the correlation factor close to one are desirable.

- The `FitPearson` command is used to extract the best Pearson parameters of a profile.
- The `FitPearsonFloor` command is a modification of `FitPearson` and is used to set a floor for the data value so that only data points with values greater than the given floor are used for the Pearson fit.

An example of using this command is one that contains the command `PearsonProfile`, which can be called to create a Pearson–IV, Pearson–V, or Pearson–VI profile depending on the parameters sent. It takes as its arguments the name of the data field to be created and a list of parameters in this order: dose [ $\text{cm}^{-2}$ ], projected range, standard deviation, skewness, and kurtosis. `FitPearsonFloor` takes the minimum value and a list of  $x$  values, which are to be fit to a Pearson. It returns parameters in the same order as the list of parameters for `PearsonProfile`:

```
sprocess> PearsonProfile Arsenic {1e14 0.0650 0.0228 0.577 3.4390}
                                         ;# Corresponds to 100keV As implant
sprocess> select z= Arsenic
sprocess> FitPearsonFloor 1.0e10 [lindex [slice silicon] 0]
9.99999659675e+13 0.0649998507454 0.0227994405041 0.576718866676
3.4368839917
sprocess>
```

---

## Resistivity

The background concentration of the wafer can be defined using the resistivity of the wafer. You can define the resistivity of the wafer with the `init` command, which requires a field name to calculate the background concentration. For example:

```
line x location = 0 tag=top
line x location = 10 tag=bot
region silicon xlo = top xhi = bot
init field=boron silicon resistivity=1.4
```

sets the boron concentration of the wafer to  $1.08 \times 10^{16} \text{ cm}^{-3}$  in silicon.

The resistivity is given in  $\Omega\text{cm}$ , and the resistivity is calculated by:

$$RHO = (qN\mu)^{-1} \quad (947)$$

where:

- $q$  is the electron density.
- $N$  is the background concentration.
- $\mu$  is the mobility.

Three mobility models can be selected using the command:

```
pdbSet <material> <dopant> Mobility.Model <model>
```

where <model> can be Model1 [1], or Model2 [2], or Model3 [3]. They are given as:

- Model1:

$$\mu = \mu_{\min} + \frac{\mu_{\max} - \mu_{\min}}{1 + \left(\frac{N}{N_r}\right)^\alpha} \quad (948)$$

- Model2:

$$\mu = \mu_{\min} e^{-\left(\frac{P_C}{N}\right)} + \frac{\mu_{\max} - \mu_{\min 2}}{1 + \left(\frac{N}{N_r}\right)^\alpha} - \frac{\mu_m}{1 + \left(\frac{N_s}{N}\right)^\beta} \quad (949)$$

- Model3:

$$\mu_p = \mu_{\min} e^{-\left(\frac{P_C}{N}\right)} + \frac{\mu_{\max}}{1 + \left(\frac{N}{N_r}\right)^\alpha} \quad (950)$$

$$\mu_n = 10^{\frac{A_0 + A_1 X + A_2 X^2 + A_3 X^3}{1 + B_1 X + B_2 X^2 + B_3 X^3}}$$

$$X = \log\left(\frac{N}{N_r}\right) \quad (951)$$

where  $N_r$ ,  $\mu_{\min}$ ,  $\mu_{\min 2}$ ,  $\mu_{\max}$ ,  $\mu_m$ ,  $P_C$ ,  $A_0$ ,  $A_1$ ,  $A_2$ ,  $A_3$ ,  $B_1$ ,  $B_2$ ,  $B_3$ ,  $\beta$ , and  $\alpha$  are fitting parameters for the empirical formulas.

The fitting parameters can be set using the following commands:

```

pdbSet <material> <dopant> uMin {<n>}
pdbSet <material> <dopant> uMin2 {<n>}
pdbSet <material> <dopant> uMax {<n>}
pdbSet <material> <dopant> uM {<n>}
pdbSet <material> <dopant> uNr {<n>}
pdbSet <material> <dopant> uNs {<n>}

```

## 13: Extracting Results

### Sheet Resistance

```
pdbSet <material> <dopant> uPC {<n>}
pdbSet <material> <dopant> uBeta{<n>}
pdbSet <material> <dopant> uAlpha {<n>}
pdbSet <material> <dopant> A0 {<n>}
pdbSet <material> <dopant> A1 {<n>}
pdbSet <material> <dopant> A2 {<n>}
pdbSet <material> <dopant> A3 {<n>}
pdbSet <material> <dopant> B1 {<n>}
pdbSet <material> <dopant> B2 {<n>}
pdbSet <material> <dopant> B3 {<n>}
```

In addition to these models, a user-defined mobility model can be set using the command:

```
pdbSet <material> <dopant> Mobility.Equation <String Expression>
```

For example, the `Mobility1` model for boron in silicon can be set using the command:

```
pdbSet Silicon Boron Mobility.Equation \
"(49.705+(467.729-49.705)/(1+abs(tNetActive/1.606e+17)^0.7))"
```

`tNetActive` is the internal name for  $N$ .

---

## Sheet Resistance

The sheet resistance and p-n junction depth of a semiconductor layer in the vertical direction are calculated using the command:

```
SheetResistance <args>
```

where `<args>` must be the y-cross section in 2D, and the y- and z-cross sections in 3D. For example, in 3D:

```
SheetResistance y=0.4 z=-0.1
```

The sheet resistance formula is given by:

$$R_s = \frac{1}{pn_{i+1} \int_{pn_i} q(\mu_n n + \mu_p p) dx} \quad (952)$$

where  $\mu_x$  is mobility of the holes ( $p$ ) or electrons ( $n$ ) given in [Eq. 948](#) or [Eq. 949](#) or [Eq. 950](#). The active concentration of dopants is calculated at the last diffusion temperature. The electron,  $n$ , and hole,  $p$ , concentrations are calculated assuming charge neutrality at a temperature of 300 K.

Sheet resistance can be calculated only after a diffusion statement or activation step. For example:

```
diffuse time=0.0 temperatur=1000  
SheetResistance y=9.4 z=-0.1
```

Since not all data fields are stored in the TDR file, the sheet resistance may not be calculated after loading the TDR file even though the last command was a diffusion command.

---

## References

- [1] D. A. Antoniadis, A. G. Gonzalez, and R. W. Dutton, “Boron in Near-Intrinsic <100> and <111> Silicon under Inert and Oxidizing Ambients—Diffusion and Segregation,” *Journal of the Electrochemical Society*, vol. 125, no. 5, pp. 813–819, 1978.
- [2] G. Masetti, M. Severi, and S. Solmi, “Modeling of Carrier Mobility Against Carrier Concentration in Arsenic-, Phosphorus-, and Boron-Doped Silicon,” *IEEE Transactions on Electron Devices*, vol. ED-30, no. 7, pp. 764–769, 1983.
- [3] W. R. Thurber *et al.*, *The Relationship Between Resistivity and Dopant Density for Phosphorus- and Boron-Doped Silicon*, National Bureau of Standards Special Publication 400-64, Washington, DC, USA, May 1981.

## 13: Extracting Results

### References

*This chapter discusses numerics-related issues, time integration methods, and the linear solvers used in Sentaurus Process.*

---

### Overview

In Sentaurus Process, during the simulation of diffusion steps, three different sets of nonlinear partial differential equations must be solved:

- Oxidant diffusion and reaction
- Dopant diffusion and reaction
- Stress equations

In the case of silicidation, the transport and reactions of dissolved silicon or dissolved metal is handled similar to the oxidant diffusion and reaction.

The oxidant, dopant, and point-defect equations are solved on the simulation mesh using a trapezoidal rule/backward differentiation formula (TRBDF) time discretization, a finite volume (box) method for the spatial integration, and a Newton method to solve the nonlinear equations.

For the discretization of the nonlinear stress equations, piecewise linear finite elements are used. If stress history is tracked, the stress equations are solved, not only during the simulation of diffusion steps, but also at the end of etch and deposit steps.

Various direct and iterative solvers are integrated in Sentaurus Process to solve the large systems of linear equations in each Newton iteration. By default, for all equations in 1D simulations and for mechanics equations in 2D simulations, the parallel direct solver PARDISO is used. For diffusion equations in two dimensions and for all equations in three dimensions, the iterative solver ILS is used. The solver can be selected using the `math` command:

```
math ils
```

This command selects the solver ILS for all types of equation in 1D, 2D, and 3D. Separate selections can be made for the various spatial dimensions and for the solution of mechanics equations and diffusion equations (the same settings are used for both oxidant and dopant–point defect equations).

## 14: Numerics

### Setting Parameters of the Iterative Solver ILS

The parameters `Flow` and `diffuse` select the type of equation, and the parameter `dim` specifies the spatial dimension:

```
math Flow    dim=2 ils
math diffuse dim=2 pardiso
math Flow    dim=3 pardiso
```

If a direct solver is used, a modified Newton method is used by default; Sentaurus Process tries to avoid the recomputation and factorization of a new matrix and will reuse the last factorized matrix, as long as the convergence rate remains sufficiently high. For the iterative solvers, by default, a modified Newton scheme is used as well.

The `math` command is used to specify various parameters for the Newton iterations and to define resources and specifications for the linear solvers (see [math on page 984](#)).

For the default settings for ILS, refer to the parameter database browser (PDB). More detailed settings for ILS can be made using `pdbSet` commands as described in the next section.

---

## Setting Parameters of the Iterative Solver ILS

The iterative solver ILS is used by default to solve the linear systems for `diffuse` in 2D simulations and for both `Flow` and `diffuse` in 3D simulations. Default parameters for ILS have been added to the parameter database. To specify modified parameters for ILS, such as the type of iterative scheme, the number of iterations, the output verbosity, or the memory resources, use the `pdbSet` commands.

**NOTE** In the `pdbSet` commands, parameters must be specified separately for each type of problem (`Flow` or `diffuse`) and for each dimension (1D, 2D, or 3D).

**NOTE** ILS is not recommended for use in 1D simulations because of the simple structure of matrices arising in 1D cases. The default direct solver PARDISO is the correct choice for 1D simulations.

Different ILS parameters can be specified for `diffuse` and `Flow`, both in 2D or 3D. In general, the `pdbSet` command for the ILS parameters has the form:

```
pdbSet Math [diffuse | Flow] [2D | 3D] ILS.[command] [value]
```

The following ILS commands are available:

<code>ILS.compact</code>	Boolean
<code>ILS.fgmres.restart</code>	Double
<code>ILS.gmres.restart</code>	Double
<code>ILS.fit</code>	Double



ILS.ilut.tau	Double
ILS.leftPreconditioner	Boolean
ILS.maxit	Double
ILS.method	String
ILS.nonsymmOrdering	String
ILS.okayForModNewton	Boolean
ILS.preconditioner	String
ILS.recompute.ordering	Double
ILS.refine.residual	Double
ILS.refine.iterate	Double
ILS.scaling	String
ILS.symmOrdering	String
ILS.tolabs	Double
ILS.tolrel	Double
ILS.tolunprec	Double
ILS.useILSRCFile	Boolean
ILS.verbose	Double

To select the GMRES method, for example, `gmres(60)`, use:

```
pdbSet Math diffuse 3D ILS.method          gmres
pdbSet Math diffuse 3D ILS.gmres.restart  60
```

To specify the FlexibleGMRES method, for example, `fgmres(40)`, to solve the stress equations, use:

```
pdbSet Math Flow 3D ILS.method          fgmres
pdbSet Math Flow 3D ILS.fgmres.restart  40
pdbSet Math Flow 3D ILS.fit             5
```

To select the efficient reuse mode (on each 3D diffuse time step, the costly reordering is applied only once to a first Jacobian system), specify:

```
pdbSet Math diffuse 3D ILS.recompute.ordering 2
```

and to return to reordering for every system, use:

```
pdbSet Math diffuse 3D ILS.recompute.ordering 1
```

To improve the accuracy and convergence of iterative linear solvers, use an enhanced option available in Version H-2013.03 by specifying (default value is 0):

```
pdbSet Math [diffuse | Flow] [2D | 3D] ILS.refine.iterate 1
```

To use the 3D diffuse gmres solver in the advanced parallel implementation, specify:

```
pdbSet Math diffuse 3D ILS.hpc.mode 3
```

## 14: Numerics

### Partitioning and Parallel Matrix Assembly

In this command, the value 3 activates algorithmic improvements made in Version H-2013.03, while the value 2 corresponds to Versions G-2012.06 and F-2011.09, and the value 1 corresponds to Version E-2010.12.

To select the solvers for mechanics, STS2 or STCG2 for 2D, and STS3 or STCG3 for 3D, for example, `sts3`, use:

```
pdbSet Math Flow 3D ILS.method          sts3
pdbSet Math Flow 3D ILS.tolrel          1e-10
pdbSet Math Flow 3D ILS.ilut.tau        5e-4
pdbSet Math Flow 3D ILS.scaling         diagsym
pdbSet Math Flow 3D ILS.nonsymmOrdering none
```

For the mechanics solvers STS2, STS3, STCG2, and STCG3, it is mandatory to specify `ILS.scaling` as `diagsym`, and `ILS.nonsymmOrdering` as `none`. It is also recommended to specify the value for the parameter `ILS.ilut.tau` in the range of  $5 \times 10^{-4}$ – $5 \times 10^{-5}$ .

To improve convergence of the mechanics solver STS2 or STS3, use an enhanced version of the solver by specifying, respectively (default value is 0):

```
pdbSet Math Flow 2D ILS.refine.sts 1
```

or:

```
pdbSet Math Flow 3D ILS.refine.sts 1
```

The enhanced version takes advantage of results from previous solve steps, so the actual performance gain can vary depending on the simulation setup, and it performs best when there is a sequence of mechanical solve steps, as in temperature ramps.

---

## Partitioning and Parallel Matrix Assembly

Sentaurus Process can assemble the diffusion and mechanics matrices in parallel on multicore machines. To switch on the parallel assembly, use:

```
math { numThreads = <n> | numThreadsAssembly = <n> }
```

where `numThreads` is the number of threads that would be used during the matrix assembly. `numThreads` is a general keyword (see [math on page 984](#)) used by both implant and linear solvers. If you want to use a different number of threads for diffusion matrix assembly, use the keyword `numThreadsAssembly`. If the number of threads is greater than 1, Sentaurus Process first creates the threads.

To modify the thread stack size, use:

```
math threadStackSize = <n>
```

**NOTE** Parallel assembly of the matrix is performed only for inert anneals. It is recommended that `numThreadsAssembly` does not exceed the number of actual cores of the computer. Parallel assembly of the matrix is not available for moving-boundary problems such as oxidation and silicidation.

Sentaurus Process then partitions the mesh structure into levels, and each level is divided into different domains at the beginning of the diffusion step. For example, [Figure 175](#) shows a structure with three levels. The first level (blue) (L0) has four domains: D0, D1, D2, and D3. Elements belonging to each domain on the same level do not cross over to the other domains. The second level (orange) (L1) also has four domains: D0, D1, D2, and D3. Again, the elements on the same level do not cross over to the other domains. The third level (green) (L2) has only one domain: D0. This is the last level and contains all the elements not included in the previous levels.

To control the partitioning, use:

```
math { maxNumberOfDomains=<n> | NumberOfElementsPerDomain=<n> }
```

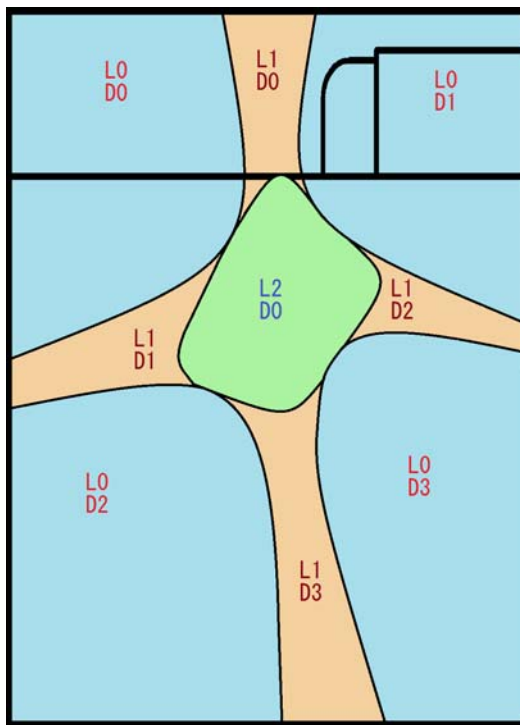


Figure 175 Partitioned mesh structure

## 14: Numerics

### Matrix Size Manipulation

**NOTE** `maxNumberOfDomains` is the maximum number of domains that each level of partition can have. It is recommended that `maxNumberOfDomains` equals or is greater than the number of threads used. `NumberOfElementsPerDomain` is the number of elements that should go to each domain.

The final number of domains at each level is determined by:

$$domains = \min(\text{maxNumberOfDomains}, \frac{\text{Number of Edges}}{\text{NumberOfElementsPerDomain}}) \quad (953)$$

To partition the mesh, based on material type, give weight to each material using the command:

```
pdbSet <material> PartitionWeight <n>
```

For example:

```
pdbSet Silicon PartitionWeight 10
pdbSet Gas PartitionWeight 0
```

gives more weight to silicon mesh elements than the gas mesh elements during partitioning. This allows Sentaurus Process to distribute the work among the threads more evenly since there is no matrix assembly for the gas mesh.

Partition weights for mechanics assembly can be specified separately with:

```
pdbSet <material> Mechanics PartitionWeight <n>
```

This allows balancing the workload among threads according to the stress analysis methods for different material behaviors. If the partition weights for mechanics assembly are not defined, the partition weights for diffusion assembly are used by default.

---

## Matrix Size Manipulation

The size of the matrix used during diffusion assembly is automatically determined based on the number of solution variables and nodes in the structure. In most cases the allocated matrix size is more than sufficient. If the matrix size becomes insufficient during the assembly, the matrix size will be increased automatically by 10%. You can change the default 10% value by using the command:

```
pdbSet Math Matrix.Size.Scale <n>
```

where the value `<n>` should be greater than one.

You also can increase the automatically determined matrix size using the command:

```
pdbSet Math Assembly.Matrix.Size.Scale <n>
```

where the value <n> should be greater than one.

**NOTE** Be careful when choosing the matrix scaling values because it can exhaust the computer memory for large scaling values.

---

## Node and Equation Ordering

Because the order of nodes in meshes does not follow a specific order by default, adjacent nodes may be far from each other in the internal node list. The order may not have much effect on simulation time for small examples (such as 2D), but it may degrade 3D results. The nodes in the structure can be ordered meshwise or globally using the command:

```
pdbSet Math < 1D | 2D | 3D > Reorder.Nodes <model>
```

where <model> is None (default), Mesh, or Global.

The default order of equation numbering in the structure is based on the meshes. Each node in the mesh receives an equation number from a solution variable and the same is repeated for the next solution. This may create many distributed entries in the assembly matrix. Again, the order may not greatly affect the simulation time for small examples (such as 2D), but it may degrade 3D results. It is possible to number equations based on solutions by taking a node in the mesh, numbering it for each solution variable, and moving to the next node in the mesh. This creates better-distributed entries in the assembly matrix. The order can be changed using the command:

```
pdbSet Math < 1D | 2D | 3D > Reorder.Equations <model>
```

where <model> is None (default) or Solution.

---

## Time Integration

The TRBDF method [1] is used for time integration by default for time-dependent problems. It also is possible to choose the backward Euler method for the time integration. The following command can be used to switch between methods:

```
math {tr_bdf | euler}
```

## 14: Numerics

### Time-Step Control

A TRBDF integration step consists of a trapezoidal step followed by a backward difference step. A second trapezoidal solution is used to estimate the local truncation error and to determine the size of the next time step.

The local truncation error can be estimated by either a Milne's device (the default method) or the divided difference method. The following command switches between methods:

```
math {milne | difference}
```

The local truncation error for the next time-step estimation can be modified using the command:

```
pdbSet Math Time.Step.Function {<model>}
```

where `<model>` is `Damped`, `UnDamped`, or `Linear`. The `Damped` model applies a logarithmic damping function to the truncation error if the error is greater than 1.0. The `UnDamped` model does not modify the error. The `Linear` model applies a linear damping function to the truncation error if the error is greater than 1.0. The `Linear` model matches that of TSUPREM-4.

When the geometry of a simulation structure evolves, one cycle of the TRBDF time integration requires the geometric coefficients at three incidents, that is,  $t = t_0, t_0 + \Delta t_{TR}, t_0 + \Delta t$ . To reduce the computational time to calculate the geometric coefficients, especially in three dimensions, the geometric coefficients at  $t = t_0 + \Delta t_{TR}$  can be set to the interpolated values by assuming that the coefficients change linearly during  $\Delta t$ , which reduces the number of the box method calls by one third:

```
pdbSet Math 3D Use.Interpolated.Geom.Coeff 1
```

or:

```
math dimension=3 use.interpolated.geom.coeff
```

---

## Time-Step Control

This section discussed different time-step controls.

---

### Time-Step Control for PDEs

Sentaurus Process provides automatic time-step control. You can modify some of the control parameters.

The first time step of the `diffuse` command uses the initial time given with the `diffuse` command (see [diffuse on page 875](#)).

In an ideal situation, oxidation, mechanics, and diffusion time steps are equal to each other, and the next time step is increased by the `IncreaseRatio`:

$$t_{n+1} = I_{\text{ratio}} t_n \quad (954)$$

where  $t_{n+1}$  is the next diffusion time step,  $t_n$  is the current time step, and  $I_{\text{ratio}}$  is the `IncreaseRatio`. The default for `IncreaseRatio` is 2.

Use the following command to change `IncreaseRatio`:

```
pdbSet Diffuse IncreaseRatio {<n>}
```

In some cases, the ideal time step can be solution limited, grid limited, or reduced:

- *Solution limited* is the case when the time step is shortened to decrease the local truncation error; in a log file, such steps are marked by (s).
- *Grid limited* is the case when the time step is reduced because of a grid motion; in a log file, such steps are marked by (g).
- *Reduced* is the case when the time step is reduced to prevent overstepping of oxidation or mechanics steps; in log files, such steps are marked by (r).

If convergence is not achieved, the next time step is reduced by the `ReduceRatio`:

$$\tilde{t}_{n+1} = R_{\text{ratio}} t_{n+1} \quad (955)$$

The following command can be used to change `ReduceRatio`:

```
pdbSet Diffuse ReduceRatio {<n>}
```

For more information about the convergence during diffusion, use the command:

```
pdbSet Diffuse Convergence.Info {1 | 0}
```

Typical output with information `level=2` will look like:

Iter	Potential	Boron	Arsenic	Int	Vac	B4
1	4.345e-02	2.244e+01	2.512e+00	5.096e+03	1.835e+02	2.599e-06
-----						
Mesh:	bulk	Mater: Silicon				
	Org. Val.	Org. Updt.	Org.-Updt	Apld. Updt.	Error	Location
Boron	5.7e+18	1.8e+17	5.5e+18	5.5e+18	3.1e+02	( 1.7e-5, 0.0, 0.0 )
Arsenic	7.2e+16	3.1e+14	7.2e+16	7.2e+16	4.3e+01	( 1.7e-5, 0.0, 0.0 )
Int	2.8e+12	-1.3e+13	1.5e+13	1.5e+13	4.5e+04	( 1.5e-5, 0.0, 0.0 )
Vac	3.5e+14	5.5e+13	2.9e+14	2.9e+14	1.5e+03	( 1.7e-5, 0.0, 0.0 )

## 14: Numerics

### Time-Step Control

Largest update: Int in Silicon @ ( 1.5e-5, 0.0, 0.0 )

where:

- `Org.Val` is the original value at the node.
- `Org.Updt` is the original update at the node.
- `Org.-Updt` is the Original Value – Original Update.
- `Apld.Updt.` is the applied update.

Sentaurus Process provides three time-step control models (TSCMs):

- A local model (LTS) based on the current time step and described above.
- Two history-based models involving all previous time steps within the `diffuse` command: BPTS and NGLTS.

BPTS uses the *biggest previous time step* from the history, such that Eq. 954 is modified as:

$$t_{n+1} = I_{\text{ratio}} t_{\text{BPTS},n} \quad (956)$$

NGLTS uses the latest *nongrid limited time step*, and Eq. 954 is modified as:

$$t_{n+1} = I_{\text{ratio}} t_{\text{NGLTS},n} \quad (957)$$

Use the following command to choose the TSCM:

```
pdbSet Diffuse TSCM <model>
```

where `<model>` can be LTS, BPTS, or NGLTS.

---

## Error Control for PDEs

To control errors during transient simulation, Sentaurus Process uses the following to calculate the error:

$$e = \left( \frac{1}{N} \sum_{i=1}^N \left( \frac{|u_i|}{|sol_i| \times \text{TransRelErr} + \text{AbsErr}} \right)^2 \right)^{1/2} \quad (958)$$

where the sum is taken over all solution variables, and  $u_i$  is the update for solution  $sol_i$ . `TransRelErr` and `AbsErr` are the transient relative error and absolute error for the solution variables, respectively. They can be set using the commands:

```
pdbSet <mater> <solution> Transient.Rel.Error <n>  
pdbSet <mater> <solution> Abs.Error <n>
```



where `<mater>` is the material name.

To control errors during nonlinear Newton iterations, Sentaurus Process uses the following to calculate the error:

$$e = \left( \frac{1}{N} \sum_{i=1}^N \left( \frac{|u_i|}{|\text{sol}_i| \times \text{RelErr} + \text{AbsErr}} \right)^2 \right)^{1/2} \quad (959)$$

where RelErr is the relative error for the solution variables. It can be set using the command:

```
pdbSet <mater> <solution> Rel.Error <n>
```

**NOTE** If the error control parameter is not defined in the PDB for a material or a solution, the long-hand command `pdbSetDouble` must be used.

---

## Time-Step Control for Mechanics

Automatic time-step control for mechanics is activated only if the structure contains certain nonlinear features that require Newton iterations, such as plasticity, viscoplasticity, and creep. The size of the time step is adjusted based on satisfaction of certain convergence criteria.

### Convergence Criteria

To check the convergence of Newton iterations for mechanics equations [2][3], the criteria are:

- Force residual
- Energy
- Displacement

The force residual criterion checks the satisfaction of force equilibrium by comparing the maximum norm of the residual ( $R = F^{\text{external}} - F^{\text{internal}}$ ) against a reference value:

$$\|R_{n+1}^i\|_{\infty} \leq \epsilon_R \|R_{n+1}^1\| \quad (960)$$

The reference value of the force residual is computed automatically by taking a norm of the element force residual vector at the first Newton iteration in a time step.

The energy criterion checks the satisfaction of the minimization of energy at equilibrium by comparing the change in energy against a reference value:

$$\sqrt{|\Delta u_{n+1}^i \cdot R_{n+1}^i|} \leq \epsilon_E \sqrt{|\Delta u_n \cdot R_{n+1}^1|} \quad (961)$$

## 14: Numerics

### Time-Step Control

The reference value of energy is computed automatically by taking a dot product of the force residual and the displacement increment ( $\Delta u = v\Delta t$ ) vector at the first Newton iteration in a time step.

The displacement criterion checks the satisfaction of the solution accuracy by comparing the maximum norm of the displacement increment against a reference value:

$$\|\Delta u_{n+1}^i\|_{\infty} \leq \epsilon_u \|\Delta u_n\| \quad (962)$$

The reference value of displacement is computed automatically by taking a norm of the displacement increment vector at the start of the first Newton iteration in a time step.

The force residual and the energy criteria are checked by default. Optionally, the energy criterion may be replaced by the displacement criterion. Use the following parameters to activate or deactivate any of the convergence criteria:

```
pdbSet Mechanics Convergence.Force.Check <n>
pdbSet Mechanics Convergence.Energy.Check <n>
pdbSet Mechanics Convergence.Displacement.Check <n>
```

where <n> is either 0 (deactivate) or 1 (activate).

The choices for the force residual and the displacement reference value norms that can be set using the following command are:

```
pdbSet Mechanics Convergence.Check.Norm [RMS | ABS]
```

where RMS refers to the root mean square value (default) and ABS refers to the mean absolute value.

The reference values for any of the convergence criteria can be changed by using the commands:

```
pdbSet Mechanics Convergence.Force.RefVal <n>
pdbSet Mechanics Convergence.Energy.RefVal <n>
pdbSet Mechanics Convergence.Displacement.RefVal <n>
```

where <n> is a suitable positive value.

By default, the tolerance for each of the convergence criteria is set to 0.001 and can be changed by using the commands:

```
pdbSet Mechanics Convergence.Force.Tolerance <n>
pdbSet Mechanics Convergence.Energy.Tolerance <n>
pdbSet Mechanics Convergence.Displacement.Tolerance <n>
```

where <n> is a value between 0.0 and 1.0.

Convergence criteria are checked in every iteration until either they are satisfied or the maximum number of Newton iterations is reached. The default value for the maximum number of Newton iteration is 8, and this can be changed using the command:

```
pdbSet Mechanics MaxIterations <n>
```

where <n> is a value greater than zero.

## Time-Step Adjustment

The first time step for solving mechanics equations is set to the initial time given with the `solve` command. The size of subsequent time steps is decided based on the convergence history of the preceding time step. The time-step size is extended if the preceding time step converges quickly. The maximum value is limited to the maximum time given with the `solve` command. The time-step size is reduced if the preceding time step takes too many iterations to converge; it remains unchanged if the preceding time step takes a moderate number of iterations to converge.

The time-step size also is adjusted to keep the viscoplastic or creep strain error or value within tolerance when using such material models. Use the following commands to change the default settings for the viscoplastic or creep strain error or value:

```
pdbSet Mechanics StrainVP.Error.Tolerance <n>  
pdbSet Mechanics StrainVP.Value.Tolerance <n>  
pdbSet Mechanics StrainCr.Error.Tolerance <n>  
pdbSet Mechanics StrainCr.Value.Tolerance <n>
```

where <n> is a value between 0.0 and 1.0 for both. By default, only the viscoplastic or creep strain error criterion is used with a tolerance of 0.02.

## Time-Step Cutback

An automatic time-step cutback procedure interrupts the Newton iteration loop and restarts the time step with a smaller size when any of the following issues is encountered:

- Convergence criteria are not satisfied within the maximum number of Newton iterations.
- The solution converges very slowly over several iterations.
- The solution diverges over several iterations.
- Convergence criteria are satisfied, but viscoplasticity equations fail to converge.
- Convergence criteria are satisfied, but the viscoplastic or creep strain error or value is greater than the tolerance.

To check convergence details during solve steps, specify `info=1` in the `solve` command.

## References

- [1] R. E. Bank *et al.*, “Transient Simulation of Silicon Devices and Circuits,” *IEEE Transactions on Electron Devices*, vol. ED-32, no. 10, pp. 1992–2007, 1985.
- [2] O. C. Zienkiewicz and R. L. Taylor, *The Finite Element Method*, Butterworth-Heinemann: Oxford, 5th ed., 2000.
- [3] K. J. Bathe and A. P. Cimento, “Some Practical Procedures for the Solution of Nonlinear Finite Element Equations,” *Computer Methods in Applied Mechanics and Engineering*, vol. 22, no. 1, pp. 59–85, 1980.

*This appendix describes the commands used in Sentaurus Process.*

---

## Example Layout of Commands

The commands are presented in the layout that follows. An example is included here to familiarize users with the placement of information.

**Function:** The uses of this command are stated briefly.

**Syntax:** The syntax of the command is presented here, for example:

```
param1=<n>[<unit1>|<unit2>]
(param2=<n>[<unit3>|<unit4>] | param3=<c>)
<material>
[<field>]
[param4=<n>] [param5=<n>] [param6=<i>]
[param7= <list>] [param8 | param9]
[param10]
[param11=<c> & (param12=<n> | param13=<n>)]
```

**Description:** This section describes the syntax. In the syntax definition, brackets denote optional parameters, angle brackets denote a specific type of input, and parentheses denote grouping. The way in which to read this syntax is that `param1` is a required parameter that takes a number (that is, `<n>`) as its value.

The unit `<unit1>` or `<unit2>` can be specified. Do not use a space between the unit and its number.

**NOTE:** The angle brackets must be included in the unit specification.

In addition to `param1`, either `param2` or `param3` is required; `param3` takes a string for its value (`<c>`). On the command line, a material must be specified. A field can be specified, but is not required. A field is typically a solution but can be a data field such as a calculated quantity or a term. The parameters `param4` and `param5` are optional, and `param6` takes an integer for its value (`<i>`). Parameter `param7` takes a Tcl list as its argument and must be enclosed in braces, and elements are separated with a space.

## A: Sentaurus Process Commands

### Example Layout of Commands

- Description:** The parameters `param8` and `param9` are Boolean; either can be specified but not both. The parameter `param10` is also a Boolean (if a Boolean is on the command line, it denotes ‘true’; if it is preceded by ‘!’, its value is ‘false’). The parameters `param11`, `param12`, and `param13` are optional but, if `param11` is specified, either `param12` or `param13` also must be specified. Conversely, if either `param12` or `param13` is specified, `param11` must also be specified. The order of parameters is unimportant.
- Options:** The options of the command are listed.
- Examples:** This section illustrates the use of the command. The backslash (\) is a line continuation character in Sentaurus Process, for example:
- ```
command param1=1.0<unit1> param2=1.0 !param10 param9 \  
  param3= "string for param3" \  
  param7= { element1 element2 element3 }
```
- See:** This section lists cross-references to other relevant commands or documentation.

## Common Parameters

**Function:** Parameters common to all commands.

**Syntax:** <command> [info=<n>] [parameters]

**Description:** Nearly all commands in Sentaurus Process (with the exception of those implemented as Tcl procedures as well as a few others) support two common parameters:

- `info` sets the amount of information to be printed to the screen and the log file. The default is 0, which is the minimum amount. Higher levels give more details about the status of the simulation as well as model and parameter selection information. Recommended values are 0, 1, or 2. This parameter can be used with any other parameter combination for nearly all commands that are not Tcl procedures.
- `parameters` prints all available parameters for this command.

**NOTE** Some parameters are only intended for internal use and as such are not documented. In a future release, these parameters will not be shown as output. These parameters should not be used with any other parameter of the command.

---

## alias

**Function:** Sets and prints aliases.

**Syntax:** `alias <c> [<c>]`

**Description:** Interactive mode command used to view or set aliases.

In the case of two arguments, a new alias is set. If the number of arguments is equal to one, aliases are printed. If the first argument is `-list`, a list of allowed aliases is printed. Otherwise, only one alias corresponding to the first argument is printed.

**Examples:** `alias V Vacancy`  
Sets a new alias of `Vacancy`.

`alias -list`  
Prints the list of allowed aliases.

`alias Vac`  
Prints an alias of `Vac`.



---

## ambient

**Function:** Creates new ambients for material growth reactions, such as oxidation or silicidation, or creates a new epi growth mode.

**Syntax:**

```
ambient
  name=<c>
  [react | inert | epi]
  (list | print | clear | delete | add)
```

**Description:** Creates ambients. The ambient names can be used in the `diffuse`, `gas_flow`, `reaction`, and `temp_ramp` commands. The default list of ambients is given in [Table 63 on page 605](#).

**Options:**

|                                |                                                                                                                                                                                             |
|--------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>add</code>               | Creates a new ambient.                                                                                                                                                                      |
| <code>clear</code>             | Clears all known ambients (only useful for very special situations).                                                                                                                        |
| <code>delete</code>            | Deletes named ambient.                                                                                                                                                                      |
| <code>list</code>              | Returns a Tcl list of all available ambients.                                                                                                                                               |
| <code>name</code>              | Defines the ambient name. This name can be used in the <code>diffuse</code> , <code>gas_flow</code> , <code>temp_ramp</code> , and <code>reaction</code> commands to identify this ambient. |
| <code>print</code>             | Prints all available ambients.                                                                                                                                                              |
| <code>react, inert, epi</code> |                                                                                                                                                                                             |

When creating a new ambient, these parameters set the ambient type:

- `react` is used to create an active ambient and can be used to define a material growth reaction such as oxidation.
- `inert` ambients are used in `gas_flow` commands to create gas reactions or to dilute active ambients.
- `epi` ambients are used to create new epi growth modes or models.

**Examples:**

```
ambient name= MyO2 add react
Creates a new ambient for a new oxidation model.
```

```
ambient name= MyEpi add epi
Creates a new ambient for a new epi growth model or mode.
```

```
ambient list
Lists the known ambients.
```

---

## ArrBreak

**Function:** Computes one of two Arrhenius expressions depending on a 'break' temperature.

**Syntax:** ArrBreak <n> <n> <n> <n> <n>

**Description:** Creates two Arrhenius expressions and switches from the first one to the second one at the given break temperature. The first argument is the prefactor, and the second one is the activation energy [eV] of the first Arrhenius expression. The third argument is the prefactor, and the fourth argument is the activation energy [eV] of the second Arrhenius expression. The final argument is the break temperature [ $^{\circ}\text{C}$ ].

The first Arrhenius expression is computed when the temperature is below the break temperature, and the second Arrhenius expression is computed when the temperature is above the break temperature.

**Examples:** ArrBreak 5.0 0.5 4 0.4 825  
Creates two Arrhenius expressions  $5.0 \cdot \exp(-0.5/kT)$  and  $4.0 \cdot \exp(-0.4/kT)$  with a break temperature of  $825^{\circ}\text{C}$ .  $5.0 \cdot \exp(-0.5/kT)$  is computed when  $T < 825.0^{\circ}\text{C}$  and  $4.0 \cdot \exp(-0.4/kT)$  is computed when  $T \geq 825.0^{\circ}\text{C}$ .

## Arrhenius

- Function:** Creates an Arrhenius expression.
- Syntax:** `Arrhenius <n> <n>`
- Description:** Creates Arrhenius expressions. The first argument is the prefactor and the second one is the activation energy [eV].
- Examples:** `Arrhenius 5.0 0.5`  
Creates an Arrhenius expression  $5.0 * \exp(-0.5/kT)$ .

---

## beam

|                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>       | Creates a beam for multiple-beam etching.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| <b>Syntax:</b>         | <pre>beam   name=&lt;c&gt;   (incidence=&lt;n&gt;   direction= {&lt;x&gt; &lt;y&gt;})   factor=&lt;n&gt;   list</pre>                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| <b>Description:</b>    | Defines the direction and relative strength of etchant beams. The beam name is referenced in the <code>etch</code> command. The angle of incidence of the beam can be given using the <code>incidence</code> keyword or by a <code>direction</code> vector, which is normalized automatically to unit length. The relative strength <code>factor</code> is used to mix the strength of different beams. Etchant beams are assumed to be collimated, that is, a slight angular spread of beam direction is not taken into account.                                               |
| <b>Options:</b>        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| <code>direction</code> | Another way to define the beam incidence angle is by a direction vector defined with <code>direction</code> . The direction vector given by users is normalized to unit length internally.                                                                                                                                                                                                                                                                                                                                                                                      |
| <code>factor</code>    | If multiple beams are defined, the relative strength of each beam can be defined through <code>factor</code> , which is a relative strength factor.                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>incidence</code> | Defines the angle of incidence of the beam. An angle of 0 is vertical. The angle is measured counterclockwise, that is, a positive angle implies a beam ray entering from the upper left towards the lower right. A negative angle implies a beam ray entering from the upper right towards the lower left.                                                                                                                                                                                                                                                                     |
| <code>list</code>      | Returns a Tcl list of known beams.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <code>name</code>      | Specifies the beam name to be referenced using the <code>sources</code> option in the <code>etch</code> command.                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| <b>Examples:</b>       | <pre>beam name=source1 incidence=0 factor=1 beam name=source2 incidence=10 factor=0.5 beam name=source3 direction= {1 -0.1} factor=0.1</pre> <p>Defines a vertical beam called <code>source1</code> and a beam called <code>source2</code> at half the strength of <code>source1</code> at an angle of <math>10^\circ</math> (positive angle implies that the beam travels from the upper left to the lower right). A third beam called <code>source3</code> at one-tenth the strength of <code>source1</code> enters from the upper right slightly towards the lower left.</p> |

---

## bound

**Function:** Extracts the boundary of a material or region, and returns the outline as a list of coordinates.

**Syntax:** bound  
[<material> | region=<c>]

**Description:** Extracts the boundary of a material or region, and returns the outline as a list of coordinates. This command is used to plot the limits of the regions for other processing. The return is a list of lists of coordinates of the boundary. The outer lists are distinct pieces of the regions. Each outer list comprises a complete circle around the piece. Each inner list contains coordinate pairs in order around the regions. The coordinate pairs are written in xy order around the material.

**NOTE:** This command is not available for 3D simulations.

**Options:**

<material> Either a material or a region must be specified. Specifying a material will extract the boundary of all regions of the specified material. For information about specifying materials, see [Material Specification on page 50](#).

region Either a material or a region must be specified. Specifying a region will extract the boundary of that region.

**Examples:** bound oxide  
Returns the boundary of the oxide material.

bound region=Silicon\_1  
Returns the boundary of the region named silicon\_1.

## Compatibility

- Function:** Applies parameters consistent with the defaults in a previous release.
- Syntax:** `Compatibility <release>`
- Description:** Changes parameters to the default values from a previous release. If used, this command must be the first command in the command file so that all subsequent commands that depend on the defaults take into account the compatibility setting (see [Compatibility with Previous Releases on page 52](#)).
- Options:**
- `<release>` Applies parameters consistent with the specified release. Aliases are available for the release name so that it is not necessary to know the release foundation letter. For example, `2011.09` can be used instead of `F-2011.09`.
- Examples:** `Compatibility 2010.12`  
Applies parameters consistent with Version E-2010.12.

## contact

**Function:** Defines a contact for subsequent device simulation. Intended only for adding contacts to structures created for device simulation.

**Syntax:**

```

contact
  [add] [list] [clear]
  [depth=<n>]
  [name=<c>]
  [new.name=<c>]
  [print]
  [sidewall]
  [width=<n>]
  [region=<c>]
  [left] [right] [back] [front] [top] [bottom]
  (
    {box <material> [adjacent.material=<c>]
     xlo=<n>[<m>|<cm>|<um>|<nm>]
     xhi=<n>[<m>|<cm>|<um>|<nm>]
     [ylo=<n>][<m>|<cm>|<um>|<nm>]
     [yhi=<n>][<m>|<cm>|<um>|<nm>]
     [zlo=<n>][<m>|<cm>|<um>|<nm>]
     [zhi=<n>][<m>|<cm>|<um>|<nm>]} |
     [cut.mesh]
     {point
      x=<n>[<m>|<cm>|<um>|<nm>]
      [y=<n>][<m>|<cm>|<um>|<nm>]
      [z=<n>][<m>|<cm>|<um>|<nm>]
      [replace]}
    )
  [SearchRadius=<n>][<m>|<cm>|<um>|<nm>]

```

**Description:** Defines new contacts, deletes contacts, and prints contact information. The `contact` command can be called multiple times with the same name if the `add` parameter is specified. In this case, the contact will have multiple parts. Contacts are written to TDR files in the `struct` command. They are not otherwise used in Sentaurus Process.

**NOTE:** Contacts are only intended for structures written for device simulation. They should be specified immediately before the final `struct` command used to write a structure for device simulation.

**NOTE:** Contacts are not transformed during the `transform` command.

**NOTE:** If a TDR file, containing a boundary or mesh, is read into Sentaurus Process (during the `init` command), contacts defined in these files are added to the list of contacts.

## A: Sentaurus Process Commands

### contact

#### Options:

`add` If the `contact` command is called multiple times with the same name, it will overwrite the previous definition by default. If `add` is used also, it will instead add to the existing contact indicated by the `name` parameter or create a new contact if it does not already exist.

`adjacent.material`

Specifies a second material for the contact. Only elements at the interface between the two materials are allowed for the contact.

`left, right, back, front, top, bottom`

These optional parameters selectively switch on certain outer boundaries. These outer boundaries are the simulation outer domain and *not* the bulk nongas outer boundary. Nongas outer boundaries are treated like interfaces and can be specified with `adjacent.material=gas`. By default, only `top` and `bottom` are switched on, and the rest are switched off. If any of these parameters are specified, internal interfaces are switched off. In addition, the `sidewall` parameter is equivalent to specifying all of these parameters.

`box, point`

Selects one of the supported contact types:

- A box-type contact consists of elements at the surface of one region or material inside the box, defined for the contact. When choosing a box-type contact, the mesh will be cut where the box intersects the chosen region to give an accurate size for the contact. Occasionally, this cutting can produce bad mesh elements, so for those cases, cutting can be switched off with `pdbSet Grid Cut.At.Contacts 0`. Use the `line` command to insert lines in the mesh if desired to retain contact size accuracy.
- A point-type contact contains all the boundary elements of one region. The region can be specified or the material and the x-, y-, and z-coordinates of one point can be specified to select the region.

`clear`

Clears the list of all contacts. If `name` is specified, removes only the specified contact.

`cut.mesh`

By default when a box contact is created, the mesh is cut at the contact borders to ensure accurate contact dimensions. Specifying `!cut.mesh` will switch off mesh cutting, providing better element quality at the contact borders, but possibly sacrificing accuracy of the contact borders. The contact will only include nodes of the existing mesh within the contact borders.

`depth`

Depth of the contact in micrometers.

`list`

Prints a list of currently defined contacts.



|                              |                                                                                                                                                                                                                                                                                                                                                                                             |
|------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <material>                   | Specifies the material for the contact. Contacts in DF-ISE and TDR files are always defined as a set of surface elements. Only elements at the surface of volume regions of the specified material are selected. For information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                        |
| name                         | Name of the contact.                                                                                                                                                                                                                                                                                                                                                                        |
| new.name                     | Used with the name parameter to change the name of a contact from that specified by name to that specified by new.name.                                                                                                                                                                                                                                                                     |
| print                        | Prints the contact information.                                                                                                                                                                                                                                                                                                                                                             |
| region                       | Name of the volume region to be used for the contact. Only surface elements of that region will be selected for the contact.                                                                                                                                                                                                                                                                |
| replace                      | If specified, in the DF-ISE or TDR file, the material of the region of a contact is replaced by gas for point contacts.<br><b>NOTE:</b> Sometimes, regions of material gas are not saved. The material of the region in the subsequent simulation is not affected.                                                                                                                          |
| SearchRadius                 | If contacts have been read from a DF-ISE or TDR file, they are added to the current list of contacts defined in Sentaurus Process. When saving the current structure to a DF-ISE or TDR file, surface elements from the current simulation mesh are selected for the contacts if all their points are in the vicinity of the original contact elements. The default unit is $\mu\text{m}$ . |
| sidewall                     | Allows only surface elements on the external boundary of the simulation domain (left, right, front, back) to be selected for a contact. By default, only surface elements at material interfaces and surface elements at the top and bottom of the simulation domain are selected for contacts. The default is false.                                                                       |
| width                        | Width of the contact in micrometers.                                                                                                                                                                                                                                                                                                                                                        |
| x, y, z                      | Define the coordinates of a point for the point contact. If some coordinates of the point are omitted, the region is selected using the specified coordinates only. The default unit is $\mu\text{m}$ .                                                                                                                                                                                     |
| xlo, xhi, ylo, yhi, zlo, zhi | Define the low and high values in each of the coordinate directions for the box contact. If some coordinates are omitted, the current extensions of the simulation domain are used. The default unit is $\mu\text{m}$ .                                                                                                                                                                     |

## A: Sentaurus Process Commands

### contact

**Examples:**

```
contact list
```

Lists all available contacts.

```
contact name=gate x=-0.05 y=0.0 replace point
```

Defines a contact named `gate`. It will consist of boundary elements of the region containing the point `(-0.05,0.0)`. The region material will be replaced by gas.

```
contact box xlo=-0.01 ylo=-0.46 xhi=0.1 yhi=-0.16 name=source Aluminum
```

Defines a box-type contact containing the surface elements of an aluminum region inside the specified box.

```
contact bottom name=substrate
```

Defines the substrate contact at the bottom of the simulation domain. Switches off interior interfaces.

```
contact left front name=lfcontact xlo=0 ylo=0 zlo=0 xhi=1 yhi=1 zhi=1
```

Defines a contact named `lfcontact` on the left side (minimum Y-coordinate) and the front (maximum Z-coordinate) of the simulation domain for that part of the simulation domain inside the box `(0,0,0) -> (1,1,1)` and not on any interior interfaces.

**See:**

[integrate on page 945](#), [struct on page 1086](#)

---

## contour

|                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>     | Plots contours in the selected variable on a 2D plot.                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <b>Syntax:</b>       | <pre>contour   [name=&lt;c&gt;] [value=&lt;n&gt;]   [x=&lt;n&gt;][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]   [y=&lt;n&gt;][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]   [z=&lt;n&gt;][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]   [color=&lt;c&gt;] [print]</pre>                                                                                                                                                                                                                                            |
| <b>Description:</b>  | Draws a contour in the selected variable or a named data field at the value specified. The value must be specified in the range of the computed variable. For example, if plotting log boron, the value should be in the range 10 to 20 and <i>not</i> 1e10 to 1e20. The <code>contour</code> command assumes that a <code>plot.2d</code> command has been specified, and that the screen is configured for plotting a 2D graphic. If this has not been set, the routine most likely will produce useless results. |
| <b>Options:</b>      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <code>color</code>   | Line color for the contour. It can be any color supported by X11 hardware and named in the color database.                                                                                                                                                                                                                                                                                                                                                                                                         |
| <code>name</code>    | Name of data field. This allows plots without using the <code>select</code> command. The default is <code>Z_Plot_Var</code> .                                                                                                                                                                                                                                                                                                                                                                                      |
| <code>print</code>   | Indicates that the contour values should be printed, not plotted. The output is compatible with <code>xgraph</code> . In addition, a set of Tcl lists is returned.                                                                                                                                                                                                                                                                                                                                                 |
| <code>value</code>   | This floating parameter expresses the value at which the contour line should be plotted. If boron has been selected, a value of 1.0e16 would produce a line of constant boron concentration at that concentration.                                                                                                                                                                                                                                                                                                 |
| <code>x, y, z</code> | Specify the plane on which contouring is performed. In two dimensions, they need not be specified. In three dimensions, two parameters must be specified to indicate the plane of calculation of the contour. The default unit is $\mu\text{m}$ .                                                                                                                                                                                                                                                                  |
| <b>Examples:</b>     | <pre>contour val=1e10</pre> Draws a line at an isoconcentration of $10^{10}$ .                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| <b>See:</b>          | <a href="#">Compatibility on page 860</a> , <a href="#">plot.2d on page 1013</a> , <a href="#">slice on page 1073</a>                                                                                                                                                                                                                                                                                                                                                                                              |

---

## CutLine2D

**Function:** Computes the slice angle when given a cut in wafer coordinates.

**Syntax:** `CutLine2D <x1> <y1> <x2> <y2>`

**Description:** Given a cut in wafer coordinates defined by the endpoints  $(x1, y1)$  and  $(x2, y2)$ , this command computes the slice angle.

**Options:**

`<x1> <y1> <x2> <y2>`

Endpoints of simulation cutline in wafer coordinates.

**Examples:** `init slice.angle= [CutLine2D 0 0 1.0 0]`  
Sets the cutline for the simulation from (0,0) to (1,0).

**See:** [Understanding Coordinate Systems on page 64](#)

## define

- Function:** Defines a Tcl variable.
- Syntax:** `define <name> <value>`
- Description:** This is equivalent to the Tcl command `set`, except that variables defined with `set` are not saved or restored in TDR files. Variables defined using the `define` command are saved or restored.
- Options:**
- <name> Any user-defined parameter name.
- <value> Any number or string value.
- Examples:** `define LG 0.02`  
Defines the Tcl variable `LG`, which is stored in and loaded from a TDR file. It can be used in any Tcl expression.
- See:** Tcl documentation for description of `set` syntax. The `define` and `fset` commands are equivalent.

---

## defineproc

**Function:** Defines a Tcl procedure.

**Syntax:**

```
defineproc name { arguments of procedure } {  
    body of procedure  
}
```

**Description:** This is equivalent to the Tcl command `proc`, except that procedures defined with `proc` are *not* saved or restored in TDR files. Procedures defined using `defineproc` are saved or restored.

**Examples:**

```
defineproc relerr { newVal RefVal name my_err } {  
    upvar my_err fl  
    set denom [ expr abs($newVal)+abs($RefVal)+1e-20 ]  
    set deviation [expr 100*abs(($RefVal - $newVal)/$denom)]  
    if { $deviation > 0.5 } {  
        LogFile IL0 "Compare: $name = $newVal, ref = $RefVal, relerr = \  
            $deviation  
            \n --> failed\n"  
        set fl [ expr $fl+1 ]  
    } else {  
        LogFile IL0 "Compare: $name = $newVal, ref = $RefVal, relerr = \  
            $deviation ok\n"  
    }  
}
```

Defines the Tcl procedure `relerr`, which is stored in and loaded from a TDR file.

**See:** Tcl documentation for description of `proc` syntax. The `defineproc` and `fproc` commands are equivalent.

## DeleteRefinementboxes

- Function:** Deletes a set of refinement boxes based on a name pattern.
- Syntax:** DeleteRefinementboxes pattern= "<pattern>"
- Description:** Finds all refinement boxes with names that match the defined pattern and deletes them. The pattern is expanded according to standard Tcl rules.
- Options:**
- pattern      Pattern to use.
- Examples:** DeleteRefinementboxes pattern= "root\*"   
Deletes all refinement boxes that have names like root\_1, root\_2 and root\_3, and so on.

---

## deposit

**Function:** Deposits a new layer.

**Syntax:**

```
deposit
{ [material>] [isotropic | anisotropic | fill | fourier | crystal]
  [thickness=<n>][<m>|<cm>|<um>|<nm>]
  [coord=<n>][<m>|<cm>|<um>|<nm>] }
[material=<c>]
[selective.materials= <material list>]
[type=isotropic | anisotropic | fill | polygon | directional | fourier]
[rate=<n>]
[1D]
[time=<n>][<hr>|<min>|<s>]
[direction= <numeric list>]
[coord=<n>][<m>|<cm>|<um>|<nm>]
[direction= <numeric list>]
[polygon= <numeric list>]
[coeffs= {<A0> <A1> <A2> ... <An>}]
[mat.coeffs= {
  <material1>= {<A0> <A1> <A2> ... <An>}
  <material2>= {<A0> <A1> <A2> ... <An>}
  ...
}]
[crystal.rate= {"<100>="<n> "<110>="<n> "<111>="<n>}]
[Strained.Lattice]
[region.name=<c>]
[temperature=<n>][<C>|<K>]
[remesh] [Adaptive] [force.full.levelset]
[repair]
[sde=<c>] [steps=<n>] [mask=<c>]
{[doping= <name list>]}
{[<field name>] | [species=<c>]
  [concentration=<n>][<m-3>|<cm-3>|<um-3>|<nm-3>]}
[fields.values= <parameter list>]
[sources= {<beam1> <beam2> ... <beamn>}]
[shadowing] [shadowing.nonisotropic] [fill.buried]
```

**Description:** Simulates a deposition step.

**Options:**

**1D** Usually, a polygon deposit automatically increases the dimension to 2D before performing the operation; setting 1D prevents this behavior.

**Adaptive** Specifies with or without adaptive meshing for this deposition. Parameters for adaptive meshing are described in [Adaptive Refinement on page 679](#). The default is the return value of `pdbGet Grid Adaptive`.

**coeffs** List of single-material coefficients  $A_0, A_1, \dots, A_n$  used in Fourier deposition.



|                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|---------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>crystal.rate</code>                               | List of deposition rates defined per crystallographic direction in the format:<br>{ "<100>"=<etch rate> "<110>"=<etch rate> "<111>"=<etch rate> }                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <code>crystal</code>                                    | Specify crystal deposition.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| <code>coord</code>                                      | The x-coordinate for <code>type=fill</code> . The default unit is $\mu\text{m}$ .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <code>direction</code>                                  | Specifies the direction for directional deposition as x- and y-coordinates of the deposition vector. The x-coordinate must be positive. Positive-y indicates a right-pointing deposition beam, and negative-y indicates a left-pointing beam.                                                                                                                                                                                                                                                                                                                        |
| <code>&lt;field name&gt;, species, concentration</code> | These parameters allow a doped layer to be deposited. The <code>species</code> parameter specifies the name of the data field to be incorporated (you can add a new user species this way). Instead of specifying <code>species</code> , you can specify a field name by name (for example, boron, arsenic, phosphorus, and indium). The default value and unit for concentration is $10^{10} \text{ cm}^{-3}$ .                                                                                                                                                     |
| <code>doping</code>                                     | String array of names of doping profiles that have been previously defined with the <code>doping</code> command.                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| <code>fields</code>                                     | List of fields to be introduced in the deposited layer. The data values for these fields are specified with the <code>values</code> parameter. For stresses, use the field names <code>StressELXX</code> , <code>StressELXY</code> , <code>StressELYY</code> , <code>StressELZZ</code> , <code>StressELXZ</code> , <code>StressELYZ</code> . It is not necessary to specify all stress components. Those that are not specified are assumed to be zero initially and are updated during the stress rebalance at the end of deposition. This parameter is deprecated. |
| <code>fields.values</code>                              | Takes a list of parameters where the parameter name is the name of the field to be introduced in the deposited layer, and the value is the initial value. A list of fields of any name can be initialized with this parameter and, for solution variables or stress components, units are accepted. For example:<br><code>fields.values= { boron=1e18&lt;cm-3&gt; }</code>                                                                                                                                                                                           |
| <code>fill.buried</code>                                | By default, the material is deposited on the surface exposed to the upper gas region. If the structure has buried gas bubbles, they are untouched. Use <code>fill.buried</code> to deposit inside those gas bubbles.                                                                                                                                                                                                                                                                                                                                                 |
| <code>force.full.levelset</code>                        | By default, the simplest algorithm is chosen to perform the etching. However, sometimes the algorithm chosen will not give correct results if the topology of the structure is complicated. Specifying this parameter switches on the general level-set time-stepping algorithm which correctly handles these structures.                                                                                                                                                                                                                                            |

## A: Sentaurus Process Commands

### deposit

|                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|-------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>fourier</code>                      | Specify Fourier deposition type. When using Fourier deposition, the coefficients must be specified using <code>coeffs</code> or <code>mat.coeffs</code> parameters.                                                                                                                                                                                                                                                                                                                                                                                                            |
| <code>isotropic, anisotropic, fill</code> | <p>Specify the type of deposition:</p> <ul style="list-style-type: none"><li>• <code>isotropic</code> implies the same rate in all directions.</li><li>• <code>anisotropic</code> defaults to vertically downward deposition (directional deposition cannot be performed with quick commands).</li><li>• <code>fill</code> is used to fill the structure with the specified material up to the specified coordinate.</li></ul> <p>These deposition types must be used with <code>thickness</code> or <code>coord</code>, not with <code>rate</code> and <code>time</code>.</p> |
| <code>mask</code>                         | <p>Name of a mask to be used for the deposition.</p> <p><b>NOTE:</b> The material is deposited outside of the mask. If deposition inside the mask is required, the parameter <code>negative</code> must be specified in the <code>mask</code> command.</p>                                                                                                                                                                                                                                                                                                                     |
| <code>mat.coeffs</code>                   | List of multimaterial coefficients $A_0, A_1, \dots, A_n$ used in Fourier deposition with a different set of coefficients defined for each material.                                                                                                                                                                                                                                                                                                                                                                                                                           |
| <code>&lt;material&gt;</code>             | Allows the specification of the deposited material. For information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <code>material</code>                     | Defines the material to be deposited. Overrides the <code>&lt;material&gt;</code> specification.                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| <code>polygon</code>                      | A list of x- and y-coordinates can be defined for the deposition. This is used only for 2D deposition with <code>type=polygon</code> . The list of coordinates must define a single polygon with no self-intersections. The first and last points are connected implicitly to close the polygon. The specified material is deposited inside the polygon. The default unit for the coordinates is $\mu\text{m}$ .                                                                                                                                                               |
| <code>rate</code>                         | Deposition rate. The default unit is $\mu\text{m}/\text{minute}$ .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>region.name</code>                  | Name of the region created by the <code>deposit</code> command. The name must not contain an underscore ( <code>_</code> ) or a period ( <code>.</code> ) because these characters have special meaning.                                                                                                                                                                                                                                                                                                                                                                       |
| <code>remesh</code>                       | Performs a remeshing after the deposition.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| <code>repair</code>                       | In MGOALS3D mode, small regions are removed automatically by default. Sometimes, this can cause small gas bubbles in the structure or other problems. Use <code>!repair</code> to switch off the small region removal.                                                                                                                                                                                                                                                                                                                                                         |

|                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| sde                    | String to specify parameters and to select algorithms for 3D Sentaurus Structure Editor. By default, the parameters <code>rate</code> , <code>time</code> , <code>thickness</code> , <code>type</code> , and so on are translated into appropriate Sentaurus Structure Editor commands. If an algorithm is specified in the <code>sde</code> parameter, it overwrites the algorithm used by default for isotropic or anisotropic deposition., for example:<br><pre>sde= {"algorithm" "lopX"} sde= {"algorithm" "lopX" "radius" 0.07}</pre> |
| selective.materials    | Specifies that deposition will occur only on selected materials. In 2D, MGOALS is used and multiple materials can be selected. In 3D, the Sentaurus Structure Editor interface is called and only one material can be selected. In addition, in either case, only one material can be deposited.                                                                                                                                                                                                                                           |
| shadowing              | In 2D, switches on the inclusion of shadowing effects if <code>force.full.levelset</code> is specified or for Fourier deposition. The visibility of each surface area to each beam is calculated at every level-set time step. In MGOALS3D, this parameter enables shadowing effects on both directional and anisotropic deposition. The interface to Sentaurus Structure Editor ignores this parameter.                                                                                                                                   |
| shadowing.nonisotropic | Use instead of <code>shadowing</code> to allow the 0th-order Fourier coefficient to deposit in areas where the beam is shadowed.                                                                                                                                                                                                                                                                                                                                                                                                           |
| sources                | Defines the source beams for level-set deposition.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| steps                  | Used to subdivide a deposition into more than one step. If necessary, stress relaxation is calculated at the end of each step. The default value is 1.                                                                                                                                                                                                                                                                                                                                                                                     |
| Strained.Lattice       | Specifies strained deposition.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| temperature            | Deposition temperature used for stress relaxation only. The default value and unit is 26.85°C .                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| thickness              | Thickness of the deposited layers. The default unit is $\mu\text{m}$ .                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| time                   | Deposition time. It must be specified if the <code>rate</code> parameter is used. The default unit is minute.                                                                                                                                                                                                                                                                                                                                                                                                                              |

## A: Sentaurus Process Commands

### deposit

**type** Explicitly specifies the type of deposition to be performed:

- `type=isotropic` performs isotropic deposition, which must be used with the `rate` and `time` arguments.
- `type=anisotropic` performs deposition in the vertical direction only, which must be used with the `rate` and `time` arguments.
- `type=fill` performs a fill of a specified material up to the coordinate specified with the `coord` argument.
- `type=polygon` performs a polygonal deposition (in 2D), which requires the `polygon` argument.
- `type=directional` performs anisotropic etching using a specified direction.
- `type=fourier` performs Fourier deposition, which requires the coefficients to be specified with either `coeffs` or `mat.coeffs`.
- `type=crystal` performs crystallographic deposition, which requires `crystal.rate` also to be specified.

**values** Data values of the fields introduced in the deposited layer by the `fields` parameter. This parameter is deprecated.

**Examples:** `deposit thickness=0.2 oxide isotropic`  
Isotropic deposition of a 0.2  $\mu\text{m}$  oxide layer.

`deposit rate= {0.2} material= {oxide} type=isotropic time=1`  
Same as above; thickness is defined by `rate` and `time`.

`deposit thickness=0.1 nitride \  
fields.values= { StressELXX=1e9<Pa> StressELYY=1e9<Pa> \  
StressELZZ=1e9<Pa> }`

In this example, an intrinsic isotropic stress of  $10^9$  Pa is added to the deposited nitride layer before the post-deposit mechanics rebalancing step.

**See:** [doping on page 883](#), [mask on page 977](#), [mgoals on page 992](#)

## diffuse

**Function:** Simulates thermal annealing, densification, and any material growth process during annealing – oxidation, silicidation, and epitaxy.

**Syntax:**

```
diffuse
  {temp.ramp=<c>} |
  {time=<n>[<hr>|<min>|<s>] temperature=<n>[<C>|<K>] | }
  [ramprate=<n>][<C/s>|<K/s>|<C/min>|<K/min>]
  [t.final=<n>][<C>|<K>]
  [(<ambient> by default one of O2 | H2O | N2O | N2 | Epi | LTE |
    H2 | HCl)]
  [flow<ambient>=<n>][<l/min>]
  [flows= {
    [<ambient1>=<n>][<l/min>]
    [<ambient2>=<n>][<l/min>]
    ...}]
  [gas.flow=<c>]
  [p<ambient>=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [partial.pressure= {
    [<ambient1>=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
    [<ambient2>=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
    ...}]
  [pressure=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [ISSG]
  [epi.layers=<i>]
  [epi.doping= <parameter list>]
  [epi.doping.final= <parameter list>]
  [epi.model=<i>]
  [epi.resist= {[<dopant1>=<n>[<ohm-cm>]] [<dopant2>=<n>[<ohm-cm>]] ...}]
  [epi.thickness=<n>][<m>|<cm>|<um>|<nm>]
  [angles.factors= {
    [<interface_mat1>= <numeric list>]
    [<interface_mat2>= <numeric list>]
  }]
  [sources= {<beam1> <beam2> ... <beamn>}]
  [deposit.type=<c>]
  [crystal.rate= {"<100>"=<n> "<110>"=<n> "<111>"=<n>}]
  [coeffs= {<A0> <A1> <A2> ... <An>}]
  [mat.coeffs= {
    <material1>= {<A0> <A1> <A2> ... <An>}
    <material2>= {<A0> <A1> <A2> ... <An>}
    ...
    <materialn>= {<A0> <A1> <A2> ... <An>} }]
  [repair]
  [auto.doping= <string list>]
  [density.increase= [<regionName>=<n> | <material>=<n>]]
```

## A: Sentaurus Process Commands

### diffuse

#### Syntax (continued)

```
[isolve]
[init=<n>][<hr>|<min>|<s>]
[maxstep=<n>][<hr>|<min>|<s>]
[delT=<n>][<C>|<K>]
[delNT=<n>][<C>|<K>]
[delTox=<n>][<C>|<K>]
[minT=<n>][<C>|<K>]
[movie=<c>]
[stress.relax]
[laser]
[write.temp.file=<c>]
[(mgoals.native) | (ts4.native) | (sp.native)]
[kmc] [kmc.stress] [lkmc] [Adaptive]
[eqnInfo]
[reload] [reloadHeat] [reloadReact]
```

**Description:** Performs annealing (either continuum or KMC) or, if the diffusion time is set to 0, this command activates dopants and performs a stress update. The command options set diffusion conditions as well as time-stepping options. Diffusion model and parameter setting are performed with the `pdbSet` command. The basic settings are `pdbSet <material> Dopant DiffModel <model>`, where `<model>` can be any of `Constant`, `Fermi`, `Pair`, `React`, `ChargedFermi`, `ChargedPair`, or `ChargedReact`. Temperature ramps are specified by first creating a list of ramping steps using the `temp_ramp` command. Then, the ramp is applied with the parameter `temp.ramp`. All `temp_ramp` command parameters can be specified with the `diffuse` command.

To specify an oxidizing ambient, there are numerous methods:

- Use the shorthand `<ambient>` flags.
- Use the `flow<ambient>` or `p<ambient>` parameters.
- Use the `gas_flow` command and set the parameter `gas.flow` to the name set in the `gas_flow` command.
- Use `gas_flow` inside the `temp_ramp` command, and use `temp.ramp` to set the name of the `temp_ramp` to be used.

The list of ambients is given in [Table 63 on page 605](#) and includes  $O_2$ ,  $H_2O$ ,  $HCl$ ,  $N_2$ ,  $H_2$ , and  $N_2O$ , which can be used in oxidation specification, as well as two epi ambients `Epi` and `LTE` for specifying epitaxial growth. For more information on `Epi` and `LTE`, see [Epitaxy on page 270](#).

**Options:**

- Adaptive** Specifies with or without adaptive meshing for this diffusion step. Parameters for adaptive meshing are described in [Adaptive Meshing during Diffusion on page 687](#). The default is the return value of `pdbGet Grid Adaptive`.
- <ambient>** Shorthand specification to set the ambient partial pressure the same as the total pressure. If an ambient is specified this way, it must be the only ambient set in the `diffuse` command. In addition to the oxidation-type ambients (O2, H2O, N2O, ISSG), the epitaxial ambients `Epi` and `LTE` are available.
- angles.factors** Specifies interface-specific anisotropic epi growth rate factors. This parameter specifies a piecewise linear growth rate factor versus angle for each growing interface (the factors must be between 0 and 1). For example, to create a 30° silicon facet and a 40° polysilicon facet, specify:  

```
angles.factors= {
  EpiOnSilicon_Gas= { 0.0 1.0 25.0 1.0 30 0.0 }
  EpiOnPolySilicon_Gas= { 0.0 1.0 35.0 1.0 40 0.0 } }
```
- auto.doping** List of species for which the auto-doping model will be switched on during epitaxial growth.
- coeffs** List of single-material coefficients  $A_0, A_1, \dots, A_n$  used in Fourier deposition when `epi.model=1` and `deposit.type=fourier`.
- crystal.rate** List of etching rates defined per crystallographic direction in the format: `{"<100>"=<dep rate> "<110>"=<dep rate> "<111>"=<dep rate>}` used for crystallographic deposition when `epi.model=1` and `deposit.type=crystal`.
- delNT** Defines the maximum temperature step during a temperature ramp down if specified. The default unit is degree Celsius. It also can be defined globally with the command: `pdbSet Diffuse delNT {<n>}`
- delT** Defines the maximum temperature step during a temperature ramp-up if specified. The default unit is degree Celsius. It also can be defined globally with the command: `pdbSet Diffuse delT {<n>}`
- delTox** Defines the maximum temperature step during a temperature ramp for oxidation/growth if specified. The default unit is degree Celsius. It also can be defined globally with the command: `pdbSet Diffuse delTox {<n>}`
- density.increase** The density increase. The increase value can be specified per region `<regionName>=<n>` or per material `<material>=<n>`.

## A: Sentaurus Process Commands

### diffuse

- `deposit.type` When `epi.model=1`, epitaxy is solved as a series of alternating deposit and diffuse steps. This parameter specifies the deposition type, and allowed values are:
- `isotropic` (default).
  - `fourier` (in which case, either `coeffs` or `mat.coeffs` must be specified).
  - `crystal` (in which case, `crystal.rate` must be specified).
- `epi.dopants` Deprecated in favor of `epi.doping`. This is a list of the data fields to be incorporated into the epitaxial layer.
- `epi.doping` Takes a list of parameters where the parameter name is the name of the species to be initialized and the value is the initial value. A list of fields of any name can be initialized with this parameter and, for solution variables, units are accepted. For example:
- ```
epi.doping= { boron=1e18<cm-3> GSize=1<nm> myfield=1 }
```
- `epi.doping.final`
- Takes a list of parameters where the parameter name is the name of the species to be initialized and the value is the final value. A list of fields of any name can be initialized with this parameter and, for solution variables, units are accepted. For example:
- ```
epi.doping.final= { boron=1e18<cm-3> GSize=1<nm> myfield=1 }
```
- `epi.layers` Number of layers of mesh lines required during epitaxial growth (for both `epi.model=0` and `epi.model=1`). The default is `-1`, which indicates that 10 layers should be used if `epi.model=1`, and 40 layers should be used if `epi.model=0`. However, if the global parameter given by:
- ```
pdbSet Silicon Grid epi.perp.add.dist <n>
```
- is set to a positive number, `epi.layers` is ignored (whether set or not), and `epi.perp.add.dist` is used to determine the distance between mesh lines. For `epi.model=1`, the number of layers is adjusted if the deposited layer thickness is less than the parameter `Grid MinEpiDepositThickness` in SDE mode or `Grid MinEpiDepositThicknessMGoals3D` in MGOALS3D mode.
- `epi.model` The two methods described above can be chosen using this parameter:
- `epi.model=0` (default) applies a moving-boundary algorithm similar to oxidation.
  - `epi.model=1` uses alternating doped deposition and inert annealing steps.
- In 3D, `epi.model=0` is not as stable or robust as `epi.model=1`, so `epi.model=1` is recommended.



<code>epi.resist</code>	List of parameters with dopant name and resistivity to calculate the background dopant concentration. If more than one dopant name appears in the list, the doping concentration is calculated individually for each dopant by ignoring the other ones.
<code>epi.thickness</code>	Sets the epitaxial layer thickness to be deposited. The default unit is $\mu\text{m}$ .
<code>eqnInfo</code>	Allows equation updates to be printed to the log file during the Newton iteration.
<code>flow&lt;ambient&gt;, flows</code>	<p>List of gas flows in the reaction chamber. The gas flows are used to compute the partial pressures of the active ambients (those causing material growth). Flows can be specified using either a parameter name composed of <code>flow + &lt;ambient&gt;</code> (for example, <code>flowO2</code> and <code>flowHCl</code> where <code>O2</code> and <code>HCl</code> are ambient names) or the <code>flows</code> parameter that takes a list of parameters with names of the ambients, for example:</p> <pre>flows= { O2 = 1.0&lt;l/min&gt; HCl = 1.0&lt;l/min&gt; }</pre> <p>The list of default ambients is given in <a href="#">Table 63 on page 605</a>, but this list can be extended by using the <code>ambient</code> command. When a gas flow is specified as a combination of flows (and not when using partial pressures), a complete reaction of the ambients is assumed to occur, for example, <math>\text{O}_2 + 2\text{H}_2 \rightarrow 2\text{H}_2\text{O}</math>. Besides gas reactions, the addition of inert gases also changes the partial pressure of the material growing ambients. For example, if the flows of only <math>\text{N}_2</math> and <math>\text{O}_2</math> are specified and are equal, then the partial pressure of <math>\text{O}_2</math> will be <math>\text{&lt;total pressure&gt;/2.0}</math> where <math>\text{&lt;total pressure&gt;}</math> is given by the <code>pressure</code> parameter (see below).</p> <p><b>NOTE:</b> Flows and partial pressures must not be specified in the same <code>gas_flow</code> together.</p>
<code>gas.flow</code>	Specifies a <code>gas.flow</code> to be used for this diffusion step. (Do not use with other <code>gas_flow</code> command parameters or with the <code>temp_ramp</code> command.)
<code>init</code>	First time step. The default is 0.0001 s, which is sometimes inappropriate for defect simulations, particularly in cases of damage. The default unit is minutes.
<code>isolve</code>	Switches off initial solve for models that need to have an equation solved to set the initial conditions. In these cases, it is possible to set an initial condition and switch off the default initialization.
<code>ISSG</code>	Switches on <i>in situ</i> steam-generated (ISSG) oxidation.
<code>kmc</code>	Allows the <code>diffuse</code> command to use Sentaurus Process KMC.

## A: Sentaurus Process Commands

### diffuse

<code>kmc.stress</code>	Switches on the stress effect for Sentaurus Process KMC.
<code>laser</code>	Switches on laser annealing.
<code>lkmc</code>	Invokes the lattice kinetic Monte Carlo (LKMC) model during epitaxial growth without the need to use a <code>SetAtomistic</code> simulation. The generation of the grown epitaxial surface is performed by atomistic LKMC in a way that is transparent to users. Use this parameter for standard continuum simulations with epitaxial LKMC growth.
<code>mat.coeffs</code>	List of multimaterial coefficients $A_0, A_1, \dots, A_n$ used in Fourier deposition when <code>epi.model=1</code> and <code>deposit.type=fourier</code> .
<code>maxstep</code>	Maximum time step. The default unit is minute.
<code>mgoals.native</code>	Allows you to use the MGOALS library to deposit a native oxide layer that helps in the case of complex structures with several triple points. The default is true for 1D oxidation and 2D silicidation cases.
<code>minT</code>	Minimum annealing temperature. If the diffusion temperature falls below this value, the diffusion solver is switched off. If it occurs during a ramp, the time-stepping is altered such that diffusion switches on or off exactly at this temperature. The default value and unit is 450°C.
<code>movie</code>	Allows you to specify actions that occur during the anneal step. For every time step of the diffusion, the character string value of the <code>movie</code> parameter is executed.

`p<ambient>`, `partial.pressure`

List of the partial pressures of active ambients. Partial pressure specifications must not be used with `flow`, `flow<ambient>`, or `pressure` specifications. Specify partial pressures using either a parameter name composed of `p` + `<ambient>` (for example, `pO2` and `pN2O` where `O2` and `N2O` are active ambient names) or the parameter `partial.pressure` that takes a list of parameters with names of the ambients, for example:  
`partial.pressure= { O2 = 1.0<atm> N2O= 1.0<atm> }`

The list of default ambients is given in [Table 63 on page 605](#), but this list can be extended by using the `ambient` command. These partial pressures are assumed to contribute to the oxidation or user-defined reaction processes. No reaction between the species is assumed. The default unit is atm.

**NOTE:** Only the partial pressures of the active ambients are used directly in the oxidation reaction equations, so setting the partial pressure of inactive (in the sense that they cause the material growth reaction) ambients such as  $N_2$  or HCl has no effect.

<code>pressure</code>	The (total) pressure of the ambient gas. The default value and unit is 1.0 atm. This setting takes effect only if <code>flows</code> or <code>flow&lt;ambient&gt;</code> is defined explicitly. If <code>gas.flow</code> is specified, the pressure is set in the corresponding <code>gas_flow</code> command.
<code>ramprate</code>	Temperature change during anneal. The default value and unit is 0.0°C/s.
<code>reload</code> , <code>reloadHeat</code> , <code>reloadReact</code>	Allows diffusion, laser annealing, or reaction equation to be parsed at each time step.
<code>repair</code>	In MGOALS3D mode, small regions are removed automatically by default. Sometimes, this can cause small gas bubbles in the structure or other problems. Use <code>!repair</code> to switch off the removal of small regions.
<code>sources</code>	Defines deposition sources used in Fourier deposition when <code>epi.model=1</code> and <code>deposit.type=fourier</code> are specified.
<code>sp.native</code>	Allows the use of the native library to deposit a native oxide layer. The default is true for 3D oxidation and silicidation cases.
<code>stress.relax</code>	This Boolean parameter is used to switch off relaxation of stresses during diffusion with an inert ambient. The default is true for two dimensions and false for three dimensions.
<code>t.final</code>	Final temperature for a temperature ram-up or ramp-down. It is used if the <code>ramp rate</code> is not given. The ramp time is calculated automatically.
<code>temp.ramp</code>	Name of a temperature ramp created with the <code>temp_ramp</code> command.
<code>temperature</code>	Annealing temperature. The default unit is degree Celsius.
<code>time</code>	Annealing time. The default unit is minute.
<code>ts4.native</code>	Allows you to use the TS4 library to deposit a native oxide layer. The default is true for 2D oxidation cases.
<code>write.temp.file</code>	Stores the thermal profile created during laser annealing. The format of the file is two columns: time (in seconds) and temperature (in degree Celsius). This file can be used to create a <code>temp_ramp</code> to allow subsequent simulations to use the computed temperature profile without the need to simulate laser annealing again.

## A: Sentaurus Process Commands

### diffuse

**Examples:**

```
diffuse time=30<s> temp=900
```

A simple low temperature 900°C anneal for 30 s.

```
diffuse time=90 temperature=1000 H2O
```

An oxidation step for a thick isolation oxide.

```
diffuse temp.ramp = spike
```

Performs a diffusion step using the temperature ramp named `spike`.

**See:**

[gas\\_flow](#) on page 901, [term](#) on page 1099

## doping

**Function:** Defines a named piecewise linear doping profile that can be used with the `deposit` command.

**Syntax:**

```
doping
  name=<c> field=<c>
  values= <numeric list>
  depths= <numeric list>
  [location=vertex | element] [list] [clear] [log.grad]
```

**Description:** Allows a doping profile specification that can be used inside the `deposit` command to add doping and other fields to the newly deposited layer (on either vertices or elements).

**Options:**

`clear` Clears all doping specifications.

`depths` A Sentaurus Process–style list of the depths at which the values are applied.

`field` Name of the field; it can be the name of the dopant. For stresses, use the field names:

- StressELXX
- StressELXY
- StressELYY
- StressELZZ
- StressELXZ
- StressELYZ

It is not necessary to specify all stress components. Those that are not specified are assumed to be zero initially and are updated during the stress rebalance at the end of deposition.

`list` List the names of all doping specifications.

`location` Location where the field is to be applied.  
The options are `vertex` (default) or `element`.

`log.grad` Specifies a piecewise logarithmic doping profile.

`name` Name of the profile to be used in the `deposit` command.

`values` A Sentaurus Process–style list of the values of the field.

## A: Sentaurus Process Commands

### doping

**Examples:**

```
doping name=init_boron field=Boron values= {1e10 1e20} depths= {0 0.1}
```

Creates a doping profile definition with the name `init_boron` and consists of a boron profile linearly increasing from  $1 \times 10^{10}$  at the starting surface to  $1 \times 10^{20}$  at  $0.1 \mu\text{m}$  and beyond in the deposited layer. This doping profile definition can be used with the `deposit` command to create the specified profile.

```
doping name= film_stress_xx field = StressELXX values= 1e9
```

```
doping name= film_stress_yy field = StressELYY values= 1e9
```

```
doping name= film_stress_zz field = StressELZZ values= 1e9
```

In this example, an intrinsic isotropic stress of  $10^9$  Pa is added to the deposited layer before the post-deposit mechanics rebalancing step.

**See:**

[deposit on page 870](#)

---

## element

**Function:** Extracts the grid of a material and returns a list of coordinates.

**Syntax:** element  
    <material> [region]

**Description:** Extracts the grid for a specified material and returns the grid as a list of coordinates. This can be used to plot the grid. The return is a list of coordinates that defines the grid. Each of the outer lists makes up a continuous line through the grid. Each inner list contains coordinate pairs in order for that line.

**NOTE:** This command is not available for 3D simulations.

**Options:**

<material> A material must be specified. For information about specifying materials, see [Material Specification on page 50](#).

region Option to limit output to only one region.

**Examples:** element oxide  
Returns the grid of the oxide material.

## Enu2G

- Function:** Computes the shear modulus from Young's modulus and the Poisson ratio.
- Syntax:** Enu2G <n> <n>
- Description:** Computes the shear modulus from Young's modulus (the first value) and the Poisson ratio (the second value).  
The same units are assumed for all moduli.
- Examples:** Enu2G 1.620e12 0.28  
Computes the shear modulus from Young's modulus (1.620e12 dyn/cm<sup>2</sup>) and the Poisson ratio (0.28).



## Enu2K

- Function:** Computes the bulk modulus from Young's modulus and the Poisson ratio.
- Syntax:** `Enu2K <n> <n>`
- Description:** Computes the bulk modulus from Young's modulus (the first value) and the Poisson ratio (the second value).  
The same units are assumed for all moduli.
- Examples:** `Enu2K 1.620e12 0.28`  
Computes the bulk modulus from Young's modulus (1.620e12 dyn/cm<sup>2</sup>) and the Poisson ratio (0.28).

---

## equation

- Function:** Allows test parsing and resolution of a sample expression.
- Syntax:** `equation [eqn=<c>] [nodal]`
- Description:** Allows testing of an equation string. It is parsed, broken into pieces, and derivatives are taken and printed. It is useful for debugging problems with the resolver and parsing, as equation strings can be tried before being run.
- Options:**
- `eqn` String to be checked.
- `nodal` Returns the nodal part of the string given with the `eqn` parameter.
- Examples:** `equation eqn= "exp(Potential*$Vti)"`  
Parses and resolves the string `"exp(Potential*$Vti)"`.
- See:** [solution on page 1076](#)

## etch

**Function:** Removes part or all of an exposed layer.

**Syntax:**

```
etch
[time=<n>][<hr>|<min>|<s>]
[etchstop= {<mat1> <mat2> ...} [etchstop.overetch=<n>]]
[mask=<c>]
[temperature=<n>][<C>|<K>]
[<material>]
[isotropic | anisotropic | cmp | trapezoidal]
[thickness=<n>][<m>|<cm>|<um>|<nm>]
[coord=<n>][<m>|<cm>|<um>|<nm>]
[material= <string list>]
[type=isotropic | anisotropic | cmp | directional | polygon |
    fourier | crystal | trapezoidal | angles.rates]
[rate= <numeric list>]
[crystal.rate= {"<100>="<n> "<110>="<n> "<111>="<n>}]
[direction= <numeric list>]
[polygon= <numeric list>]
[1D] [Adaptive] [force.full.levelset] [remesh] [repair]
[isotropic.overetch=<n>]
[sde=<c>]
[coeffs= {<A0> <A1> <A2> ... <An>}]
[mat.coeffs= {
    <material1>= {<A0> <A1> <A2> ... <An>}
    <material2>= {<A0> <A1> <A2> ... <An>}
    ...
    <materialn>= {<A0> <A1> <A2> ... <An>} }]
[angles.rates= {
    materialA= { angleA0 rateA0 angleA1 rateA1 ... angleAn rateAn }
    materialB= { angleB0 rateB0 angleB1 rateB1 ... angleBn rateBn }
    ... }]
[sources= {<beam1> <beam2> ... <beamn>}]
[shadowing] [undercut=<n>] [angle=<n>]
[shadowing.nonisotropic]
[bottom.thickness=<n>] [bottom.angle=<n>]
[roundness=<n>] [ambient.rate=<n>] [levelset.upwind]
```

**Description:** Etches a layer exposed to the top gas. Several materials can be etched at the same time. Sentaurus Process has several modes to perform etching:

- The MGOALS mode uses either an analytic or a level-set method performed by the MGOALS library.
- A general level-set time-stepping mode is available for handling more sophisticated etching capabilities such as multimaterial etching, Fourier etching, multiple beam, and shadowing.

## A: Sentaurus Process Commands

### etch

#### Options:

1D	Usually, a polygon etch automatically increases the dimension to 2D before performing the operation; setting 1D prevents this behavior.
Adaptive	Specifies with or without adaptive meshing for this etch step. Parameters for adaptive meshing are described in <a href="#">Adaptive Refinement on page 679</a> . The default is the return value of <code>pdbGet Grid Adaptive</code> .
ambient.rate	Used with <code>type=trapezoidal</code> and <code>force.full.levelset</code> to approximate the underetch effect.
angle	Specifies the etching angle for <code>type=trapezoidal</code> .
angles.rates	Specifies a set of angle rate pairs that gives a piecewise linear etch rate versus angle. To be stable, smaller angles should have a higher etch rate. Specify the etching rate to go to zero above some angle produces facets.
anisotropic	Specifies anisotropic etching.
bottom.angle	Specifies the angle for the bottom of a trapezoidal etching in 3D.
bottom.thickness	Specifies the thickness for the bottom of a trapezoidal etching in 3D.
cmp	Specifies chemical mechanical polishing.
coeffs	List of single-material coefficients $A_0, A_1, \dots, A_n$ used in Fourier etching.
coord	The x-coordinate to work with the <code>cmp</code> type. The default unit is $\mu\text{m}$ .
crystal.rate	List of etching rates defined per crystallographic direction in the format: { "<100>"=<etch rate> "<110>"=<etch rate> "<111>"=<etch rate> }
direction	List of x-, y-, and z-values specifying the etching direction for <code>type=directional</code> .

**NOTE:** Always all three values must be specified. In 2D, the z-value must always be zero.

etchstop	Materials, instead of time, can be given as etch-stopping criteria. In this case, etching continues until any of the given <code>etchstop</code> materials is exposed. An additional overetch is performed, with a time equal to <code>etchstop.overetch</code> (default: 10%) multiplied by the accumulated time required to expose the first <code>etchstop</code> material. In 3D, <code>etchstop</code> is ignored when Sentaurus Structure Editor is used.
----------	--

**NOTE:** Materials, in addition to time, can be given as etch-stopping criteria for Fourier etching. If both `time` and `etchstop` are given, Fourier etching stops when either of the two criteria is first met.

`etchstop.overetch`

When `etchstop` is defined, an additional `overetch` is performed when the first `etchstop` material becomes exposed to gas. The duration of this `overetch` step is the already performed etching time multiplied by `etchstop.overetch`. The default value is 0.1 (10%).

`force.full.levelset`

By default, the simplest algorithm is chosen to perform the etching. However, sometimes, the algorithm chosen will not give correct results if the topology of the structure is complicated. Specifying this parameter switches on the general level-set time-stepping algorithm, which correctly handles these structures.

`isotropic` Specifies isotropic etch.

`isotropic.overetch`

Specifies a required amount of isotropic etch following an anisotropic etch. The thickness is specified as a fraction of the anisotropic component. This parameter is not implemented in MGOALS3D.

`levelset.upwind` Used with `force.full.levelset` to choose the Upwind formulation of the full level-set algorithm. The Upwind algorithm is less stable and less robust than the Lax–Friedrichs algorithm, which is the default.

`mask` Name of the mask to be used for the etch.

`mat.coeffs` List of multimaterial coefficients  $A_0, A_1, \dots, A_n$  used in Fourier etching with a different set of coefficients defined for each material.

`<material>` Specifies the material to be etched. For information about specifying materials, see [Material Specification on page 50](#).

`material` Defines a list of materials for multimaterial etching.

`polygon` Defines a list of x- and y-coordinates for `type=polygon`. The list of coordinates  $\{x_0 \ y_0 \ x_1 \ y_1 \ x_2 \ y_2 \ \dots \ x_n \ y_n\}$  defines a single polygon that must not be self-intersecting. The first and last points are connected implicitly to close the polygon. The material inside the polygon is etched. The default unit of the coordinates is  $\mu\text{m}$ .

`rate` Defines a list of etching rates. The default unit is  $\mu\text{m}/\text{minute}$ .

`remesh` Performs remeshing after the etch.

## A: Sentaurus Process Commands

### etch

<code>repair</code>	<p>In MGOALS3D mode, small regions are removed automatically by default.</p> <p><b>NOTE:</b> Sometimes, this causes small gas bubbles in the structure or other problems. Use <code>!repair</code> to switch off small region removal.</p>
<code>roundness</code>	<p>Tuning parameter for the curvature of etch sidewalls in the case of trapezoidal etching when <code>force.full.levelset</code> is used. The default value is 1.0. Increased values up to 2.0 or 3.0 increase the curvature of the etch sidewall calculated by the level-set solver.</p>
<code>sde</code>	<p>String used to specify parameters and select algorithms for 3D Sentaurus Structure Editor. By default, the parameters <code>rate</code>, <code>time</code>, <code>thickness</code>, <code>type</code>, and so on are translated into appropriate Sentaurus Structure Editor commands. If an algorithm is specified in the <code>sde</code> parameter, it overwrites the algorithm used by default for isotropic or anisotropic etching, for example:</p> <pre>sde= {"algorithm" "lopx"} sde= {"algorithm" "lopx" "radius" 0.07}</pre>
<code>shadowing</code>	<p>In 2D, it switches on the inclusion of shadowing effects if <code>force.full.levelset</code> is specified or for Fourier etching. The visibility of each surface area to each beam is calculated at every level-set time step. In MGOALS3D, this parameter enables the shadowing effects on both directional and anisotropic etching. The interface to Sentaurus Structure Editor ignores this parameter.</p>
<code>shadowing.nonisotropic</code>	<p>Used instead of shadowing to allow the 0th-order Fourier coefficient to etch areas where the beam is shadowed.</p>
<code>sources</code>	<p>Defines the etching source beams for level-set etching.</p>
<code>temperature</code>	<p>Etching temperature. The default value and unit is 26.85°C.</p>
<code>thickness</code>	<p>Thickness that is removed in the etching. The default unit is <math>\mu\text{m}</math>.</p>
<code>time</code>	<p>Refers to etching time. It must be specified if the <code>rate</code> parameter is used. The default value and unit is 1.0 minute.</p> <p><b>NOTE:</b> If both <code>time</code> and <code>etchstop</code> are given for Fourier etching, the Fourier etching stops when either of the two criteria – time or material <code>etchstop</code> – is met.</p>
<code>trapezoidal</code>	<p>Specifies trapezoidal etching.</p>

`type` Specifies the type of etching to be performed:

- `type=isotropic` performs isotropic etching, which must be used with the `rate` and `time` arguments.
- `type=anisotropic` performs etching in the vertical direction only and must be used with the `rate` and `time` arguments.
- `type=cmp` performs chemical-mechanical polishing (CMP) and is used with the argument `coord`.
- `type=directional` performs anisotropic etching in other directions and must be used with the `direction`, `rate`, and `time` arguments.
- `type=polygon` performs polygonal etching in 2D and is used with the `polygon` argument.
- `type=fourier` performs angle-dependent etching in 2D or 3D where the rate-versus-angle functions are defined by a cosine series using the `coeffs` or `mat.coeffs` parameter.
- `type=crystal` performs etching in 2D or 3D using etching rates dependent on the crystallographic direction defined by the `crystal.rate` argument.
- `type=trapezoidal` performs TSUPREM-4-like trapezoidal etching in 2D defined by the `thickness`, `undercut`, and `angle` parameters, and in 3D defined by the `thickness`, `angle`, `bottom.thickness`, and `bottom.angle` parameters.

`undercut` Distance to etch below the nonetchable material in 2D trapezoidal etching.

**Examples:**

```
etch time=2.0 rate= {0.1} material= {silicon} type=directional \
  direction= {1.0 1.0 0.0} mask=m1
```

A 0.2  $\mu\text{m}$  silicon layer will be etched anisotropically in the direction indicated by the parameter `direction`, and a mask called `m1` is used during etching.

```
beam name=source1 factor=1.0 incidence=-30
etch material= {silicon} shadowing sources= {source1} type=fourier \
  coeffs= {0.1 0 0 1} time=0.1
```

Etches silicon for 0.1 minute at a rate of 1  $\mu\text{m}$  per minute, using `source1` as the etching beam, including shadowing effects, and with a Fourier response to the etchant defined by  $A_0 = 0.1$  and  $A_3 = 1$ .

```
beam name=source_beam factor=1.0 incidence=-30
etch material= {Silicon Nitride Oxide PolySi} sources= {source_beam} \
  mat.coeffs= { Silicon= {0 0.5} Nitride= {0 1} Oxide= {0 0.75} \
  PolySilicon= {0.5} } type=fourier time=0.2
```

Defines multimaterial Fourier etching for 0.2 minute. The Fourier  $A$  coefficients for each material are given separately within the `mat.coeffs` option.

**See:** [deposit on page 870](#), [mask on page 977](#), [mgoals on page 992](#)

---

## exit

- Function:** Terminates the execution of Sentaurus Process.
- Syntax:** exit
- Description:** Terminates the execution of Sentaurus Process. It can be used in the interactive mode and in command files.
- Examples:** exit  
This interactive mode command terminates Sentaurus Process.
- See:** [fbreak on page 896](#), [fcontinue on page 897](#)



---

## extract

- Function:** Extracts historical data during diffuse step.
- Syntax:**
- ```
extract
    [clear] [print] [name=<c>]
    [command= {<c> <c> ...}]
    [syntax.check.value]
```
- Description:** Specifies the Sentaurus Process commands for data extraction during a diffuse step. The extracted historical data can be returned as a Tcl list.
- Options:**
- `clear` Clears the stored historical data.
- `command` List of Sentaurus Process commands for data interpolation.
- `name` Name of data extraction.
- `print` Returns the extracted data values as a Tcl list with all interpolated variables.
- `syntax.check.value`
- Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during the normal run mode. Setting this value avoids such problems.
- Examples:**
- ```
extract name=etest command= { \
    sel z=Boron \
    interpolate Silicon x=0.04 \
}
```
- Extracts and stores the boron concentration at the position 0.04  $\mu\text{m}$  in the silicon for each diffuse step.
- ```
extract print name=etest
```
- Returns the extracted data values with the extraction name `etest` in a Tcl list. For example, if two values are extracted in `etest`, the Tcl list takes the format:
- ```
<time1> <value1_1> <value2_1> <time2> <value1_2> <value2_2> ...
```
- ```
extract clear
```
- Clears all stored historical data.
- See:** [interpolate on page 950](#) and [Extracting Values during diffuse Step: extract on page 830](#)

---

## fbreak

- Function:** Enters interactive mode.
- Syntax:** fbreak
- Description:** Interrupts the execution of a command file and starts an interactive mode.
- Examples:** fbreak  
This command inside the command file starts an interactive mode.
- See:** [exit on page 894](#), [fcontinue on page 897](#)

## fcontinue

- Function:** Resumes execution of command files.
- Syntax:** `fcontinue`
- Description:** This interactive mode command is used to resume the program execution in the batch input mode.
- Examples:** `fcontinue`  
This command resumes the execution of a command file.
- See:** [exit on page 894](#), [fbreak on page 896](#)

---

## fexec

- Function:** Executes system commands.
- Syntax:** `fexec`
- Description:** Executes system calls through the Tcl command `exec` (with exactly the same syntax). Using `fexec`, the system calls are not executed during syntax-checking as they would be if the plain `exec` command were used.
- Examples:** `fexec ls`  
Lists the contents of the current directory.
- See:** Tcl documentation for description of `exec` syntax.

---

## fproc

**Function:** Defines a Tcl procedure.

**Syntax:**

```
fproc name { arguments of procedure } {  
    body of procedure  
}
```

**Description:** This is equivalent to the Tcl command `proc`, except that procedures defined with `proc` are *not* saved or restored in TDR files. Procedures defined using `fproc` are saved or restored. If a procedure is defined using both `fproc` and `proc`, the latter overwrites the previous one, but `fproc` stays in the memory and is saved in TDR files.

**Examples:**

```
fproc relerr { newVal RefVal name my_err } {  
    upvar my_err fl  
    set denom [ expr abs($newVal)+abs($RefVal)+1e-20 ]  
    set deviation [expr 100*abs(($RefVal - $newVal)/$denom)]  
    if { $deviation > 0.5 } {  
        LogFile IL0 "Compare: $name = $newVal, ref = $RefVal, relerr = \  
            $deviation  
            \n --> failed\n"  
        set fl [ expr $fl+1 ]  
    } else {  
        LogFile IL0 "Compare: $name = $newVal, ref = $RefVal, relerr = \  
            $deviation ok\n"  
    }  
}
```

Defines the Tcl procedure `relerr`, which is stored in and loaded from a TDR file.

**See:** Tcl documentation for description of `proc` syntax. The `defineproc` and `fproc` commands are equivalent.

## fset

See [define on page 867](#).

## gas\_flow

**Function:** Specifies a gas mixture for use with the `diffuse` or `temp_ramp` command.

**Syntax:**

```
gas_flow
(list | clear | print | name=<c>)
[<ambient>]
[flow<ambient>=<n>][<l/min>]
[flows= {
  [<ambient1>=<n>][<l/min>]
  [<ambient2>=<n>][<l/min>]
  ...}]
[ISSG]
[p<ambient>=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
[partial.pressure= {
  [<ambient1>=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [<ambient2>=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  ...}]
[pressure=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
```

**Description:** Specifies a gas mixture for thermal oxidation or user-defined gas material reactions, and can be set in the `diffuse` command or `temp_ramp` command. Specification in a multiple `temp_ramp` command allows changing the gas flow during a temperature ramp. If gas flows are specified by `flows` (see below), a complete gas reaction between the contributing gas types is assumed. The partial pressure of the active ambients (for example, material-growing ambients  $O_2$ ,  $H_2O$ , and  $N_2O$ ) are the quantities directly needed to compute oxidation rates. If `flows` is specified, the partial pressures are computed from gas reactions, the mix of remaining gases after the reaction, and the total pressure. If partial pressures of the active ambients are specified, they are used directly. The default value is 0 for all parameters, except pressure. The list of ambients is given in [Table 63 on page 605](#) and includes  $O_2$ ,  $H_2O$ ,  $HCl$ ,  $N_2$ ,  $H_2$ , and  $N_2O$  as well as two epi ambients `Epi` and `LTE` that do not apply to this command.

**Options:**

`<ambient>` Shorthand specification to set the ambient partial pressure the same as the total pressure. Only active ambients can be specified in this way, and only one ambient can be specified. The active ambients are `O2`, `H2O`, and `N2O`.

`clear` Clears the global list of gas mixtures.

## A: Sentaurus Process Commands

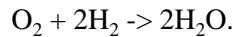
### gas\_flow

flow<ambient>, flows

List of gas flows in the reaction chamber. The gas flows are used to compute the partial pressures of the active ambients (those causing material growth). You can specify flows using either a parameter name composed of flow + <ambient> (for example, flowO2 and flowHCl where O2 and HCl are ambient names) or the flows parameter that takes a list of parameters with names of the ambients, for example:

```
flows= { O2 = 1.0<l/min> HCl = 1.0<l/min> }
```

The list of default ambients is given in [Table 63 on page 605](#), but this list can be extended by using the ambient command. When a gas flow is specified as a combination of flows (and not when using partial pressures), a complete reaction of the ambients is assumed to occur, for example:



Besides gas reactions, the addition of inert gases also changes the partial pressure of the material-growing ambients. For example, if the flows of only N<sub>2</sub> and O<sub>2</sub> are specified and are equal, the partial pressure of O<sub>2</sub> will be <total pressure>/2.0 where <total pressure> is given by the pressure parameter (see below).

**NOTE:** Flows and partial pressures must not be specified together in the same gas\_flow.

|      |                                                                                                                                                                                                                                                                                                                                   |
|------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| ISSG | Switches on <i>in situ</i> steam-generated (ISSG) oxidation.                                                                                                                                                                                                                                                                      |
| list | This Boolean parameter generates a list of gas mixtures and returns a Tcl list that can be operated on as such. The default action for commands is to print the return, so if no handling is required, this prints a list of names of defined gas mixtures. If a name is specified, that gas mixture only is listed with details. |
| name | Identifies the gas mixture description and specifies it in a diffuse or temp_ramp command.                                                                                                                                                                                                                                        |



p<ambient>, partial.pressure

List of the partial pressures of active ambients. Partial pressure specifications must not be used with flows, flow<ambient>, or pressure specifications. You can specify partial pressures using either a parameter name composed of p + <ambient> (for example, pO2 and pN2O where O2 and N2O are active ambient names) or the parameter partial.pressure that takes a list of parameters with names of the ambients, for example:

```
partial.pressure= { O2 = 1.0<atm> N2O= 1.0<atm> }
```

The list of default ambients is given in [Table 63 on page 605](#), but this list can be extended by using the ambient command. These partial pressures are assumed to contribute to the oxidation or user-defined reaction processes. No reaction between the species is assumed. The default unit is atm.

**NOTE:** Only the partial pressures of the active ambients are used directly in the oxidation reaction equations, so setting the partial pressure of inactive (in the sense that they cause the material growth reaction) ambients such as N<sub>2</sub> or HCl have no effect.

pressure The (total) pressure of the ambient gas. The default value and unit is 1.0 atm.

print Prints the gas flow information.

**Examples:**

```
gas_flow name=myflow pressure=0.8 flows= {O2=3.1 H2O=1.2 H2=0.8}
gas_flow name=myflow pressure=0.8 flowO2=3.1 flowH2O=1.2 flowH2=0.8
gas_flow name=myflow pressure=0.8 flowO2=3.1 flows= {H2O=1.2 H2=0.8}
```

These are three equivalent flow specifications for the gas mixture myflow.

```
gas_flow name=mypp partial.pressure= {O2=3.1 H2O=1.2}
gas_flow name=mypp pO2=3.1 pH2O=1.2
gas_flow name=mypp pO2=3.1 partial.pressure= {H2O=1.2}
```

Similar syntax for partial pressures: Three equivalent specifications for the gas mixture mypp. When setting partial pressures, pressure, flow<ambient>, and flows must not be used.

**See:** [diffuse on page 875](#), [term on page 1099](#)

---

## graphics

**Function:** Updates or initiates Sentaurus Process graphics specified by the command option.

**Syntax:**

```
graphics
  [on | off] [cmd= <command>]
  [connect] [maxdepth] [update]
  [host=<c>] [display=<c>] [configure= <command>]
```

**Description:** Controls automatic graphics updating or specifies a Sentaurus Process command sequence that will be called automatically after structure- or data-changing steps. The default display uses an interface to Tecplot SV. To use the interface, you must open an interprocess communication-enabled Tecplot SV first from the UNIX command line:

```
unix:> tecplot_sv -s:ipc
```

After the main window has opened, subsequent runs of Sentaurus Process connect to it and open a new frame if the command `graphics on` is issued.

### Options:

|                        |                                                                                                                                                                                  |
|------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cmd</code>       | Specifies the <code>update</code> command. The default value is <code>plot.tec grd data</code> .                                                                                 |
| <code>configure</code> | Runs a <code>plot.tec</code> configuration command. Any valid <code>plot.tec</code> option can be specified.                                                                     |
| <code>connect</code>   | Allows connection.                                                                                                                                                               |
| <code>display</code>   | Specifies the display for Tecplot SV. The default is the value of the <code>DISPLAY</code> environment variable.                                                                 |
| <code>host</code>      | Specifies the host on which Tecplot SV is to run. The default behavior is explained in <a href="#">Tecplot SV User Guide, Launching or Connecting to Tecplot SV on page 13</a> . |
| <code>maxdepth</code>  | Specifies the command depth limit.                                                                                                                                               |
| <code>off</code>       | Disables automatic updating of graphics.                                                                                                                                         |
| <code>on</code>        | Enables automatic updating of graphics using the command given by the <code>cmd</code> option.                                                                                   |
| <code>update</code>    | Runs the <code>update</code> command.                                                                                                                                            |

**Examples:**

```
graphics configure= "xyshow=Boron* Stress*"
Specifies the datasets to display.
```

```
graphics on
Switches graphics on and uses the Tecplot SV interface.
```

```
graphics on cmd= "plot.2d grid gas"
Automatically calls the old 2D graphics display for data- or structure-
changing steps.
```

---

## grid

**Function:** Performs grid operations and computes statistics about the mesh.

**Syntax:** `grid`

```
[remesh [Adaptive]] | (2D | 3D | FullD) | refine.check]
[merge] [interpolate]
[mesh.stats]
[<material>] [Gas]
[sano.remesh] [sano.smooth] [sano.list] [sano.materials]
[mingrid=<n>][<m>|<cm>|<um>|<nm>]
[syntax.check.value=<c>]
[rename [print.names]] [set.volume] [set.min.edge] [interface.area]

[bbox | bbox.um | bbox.cm | bulk.nodes | bulk.regions | dimension |
elements | interface.nodes | interface.regions | max.angle |
max.connectivity | max.edge | max.volume | max.volume.ratio |
max.volume.ratio.location | min.angle | min.edge |
min.edge.vertices | min.volume | min.volume.location | nodes |
obtuse | total.nodes | total.volume | vertices | brep.faces |
brep.min.angle | brep.min.angle.location | brep.min.edge |
brep.min.edge.location | brep.stats | brep.vertices]
```

**Description:** Allows you to:

- Remesh.
- Merge regions.
- Extrude.
- Rename regions.
- Measure and report on various mesh statistics.
- Measure and report on various boundary representation (referred to as *brep*) statistics.
- Convert KMC particles into FE fields using the Sano method.
- Remesh while adaptively refining Sano fields.

To retrieve mesh or brep statistics, use one of the following options:

- In a single pass, all the statistics can be computed and returned in a Tcl array that can be accessed by the name of the measured value, for example:

```
array set returnArray [grid mesh.stats]
set numNodes $returnArray(total.nodes)
set numElements $returnArray(elements)
```

- To retrieve only the required parameter, use:

```
set numNodes [grid nodes]
```

**NOTE:** If you are interested in several mesh statistics, it is more efficient to retrieve all the statistics in one pass and read them from a Tcl array.

**Description:** **NOTE:** To limit grid or brep statistics to a certain material or interface, specify the material on the command line. For example:

- To limit brep statistics to silicon, use: `grid brep.stats Silicon`
- To limit brep statistics to the oxide–silicon interface, use:  
`grid brep.stats Silicon /Oxide`

Several mesh statistics parameters compute a measure of element quality including:

- `avg.element.quality` (average element quality)
- `best.element.quality`
- `worst.element.quality`
- `lt3.element.quality` (percentage of elements whose quality is less than 0.3)
- `gt6.element.quality` (percentage of elements whose quality is greater than 0.6)

These parameters are computed and returned as part of `mesh.stats`, but they are not separately available.

**NOTE:** For the purpose of this command, quality is defined as:

- Triangles:  $4.0 * \sqrt{3.0} * \text{area} (\text{sum of side lengths})^2$ .
- Tetrahedra: The ratio of the radius of the inscribed sphere to the radius of the circumsphere.

**Options:**

**Regriding, renaming, refinement, and so on**

|                            |                                                                                                                                                                                                                                                                                                 |
|----------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>2D, 3D, FullD</code> | Extrudes grid to higher dimension. The line commands must be issued before extruding to a higher dimension. For 2D, at least two y-lines must have been specified. For 3D, two y-lines and two z-lines must have been specified. <code>FullD</code> extrudes to the highest possible dimension. |
| <code>Adaptive</code>      | Specifies adaptive meshing if <code>remesh</code> is chosen.                                                                                                                                                                                                                                    |
| <code>interpolate</code>   | Performs interpolation if <code>remesh</code> is chosen.                                                                                                                                                                                                                                        |
| <code>merge</code>         | Merges adjacent regions of the same material into one region. Do not use in combination with other options.                                                                                                                                                                                     |
| <code>mingrid</code>       | Specifies the minimum-allowed grid spacing. The default unit is $\mu\text{m}$ .                                                                                                                                                                                                                 |
| <code>print.names</code>   | Prints the region names if the option <code>rename</code> is chosen.                                                                                                                                                                                                                            |
| <code>refine.check</code>  | Returns 1 if remeshing is needed based on refinement criteria; otherwise, it returns 0.                                                                                                                                                                                                         |
| <code>remesh</code>        | If this option is selected, Sentaurus Process recreates the mesh using the currently active mesh generator.                                                                                                                                                                                     |

## A: Sentaurus Process Commands

### grid

- `rename` Renames all regions of the structure according to the material they contain and the smallest y-coordinate point of the region, that is, from the bottom of the structure upwards. Multiple regions of the same material with the smallest y-coordinate within the given coordinate interval will increase the associated index towards the positive x-axis, from left to right.
- `set.min.edge` Must be used by itself. When specified, Sentaurus Process computes the smallest edge length in each direction and saves it in three fields: `MinXEdgeLength`, `MinYEdgeLength` (for 2D or 3D structures), and `MinZEdgeLength` (for 3D structures). In addition, this parameter stores the element volumes in a field `ElementVolume`. When this parameter is set, the average edge length in each direction is returned and can be used to set a Tcl variable, for example:  
`set aveEdgeLength [grid set.min.edge]`
- `set.volume` Sets element volumes as element values over the mesh. This field is not updated automatically.
- `syntax.check.value`  
  
Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during the normal run mode. Setting this value avoids such problems.

#### Grid statistics

- `Gas` By default, `quality` (except `volume`) and `bbox` measures include the gas mesh. To exclude gas in the `quality` or `bbox` measure, use `!Gas`.
- `<material>` If specified, limits the measured grid statistics to the specified material.

#### Grid statistics reporting

- `bbox` Prints the bounding box of the structure (coordinates in  $\mu\text{m}$ ).
- `bbox.cm` Prints the bounding box of the structure (coordinates in cm).
- `bbox.um` Prints the bounding box of the structure (coordinates in  $\mu\text{m}$ ).
- `bulk.nodes` Returns the number of bulk nodes.
- `bulk.regions` Returns the number of bulk regions.
- `dimension` Returns the current simulation dimension.
- `elements` Returns the number of elements.

`interface.area`

Computes the area of interfaces. It can be limited to one particular interface by specifying a material interface such as "Silicon /Oxide" ( $\mu\text{m}$  in 2D,  $\mu\text{m}^2$  in 3D).

`interface.nodes`

Returns the number of interface nodes.

`interface.regions`

Returns the number of interface regions.

`max.angle` Returns the maximum angle in degrees between edges (2D) or faces (3D).

`max.connectivity`

Returns the maximum number of edges connected to a single node.

`max.edge` Returns the maximum edge length in  $\mu\text{m}$ .

`max.volume` Returns the maximum element volume ( $\mu\text{m}^2$  in 2D,  $\mu\text{m}^3$  in 3D).

`max.volume.ratio`

Returns the maximum ratio of volumes of two elements that share the same face (3D only).

`max.volume.ratio.location`

Returns the location where the maximum volume ratio occurs (coordinates in  $\mu\text{m}$ ).

## A: Sentaurus Process Commands

### grid

|                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|--------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>mesh.stats</code>        | <p>Indicates that all bulk mesh statistics must be printed. Here, all mesh statistics are listed as command parameters if they can be individually queried. They also are printed with the <code>mesh.stats</code> parameter or are listed below if they are available only by using the <code>mesh.stats</code> parameter:</p> <ul style="list-style-type: none"><li>• <code>dimension</code>: Simulation dimension.</li><li>• <code>vertices</code>: Number of vertices in mesh.</li><li>• <code>nodes</code>: Total number of nodes in mesh. (At interfaces, there are three nodes for each vertex. In the bulk, there is one node for each vertex.)</li><li>• <code>bulk.nodes</code>: Number of nodes in mesh excluding those in the interface meshes (this gives two nodes for each vertex on an interface and one node for each bulk vertex).</li><li>• <code>interface.nodes</code>: Number of interface nodes in mesh. This will be the same as the number of interface vertices.</li><li>• <code>total.nodes</code>: Same as <code>nodes</code>, that is, the total number of nodes in mesh.</li><li>• <code>elements</code>: Number of elements in the mesh.</li><li>• <code>bulk.regions</code>: Number of regions in the mesh.</li><li>• <code>interface.regions</code>: Number of interface regions in the mesh.</li><li>• <code>bbox</code>: Bounding box (minimum and maximum extents) of the mesh.</li><li>• <code>min.edge</code>: Length of minimum edge in the mesh (in micrometers).</li><li>• <code>min.edge.vertices</code>: Endpoints of minimum edge.</li><li>• <code>max.edge</code>: Length of maximum edge in the mesh (in micrometers).</li><li>• <code>total.volume</code>: Volume of mesh (in <math>\mu\text{m}^D</math> where <math>D</math> is the dimension).</li><li>• <code>min.angle</code>: Minimum of all angles of all elements in the mesh.</li><li>• <code>max.angle</code>: Maximum of all angles of all elements in the mesh.</li><li>• <code>max.connectivity</code>: Maximum number of edges sharing one vertex in the mesh.</li><li>• <code>min.volume</code>: Minimum element volume (in <math>\mu\text{m}^D</math> where <math>D</math> is the dimension).</li><li>• <code>min.volume.location</code>: Location of the center of the element with the minimum volume.</li><li>• <code>max.volume</code>: Maximum element volume (in <math>\mu\text{m}^D</math> where <math>D</math> is the dimension).</li><li>• <code>max.volume.ratio</code>: Maximum ratio of volumes (larger volume to smaller volume) of neighboring elements.</li><li>• <code>max.volume.ratio.location</code>: Location where maximum ratio of volumes occurs.</li><li>• <code>obtuse</code>: Percentage of triangles or tetrahedra that have obtuse angles.</li></ul> |
| <code>min.angle</code>         | Returns the minimum angle in degrees between edges (2D) or faces (3D).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <code>min.edge</code>          | Returns the minimum edge length in $\mu\text{m}$ .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>min.edge.vertices</code> | Returns the vertices of the minimum edge.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |



|                                      |                                                                                                                                                                                                        |
|--------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>min.volume</code>              | Returns the element with the smallest area in 2D (in $\text{cm}^2$ ) or the smallest volume in 3D (in $\mu\text{m}^3$ ).                                                                               |
| <code>min.volume.location</code>     | Prints the location of the smallest element (coordinates in $\mu\text{m}$ ).                                                                                                                           |
| <code>nodes</code>                   | Same as <code>bulk.nodes</code> .                                                                                                                                                                      |
| <code>obtuse</code>                  | Returns the percent of triangles or tetrahedra that have obtuse angles.                                                                                                                                |
| <code>total.nodes</code>             | Returns the total number of nodes in the mesh. Note the difference between points and nodes: there is a node for each region sharing an interface point in addition to each point not on an interface. |
| <code>total.volume</code>            | Returns the total volume of the bounding box (cm in 1D, $\text{cm}^2$ in 2D, and $\text{cm}^3$ in 3D). The unit of the angles reported is degree. If none of these is chosen, all values are reported. |
| <code>vertices</code>                | Returns the total number of vertices in the mesh.                                                                                                                                                      |
| <b>Brep statistics reporting</b>     |                                                                                                                                                                                                        |
| <code>brep.faces</code>              | Returns the number of faces in the brep.                                                                                                                                                               |
| <code>brep.min.angle</code>          | Returns the brep minimum angle in degrees.                                                                                                                                                             |
| <code>brep.min.angle.location</code> | Returns the coordinates of the minimum angle (coordinates in $\mu\text{m}$ ).                                                                                                                          |
| <code>brep.min.edge</code>           | Returns the minimum edge length (in $\mu\text{m}$ ) (3D only).                                                                                                                                         |
| <code>brep.min.edge.location</code>  | Returns the coordinates of the minimum edge length (3D only) (coordinates in $\mu\text{m}$ ).                                                                                                          |

## A: Sentaurus Process Commands

grid

`brep.stats` Indicates that all brep statistics should be printed. In this section, all brep statistics are listed as command parameters if they can be individually queried. They also are printed with the `brep.stats` parameter or are listed below if they are available only by using the `brep.stats` parameter:

- `brep.are.all.boundaries.on.bbox`: Returns true if all outer boundaries are on a flat bounding box; otherwise, false.
- `brep.bbox`: Returns the bounding box of the brep.
- `brep.conformal`: Returns true if the brep is conformal; otherwise, false.
- `brep.dimension`: Returns the dimension of the brep.
- `brep.max.angle`: Returns the brep maximum angle in degrees.
- `brep.max.angle.from.flat`: Returns  $180^\circ$ -brep maximum angle (3D only).
- `brep.max.angle.location`: Returns the coordinates (in  $\mu\text{m}$ ) of the maximum angle (3D only).
- `brep.min.dihedral.angle`: Returns the minimum dihedral angle in degrees in the brep (3D only).
- `brep.min.dihedral.angle.location`: Returns the coordinates of the minimum dihedral angle (3D only) (coordinates in  $\mu\text{m}$ ).
- `brep.min.dihedral.angle.material`: Returns the material where the minimum dihedral angle is located (3D only).
- `brep.regions`: Returns the number of regions in the brep.
- `brep.total.area`: Returns the total brep interface area in 3D or the bulk area in 2D (in  $\mu\text{m}^2$ ).
- `brep.total.volume`: Returns the brep volume (3D only) (in  $\mu\text{m}^3$ ).

`brep.vertices` Returns the number of vertices in the brep.

### Sano smoothing and remeshing

`sano.list` Sets the list of fields for `sano.remesh` or `sano.smooth` operations. By default, the list contains the active dopant concentrations. The field `NetActive` (Doping Concentration) is updated automatically during Sano operations and does not need to be explicitly included here.

`sano.materials`

Sets the list of materials where the Sano method is applied. The default is `Silicon`. It is not recommended to include other materials unless special care is taken to configure KMC for those materials because, by default, KMC models are simplistic in materials other than silicon.

`sano.remesh` Switches on a special Sano remesh mode. Usually, remeshing based on Sano fields and Sano field creation are performed with the `UnsetAtomistic` command (see [UnsetAtomistic on page 1110](#)), which calls `grid sano.remesh` and `grid sano.smooth`. More detail is provided here if nonstandard behavior is required. During `grid sano.remesh`, certain fields, called Sano fields, can be the target of adaptive refinement. By default, the list of Sano fields contain active dopants.

**NOTE:**

- `NetActive` is updated automatically using Sano active fields during `sano.remesh`.
- This mode does not create any new fields in the structure. Sano fields can be created using `sano.smooth` in a separate `grid` command.
- This mode does not automatically switch on adaptive meshing.

`sano.smooth` Converts KMC particle distributions to FE fields using the Sano method. Usually, this conversion is performed with the `UnsetAtomistic` command (see [UnsetAtomistic on page 1110](#)), which calls `grid sano.remesh` and `grid sano.smooth`. More detail is provided here if nonstandard behavior is required. The list of fields that are converted by default contains the active dopants that are present. To change this list, use the `sano.list` parameter.

**NOTE:**

- `NetActive (DopingConcentration)` is updated automatically using Sano fields during `sano.smooth`.
- This parameter specifies that only KMC particles are converted to new FE fields on the existing mesh; no remeshing occurs.

## A: Sentaurus Process Commands

### grid

**Examples:**

```
grid remesh
```

Recreates the mesh using currently specified refinements.

```
grid obtuse silicon
```

Reports the percentage of obtuse elements in silicon.

```
array set returnArray [grid mesh.stats]  
set numNodes $returnArray(total.nodes)  
set numElements $returnArray(elements)
```

First, computes all mesh statistics, and then reads the number of nodes and the number of elements from the statistics array into `numNodes` and `numElements`, respectively. To have different Sano lists for remesh versus smoothing, use the following commands:

```
KMC2PDE  
grid sano.remesh sano.list= BActive  
grid sano.smooth sano.list= { AsActive BActive }  
pdbSet Diffuse KMC 0  
pdbSet Implant MC 0  
pdbSet AtomisticData 0  
kmc off
```

**See:**

[line on page 969](#)

## help

- Function:** Prints a list of all the commands available in Sentaurus Process.
- Syntax:** help
- Description:** Prints a list of all Sentaurus Process commands. It can be used in the interactive mode and in the command files.

---

## icwb

**Function:** IC WorkBench (ICWB)-related functions.

**Syntax:**

```
icwb
  bbox { xmin | xmax | ymin | ymax | left | right | front | back } |
  create.all.masks | dimension | domain= "<domain name>" |
  domain= [list "<domain name 1>" "<domain name 2>" ... \
    "<domain name n>"] |
  filename= "<filename.mac>" [scale=<scale>] |
  gds.file=<c> cell=<c> layer.numbers= {<n>} layer.names= {<c>} \
    [domain.name=<c>] sim2d | sim3d= {<n>} [stretches= {<c>= {<n>}}] \
    [scale=<n>] |
  layer.name= "<layer name>" list polygon.names |
  list { domains | layerIDs | layerNames } |
  list polygon.bounding.bboxes layer.name= "<layer name>" |
  list polygon.tessellations layer.name= "<layer name>" |
  polygon.name= "<polygon name>" list.segments |
  stretch name= "<stretch name>" value=<amount> | slice.angle.offset
```

**Description:** The keyword `icwb` introduces commands used to operate with ICWB TCAD layout files. The different uses of the keyword `icwb` are given here, along with their syntax and corresponding descriptions.

**Detailed descriptions:**

`icwb bbox <option>`

Returns corresponding coordinate where `<option>` can be the following in either ICWB coordinates (`xmin`, `xmax`, `ymin`, `ymax`) or Sentaurus Process coordinates (`left`, `right`, `front`, `back`).

`icwb create.all.masks`

Faster version of the `icwb.create.all.masks` command; intended to create large masks from complex layouts.

`icwb dimension`

Returns dimension of current domain. For the following domain types, the corresponding value for `dimension` is returned:

- Point: 1
- Gauge: 2
- Highlight: 3

```
icwb domain= "<domain name>"
icwb domain= [list "<domain name 1>" "<domain name 2>" ... "<domain name n>"]
```

Defines the current domain. Setting the current domain is a prerequisite for other ICWB commands that implicitly depend on the current domain being defined.

The second variation allows for the concatenation of multiple “gauge” domains, reorientated into one linear simulation domain.

```
icwb filename= "<filename.mac>" [scale=<scale>]
```

Reads an ICWB TCAD layout file. Coordinates in the ICWB file are multiplied by the optional parameter `scale` as the file is read. The ICWB TCAD layout file must be read as a prerequisite to other ICWB commands that act on the domains and masks defined in that file.

```
icwb gds.file=<c> cell=<c> layer.numbers= {<n>} layer.names= {<c>} [domain.name=<c>]
sim2d | sim3d= {<n>} [stretches= {<c>= {<n>}}] [scale=<n>]
```

Reads a GDSII layout file.

The `gds.file` parameter specifies the input GDSII file name, and the `cell` parameter specifies the cell name. The `layer.numbers` is a list of selected layers from the GDSII file, and `layer.names` is a list of names for those layers.

The `domain.name` parameter defines the name of the simulation domain. If no name is specified, `SIM3D` is used for a 3D domain, and `SIM2D` is used for a 2D domain. The domain will be set to be the current domain automatically, so you do not need to call `icwb domain=<c>` before using other `icwb` commands. However, you can call `icwb domain=<c>` to set another preferred current domain.

`sim2d | sim3d` indicates whether it is a 2D or 3D simulation domain. The simulation domain is defined by two points, with each point defined by x- and y-coordinates in the GDSII coordinate system. For two dimensions, the two points are endpoints of a segment. The segment must be horizontal or vertical in the GDSII coordinate system. For three dimensions, the two points are the two opposite corners of the simulation domain. The first point is the left-back corner and the second point is the right-front corner in the internal coordinate system. Either `sim2d` or `sim3d` must be specified.

The `stretches` parameter is a list of stretches, with each stretch having a name and being defined by a segment with two points. For a 3D domain, the segment must cross the bounding box of the domain. For a 2D domain, the segment must intersect with the 2D domain.

## A: Sentaurus Process Commands

### icwb

The `scale` parameter is the same as that in the command `icwb filename=<c> [scale=<n>]`. Coordinates in the GDSII file are multiplied by this parameter as the file is read in to Sentaurus Process.

This `icwb` command can be called multiple times to set multiple simulation domains. The GDSII layout file or the ICWB TCAD layout file must be read as a prerequisite to other ICWB commands that act on the domains and masks defined in that file.

```
icwb layer.name= "<layer name>" list polygon.names
```

Lists polygon names given a layer name.

```
icwb list domains
```

Queries the names of the current domains.

```
icwb list { layerIDs | layerNames }
```

Returns a list of ICWB TCAD layout file layer IDs or layer names.

```
icwb list polygon.bounding.bboxes layer.name= "<layer name>"
```

Returns the bounding box rectangle for each polygon in the layer.

```
icwb list polygon.tessellations layer.name= "<layer name>"
```

Breaks each polygon in the layer into a set of rectangles, and then returns these rectangles,

```
icwb polygon.name= "<polygon name>" list.segments
```

Lists polygon segments given a polygon name.

```
icwb slice.angle.offset
```

Returns the relative angle of the active simulation domain.

```
icwb stretch name= "<stretch name>" value=<amount>
```

Applies the given stretch by the given amount to the current domains. The order of applied stretches matters since the location of other stretches can change given the application of one stretch.



---

## icwb.contact.mask

|                     |                                                                                                                                                           |
|---------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>    | Layout-driven contact placements.                                                                                                                         |
| <b>Syntax:</b>      | <pre>icwb.contact.mask<br/>  layer.name= (&lt;string&gt;   &lt;string list&gt;) [name= &lt;string&gt;] &lt;other options&gt;<br/>  [info=&lt;n&gt;]</pre> |
| <b>Description:</b> | Creates contacts for subsequent device simulations that are tied to a layer in the ICWB TCAD layout file.                                                 |

The command serves as an interface between the ICWB TCAD layout and the Sentaurus Process `contact` command by automatically obtaining the lateral placement of the contact from the specified ICWB layer, taking the vertical placement from the argument list and passing all other options directly to the `contact` command.

The command supports both box-type and point-type contacts:

- A box-type contact consists of elements at the surface of one region or material inside the box. The lateral extent of the box is determined automatically from the layer segment (2D) or the polygon bounding box (3D), while the vertical extent is taken from the `contact` command keywords `xlo` and `xhi`.
- A point-type contact contains all the boundary elements of one region. The lateral position of the point is determined automatically as the midpoint of the layer segment (2D) or the polygon bounding box (3D), while the vertical position is taken from the `contact` command keyword `x`.

For details on how to define contacts, see [contact on page 861](#).

**NOTE:** A layer used for layout-driven contact placements can consist of only a single segment or polygon in each ICWB simulation domain. It may be necessary to create auxiliary layers in ICWBEV Plus for the placement of contacts.

**NOTE:** For 3D simulations, sometimes the placement of contacts in Sentaurus Process causes meshing problems. In this case, use the similar layout-driven contact placement feature in Sentaurus Structure Editor.

|                         |                                                                     |
|-------------------------|---------------------------------------------------------------------|
| <b>Options:</b>         |                                                                     |
| <code>info</code>       | Specifies the information level. Select 1 or 2 for detailed output. |
| <code>layer.name</code> | Name of a layer in the ICWB TCAD layout file.                       |

## A: Sentaurus Process Commands

icwb.contact.mask

**name**                   Optional contact name. The name defaults to the layer name.

**<other options>**   Any other options supported by the contact command.

**Examples:**           icwb.contact.mask layer.name= emitter box polysilicon \  
                          adjacent.material=oxide xlo= -2.05 xhi=-1.95  
                          icwb.contact.mask layer.name= pdrain name= drain \  
                          point aluminum replace x= -2.0

**See:**                   [contact on page 861](#)

---

## icwb.create.all.masks

**Function:** Creates positive and negative mask versions for all layers found in the currently active ICWB simulation domain.

**Syntax:** `icwb.create.all.masks [info=<n>]`

**Description:** Creates a positive and a negative mask for each layer found in the currently active ICWB simulation domain. The names of the masks are given by the layer names and the postfix `_p` for the positive and `_n` for the negative version of the mask. For example, if the TCAD layout contains a layer with the layer name `TRENCH`, the corresponding mask names are `TRENCH_p` and `TRENCH_n`.

**NOTE:** Use the command-line option `-n` to suppress automatic syntax-checking in Sentaurus Process when using this feature. The syntax-checker cannot determine which masks are available and, therefore, may incorrectly flag the use of an unknown mask.

**Options:**

`info` Specifies the information level. Select 1 or 2 for detailed output.

**Examples:** `icwb.create.all.masks`

---

## icwb.create.mask

**Function:** Creates a mask for subsequent use in `etch`, `deposit`, or `photo` commands from one or more ICWB layers.

**Syntax:** `icwb.create.mask`  
`layer.name= (<string> | <string list>)`  
`[name= <string>] [polarity= positive | negative] [info=<n>]`  
`[shift= {dy dz}] [stretchypos= {yo dy}] [stretchyneg= {yo dy}]`  
`[stretchzpos= {zo dz}] [stretchzneg= {zo dz}]`

**Description:** Serves as an interface between the ICWB TCAD layout and the Sentaurus Process mask and `polygon` commands, and provides a convenient way to generate 1D, 2D, and 3D masks consisting of the points, segments, or polygons from one or more ICWB layers based on a dimension-independent syntax. The command automatically determines the dimension of the currently active ICWB simulation domain.

### Options:

`info` Specifies the information level. Select 1 or 2 for detailed output.

`layer.name` Name of one or more layers in the ICWB TCAD layout file. If more than one layer name is given, the resulting mask is the union of the polygons (3D) or segments (2D) from all the layers listed. (Use the command `icwb list layerNames` to obtain a list of all layer names.)

`name` Optional mask name. The mask name defaults to the layer name. If the layer name list contains more than one entry, the first layer name is used.

`polarity` Sets the polarity to negative to invert a mask. The polarity is assumed to be positive by default (that is, points inside the mask are considered masked).

`shift` Shifts the layers by the specified amount before creating the mask.

`stretchypos`, `stretchyneg`, `stretchzpos`, `stretchzneg`

Stretches the layer before creating the mask. The last four characters of the keywords determine if the stretch is applied along the y- or z-direction and if the layer is stretched to the positive or negative side of the stretch position.

More than one `shift` and `stretch` keyword can be used in a `icwb.create.mask` command. As these operations may not commute, it is important to note the order in which these operations are applied if more than one is used. First, the `shift` is applied, and then `stretchypos`, `stretchyneg`, `stretchzpos`, and finally `stretchzneg` are applied.

**Examples:**

```
icwb.create.mask layer.name= NWELL polarity= negative
icwb.create.mask layer.name= NWELL name= NOTNWELL
icwb.create.mask layer.name= "NPDIFF PPDIFF NPLUG PBASE" name=STI info=1
icwb.create.mask layer.name= 1:0 stretchyneg= {1.2 -0.25}
```

---

## icwb.refine.mask

|                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|---------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>    | Layout-driven refinement specifications.                                                                                                                                                                                                                                                                                                                                                                                                                           |
| <b>Syntax:</b>      | <pre>icwb.refine.mask   layer.name= (&lt;string&gt;   &lt;string list&gt;) [name= &lt;string&gt;] [oversize=&lt;n&gt;]   xtop=&lt;n&gt; xbot=&lt;n&gt; &lt;other options&gt; [info=&lt;n&gt;]</pre>                                                                                                                                                                                                                                                                |
| <b>Description:</b> | Creates refinement boxes that are tied to layers in the ICWB TCAD layout file. The command serves as an interface between the ICWB TCAD layout and the Sentaurus Process <code>refinebox</code> command by automatically obtaining the lateral dimension of the refinement box from the specified ICWB layers, taking the vertical refinement box dimensions from the argument list, and passing all other options directly to the <code>refinebox</code> command. |

For a 2D or 3D ICWB simulation domain, a refinement box is created for each segment or polygon found in the specified layers. For 3D, the lateral extent of respective refinement boxes is given by an axis-aligned tessellation of the polygon.

Using the `oversize` keyword increases the area of refinement beyond the extent of the actual segments or polygon bounding boxes. The nonzero `oversize` value is subtracted from or added to the minimum and maximum segment or polygon bounding box coordinates, respectively.

**NOTE:** Layout-driven refinement is available only for the area under the given layer itself, not for the inverse of a layer. If refinement is needed in an area not covered by the layer, you must create the inverse of the layer as an auxiliary layer explicitly in ICWBEV Plus.

For details on how to define refinement boxes, see [refinebox on page 1040](#).

|                                    |                                                                                                                                                                                                                                                                |
|------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Options:</b>                    |                                                                                                                                                                                                                                                                |
| <code>info</code>                  | Specifies the information level. Select 1 or 2 for detailed output.                                                                                                                                                                                            |
| <code>layer.name</code>            | Name of one or more layers in the ICWB TCAD layout file. If more than one layer name is given, refinement boxes are created for the polygons (3D) or segments (2D) from all mentioned layers.                                                                  |
| <code>name</code>                  | Optional refinement box name. The name defaults to the layer name. If the layer name list contains more than one entry, the first layer name is used. If more than one polygon (3D) or segment (2D) is found, an index is appended to the refinement box name. |
| <code>&lt;other options&gt;</code> | Any other options supported by the <code>refinebox</code> command.                                                                                                                                                                                             |

`oversize` To refine an area wider than the polygon bounding box (3D) or the segment (2D), specify a nonzero `oversize` parameter (unit is micrometer). This value is used to increase the refinement boxes beyond the extent given by the polygon bounding boxes or segments.

`xbot` Bottom or maximum x-coordinate of the refinement box extent.

`xtop` Top or minimum x-coordinate of the refinement box extent.

**Examples:**

```
icwb.refine.mask name=UnderPoly layer.name=POLY \  
oversize=0.1 xtop=-1.51 xbot=-1.35 xrefine=0.02 yrefine=0.02  
icwb.refine.mask name=SiOxPo layer.name=POLY \  
oversize=0.1 xtop=-1.51 xbot=-1.35 min.normal.size=0.005 \  
interface.mat.pairs= {Silicon Oxide Silicon Polysilicon}
```

**See:** [refinebox on page 1040](#)

---

## implant

**Function:** Specifies implantation model parameters and implants an ion species into a wafer.

**Syntax:**

```
implant
  {[tables=Default | Dios | Tasch | AdvCal | Taurus] [data.suf=<c>]
  [dam.suf=<c>] [ts4.prefix=<c>]} |

  {[species=<c>]
  [tables=Default | Dios | Tasch | AdvCal | Taurus | TSuprem4]
  [data.suf=<c>] [dam.suf=<c>] [ts4.prefix=<c>]}
  [energy=<n>] [tilt=<n>] [en.stdev=<n> [tilt.stdev=<n>]] |

  {[<material>] [species=<c>] [dataset=<c>]
  [imp.table=<c>] [dam.table=<c>]
  [ts4.species=<c>] [ts4.material=<c>]
  [gaussian | pearson | pearson.s | dualpearson | point.response]
  [damage]
  [file=<c>] [y.position=<n>] [z.position=<n>]
  [rp=<n>][<m>|<cm>|<um>|<nm>]
  [rp2=<n>][<m>|<cm>|<um>|<nm>]
  [stdev=<n>][<m>|<cm>|<um>|<nm>]
  [stdev2=<n>][<m>|<cm>|<um>|<nm>]
  [gamma=<n>] [gamma2=<n>]
  [beta=<n>] [beta2=<n>]
  [lexp=<n>] [lexp2=<n>]
  [lat.stdev=<n>][<m>|<cm>|<um>|<nm>]
  [lat.stdev2=<n>][<m>|<cm>|<um>|<nm>]
  [lat.scale=<n>][<m>|<cm>|<um>|<nm>]
  [lat.scale2=<n>][<m>|<cm>|<um>|<nm>]
  [ratio=<n>] [eff.caplayer.thick=<n>]
  [angle.dependent] [cap.dependent] [depth.dependent]
  [min.conc=<n>][<m-3>|<cm-3>|<um-3>|<nm-3>]}

  [eff.channeling.suppress] [ge.effect]
  [i.plus.offset= {<n> <n> <n>}] [v.plus.offset= {<n> <n> <n>}]
  [frenkel.pair.offset= {<n> <n> <n>}]

  {[<species>]
  [energy=<n>][<eV>|<keV>|<MeV>]
  [dose=<n>][<cm-2>]
  [dose.rate=<n>][<cm-2/s>]
  [tilt=<n>][<degree>] [rotation=<n>][<degree>] [mult.rot=<i>]
  [primary= beam | wafer]
  [beam.dose] [temperature=<n>] [current=<n>]
  [contamination= {energy=<n> dose.fraction=<n>}]
  [preprocess] [postprocess] [postprocessonly] [extrude]
  [defect.model= plus.one | effective.plus.n | frenkel.pair |
  user.defined]
```



**Syntax:**

```
[Adaptive] [average]
[backscattering] [ts4.backscattering]
[match= no | range | dose]
[pai] [range.sh] [profile.reshaping]
[get.moments] [material=<c>]
[oxide.thickness=<n>][<m>|<cm>|<um>|<nm>]
[extract.moments] [data.file=<c>]
[data.xcol=<n>] [data.col=<n>]
[data.xlo=<n>] [data.xhi=<n>] [data.min=<n>] [data.max=<n>]
[data.units=<c>] [max.iter=<n>] [tolerance=<n>] [rp.offset]
[crystaltrim | sentaurus.mc]
[particles=<n>]
[cascades] [iBCA] [recoils] [point.implant] [randomize]
[KMC] [full.molecular] [secondary.ions]
[plasma] [conformity=<n>]
[plasma.source= {<species1>=<n> <species2>=<n> ...}]
[plasma.deposit= {material=<c> thickness=<n> steps=<n>}]
[en.stdev=<n>] [tilt.stdev=<n>] [conformity=<n>]
[ifactor=<n>] [vfactor=<n>] [dfactor=<n>]
[fp.ifactor=<n>] [fp.vfactor=<n>]
[crit.dose=<n>][<cm-2>]
[mc.ifactor=<n>] [mc.vfactor=<n>] [mc.dfactor=<n>]
[smooth] [smooth.field= {<list of fields>}]
[smooth.distance= {<double array>}]
[load.mc]
[shift=<n>] [flip] [left] [right] [multiply=<n>]
[saveld] [saveld.file=<c>] [saveld.unit=<c>]
[igrd.file] [predamage.igrd] [keepdamage.igrd]
[mpp] [ion.movie] [info=<n>}]
```

**Description:** There are two main branches to this command. The first allows you to specify parameters for the analytic model. It can be performed by specifying tables or species parameters. The second performs an implantation into the current structure. Either analytic functions or Monte Carlo simulations (Crystal-TRIM or Sentaurus MC) can be used.

**Options:**

**Specifying parameters**

- angle.dependent  
Declares the tilt- and rotation-dependent range parameters in the implant table used. By default, the Dios tables are all set to angle independent. For all other tables, angle-dependent moments are assumed by default.
- beta  
Overwrites the kurtosis found in the specified implant table.
- beta2  
Overwrites the second kurtosis found in the specified implant table for the dual Pearson model.

## A: Sentaurus Process Commands

### implant

|                                      |                                                                                                                                                                                                                                                                                                                                         |
|--------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cap.dependent</code>           | Specifies that the implant moments are cap (screening) layer dependent in the dual Pearson model.                                                                                                                                                                                                                                       |
| <code>dam.suf</code>                 | Specifies the file name suffix for Taurus tables that contain the required implant damage data in the format <code>&lt;ion&gt;_damage_in_&lt;material&gt;_&lt;suffix&gt;</code> .                                                                                                                                                       |
| <code>dam.table</code>               | Defines the implantation table containing moments for the primary and lateral damage distributions.                                                                                                                                                                                                                                     |
| <code>damage</code>                  | Switches on or off the damage calculation based on the Hobler model.                                                                                                                                                                                                                                                                    |
| <code>data.suf</code>                | Specifies the file name suffix for Taurus tables that contain the required implant data in the format <code>&lt;ion&gt;_in_&lt;material&gt;_&lt;suffix&gt;</code> .                                                                                                                                                                     |
| <code>dataset</code>                 | Used for the data name that is created when an implant is performed.                                                                                                                                                                                                                                                                    |
| <code>depth.dependent</code>         | Switches on or off the lateral standard deviation depth dependency.                                                                                                                                                                                                                                                                     |
| <code>eff.caplayer.thick</code>      | Efficiency factor for the summation of layer thicknesses to calculate the total screening (cap) layer thickness. The default is 1.                                                                                                                                                                                                      |
| <code>eff.channeling.suppress</code> | Logical switch for the effective channeling suppression model. The default is 1 for the Taurus/TSUPREM-4 mode, and 0 otherwise.                                                                                                                                                                                                         |
| <code>energy</code>                  | Specifies the plasma implantation energy for the species. If this parameter is specified for a given ion species, the energy as specified will be used for this species instead of the common energy as specified in the performing branch of the <code>implant</code> command. Used for plasma implantation only.                      |
| <code>en.stdev</code>                | Specifies the standard deviation of plasma implantation energy for the species. If this parameter is specified for a given ion species, the value as specified will be used for this species instead of the common energy as specified in the performing branch of the <code>implant</code> command. Used for plasma implantation only. |
| <code>file</code>                    | Name of the file used in the <code>point.response</code> implant model and the <code>load.mc</code> mode.                                                                                                                                                                                                                               |
| <code>frenkel.pair.offset</code>     | Specifies the amount of spatial shift for <code>frenkel.pair</code> . The actual shift occurs for interstitials. This parameter takes a list of numeric values. The first, second, and third values in the list are taken as the x-, y-, and z-value, respectively. The missing value is treated as zero.                               |

|                                                                        |                                                                                                                                                                                                                                                   |
|------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>gamma</code>                                                     | Overwrites the skewness found in the specified implant table.                                                                                                                                                                                     |
| <code>gamma2</code>                                                    | Overwrites the second skewness found in the specified implant table for the dual Pearson model.                                                                                                                                                   |
| <code>gaussian, pearson, pearson.s, dualpearson, point.response</code> | Specifies which type of distribution to use.                                                                                                                                                                                                      |
| <code>ge.effect</code>                                                 | Specifies that the effect of Ge needs to be taken into account if its concentration is sufficiently large. Default is false.                                                                                                                      |
| <code>i.plus.offset</code>                                             | Specifies the amount of spatial shift for <i>plus</i> interstitials and takes a list of numeric values. The first, second, and third values in the list are taken as the x-, y-, and z-value, respectively. The missing value is treated as zero. |
| <code>imp.table</code>                                                 | Defines the implantation table containing moments for the primary and lateral dopant distributions.                                                                                                                                               |
| <code>lat.scale</code>                                                 | Scaling factor for the lateral standard deviation. The default is 1.                                                                                                                                                                              |
| <code>lat.scale2</code>                                                | Scaling factor for the second lateral standard deviation. The default is 1.                                                                                                                                                                       |
| <code>lat.stdev</code>                                                 | Overwrites the lateral standard deviation found in the specified implant table. The default unit is $\mu\text{m}$ .                                                                                                                               |
| <code>lat.stdev2</code>                                                | Overwrites the second lateral standard deviation found in the specified implant table for the dual Pearson model. The default unit is $\mu\text{m}$ .                                                                                             |
| <code>lexp</code>                                                      | Overwrites the linear exponential tail length found in the specified implant table.                                                                                                                                                               |
| <code>lexp2</code>                                                     | Overwrites the second linear exponential tail length found in the specified implant table.                                                                                                                                                        |
| <code>&lt;material&gt;</code>                                          | Specifies a material for which specification of model parameters is performed. For information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                |
| <code>min.conc</code>                                                  | Minimum concentration of the implanted species. The default unit is $\text{cm}^{-3}$ .                                                                                                                                                            |
| <code>ratio</code>                                                     | Ratio between the amorphous part of the dose and the total dose for the dual Pearson model.                                                                                                                                                       |
| <code>rp</code>                                                        | Overwrites the projected range found in the specified implant table. The default unit is $\mu\text{m}$ .                                                                                                                                          |
| <code>rp2</code>                                                       | Overwrites the second projected range found in the specified implant table for the dual Pearson model. The default unit is $\mu\text{m}$ .                                                                                                        |
| <code>species</code>                                                   | Name of one of the solution variables of the simulation, for example, Boron.                                                                                                                                                                      |

## A: Sentaurus Process Commands

### implant

|                            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>stdev</code>         | Overwrites the standard deviation found in the specified implant table. The default unit is $\mu\text{m}$ .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| <code>stdev2</code>        | Overwrites the second standard deviation found in the specified implant table for the dual Pearson model. The default unit is $\mu\text{m}$ .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <code>tables</code>        | <p>Changes the implant tables and model switches in all materials. The settings will be overwritten for one particular species if there is the <code>species</code> keyword. Otherwise, the implant tables and model switches will be overwritten for all species in all materials. The options that correspond to different available tables are:</p> <ul style="list-style-type: none"><li>• <code>Default</code> (tables extracted from Monte Carlo simulations with Crystal-TRIM).</li><li>• <code>Dios</code> (tables used by default in Dios).</li><li>• <code>Tasch</code> (University of Texas implant tables).</li><li>• <code>AdvCal</code> (makes the <code>Default</code> table data available in the Taurus Process table format).</li><li>• <code>Taurus</code> (the Taurus Process table set).</li><li>• <code>TSuprem4</code> (TSUPREM-4 native implant tables).</li></ul> |
| <code>tilt</code>          | Specifies the tilt angle for the species. If this parameter is specified for a given ion species, the tilt angle as specified will be used for this species instead of the common tilt as specified in the performing branch of the <code>implant</code> command. Used for plasma implantation only.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| <code>tilt.stdev</code>    | Specifies the standard deviation of the tilt angle for the species. If this parameter is specified for a given ion species, the value as specified will be used for this species instead of the common value of <code>tilt.stdev</code> as specified in the performing branch of the <code>implant</code> command. Used for plasma implantation only.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| <code>ts4.material</code>  | Specifies the name of the material as used in TSUPREM-4. This is used for TS4-style tables only.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| <code>ts4.prefix</code>    | Specifies the prefix used in TSUPREM-4 native implant tables. Valid prefixes include <code>default</code> , <code>none</code> , <code>ch</code> , <code>dual</code> , <code>le</code> , <code>tr</code> , <code>ut</code> , and <code>scr</code> .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <code>ts4.species</code>   | Specifies the TS4 implant table name for the dopant, for example, <code>chboron</code> , <code>tr.arsenic</code> . This is used for TS4-style tables only.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| <code>v.plus.offset</code> | Specifies the amount of spatial shift for <i>plus</i> vacancies and takes a list of numeric values. The first, second, and third values in the list are taken as the x-, y-, and z-value, respectively. The missing value is treated as zero.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <code>y.position</code>    | Point of reference in y for the automated 1D Monte Carlo run.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <code>z.position</code>    | Point of reference in z for the automated 1D Monte Carlo run.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |

### Performing an implantation

|                |                                                                                                                                                                                                                                                                                                                                                                                                                                |
|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Adaptive       | Specifies with or without adaptive meshing for both analytic and Monte Carlo implantation. Parameters for adaptive meshing are described in <a href="#">Adaptive Meshing during Implantation on page 688</a> . The default is the return value of <code>pdbGet Grid Adaptive</code> .                                                                                                                                          |
| average        | Specifies whether to average the as-implanted profiles over the reflected domains in the case of <code>TrueReflect</code> boundary conditions. The default is true if the tilt angle (or <code>tilt2D</code> in the case of a 2D structure) is less than $2^\circ$ , and false otherwise.                                                                                                                                      |
| backscattering | Switches on or off the integration algorithm that accounts for particles backscattered from the surface. The default is true.                                                                                                                                                                                                                                                                                                  |
| beam.dose      | Switches to beam dose control. The default is 1 for the Taurus/TSUPREM-4 mode, and 0 otherwise.                                                                                                                                                                                                                                                                                                                                |
| cascades       | Runs Monte Carlo simulations in a full-cascade mode. The default is false.                                                                                                                                                                                                                                                                                                                                                     |
| conformity     | Specifies the conformal doping fraction between 0 and 1: <ul style="list-style-type: none"> <li>• <code>conformity=0</code> is the standard implantation.</li> <li>• <code>conformity=1</code> is fully conformal doping.</li> </ul>                                                                                                                                                                                           |
| contamination= | <code>{energy=&lt;n&gt; dose.fraction=&lt;n&gt;}</code><br>Specifies the energy contamination implantation parameters, where <code>energy</code> is the contaminated energy, and <code>dose.fraction</code> is the fraction of the specified dose. The contaminated dose is <code>dose.fraction</code> $\times$ <code>dose</code> , while the main implantation dose is then $(1 - \text{dose.fraction}) \times \text{dose}$ . |
| crit.dose      | Defines a parameter used for the point-defect profile calculation in the <code>plus.one</code> and <code>frenkel.pair</code> models in the case of analytic implantation. The default unit is $\text{cm}^{-2}$ .                                                                                                                                                                                                               |
| crystaltrim    | Selects simulation of ion implantation using the Monte Carlo simulator Crystal-TRIM.                                                                                                                                                                                                                                                                                                                                           |
| current        | Beam line current. The default value and unit is 0 A.                                                                                                                                                                                                                                                                                                                                                                          |
| data.col       | Specifies the column number of concentration data in <code>data.file</code> used by <code>extract.moments</code> . The default column number is 2.                                                                                                                                                                                                                                                                             |
| data.file      | Specifies the file name of the data for <code>extract.moments</code> .                                                                                                                                                                                                                                                                                                                                                         |
| data.max       | Specifies the maximum value of the concentration data to be loaded from <code>data.file</code> . Concentration data above <code>data.max</code> is ignored by <code>extract.moments</code> . The default value and unit is $1 \times 10^{30} \text{ cm}^{-3}$ .                                                                                                                                                                |

## A: Sentaurus Process Commands

### implant

|                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
|------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>data.min</code>        | Specifies the minimum value of the concentration data to be loaded from <code>data.file</code> . Concentration data smaller than <code>data.min</code> is ignored by <code>extract.moments</code> . The default value and unit is $1 \times 10^{14} \text{ cm}^{-3}$ .                                                                                                                                                                                                                                                                                                                          |
| <code>data.units</code>      | Specifies the units of the depth (x-)coordinate in <code>data.file</code> . Valid values are <code>um</code> , <code>nm</code> , and <code>cm</code> . The default value is <code>um</code> .                                                                                                                                                                                                                                                                                                                                                                                                   |
| <code>data.xcol</code>       | Specifies the column number of the depth (x-)coordinate in <code>data.file</code> used by <code>extract.moments</code> . The default column number is 1.                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <code>data.xhi</code>        | Specifies the maximum value of the depth (x-)coordinate to be loaded from <code>data.file</code> . Depths greater than <code>data.xhi</code> are ignored by <code>extract.moments</code> . The default value is $1 \times 10^{10}$ .                                                                                                                                                                                                                                                                                                                                                            |
| <code>data.xlo</code>        | Specifies the minimum value of the depth (x-)coordinate to be loaded from <code>data.file</code> . Depths smaller than <code>data.xlo</code> are ignored by <code>extract.moments</code> . The default value is the first depth data in <code>data.file</code> .                                                                                                                                                                                                                                                                                                                                |
| <code>defect.model</code>    | Selects the model used to calculate point defects. Possible choices are: <ul style="list-style-type: none"><li>• The <code>plus.one</code> switch selects the +1 model.</li><li>• The <code>effective.plus.n</code> model dynamically calculates an <code>NFactor</code> using an energy-dependent and a dose-dependent fitting formula.</li><li>• For <code>frenkel.pair</code>, interstitial and vacancy profiles are calculated from the damage profile resulting from the last implantation.</li><li>• The <code>user.defined</code> model allows you to defined your own models.</li></ul> |
| <code>dfactor</code>         | Scaling factor for the damage profile calculation in analytic implant. The default is 1.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <code>dose</code>            | Dose of the implant. The default value and unit is $1 \times 10^{14} \text{ cm}^{-2}$ .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <code>dose.rate</code>       | Dose rate of the implant. The default unit is $\text{cm}^{-2}/\text{s}$ . If <code>dose.rate</code> is specified in the <code>implant</code> command, its value is used with the assumption of a uniform dose rate. If it is not specified, the dose rate is calculated from the <code>DoseRate Tcl</code> procedure in <code>Implant.tcl</code> . This parameter is useful for KMC only.                                                                                                                                                                                                       |
| <code>en.stdev</code>        | Standard deviation of implant energy for plasma implantation. The default is 0.0. Used for plasma implantation only.                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| <code>energy</code>          | Implant energy. The default value and unit is 250 keV.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| <code>extract.moments</code> | Logical switch that specifies that this command will extract the implant moments from the ASCII data file as specified by <code>data.file</code> .                                                                                                                                                                                                                                                                                                                                                                                                                                              |

|                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>extrude</code>          | Logical switch for extruding the 1D or 2D structure into pseudo-3D structure before analytic implantation. This makes 1D or 2D simulation results nearly identical to those in 3D. The default is false.                                                                                                                                                                                                                                                                  |
| <code>flip</code>             | Flips the profile loaded with <code>load.mc</code> to the left.                                                                                                                                                                                                                                                                                                                                                                                                           |
| <code>fp.ifactor</code>       | Scaling factor for the interstitial profile calculation in the <code>frenkel.pair</code> models. It is used for analytic implantation only.                                                                                                                                                                                                                                                                                                                               |
| <code>fp.vfactor</code>       | Scaling factor for the vacancy profile calculation in the <code>frenkel.pair</code> models. It is used for analytic implantation only.                                                                                                                                                                                                                                                                                                                                    |
| <code>full.molecular</code>   | Follows all particles in a Crystal-TRIM or Sentaurus MC run for a molecular species. This is the default.                                                                                                                                                                                                                                                                                                                                                                 |
| <code>get.moments</code>      | Logical switch for returning the implant moments instead of performing the actual implantation. The return value of the <code>implant</code> command is a list of key-value pairs. For example, for the Gaussian model, the return list would be “model gaussian rp <n> stdev <n>”. For the dual Pearson model, the return list would be “model dualpearson rp <n> stdev <n> beta <n> gamma <n> rp2 <n> stdev2 <n> beta2 <n> gamma2 <n> ratio <n>”. The default is false. |
| <code>iBCA</code>             | Logical switch for the improved BCA (iBCA) damage model. The default is false. This option is used in Sentaurus MC implantation only.                                                                                                                                                                                                                                                                                                                                     |
| <code>ifactor</code>          | Scaling factor for the interstitial profile calculation in the <code>plus.one</code> and <code>frenkel.pair</code> models. It is used for the <code>frenkel.pair</code> model in the case of analytic implantation only. The default is 1.                                                                                                                                                                                                                                |
| <code>igrid.file</code>       | Specifies the file name for storing the damage information in the internal grid of Crystal-TRIM. This is not used in Sentaurus MC. This parameter is deprecated.                                                                                                                                                                                                                                                                                                          |
| <code>info</code>             | Specifies the information level. Recommended values are 1...3.                                                                                                                                                                                                                                                                                                                                                                                                            |
| <code>ion.movie</code>        | Plots the positions of implanted ions during a Monte Carlo run.                                                                                                                                                                                                                                                                                                                                                                                                           |
| <code>keepdamage.igrid</code> | Keeps the damage information stored at the internal grid between two runs of Crystal-TRIM. This is not used in Sentaurus MC. This parameter is deprecated.                                                                                                                                                                                                                                                                                                                |
| <code>KMC</code>              | Switches on the KMC mode for MC implantation (both Crystal-TRIM and Sentaurus MC). In this mode, dynamic annealing is performed with Sentaurus Process KMC.                                                                                                                                                                                                                                                                                                               |

## A: Sentaurus Process Commands

### implant

|                              |                                                                                                                                                                                                                                                                                                                                                                                  |
|------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>left, right</code>     | Direction specifiers for the <code>flip</code> command.                                                                                                                                                                                                                                                                                                                          |
| <code>load.mc</code>         | Loads an external profile specified with the <code>file</code> selector. You can select either Crystal-TRIM or Sentaurus MC for an automated Monte Carlo run by setting the <code>model</code> parameter in the parameter database, for example:<br><code>pdbSet MCImplant model crystaltrim</code><br>The default is <code>sentaurus.mc</code> .                                |
| <code>match</code>           | Selects algorithms of simulation in multilayer structures using this parameter whose options are: <ul style="list-style-type: none"><li>• <code>range</code> selects the numeric range scaling algorithm. It is the used by default.</li><li>• <code>dose</code> selects the dose-matching algorithm.</li><li>• <code>no</code> switches off both algorithms.</li></ul>          |
| <code>material</code>        | Specifies the material for the <code>get.moments</code> parameter from which implant moments are extracted. The default is <code>silicon</code> .                                                                                                                                                                                                                                |
| <code>max.iter</code>        | Maximum number of iterations to extract the dual-Pearson implant moments from <code>data.file</code> . The default value is 500.                                                                                                                                                                                                                                                 |
| <code>mc.dfactor</code>      | Scaling factor for the damage profile calculated by Sentaurus MC. The default value is 1.                                                                                                                                                                                                                                                                                        |
| <code>mc.ifactor</code>      | Scaling factor for the interstitial profile calculation in the <code>frenkel.pair</code> models. It is used for Monte Carlo simulation only.                                                                                                                                                                                                                                     |
| <code>mc.vfactor</code>      | Scaling factor for the vacancy profile calculation in the <code>frenkel.pair</code> models. It is used for Monte Carlo simulation only.                                                                                                                                                                                                                                          |
| <code>mpp</code>             | Switches on or off the multiprocessing parallelization (MPP) feature for MC implants. However, if the <code>pdb</code> parameter <code>ParallelJobs</code> is equal to 1, no parallel jobs will be run even if this switch is on. The default is on. This parameter is deprecated.                                                                                               |
| <code>mult.rot</code>        | Specifies multiple stages of implants at different rotation angles. For example, <code>mult.rot=4</code> means one quarter of the dose is implanted at the first rotation angle, the next quarter at the original rotation angle plus 90°, the next quarter at the original rotation angle plus 180°, and the last quarter at the original rotation plus 270°. The default is 1. |
| <code>multiply</code>        | Profile loaded with <code>load.mc</code> is multiplied by a factor.                                                                                                                                                                                                                                                                                                              |
| <code>oxide.thickness</code> | Specifies the oxide thickness for <code>get.moments</code> parameter. For oxide thickness-dependent implant tables, the implant moments are interpolated with respect to the specified oxide thickness. The default thickness is 0.0.                                                                                                                                            |



|                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>pai</code>             | Logical switch for the preamorphization implant (PAI) mode. The PAI model takes preamorphization into account by converting the damage into effective screening layer thicknesses used for the moment lookup in screening (cap) layer-dependent tables. The default is 1 for the Taurus/TSUPREM-4 mode, and 0 otherwise.                                                                                                                                                                                      |
| <code>particles</code>       | Number of pseudoparticles that will be started per surface segment during MC simulation.                                                                                                                                                                                                                                                                                                                                                                                                                      |
| <code>plasma</code>          | Logical switch for plasma implantation. This option is valid for Sentaurus MC implantation only.                                                                                                                                                                                                                                                                                                                                                                                                              |
| <code>plasma.source=</code>  | <code>{&lt;species1&gt;=&lt;n&gt; &lt;species2&gt;=&lt;n&gt; ...}</code><br>Specifies a list of plasma ion species, where <code>&lt;species1&gt;</code> , <code>&lt;species2&gt;</code> , and so on, can be any predefined species, and the number after each species specifies the fraction of the total dose as specified by the <code>dose</code> parameter.                                                                                                                                               |
| <code>plasma.deposit=</code> | <code>{material=&lt;c&gt; thickness=&lt;n&gt; steps=&lt;n&gt;}</code><br>Specifies the parameters for deposition during plasma implantation, where <code>material</code> specifies the deposit material, <code>thickness</code> specifies the total thickness of the deposit material, and <code>steps</code> specifies the number of steps Sentaurus Process will perform alternatively between MC implantation and material deposition. The default thickness is 0.0, and the default number of steps is 1. |
| <code>point.implant</code>   | Logical switch for point implant mode, in which all particles are implanted into a central location of the implant surface. This option is valid for Sentaurus MC implantation only.                                                                                                                                                                                                                                                                                                                          |
| <code>postprocess</code>     | Switches on postprocessing of <code>*_LastImp</code> datasets. This is the default.                                                                                                                                                                                                                                                                                                                                                                                                                           |
| <code>postprocessonly</code> | Postprocesses existing <code>*_LastImp</code> datasets only (implantation itself is omitted).                                                                                                                                                                                                                                                                                                                                                                                                                 |
| <code>predamage.igrid</code> | Uses the damage from the internal grid for a Crystal-TRIM run. This is not used in Sentaurus MC. This parameter is deprecated.                                                                                                                                                                                                                                                                                                                                                                                |
| <code>preprocess</code>      | Switches on preprocessing. This is the default.                                                                                                                                                                                                                                                                                                                                                                                                                                                               |

## A: Sentaurus Process Commands

### implant

|                                |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|--------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>primary</code>           | <p>Defines the interpretation of the range and lateral range parameters. Possible choices are:</p> <ul style="list-style-type: none"><li>• <code>beam</code> switches to the beam projection mode. In this case, the primary moments are applied along the projection of the ion beam onto the simulation plane, and the lateral integration is performed perpendicular to the projection of the ion beam. This is the default in Sentaurus Process.</li><li>• <code>wafer</code> switches to the wafer normal mode. Here, the primary distribution function and the moments are interpreted orthogonally to the wafer surface.</li></ul> |
| <code>profile.reshaping</code> | <p>Logical switch for the profile reshaping model. Default is 1 for the Taurus/TSUPREM-4 mode, and 0 otherwise.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| <code>randomize</code>         | <p>Switches to randomize the random seed (by using internal clock) each time the command file is run. Therefore, each run will produce different results. This parameter is used in MC implantation only. The default is false.</p>                                                                                                                                                                                                                                                                                                                                                                                                       |
| <code>range.sh</code>          | <p>Logical switch for the proportional range shift mode. The channeling part of the profile is shifted proportionally to the ratio of the amorphous and the channeling range. The shift is the same for both contributions if the model is switched off. The default is 1 for the Taurus/TSUPREM-4 mode, and 0 otherwise.</p>                                                                                                                                                                                                                                                                                                             |
| <code>recoils</code>           | <p>Switches to recoil implant mode, such as simulating the oxygen knock-on effect. This parameter is used in Sentaurus MC implantation only. The default is false.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <code>rotation</code>          | <p>Rotation angle of the wafer in the implanter. The default value and unit is <math>-90^\circ</math>.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| <code>rp.offset</code>         | <p>Specifies the offset for the projected ranges of the first and second Pearson moments extracted by <code>extract.moments</code>. The extracted projected ranges are shifted by <code>rp.offset</code>. The default value and unit is <math>0.0 \mu\text{m}</math>.</p>                                                                                                                                                                                                                                                                                                                                                                 |
| <code>saveld</code>            | <p>Specifies that the 1D profiles as calculated by Sentaurus MC implantation will be saved in (x,y) format. These saved files have the particle names as the file name extension. Valid for 1D or quasi-1D structure only.</p>                                                                                                                                                                                                                                                                                                                                                                                                            |
| <code>saveld.file</code>       | <p>Specifies the file name for the 1D profiles as calculated by Sentaurus MC implantation. These saved files have the particle names as the file name extension. Valid for 1D or quasi-1D structure only.</p>                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>saveld.unit</code>       | <p>Specifies the unit of the x-axis for the 1D profiles as calculated by Sentaurus MC implantation. The valid units are A, nm, and <math>\mu\text{m}</math>.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |

|                                 |                                                                                                                                                                                                                                                 |
|---------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>secondary.ions</code>     | When this parameter is switched off, secondary ion fields (for example, fluorine in a $\text{BF}_2$ implantation) are not created for Monte Carlo implantation. The default is on.                                                              |
| <code>sentaurus.mc</code>       | Selects simulation of ion implantation using the Monte Carlo simulator Sentaurus MC.                                                                                                                                                            |
| <code>shift</code>              | Shifts the profile loaded with <code>load.mc</code> by a certain amount along the y-axis.                                                                                                                                                       |
| <code>smooth</code>             | Logical switch for smoothing the as-implanted profiles after MC implantation. If <code>smooth.field</code> is not specified, all the as-implanted profiles will be smoothed. The default is false.                                              |
| <code>smooth.field</code>       | Specifies a set of fields to be smoothed. The valid fields are dopant names or Damage. For example, for $\text{BF}_2$ implantation, Boron, Fluorine, or Damage are valid names.                                                                 |
| <code>smooth.distance</code>    | Specifies the smoothing distance for each field as specified in <code>smooth.field</code> parameter. The default smooth distance is 2.0 nm.                                                                                                     |
| <code>&lt;species&gt;</code>    | Any of the previously defined species names can be specified for this parameter.                                                                                                                                                                |
| <code>temperature</code>        | Implant temperature (wafer temperature). The default value and unit is $26.84^\circ\text{C}$ .                                                                                                                                                  |
| <code>tilt</code>               | Angle normal to the substrate at which the impurity was implanted. The default value and unit is $7^\circ$ .                                                                                                                                    |
| <code>tilt.stdev</code>         | Standard deviation of the tilt angle for plasma implantation. The default is 0.                                                                                                                                                                 |
| <code>tolerance</code>          | Error tolerance for convergence to extract the dual-Pearson implant moments from <code>data.file</code> . The default value and unit is 0.1%.                                                                                                   |
| <code>ts4.backscattering</code> | Switches the TS4 backscattering model on or off. In this model, the portion of the profile distribution which sticks out of the solid structure is assumed to be lost, resulting in slightly less dose than the nominal dose. Default is false. |
| <code>vfactor</code>            | Scaling factor for the vacancy profile calculation in the <code>plus.one</code> and <code>frenkel.pair</code> models. It is used for the <code>frenkel.pair</code> model in the case of analytic implantation only. The default is 1.           |

## A: Sentaurus Process Commands

### implant

**Examples:**

```
implant species=Boron tables=Dios
```

Changes all implant specifications for the species boron from the default to the Dios implantation tables and models.

```
implant species=Boron Silicon imp.table=my_table.tab pearson !damage
```

Changes the default implantation table for boron in silicon to my\_table.tab and the implant model to pearson. It also switches off the damage calculation for boron in silicon.

```
implant Phosphorus dose=1e14 energy=100
```

Specifies that a 100 keV implant of phosphorus is performed with a dose of  $1 \times 10^{14} \text{ cm}^{-2}$ . The previously assigned data files and models are used to obtain range statistics.

```
implant Arsenic dose=1e15 energy=60 tmc defect.model=frenkel.pair
```

Specifies an implant of arsenic with a dose of  $1 \times 10^{15} \text{ cm}^{-2}$  and energy of 60 keV. Sentaurus MC simulation will be used. Point-defect profiles will be calculated from the damage profile.

---

## init

|                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
|---------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>    | Sets up the mesh and background doping levels.                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| <b>Syntax:</b>      | <pre>init   [dfise=&lt;c&gt;] [tdr=&lt;c&gt;] [bnd=&lt;c&gt;] [sat=&lt;c&gt;] [sigmac=&lt;c&gt;]   [clear] [done] [load.commands] [pdb] [pdb.only]   [Adaptive] [resistivity]   [field=&lt;c&gt;] [concentration=&lt;n&gt;][&lt;m-3&gt; &lt;cm-3&gt; &lt;um-3&gt; &lt;nm-3&gt;]   [&lt;material&gt;]   [DelayFullD]   [flat.orient= &lt;numeric list&gt;] [wafer.orient= &lt;numeric list&gt;]   [caxis.tilt=&lt;n&gt;] [caxis.rotation=&lt;n&gt;]   [slice.angle=&lt;n&gt;][&lt;degree&gt;]   [top] [scale=&lt;n&gt;]</pre> |
| <b>Description:</b> | Sets up the mesh from either a rectangular specification or a file. The command also allows initialization of the background doping concentration and type.                                                                                                                                                                                                                                                                                                                                                                  |
| <b>Options:</b>     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| Adaptive            | When loading a TDR file containing geometry but no mesh, a mesh is generated automatically. This parameter determines whether adaptive meshing is used. The default is obtained from the <code>pdb</code> parameter <code>Grid Adaptive</code> .                                                                                                                                                                                                                                                                             |
| bnd                 | Selects the <code>.bnd</code> format file for reading. This command reads the boundary file (2D or 3D) and meshes it with MGOALS using the parameters and refinement boxes previously defined.                                                                                                                                                                                                                                                                                                                               |
| caxis.rotation      | Specifies the orientation of the wafer miscut, in other words, the rotation angle of the wafer normal with respect to the crystal coordinate system. This parameter is used in both analytic and Sentaurus MC implantation. The default value and unit is $0^\circ$ ; in other words, the projection of the wafer normal to the crystal plane formed by b- and c-axis is coincidental to the $\langle 110 \rangle$ direction in silicon.                                                                                     |
| caxis.tilt          | Specifies the magnitude of the wafer miscut, in other words, the tilt angle of the wafer normal from the crystal c-axis. This parameter is used in both analytic and Sentaurus MC implantation. The default value and unit is $0^\circ$ , in other words, no wafer miscut.                                                                                                                                                                                                                                                   |
| clear               | Clears all the current structure data in memory. The default is true.                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

## A: Sentaurus Process Commands

### init

|               |                                                                                                                                                                                                                                                                                                                                                                                                            |
|---------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| concentration | Concentration of the incorporated data field. The only available unit is $\text{cm}^{-3}$ , but any nodal quantity (with any internal unit) can be initialized with this parameter if no unit is specified. The default value is zero.                                                                                                                                                                     |
| dfise         | Selects a pair of DF-ISE format files for reading. The .grd, .dat or .grd.gz, .dat.gz extensions are searched for automatically. So, if dfise=filename is given, Sentaurus Process looks for filename.grd, filename.dat, or filename.grd.gz, filename.dat.gz. The DF-ISE format has a different default orientation from the internal format of Sentaurus Process. A rotation is applied to the structure. |
| done          | Returns 1 if the initialization is performed; otherwise, returns 0.                                                                                                                                                                                                                                                                                                                                        |
| DelayFullD    | By default, Sentaurus Process generates a minimum-dimensional structure, which will be extruded to higher dimensions when Sentaurus Process encounters a 'mask.' To generate a full-dimensional structure, specify !DelayFullD.                                                                                                                                                                            |
| field         | Name of data field to be initialized everywhere in the structure.                                                                                                                                                                                                                                                                                                                                          |
| flat.orient   | Crystal orientation of the wafer flat or notch. The default is flat.orient= {1 1 0}.                                                                                                                                                                                                                                                                                                                       |
| load.commands | Loads the commands in the TDR format file. The default is true.                                                                                                                                                                                                                                                                                                                                            |
| <material>    | Specifies a material for doping. Must be used with the field parameter.                                                                                                                                                                                                                                                                                                                                    |
| pdb           | Loads pdb parameters along with geometry and data in the TDR format file. The default is true.                                                                                                                                                                                                                                                                                                             |
| pdb.only      | Loads only pdb parameters without geometry and data in the TDR format file. The default is false.                                                                                                                                                                                                                                                                                                          |
| resistivity   | Sets the value of the field by requesting a resistivity. This parameter only works for fields that have the resistivity pdb parameters set (which, by default, are only As, B, P, Sb, and In in silicon).                                                                                                                                                                                                  |
| sat           | Specifies to read the structure file in the Sentaurus Structure Editor format.                                                                                                                                                                                                                                                                                                                             |
| scale         | Coordinates of the input structure are divided by the specified value. The default is 1.0e4, which converts from DF-ISE standard (micrometer) structures to Sentaurus Process internal standard (centimeter).                                                                                                                                                                                              |
| sigmac        | Specifies to read the structure file in Sigma-C 3D format.                                                                                                                                                                                                                                                                                                                                                 |
| slice.angle   | Angle of the simulation domain with respect to the wafer coordinate system. The default value and unit is $-90^\circ$ .<br>The slice.angle can be specified using a CutLine2D command:<br>init slice.angle= [CutLine2D 1.65 0.15 1.95 0.6]                                                                                                                                                                 |

`tdr` Selects the TDR format file for reading. The `_fps.tdr` extension is appended to the specified file name automatically if one is not supplied.

The TDR file can contain a variety of information depending on which tool was used to write the file. By default, Sentaurus Process writes files with enough information to restart a simulation. This includes current parameter settings, stored commands (such as `polygon`, `mask`, `contact`), bulk mesh and data, and, in 3D, a boundary (see [Saving a Structure for Restarting the Simulation on page 74](#)). If such a file is specified, all this data is read and used to restart the simulation. It is also possible to read TDR files that include only bulk mesh and data, or only a boundary. If only a boundary is available, Sentaurus Process will create a mesh using current refinement criteria. Finally, a TDR file can contain information for restarting a Sentaurus Process KMC simulation with a KMC structure and other restart information. This type of file is saved by the `kmc extract` command if the atomistic mode is switched on (see [Atomistic Mode on page 371](#) and [Using the Sentaurus Process Interface on page 529](#)).

If the `--fastMode` option is on and `init` does not find the specified file, it looks for a `.bnd` file instead.

For information about the TDR format, refer to the *Sentaurus Data Explorer User Guide*.

`top` Specifies that the gas is found at the smallest x-value (at the top of the structure). If `!top` is specified, the gas is added at the highest x-value (at the bottom). The default is `true`.

`wafer.orient` Wafer orientation. The default is `wafer.orient= {0 0 1}`.

**Examples:** `init dfise=tmp`  
Reads in a structure previously saved in `tmp.grd.gz` and `tmp.dat.gz` files.

`init field=Boron concentration=1e15`  
Finishes a rectangular mesh and sets up a boron doping of  $1 \times 10^{15}$ .

**See:** [line on page 969](#), [region on page 1047](#), [struct on page 1086](#)

---

## insert

**Function:** Inserts segments in 1D, polygons into 2D structures, and polyhedra into 3D structures.

**Syntax:**

```
insert
  [Adaptive]
  segments= {<n_1> <n_2> ...} | polyhedron=<phname> | polygon=<poname>
  [replace.materials= {<mat_1> ... <mat_n>}]
  [replace.regions= {<reg_1> ... <reg_n>}]
  [new.material=<matname>] [new.region=<regname>]
```

**Description:** Inserts segments in 1D, polygons in 2D, and polyhedra in 3D. Segments are defined using the `segments` parameter, but polygons and polyhedra must be defined using the `polygon` and `polyhedron` commands, respectively. One of the following parameters must be specified: `segments`, `polyhedron`, or `polygon`. Other parameters are optional.

When specified, `replace.materials` and `replace.regions` provide a list of materials and regions to be replaced. If neither is specified, all materials will be replaced. If both are specified, the union of them will be replaced. The parameter `new.material` changes the polyhedron material temporarily.

The `insert` command can be used to perform polyhedron or polygon etching and deposition as well as the more general polyhedron or polygon insert functionality. Polyhedron or polygon etching is performed by specifying `new.material=gas` or by creating a gas polyhedron. You also can do the same in one dimension with segments, but this is the same as `CMP` or `fill`. Polyhedron or polygon deposition is performed by specifying `replace.materials=gas` as well as having one or more bulk materials in the polyhedron or polygon, or defining them temporarily with `new.material`.

This command operates only in the `MGOALS3D` mode for polyhedra. If the `SDE` mode is switched on, calling this command will set `sde off`.

### Options:

`Adaptive` If remeshing, this parameter determines whether adaptive meshing is used. The default is obtained from the `pdb` parameter `Grid Adaptive`.

`new.material` Sets the material for the inserted segment, polyhedron, or polygon. This parameter is mandatory for all but `TDR` polyhedra or polygons.



`new.region` Sets the name of the inserted region. It works with one segment or polygon only, that is, it does not work if the segment, polygon, or polyhedron contains more than one region.

**NOTE:** This parameter is not allowed for TDR polyhedra.

`polygon` Uses `<poname>` as the polygon to insert. Only polygons created with the `xy` option are allowed (see [polygon on page 1024](#)). It fails if the simulation is 3D or if it is 1D and cannot be extruded to 2D because there are no `y`-lines available.

`polyhedron` Uses `<phname>` as the polyhedron to insert. It needs a 3D simulation or a simulation that can be extruded to 3D.

`replace.materials`

Specifies a list that indicates the materials to be replaced by the polyhedron. In addition to explicit materials, the keyword `bulk.materials` is allowed. If `bulk.materials` is used, it means that all materials in the structure, except gas, will be replaced.

`replace.regions`

Specifies a list of regions to be replaced by the polyhedron.

`segments` Segments are defined as a list of an even number of coordinates (in  $\mu\text{m}$ ). If more than two coordinates are specified, unique region names are generated for each segment/region.

**Examples:**

```
insert polyhedron=prism new.material=Gas
```

Etches the structure using a polyhedron called `prism`.

```
insert polyhedron=smallCube new.material=Oxide
```

Replaces all the materials in the structure with a polyhedron called `smallCube`. The polyhedron will be filled with oxide.

```
insert polyhedron=smallCube replace.materials= { Nitride } \
    new.material = Oxide
```

Replaces the nitride, and only the nitride, in the simulation with oxide inside the polyhedron called `smallCube`.

```
mater add name=Silicon2 new.like=Silicon alt.matname=Silicon
insert polygon=Channel new.material=Silicon2 new.region=ChannelRegion
```

Replaces all the materials in the structure with a polygon called `Channel`. The polygon will be filled with material `Silicon2` and the region is named as `ChannelRegion`. This polygon can be inserted without merging with neighboring silicon regions.

## A: Sentaurus Process Commands

insert

**See:** [Inserting Polyhedra on page 765](#), [polyhedron on page 1027](#), [polygon on page 1024](#)

## integrate

**Function:** Returns volume integration of named quantity.

**Syntax:** `integrate`  
`[name=<c>] [<material>] [region=<c>]`  
`[element] [absolute] [average] [interfaces] [skipgas]`  
`[min= {<n> <n> <n>}] [max= {<n> <n> <n>}]`  
`[mode= mesh | boundary | jagged]`  
`[syntax.check.value=<c>]`

**Description:** Integrates the field specified with the name parameter (by default, the last unnamed `select` command field) over the entire structure or within a given box specified by the `min` and `max` parameters. If `material` is specified, the integration is limited to regions of the given material. If a region is specified, the integration is limited to only the named region.

The modes for integration within a given box are:

- The `mesh` mode (default) uses a mesh-cutting algorithm.
- The `boundary` mode for three dimensions cuts the boundary to a cuboid and remeshes the cuboid using the given mesh refinements.
- The `jagged` mode simply includes all nodes contained entirely within the given box for integration.

The command by default expects the quantity to be nodal and the integration is performed nodewise, but if the `element` parameter is given, an elemental quantity is expected and the integration proceeds elementwise.

A Tcl list is returned where the first value is the integrated value. The second value is the volume of the computed regions (in `<value unit>*cm` for 1D, in `<value unit>*cm2` for 2D, and in `<value unit>*cm3` in 3D where `<value unit>` is the unit of the named quantity). The third value is the dose (the integrated value divided by the simulated area in `cm-2` in all dimensions). The fourth and fifth values are the minimum and maximum of the named quantity, respectively. If the parameter `average` is specified, the averaged result for the named quantity is appended to the returned Tcl list.

**Options:**

`absolute` Specifies that integration is performed with the absolute values of the named quantity.

`average` Specifies that the average value of the named quantity is computed and added to the returned Tcl list.

## A: Sentaurus Process Commands

### integrate

|                                 |                                                                                                                                                                                                                                                                                                      |
|---------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>element</code>            | Specifies that integration is performed elementwise. In this case, it is expected that the quantity specified by <code>name</code> is an elemental quantity.                                                                                                                                         |
| <code>interfaces</code>         | Specifies that integration is performed on interface meshes.                                                                                                                                                                                                                                         |
| <code>&lt;material&gt;</code>   | Used to limit integration to regions of the specified material. For information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                                                                                  |
| <code>max</code>                | List of numbers defining the x-, y-, and z-coordinates of the lower-right front corner of the cutting box in the internal coordinate system. For 1D, 2D, and 3D structures, a list of one, two, or three numbers is required, respectively. The possible maximum number is used for missing numbers. |
| <code>min</code>                | List of numbers defining the x-, y-, and z-coordinates of the upper-left back corner of the cutting box in the internal coordinate system. For 1D, 2D, and 3D structures, a list of one, two, or three numbers is required, respectively. The possible minimum number is used for missing numbers.   |
| <code>mode</code>               | Specifies the integration mode. Available modes are <code>mesh</code> , <code>boundary</code> , and <code>jagged</code> . The <code>boundary</code> mode is for 3D only. The default is <code>mesh</code> .                                                                                          |
| <code>name</code>               | Quantity to be integrated. The default is <code>Z_Plot_Var</code> .                                                                                                                                                                                                                                  |
| <code>region</code>             | Limits integration to only the region specified.                                                                                                                                                                                                                                                     |
| <code>skipgas</code>            | Specifies that integration is omitted on invisible meshes.                                                                                                                                                                                                                                           |
| <code>syntax.check.value</code> | Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during normal run mode. Setting this value avoids such problems.                      |

**Examples:**

```
integrate silicon name=Boron
```

Returns the integral boron in all silicon regions in the structure, the volume of all silicon regions, and the combined boron dose in all silicon regions.

```
select z= "1.0/3*(StressELXX+StressELYY+StressELZZ)"  
integrate element
```

Returns the integrated pressure elementwise in the whole structure (not including gas), the volume of the structure (not including gas), and the dose of pressure not including gas, which in this case is not necessarily a useful number.

```
integrate name=Boron average min= {0. 0.} max= {10. 0.2}
```

Returns a list of integral, volume, dose, minimum, maximum, and average values of boron within the box defined by upper-left corner (0.0, 0.0) and lower-right corner (10.0, 0.2).

```
sel z=BActive  
integrate silicon
```

Returns the integrated term `BActive`, the volume and the combined dose in all silicon regions in the structure. The term `BActive` is first converted to a temporary data field before integration.

```
integrate name=Boron mode=jagged min= {0. 0. 0.} max= {0.4 0.4 0.4}
```

Returns a list of integral, volume, dose, and minimum and maximum of boron within the cuboid defined by upper-left back corner (0.0, 0.0, 0.0) and the lower-right front corner (0.4, 0.4, 0.4).

---

## interface

|                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|---------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>    | Returns the location or the value of the selected data field at a material interface.                                                                                                                                                                                                                                                                                                                                                                                            |
| <b>Syntax:</b>      | <pre>interface   [name=&lt;c&gt;] [&lt;material&gt;]   [data] [side=&lt;c&gt;] [All]   [x=&lt;n&gt;][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]   [y=&lt;n&gt;][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]   [z=&lt;n&gt;][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]   [p1= {&lt;n&gt; &lt;n&gt; &lt;n&gt;} &amp; p2= {&lt;n&gt; &lt;n&gt; &lt;n&gt;}]   [precision=&lt;n&gt;]   [syntax.check.value=&lt;c&gt;]</pre>                                                        |
| <b>Description:</b> | Returns the position of an interface, or returns the value of the selected data field if <code>data</code> is specified. Therefore, the command can be used to prepare plots of material thickness, silicon consumption, or material growth. It also is used to provide an argument to the <code>interpolate</code> command, which returns a list if there is more than one interface. The list processing commands of Tcl, particularly <code>lindex</code> , are very helpful. |
| <b>Options:</b>     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| All                 | If specified, all interface locations are returned. Otherwise, only the first value is returned.                                                                                                                                                                                                                                                                                                                                                                                 |
| data                | If specified, the value of the selected data field at the interface will be returned.                                                                                                                                                                                                                                                                                                                                                                                            |
| <material>          | Usually works with an interface description and returns the location or value of the selected quantity at the interface.<br><b>NOTE:</b> If an interface is not specified, an error occurs. If the specified interface does not exist in the current structure, an error is reported. For information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                                        |
| name                | Specifies the name of the data field to be returned when data is specified. The default is <code>Z_Plot_Var</code> .                                                                                                                                                                                                                                                                                                                                                             |
| p1, p2              | Specify the two endpoints of a cutline; each is a list of numbers. Only the first <dim> numbers from each list is read, where <dim> is the spatial dimension of the simulation. Specifying the endpoints with <code>p1</code> and <code>p2</code> allows for nonaxis-aligned cuts. Endpoints also can be used to limit axis-aligned cuts instead of cutting through the entire structure.                                                                                        |
| precision           | Controls the number of precision digits of floating values (in scientific notation). The default value is 6.                                                                                                                                                                                                                                                                                                                                                                     |

`side` Takes its value from one of the two bulk materials consisting of the interface or the 'interface' (literally) itself. If `side` is not specified, the 'interface' itself is assumed. If `side` is specified as one of the bulk materials, the value of the selected data field for the bulk material is returned. This parameter is effective only if the parameter `data` is specified.

`syntax.check.value`

Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during normal run mode. Setting this value avoids such problems.

`x, y, z` Provide the description of a line to look for the interface. It is unnecessary in 1D simulation. In 2D, one of `x` and `y` must be specified. In 3D, two of these must be specified. The default unit is  $\mu\text{m}$ . The default values are zero.

**Examples:**

```
interface y=1.0 silicon /oxide
```

Returns the silicon–oxide interface at a lateral position of 1.0  $\mu\text{m}$ .

```
interface oxide /gas
```

Returns the top position of the oxide.

```
interface p1= { 1.0 1.0 } p2= { 1.1 1.1 } Nitride /Oxide
```

Returns any oxide–nitride interfaces between (1.0, 1.0) and (1.1, 1.1). This specification is valid for one or two dimensions, but not three dimensions. In one dimension, it returns the interfaces between 1.0 and 1.1.

**See:**

[interpolate on page 950](#), [plot.xy on page 1021](#), [point.xy on page 1023](#)

---

## interpolate

**Function:** Returns the request position or value at a specified location.

**Syntax:**

```
interpolate
  <material> [name=<c>]
  [x=<n>][<m>|<cm>|<um>|<nm>]
  [y=<n>][<m>|<cm>|<um>|<nm>]
  [z=<n>][<m>|<cm>|<um>|<nm>]
  [value=<n>] [syntax.check.value=<c>]
```

**Description:** Analyzes simulation results. (This is a powerful command.) It returns the interpolated value of one coordinate given the other two coordinates in the 3D defined by x- and y-variables, and the data field. It also works for 1D simulation by returning values as a function of one coordinate.

This function may return a Tcl list of values if more than one is found. For example, there may be several junctions found along a given line. All of these are returned and can be processed by normal Tcl list operations. For most cases, this command return a single value.

This command has multiple uses. It can return the data value at a specified position in the structure or return the position at which a specified data value occurs.

### Options:

`<material>` Mandatory. Limits the search to a single material. For information about specifying materials, see [Material Specification on page 50](#).

`name` Specifies name of a data field. This allows printing without using the `select` or `tcisel` commands. The default is `Z_Plot_Var`.

`syntax.check.value`

Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during normal run mode. Setting this value avoids such problems.



`x, y, z, value`

The combination of these parameters determines how the command operates. In 1D, you must supply either `x` or `value`. If `x` is supplied, Sentaurus Process returns the value at `x`. If `value` is supplied, Sentaurus Process returns the locations at which the selected profile crosses `value`. In 2D, two of four parameters must be given (not `z`). In 3D, three of the four parameters must be given. For example, in 2D, if `x` and `value` are given, the locations along `x` where `value` is crossed are returned. If `x` and `y` are given, the value at the location (`x, y`) is returned.

**Examples:**

```
interpolate oxide x=1.0 y=1.0
```

Returns the value of the data field at the position (1.0  $\mu\text{m}$ , 1.0  $\mu\text{m}$ ) in the oxide.

```
interpolate y=0.0 silicon value=0.0
```

Returns a list of zero crossings in silicon of the data field along the vertical line `y = 0.0  $\mu\text{m}$` .

```
interpolate silicon x=2.0 value=0.0
```

Returns a list of zero crossings in silicon along a horizontal line at a depth of 2.0  $\mu\text{m}$ .

```
interpolate x=1.0 silicon
```

Returns the value of the data field at 1.0  $\mu\text{m}$ .

```
interpolate silicon val=0.0
```

Returns a list of zero crossings in the silicon material.

**See:**

[interface on page 948](#), [plot.xy on page 1021](#), [point.xy on page 1023](#)

## KG2E

- Function:** Computes Young's modulus from bulk modulus and shear modulus.
- Syntax:** KG2E <n> <n>
- Description:** Computes Young's modulus from the bulk modulus (the first value) and the shear modulus (the second value).  
The same units are assumed for all moduli.
- Examples:** KG2E 1.2272e12 6.328e11  
Computes the Young's modulus from the bulk modulus 1.2272e12 dyn/cm<sup>2</sup> and the shear modulus 6.328e11 dyn/cm<sup>2</sup>.

## KG2nu

- Function:** Computes the Poisson ratio from bulk modulus and shear modulus.
- Syntax:** `KG2nu <n> <n>`
- Description:** Computes the Poisson ratio from the bulk modulus (the first value) and the shear modulus (the second value).  
The same units are assumed for all moduli.
- Examples:** `KG2nu 1.2272e12 6.328e11`  
Computes the Poisson ratio from the bulk modulus  $1.2272e12$  dyn/cm<sup>2</sup> and the shear modulus  $6.328e11$  dyn/cm<sup>2</sup>.

---

## kmc

**Function:** Specifies options for the atomistic kinetic Monte Carlo (KMC) mode.

**Syntax:**

```
kmc
  (add |
  (add queue name=<c> [amorphous | crystalline]
    {coordx=<n>[<m>|<cm>|<um>|<nm>]}
    {coor dy=<n>[<m>|<cm>|<um>|<nm>]}
    {coordz=<n>[<m>|<cm>|<um>|<nm>]} )
  {clustertype name=<c>} |
  {deatomize name=<c> [active] [<material>]} |
  {defects.read=<filename>} |
  {defects.write=<filename> [defectname=<c>] [materialname=<c>]} |
  {defecttypes [<material>]} |
  (extract
  (acinterface
    [coordx=<n>][<m>|<cm>|<um>|<nm>]
    [coor dy=<n>][<m>|<cm>|<um>|<nm>]
    [coordz=<n>][<m>|<cm>|<um>|<nm>])) |
  (defects
    [name=<c>] [defectname=<c>] [materialname=<c>]
    [countparticles] [countdefects] ([acinterface] [detailed])) |
  (dose
    [name=<c>] [defectname=<c>] [materialname=<c>] [countdefects]) |
  (histogram
    name=<c> [materialname=<c>] [meansize [minsize=<u>]]) |
  (materials
    [detailed]
    [coordx=<n>][<m>|<cm>|<um>|<nm>]
    [coor dy=<n>][<m>|<cm>|<um>|<nm>]
    [coordz=<n>][<m>|<cm>|<um>|<nm>]) |
  (profile
    name=<c> [timeaveraged] [materialname=<c>] [defectname=<c>]
    [coordx=<n>][<m>|<cm>|<um>|<nm>]
    [coor dy=<n>][<m>|<cm>|<um>|<nm>]
    [coordz=<n>][<m>|<cm>|<um>|<nm>]) |
  (supersaturation {name=<c>}) |
  (tdrAdd [concentrations] ([defects] | [visual=<l>]) [histogram]
    [list=<l>] [stress]) |
  (tdrClear) | (tdrWrite {filename=<c>}) | ) |
  materialtypes | off | particletypes | PDEupdated |
  present {name=<c>} | report
  )
```

**Description:** Interface to send direct instructions to Sentaurus Process Kinetic Monte Carlo (Sentaurus Process KMC), which is used for diffusion. The main options are:

- `add` to create defects in the simulation.
- `deatomize` to create fields according to the atomistic concentrations.
- `extract` to obtain physical information (mainly concentrations) on the simulation. `extract` has many different options and the most important are: `defects`, `dose`, `histogram`, `profile` and `tdrAdd`, `tdrClear`, and `tdrWrite`.

**Options:**

`acinterface` The command `kmc extract acinterface` returns the 1D coordinates of the amorphous–crystalline transitions present in the simulation. If the simulation has  $N$  dimension, it needs  $N-1$  cutlines, specified with `coordx`, `coordy`, or `coordz`.

The command `kmc extract defects acinterface` returns the atomistic position of lattice atoms in the amorphous–crystalline interface, when using the LKMC recrystallization mode.

`active` Used by `kmc deatomize` to deatomize only the active part of a dopant.

`add` Instructs Sentaurus Process KMC to add a new defect into the simulation cell. The defect to be included must be first sent to the queue, using `kmc add queue`. Here, the defect is specified with `name`, and the coordinates with `coordx`, `coordy`, and `coordz`. When all defects are in the queue, the command `kmc add`, without any other parameter, passes the defects from the queue to Sentaurus Process KMC, erasing the queue.

`amorphous` When added to `kmc add`, creates the defect and changes the material to amorphous.

`clustertype` Defines the type of defect specified in `name`. For example, `kmc clustertype name=I56` returns if this cluster is considered an amorphous pocket (AP), a {311}, or a loop.

`concentrations` Instructs Sentaurus Process KMC to generate concentration information to be included in the TDR file. It is used with `kmc extract tdrAdd`.

`coordx`, `coordy`, `coordz`

Specify the x-, y-, and z-coordinates needed for the command `kmc add queue`. They also are used to specify cutlines in the commands `kmc extract profile` and `kmc extract materials`.

## A: Sentaurus Process Commands

### kmc

|                             |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|-----------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>countdefects</code>   | Used with <code>kmc extract defects</code> to instruct Sentaurus Process KMC to count the number of defects instead of listing the particles in the defects.<br>Used with <code>kmc extract dose</code> to compute the dose of defects, not particles. For example, the dose of loops is different from the dose of particles in loops.                                                                                                                                                  |
| <code>countparticles</code> | Used with <code>kmc extract defects</code> to instruct Sentaurus Process KMC to count and return the number of particles, instead of listing them.                                                                                                                                                                                                                                                                                                                                       |
| <code>crystalline</code>    | When added to <code>kmc add</code> , creates the defect in a crystalline phase of the material, locally recrystallizing the area where the defect will be added when necessary.                                                                                                                                                                                                                                                                                                          |
| <code>deatomize</code>      | Instructs Sentaurus Process KMC to build a new data field and fill it with the concentrations taken from the KMC simulation. <code>name</code> is the field to create. For <code>deatomize</code> , the parameter name also can be <code>XTotal</code> or <code>NetActive</code> , where <code>X</code> means any dopant. It accepts the <code>active</code> flag to account for the active part of the dopant only.                                                                     |
| <code>defectname</code>     | Specifies an optional name of a defect ( <code>ThreeOneOne</code> , <code>ImpurityCluster</code> , ...) for <code>kmc extract profile</code> , <code>kmc extract defects</code> , <code>kmc extract dose</code> , and <code>kmc defects.write</code> . This option is used to further refine the option name. For example, if <code>name</code> is <code>I</code> , using this option refines these interstitials to interstitials as point defects, or in impurity clusters, and so on. |
| <code>defects</code>        | Using <code>kmc extract defects</code> returns the defects currently present in the simulation.<br>Using <code>kmc extract tdrAdd defects</code> appends to the TDR file an atomistic 3D view of the defects currently contained in the simulation, allowing visualization, and loading and continuing the simulation.                                                                                                                                                                   |
| <code>defects.read</code>   | Specifies the name of a text file from which to read its defects and insert them in the current simulation.                                                                                                                                                                                                                                                                                                                                                                              |
| <code>defects.write</code>  | Specifies the name of a text file into which to write all the current defects in the simulation. Use the parameters <code>defectname</code> and <code>materialname</code> to filter the defects written.                                                                                                                                                                                                                                                                                 |
| <code>defecttypes</code>    | Using <code>kmc defecttypes</code> returns the name of the defects that can be used by the option <code>defectname</code> .                                                                                                                                                                                                                                                                                                                                                              |

|           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| detailed  | <p>Produces different results depending on the context.</p> <ul style="list-style-type: none"> <li>• <code>kmc materials detailed</code> returns the current list of materials for each internal KMC element, including the element coordinates.</li> <li>• <code>kmc extract defects acinterface detailed</code> works as <code>extract defects acinterface</code>, but returns all the lattice atoms in the LKMC model, and not solely those ones belonging to the amorphous–crystalline interface.</li> </ul>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| dose      | <p>Using <code>kmc extract dose</code> returns doses (concentration in <math>\text{cm}^{-2}</math>). The option <code>countdefects</code> returns the dose of defects, instead of the dose of particles (which is the default). The defects and particles included in this dose are refined with the parameters <code>name</code> and <code>defectname</code>.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| extract   | <p>The command <code>kmc extract</code> retrieves information about the current status of the KMC simulation. This information is mainly concentrations, histograms, and atomistic positions and types of the defects. <code>kmc extract</code> also is used to control the information written to the TDR file. It is mandatory to use another option together with the <code>kmc extract</code> command. Available options are:</p> <ul style="list-style-type: none"> <li>• <code>defects</code> to obtain the current list of particles in the simulation.</li> <li>• <code>dose</code> to compute and return the dose of given particles or defects or both.</li> <li>• <code>histogram</code> to retrieve the number of defects depending on their size.</li> <li>• <code>materials</code> to retrieve the materials currently in the simulation.</li> <li>• <code>profile</code> to return the concentration of particles, defects, electrons, and holes in the simulation or any cutline of the simulation.</li> <li>• <code>supersaturation</code> to return the concentration relative to equilibrium for interstitials and vacancies.</li> <li>• <code>tdrAdd</code>, <code>tdrClear</code>, and <code>tdrWrite</code> to control the information to be written to the TDR file.</li> </ul> |
| filename  | <p>Specifies the name of the TDR file to be written by the command <code>kmc extract tdrWrite</code>.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| histogram | <p>The command <code>kmc extract histogram</code> returns the number of defects for each defect size. The parameter <code>name</code> determines the returned histogram. If <code>name</code> is <code>XI</code> or <code>XV</code> (<math>X</math> being a dopant or impurity), it returns the histogram of impurity clusters for that dopant with <math>I</math>s or <math>V</math>s. If the <code>name</code> is <code>I</code> or <code>V</code>, it produces the histogram of <math>I</math> or <math>V</math> extended defects. Finally, if the <code>name</code> is set to <code>IV</code>, it returns the AP histograms.</p> <p>If the option <code>meansize</code> is included, the returned value is not a list of defects and sizes, but the average size for these defects. The minimum size for computing this average is zero by default, but it can be changed using the option <code>minsize</code>.</p> <p>If <code>histogram</code> is added to the <code>kmc extract tdrAdd</code> command, it will include histogram information in the TDR file.</p>                                                                                                                                                                                                                              |

## A: Sentaurus Process Commands

### kmc

|                               |                                                                                                                                                                                                                                                                                                                                                                                                       |
|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>list</code>             | Adds a list of fields to be included in the TDR file. This parameter is used in the <code>kmc extract tdrAdd</code> command. Any specific defect name is allowed, and generic defect names (as obtained by <code>kmc defecttypes</code> ) also are allowed. For example, <code>I8</code> adds this cluster to the TDR file, but <code>AmorphousPockets</code> adds any AP existing in the simulation. |
| <code>&lt;material&gt;</code> | Specifies the material name for the options <code>deatomize</code> or <code>clustertype</code> . For information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                                                                                                                                                  |
| <code>materialname</code>     | Restricts the output to the material specified.                                                                                                                                                                                                                                                                                                                                                       |
| <code>materials</code>        | The command <code>kmc extract materials</code> returns the list of materials currently present in the simulation.<br>The command <code>kmc extract materials detailed</code> returns the coordinates and materials of the KMC elements. <code>materialname=&lt;c&gt;</code> adds a condition to the output of <code>kmc extract defects,profile,dose,</code> and <code>histogram</code> .             |
| <code>materialtypes</code>    | Returns the subset of materials allowed in the Sentaurus Process KMC simulation. Any material not listed here is assigned as 'unknown'                                                                                                                                                                                                                                                                |
| <code>meansize</code>         | Can only be used together with <code>kmc extract histogram</code> . It instructs Sentaurus Process KMC to compute the average size for the specified defect type. The minimum size needed to take the defect into account is 0, unless <code>minsize</code> is specified.                                                                                                                             |
| <code>minsize</code>          | Can only be used together with <code>kmc extract histogram meansize</code> . It instructs Sentaurus Process KMC to use the specified value as the minimum size to take any cluster into consideration when computing the average cluster size.                                                                                                                                                        |



|               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|---------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| name          | <p>Specifies the name of the field, particle, or defect for the following options. In the following, <i>X</i> is the name of a valid dopant (such as B or As). <i>Any defect</i> means very detailed defects such as B<sub>2</sub>I<sub>3</sub>, I<sub>8</sub>, I<sub>4</sub>V<sub>5</sub>, and AsV<sub>4</sub>. <i>Any particle</i> means point defects, dopants, impurities, or impurity- and dopant-paired point defects in any charge state, in other words, any name obtained with the command <code>kmc particletypes</code> (for example, I, VMM, BiP, or F):</p> <ul style="list-style-type: none"> <li>• <code>add</code> is name of the defect or particle to be added. XAmorphous and XInterface also are acceptable.</li> <li>• <code>histogram</code>: XI, XV, I, V, and IV are the only valid names.</li> <li>• <code>profile</code> is any defect or any particle. Holes, electrons, XAmorphous, and XInterface also are valid.</li> <li>• <code>defects</code> is any defect or any particle.</li> <li>• <code>dose</code> is any defect or any particle.</li> <li>• <code>supersaturation</code> allows only I or V.</li> <li>• <code>deatomize</code> is any defect or any particle. XAmorphous, XInterface, XTotal, NetActive, pNetActive, nNetActive, and tNetActive also are valid.</li> <li>• <code>present</code> is any defect or any particle. XAmorphous, XInterface, and XTotal also are acceptable.</li> <li>• <code>clustertype</code> is any defect.</li> </ul> |
| off           | <p>Using <code>kmc off</code> deletes the Sentaurus Process KMC information and removes the current KMC object from memory.<br/> <b>NOTE:</b> Use with caution.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| particletypes | <p>Returns a list of valid particle names. This list may change between simulations, depending on the dopants specified in the parameter database.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| PDEupdated    | <p>Returns true if the state of Sentaurus Process KMC did not change since the last time the PDEs were synchronized (by using <code>KMC2PDE</code>).</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| present       | <p>Returns true (1) when the species specified in <code>name</code> is in the KMC simulation.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |

## A: Sentaurus Process Commands

### kmc

|                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|-----------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| profile         | <p>Using <code>kmc extract profile</code> returns concentrations. These concentrations contain 1D, 2D, or 3D information depending on the simulation dimension. Cutlines can be specified with <code>coordx</code>, <code>coor<sub>y</sub></code>, and <code>coordz</code>. Each of these parameters reduces the dimensions of the output by 1. The concentrations in 1D simulations can be directly compared with SIMS profiles.</p> <p>The parameter <code>name</code> specifies the particle or defect from which the concentration is obtained. If <code>name</code> is a valid particle name (see <code>particletypes</code>), the parameter <code>defectname</code> can be used with a valid defect name (see <code>defecttypes</code>) to further refine <code>name</code>. When a particle is specified in <code>name</code>, <code>profile</code> returns the concentration of particles; otherwise, it returns the concentration of defects.</p> <p>Some particular names that can be used are:</p> <ul style="list-style-type: none"><li>• <code>holes</code>, <code>electrons</code>, <code>GapNarrowing</code>, and <code>gap</code> for electronic concentrations.</li><li>• <code>stressXX</code>, <code>stressXY</code>, <code>stressZZ</code>, <code>strainXX</code>, <code>strainYY</code>, <code>strainZZ</code>, <code>strainXY</code>, <code>strainXZ</code>, and <code>strainYZ</code> for mechanical properties.</li><li>• <code>dopants</code> for the net active concentration.</li><li>• <code>Ge</code> for the germanium concentration.</li></ul> |
| queue           | <p>Adds the new defect, specified with <code>name</code>, into the simulation at the coordinates <code>coordx</code>, <code>coor<sub>y</sub></code>, and <code>coordz</code>. Adding defects to the queue will not put them in the KMC simulation. To transfer the defects from the queue to the simulation, use the command <code>kmc add</code>, without any other parameter.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| report          | <p>Instructs Sentaurus Process KMC to generate a list of defects created during the simulation. This list includes the first and last time and temperature the defect was seen. If the defect is still in the simulation, the report also gives the number of defects. In addition, a report is printed automatically at the end of the <code>diffuse</code> and <code>implant</code> commands.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| stress          | <p>When added to <code>kmc extract tdrAdd</code>, it adds the stress and strain distribution as imported by Sentaurus Process KMC.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| supersaturation | <p>Using <code>kmc extract supersaturation</code> returns the value of the global supersaturation (concentration over equilibrium concentration). The parameter <code>name</code> must be specified. This parameter can only be <i>I</i> or <i>V</i>.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |

|                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|---------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>tdrAdd</code>       | <p>Using <code>kmc extract tdrAdd</code> instructs Sentaurus Process KMC to add a new ‘snapshot’ of information ready to be written into a TDR file. This information is stored in memory and is written using the command <code>kmc extract tdrWrite</code>. <code>tdrAdd</code> without options will add an empty snapshot. The <code>tdrAdd</code> options are:</p> <ul style="list-style-type: none"> <li>• <code>concentrations</code> computes and adds 1D, 2D, or 3D concentrations for each particle and defect.</li> <li>• <code>defects</code> adds atomistic 3D information. It allows you to see the defects shape and position, and to load and continue the simulation.</li> <li>• <code>histogram</code> adds histograms for extended defects and impurity clusters.</li> <li>• <code>list</code> adds user-specified defects. For example, <code>concentrations</code> only adds ‘I in ThreeOneOne’, but <code>list</code> can be used to add <code>I<sub>45</sub></code>, <code>I<sub>65</sub></code>, and so on. Specifying the name of a defect (as obtained in <code>kmc defecttypes</code>) adds all the clusters in this particular defect for each existing size in the simulation.</li> <li>• <code>stress</code> includes stress fields in the file.</li> </ul> |
| <code>tdrClear</code>     | Using <code>kmc extract tdrClear</code> removes all the snapshots previously added with <code>kmc extract tdrAdd</code> from memory.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| <code>tdrWrite</code>     | Using <code>kmc extract tdrWrite</code> instructs Sentaurus Process KMC to write all the snapshots (previously added with <code>tdrAdd</code> ) to a file. The name of the file is specified using the option <code>filename</code> .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <code>timeaveraged</code> | Must be used with <code>kmc extract profile</code> . It generates time-averaged concentrations of particles, instead of instantaneous ones. The averaging is performed between two snapshots. Since this option only makes sense for mobile particles, the parameter name must be a valid particle, not a defect.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <code>visual</code>       | <p>When added to <code>kmc extract tdrAdd</code>, it includes atomistic information that can be used for visualization purposes only, and not for restarting (in contrast with the <code>defects</code> option).</p> <p><code>visual</code> attempts to produce a file as small as possible without losing atomistic information. A list of the type of defects to be saved must accompany <code>visual</code>. The generic defects (that is, <code>ThreeOneOne</code>, <code>Void</code>), specific ones (such as <code>B2I3</code>), or materials (<code>Silicon</code>) specified act as filters for the defects to be save.</p> <p>To save all of them, use <code>visual=all</code>.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |

## A: Sentaurus Process Commands

kmc

### Examples:

```
kmc add queue coordx=10<nm> coordy=15<nm> coordz=6<nm> name=I8
kmc add queue coordx=3<nm> coordy=8<nm> coordz=7<nm> name=B2I2
kmc add queue coordx=5<nm> coordy=5<nm> coordz=5<nm> name=Bi
kmc add
```

Creates an  $I_8$  clusters, a mobile B in interstitial position and the BIC  $B_2I_2$  in the queue, and it adds the queue to the KMC simulation.

```
kmc clustertype name=I543
```

Returns whether an  $I_{543}$  is a ThreeOneOne or a Loop in this simulation.

```
kmc deatomize name=BTotAl
```

Creates a `BTotAl` data field. This field will be computed by Sentaurus Process KMC including all the boron in any defect in the simulation.

```
kmc deatomize name=As4V
```

Creates an `As4V` data field, filled with the `As4V` information taken from the KMC simulation.

```
kmc defecttypes
```

Returns a list of the different defect types modeled by Sentaurus Process KMC.

```
kmc extract defects
```

Returns a list containing the particles currently in the KMC simulation, including its defect type, defect number, and coordinates. Particles with the same defect number belong to the same defect.

```
kmc extract defects name=I
```

Returns a list of each I particle currently in the KMC simulation.

```
kmc extract defects name=B defectname=ImpurityCluster
```

Returns the B particles in impurity clusters currently in the simulation.

**Examples:**

```
kmc extract defects name=B2I3 countparticles
```

Returns the number of particles in  $B_2I_3$  defects.

```
kmc extract defects name=B2I3 countdefects
```

Returns the number of  $B_2I_3$  defects in the simulation.

```
kmc extract defects detailed
```

Returns a list of particles currently in the KMC simulation. It also returns the 'hidden' particles, which are regenerated by Sentaurus Process KMC using internal information (see [Damage Accumulation Model: Amorphous Pockets on page 420](#)).

```
kmc extract defects name=As4V
```

Returns the  $As_4V$  defects present in the simulation.

```
kmc extract profile name=electrons
```

Returns the electron concentration computed by Sentaurus Process KMC.

```
kmc extract histogram name=BI
```

Returns the BIC histograms.

```
kmc extract histogram name=I minsize=40
```

Returns the average size of I in extended defects. The minimum size to be included in this average is set to 40.

```
kmc extract profile name=I2V3
```

Returns the concentration of  $I_2V_3$  defects.

```
kmc extract profile name=holes
```

Returns the concentration of holes in the KMC simulation.

```
kmc extract profile name=B
```

Returns the concentration of boron in any defect.

```
kmc extract profile name=B defectname=PointDefect
```

Returns the concentration of substitutional boron.

```
kmc extract dose name=I defectname=ThreeOneOne
```

Returns the dose (concentration in  $cm^{-2}$ ) of interstitials in {311}s.

```
kmc extract materials
```

Returns the list of materials currently present in the simulation.

```
kmc extract materials detailed
```

Returns the coordinates of each KMC element and its material.

## A: Sentaurus Process Commands

kmc

### Examples:

```
kmc extract profile timeaveraged name=I
```

Returns the concentration of mobile interstitials in the simulation.

```
kmc extract supersaturation name=I
```

Returns the interstitial supersaturation.

```
kmc extract tdrClear
```

```
kmc extract tdrAdd concentrations defects
```

```
kmc extract tdrWrite filename=example.tdr
```

Clears all the previous stored information, adds a new snapshot with the concentration of particles and the atomistic information for any defect, and writes the information in a TDR file called `example.tdr`. Since the option `defects` is included, this file also can be used to load and continue the simulation.

```
kmc materialtypes
```

Returns the list of materials supported by Sentaurus Process KMC.

```
kmc particletypes
```

Returns the list of particles supported by Sentaurus Process KMC. This list can be changed using `pdb` commands.

```
kmc present name=BI2
```

Returns true (1) or false (0) depending on the presence of  $BI_2$  in the simulation.

```
kmc off
```

Exits Sentaurus Process KMC and removes all its associated information from memory.

```
kmc report
```

Prints a list of the simulated defects with the first and last time and temperature they were seen in the simulation.

```
kmc extract profile name=B2I2 coordx=10<nm>
```

In 1D, returns the concentration of  $B_2I_2$  at  $x = 10$  nm.

In 2D, returns the concentration of  $B_2I_2$  in the line  $x = 10$  nm.

In 3D, returns the concentration of  $B_2I_2$  in the plane  $x = 10$  nm.

```
kmc extract profile name=B2I2 coordx=10<nm> coordz=15<nm>
```

Returns the concentration in the line  $y$  with  $x = 10$  nm and  $z = 15$  nm.

```
kmc extract tdrAdd list={ThreeOneOne BI2 B2I2}
```

Creates a TDR snapshot with any  $\{311\}$  defect and the  $BI_2$  and  $B_2I_2$  defects.

**See:** [deposit on page 870](#), [diffuse on page 875](#), [etch on page 889](#),  
[implant on page 926](#), [integrate on page 945](#), [line on page 969](#),  
[photo on page 1010](#), [profile on page 1033](#), [region on page 1047](#),  
[select on page 1053](#), [stressdata on page 1081](#), [struct on page 1086](#)  
For more details on Sentaurus Process KMC, see [Chapter 5 on page 369](#).

## KMC2PDE

**Function:** Translates the atomistic KMC atomistic information to Sentaurus Process.

**Syntax:** KMC2PDE

**Description:** Translates the atomistic information stored in the KMC diffusion into continuum five-stream quantities, and transfers it into the standard Sentaurus Process mesh. Consequently, there are two transformation involved here:

- Deatomization of particles into concentrations
- Translation of the Sentaurus Process KMC field names into Sentaurus Process field names

The deatomization is performed in a standard way by calling `kmc deatomize` for each existing Sentaurus Process KMC field. If the Sentaurus Process mesh is too coarse, the continuum fields will look smooth, but some information may be lost. On the other hand, if the Sentaurus Process mesh is too fine, isolated islands of concentration may form following its corresponding atomistic concentrations.

The translation is made as accurately as possible by mapping as many KMC species into similar five-stream fields. In cases when this one-to-one map is not possible or unique, acceptable approximations can be taken. For example, `Bi` will be translated into `BoronInt`, but `B2I2`, `BI2`, and so on will be translated into only `BCluster`. A complete list of these translations is available in the file `KMC.tcl`.

**Examples:** KMC2PDE

**See:** [UnsetAtomistic on page 1110](#)



## layers

**Function:** Prints material interfaces and integrated data field values.

**Syntax:** layers  
 [<material>] [name] [region.names]  
 [x=<n>][<m>|<cm>|<um>|<nm>]  
 [y=<n>][<m>|<cm>|<um>|<nm>]  
 [z=<n>][<m>|<cm>|<um>|<nm>]  
 [merge] [precision=<n>] [print.logfile] [syntax.check.value=<c>]

**Description:** Prints the material interfaces and integrates the selected data field in each region. It is most useful for examining doping because it gives the integrated doping in each layer. This command can be simulated with the `interpolate` and `interface` commands, and it returns a Tcl list of each material.

**Options:**

<material> Used to limit the reporting of layers to regions of the specified material. For information about specifying materials, see [Material Specification on page 50](#).

merge Specifies that the adjacent regions with the same material should be merged. The default is false.

name Specifies a data field name. This allows printing without using the `select` or `tclsel` commands. The default is `Z_Plot_Var`.

precision Controls the number of precision digits of floating values (in scientific notation). The default is 12.

print.logfile Allows output to be written to the log file.

region.names Specifies that region names should be printed in addition to the material names for each region in the structure.

syntax.check.value  
 Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during normal run mode. Setting this value avoids such problems.

## A: Sentaurus Process Commands

layers

*x, y, z*

Specify the constant values of a line along which sectioning will be performed. In 1D, these parameters are not necessary. In 2D, only one of *x* or *y* can be specified for a given device. Specifying *x* produces a horizontal slice through the device, and *y* specifies a vertical slice. An easy way to remember this is that the cross section is taken at the constant value specified. For a 3D simulation, two of these three must be specified. The default unit is  $\mu\text{m}$ .

### Examples:

```
layers
```

In a 1D simulation, this lists all material interfaces.

```
layers y=0.0 name=Boron
```

In a 2D simulation, this lists all material interfaces at a lateral position of  $0.0 \mu\text{m}$  and integrates the data field named `BORON`.

### See:

[interface on page 948](#), [interpolate on page 950](#), [select on page 1053](#),  
[tclsel on page 1091](#)

---

## line

**Function:** Specifies the position and spacing of mesh lines.

**Syntax:**

```
line
  (x | y | z)
  location=<n>[<m>|<cm>|<um>|<nm>]
  [spacing=<n>][<m>|<cm>|<um>|<nm>]
  [kmc] [mgoals]
  clear [tag=<c>]
```

**Description:** Specifies the position and spacing of mesh lines. All `line` commands must precede `region` commands, which in turn must be followed by the `init` command. Lines must be given in increasing order.

When used to create the initial mesh, only rectilinear structures can be specified with the `line` and `region` commands, that is, rectangular regions in 2D and cuboid-shaped regions in 3D.

Sentaurus Process has the following coordinate system, which is the same as the unified coordinate system (UCS):  $x$  is the direction normal to the wafer with positive- $x$  oriented into the bulk of wafer;  $y$  is perpendicular to the  $x$ -direction and lies along the wafer surface;  $z$  is in the lateral direction. The  $z$ -direction is used for 3D and the direction is given by  $X \times Y$ . By default, Sentaurus Process delays promoting a structure until it is necessary (by use of a higher dimensional mask). The lines specifying the higher dimensions are stored until they are needed. During the `init` command, the line and spacing information is expanded into mesh ‘ticks’ that are stored in the PDB. These ticks are used every time a mesh is created if `UseLines` is on (see [UseLines: Keeping User-defined Mesh Lines on page 702](#)).

After an `init` command, if new lines are specified and `UseLines` is on, the `spacing` parameter is ignored, and only one tick or mesh line at a time may be added. To create an entirely new structure, the command `line clear` should first be issued to clear old lines and mesh ticks before issuing new lines, regions, and `init` commands.

**Options:**

`clear` Clears lines in preparation for a new structure definition, or removes all ticks stored for the `UseLines` method (see [UseLines: Keeping User-defined Mesh Lines on page 702](#)).

## A: Sentaurus Process Commands

### line

|                          |                                                                                                                                                                                                                                                                                                                                                              |
|--------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>kmc, mgoals</code> | Lines for KMC and MGOALS (continuum) meshes are stored separately. By default, <code>line</code> commands are applied to both KMC and continuum meshes. Use negative values for these parameters to <i>not</i> apply mesh lines to one or the other. For example, for a <code>line</code> command to apply only to a continuum mesh, use <code>!kmc</code> . |
| <code>location</code>    | Location along the chosen axis. The default unit is $\mu\text{m}$ .                                                                                                                                                                                                                                                                                          |
| <code>spacing</code>     | Local grid spacing. Each mesh line has a characteristic required spacing. Lines are graded from one spacing to the next over the interval. The default is a spacing equal to the largest interval between the neighboring lines. The default unit is $\mu\text{m}$ .                                                                                         |
| <code>tag</code>         | Lines can be labeled for later reference by <code>region</code> statements. The label can be any word.                                                                                                                                                                                                                                                       |
| <code>x, y, z</code>     | Specifies the orientation of the mesh line. Specifying <code>x</code> places a mesh line at a constant <code>x</code> -value. A series of <code>line x</code> commands would specify the horizontal grid locations during the simulation.                                                                                                                    |

**Examples:**

```
line x loc=0 spa=0.02 tag=surf
line x loc=3 spa=0.5 tag=back
line y loc=0 spa=1 tag=left
line y loc=1 spa=0.1
line y loc=2 spa=1 tag=right
```

There are three user-specified `y`-lines and two user-specified `x`-lines. Taking the `y`-lines as an example, there is a finer spacing in the center than at the edges. After processing, Sentaurus Process produces a mesh with `x`-lines at 0.0, 0.42, 0.69, 0.88, 1.0, 1.12, 1.31, 1.58, and 2.0. Around the center, the spacing is 0.12, approximately what was requested. At the edge, the spacing is 0.42 because that was as coarse as it could become without having an interval ratio greater than 1.5 (a fixed quantity). If the interval ratio was allowed to be 9, for example, there would have been one interval of 0.9 and one interval of 0.1 on each side. In this example, specifying a spacing of 1 at the edges is redundant because that is what the spacing of the user-specified lines was already.

**See:** [region on page 1047](#)

---

## line\_edge\_roughness

**Function:** Adds line edge roughness (LER) to named masks.

**Syntax:**

```
line_edge_roughness
  masks= {<string list>}
  normal= ("Y" | "Z")
  correlation.length=<n>[<m>|<cm>|<um>|<nm>]
  max.segment.length=<n>[<m>|<cm>|<um>|<nm>]
  standard.deviation=<n>[<m>|<cm>|<um>|<nm>]
  [random.seed=<n>] [random.reseed] [min.radius=<n>] [max.tries=<n>]
```

**Description:** Adds LER to the named masks, along the mask edges normal to the given normal axis ("Y" or "Z").

LER can be added to a mask only once. See [Boolean Masks on page 744](#).

**Options:**

correlation.length

Specifies the correlation length of the randomized LER. Approximately corresponds to the concept of *wavelength*. The default value and unit is 20 nm.

masks

Specifies the names of masks to receive LER defined by the other parameters in the `line_edge_roughness` command.

max.segment.length

Specifies the maximum segment length. Mask edges are subdivided into segments that are approximately this size or smaller before LER deviation is added to each. The default value and unit is 1 nm.

max.tries

Specifies the maximum number of LER mask generation attempts. For nonzero values, detection of nearly collinear points is performed after LER generation, and the LER process is restarted if decimation occurs based on the `mgoals` accuracy value. The default value is 0, meaning that the LER mask is accepted as it is, with no decimation detection.

min.radius

When `normal` is not specified, where two mask edges receiving LER meet, the corner is first rounded before LER is applied. This is to allow a well-defined application of LER and to avoid discontinuous jumps in the resulting mask shape. The rounding radius is the larger of `min.radius` and twice `correlation.length`.

## A: Sentaurus Process Commands

### line\_edge\_roughness

- `normal` Defines the normal axis. Only mask segments normal to this axis receive LER. This axis is also the reference axis along which the LER deviation is added to the given mask segment. The default is to add LER to all edges of the mask.
- `random.reseed` Before the calculation of LER, the random number generator is reseeded to ensure each call of `line_edge_roughness` results in randomized noise that is uncorrelated with other calls of `line_edge_roughness`. To switch off this random reseeding, use `!random.reseed` to reproduce the same LER from call to call. The default is true.
- `random.seed` Used to reproduce specific LER calculations from one run to the next by setting the same random seed in both runs. Ignored when `!random.reseed` is used.
- `standard.deviation`
- Specifies the standard deviation of the randomized LER. Approximately corresponds to the concept of added noise *amplitude*. The default value and unit is 2 nm.

#### Examples:

```
line_edge_roughness normal= "Z" masks= {mask1} \  
    correlation.length= 25.00<nm> standard.deviation= 5.00<nm> \  
    max.segment.length=5.00<nm>
```

Adds LER to the mask named `mask1` along mask segments normal to the z-axis. These segments are subdivided into smaller segments of length smaller than or equal to 5 nm. LER is characterized by a `correlation.length` of 25 nm and `standard.deviation` of 5 nm. The random number generator is reseeded automatically before LER is calculated.

**See:** [Line Edge Roughness Effect on page 746](#)

---

## load

**Function:** Loads data from a file and interpolates it onto the current mesh.

**Syntax:**

```
load
  (tdr=<c> | dfise=<c> | grdfile=<c> datfile=<c>)
  (sum | replace | rename | merge)
  [species= <list>] [actions= <list>] [fast.tdr.ave= <list>]
  [shift=<n>] [flip (left | right | front | back | up | down)]
  [offset= {<n> <n>}]
  [transform= {<n> <n> <n> <n> <n> <n>}]
```

**Description:** Interpolates data from TDR or DF-ISE grid and data files onto the current mesh. The file to be loaded must have the same dimension as the existing structure. There are several options for handling the new and old datasets. First, the actions can be applied individually to selected datasets using the `species` and `actions` lists. If the `species` list appears, the `actions` list must be specified and must have the same number of members as the `species` list. If this is the case, only the species in the `species` list are taken from the external datasets. If the `species` list does not appear, one of the global actions is used. The default behavior is a global `sum` where new datasets are added and, if there is an existing dataset with the same name, the external data is added (summed) with the existing dataset.

The other actions that can be performed are:

- `replace` replaces current datasets with new datasets of the same name.
- `rename` renames new datasets by appending `__load` to the name, which can be manipulated with the `select` command as required.
- `merge` takes only the new datasets that do not currently exist in the structure.
- In atomistic mode, only the options `tdr` and `replace` can be used to replace the current simulation contents with the particles stored in a TDR file.

**Options:**

`dfise` Specifies the input file name. Sentaurus Process checks for all standard suffixes for both grid files (`.grd`, `_fps.grd`, `.grd.gz`, `_fps.grd.gz`) and data files (`.dat`, `_fps.dat`, `.dat.gz`, `_fps.dat.gz`).

## A: Sentaurus Process Commands

### load

`fast.tdr.ave` Averages the data from a list of TDR files (all with identical meshes to the current mesh) and replaces the current data with the averaged data from the files. This is an option developed specifically for the distributed MC implantation feature (mpp). However, there may be other uses for it, for example, to improve KMC statistics.

**NOTE:** Do not use it with any other parameter. To use it, specify a list of files, for example:

```
fast.tdr.ave= {mydata1.tdr mydata2.tdr mydata3.tdr}
```

`flip & left | right | front | back | up | down`

For 2D structures only. Performs a flip of the data in the indicated direction about the outer boundary before interpolation. Must be used with a direction: left, right, front, back, up, down.

`grdfile, datfile`

Specifies the exact names for the DF-ISE files (should not be used with the `dfise` parameter).

`merge` Adds only new datasets that do not currently exist in the structure.

`offset` For 2D structures only. Offsets the data by a vector before loading it.

`rename` Adds new datasets and renames them by adding the suffix `load`.

`replace` Adds new datasets and replaces existing datasets with new datasets of the same name.

`shift` Shifts the data laterally before loading it.

`species, actions`

These lists specify species-by-species actions. The species name must be one of those appearing in the loaded `.dat` file. Each action in the `actions` list should be one of `sum`, `replace`, `rename`, or `merge`.

`sum` Adds new datasets and sums matching datasets.

`tdr` Specifies the input file name with TDR format. Sentaurus Process checks for standard file names with the `.tdr` extension.

`transform` This function provides a general interface for translating or rotating the structure to be loaded before interpolation. In 1D, one value must be specified – the shift in the x-coordinate. In 2D, six values must be specified: `rxx`, `ryx`, `rxz`, `ryy`, `offsetx`, `offsety`. In 3D, 12 values must be specified: `rxx`, `ryx`, `ryz`, `ryy`, `rzz`, `rxy`, `ryz`, `rzz`, `offsetx`, `offsety`, `offsetz`. First, the offset is applied, and then the rotation matrix is applied (it does not have to be an orthogonal matrix).



**Examples:**

```
load tdr=in replace
```

Replaces all existing datasets with those in the file `in_fps.tdr`.

```
load tdr=in species= {Arsenic_Implant Damage_Implant} actions= {sum replace}
```

Loads the TDR file `in_fps.tdr`, sums `Arsenic_Implant` with the existing `Arsenic_Implant` (if available), and replaces the existing `Damage_Implant` data field by the one in the `in_fps.tdr` file.

---

## LogFile

**Function:** Prints a message to the screen and to the log file.

**Syntax:** `LogFile`  
          `[IL0 | IL1 | IL2 | IL3]`  
          `(message)`

**Description:** Prints messages to the terminal window in which Sentaurus Process is running and to the log file. If one of IL0, IL1, IL2, or IL3 is given and this command is called from within a Sentaurus Process command, the message is printed only if the information level is equal to or greater than the one specified.

**Options:**

IL0, IL1, IL2, IL3

Specify the information level.

message Specifies the message to be printed to the screen and to the log file.

**Examples:** `LogFile "Step 25"`  
Writes the string "Step 25" to the log file and to the screen.

`LogFile IL2 "$DebugInfo"`  
Prints the contents of the Tcl variable `DebugInfo` only if `info=2` or higher has been specified in the calling command.

## mask

**Function:** Creates a mask for subsequent use in `etch`, `deposit`, or `photo` commands.

**Syntax:**

```
mask
  [list] [clear] [name=<c>] [negative] [bbox]
  [covered.status] [get.segments] [get.segments.z] [bool=<op>]
  (
    {[left=<n>][<m>|<cm>|<um>|<nm>]
    [right=<n>][<m>|<cm>|<um>|<nm>]
    [front=<n>][<m>|<cm>|<um>|<nm>]
    [back=<n>][<m>|<cm>|<um>|<nm>]} |

    {[polygons= <string list>]}
    {[segments= <numeric list>]}
    {[layoutfile=<c>]}
  )
  { [cut.x=<n>] [regions= <string list>] [materials= <string list>] }
```

**Description:** Allows the management and creation of masks for use with subsequent `etch`, `deposit`, or `photo` commands. Mask definitions are stored in TDR files and restored when loading a TDR file in the `init` command. Masks can be defined by rectangles, polygons, and segments, or they can be read using the ICWB interface (see [ICWBEV Plus Interface for Layout-driven Simulations on page 795](#)) or read from a DF-ISE layout format file.

Masks are created additively. If more than one `mask` command is issued with the same name, the union of the specified masks is assumed. To change a mask, clear it first and then assign a new specification (in two separate calls to the `mask` command).

**Options:**

`bbox` Returns the mask bounding box. The command returns a list of lists where the values are in centimeters: {ymin zmin} {ymax zmax}.

`bool` Performs Boolean operations between masks. The `bool` option cannot be used together with the `layoutfile`, `polygon`, and `negative` options. For more information, see [Boolean Masks on page 744](#).

`clear` Clears the list of all masks. If `name` is specified, it clears only that mask.

## A: Sentaurus Process Commands

### mask

`covered.status`

Used to obtain information about the coverage of the simulation domain. The following strings may be returned:

- `covered`: The mask completely covers the simulation domain.
- `uncovered`: The mask does not cover the simulation domain at all.
- `partial.2d`: The mask partially covers the domain, but in a way that the mask does not promote the simulation dimension (that is, the mask does not vary in the z-direction over the simulation domain).
- `partial`: The mask partially covers the simulation domain, and its use in etch or deposit forces the simulation to 3D.

`cut.x, regions, materials`

Currently, this parameter is only available in 2D. The `cut.x` parameter must be used with the `regions` or `materials` parameters to create a mask. The mask is created by taking a cut through the set of regions created by a union of regions named in the `regions` parameter and regions of one of the materials named in the `materials` parameter. The cut is taken at the x-coordinate specified in the `cut.x` parameter, and the resulting outline is used to create the mask.

`get.segments, get.segments.z`

Retrieves segments that result from cutting the mask at `z=get.segments.z`. The default value of `get.segments.z` is the midpoint of the simulation domain in the z-direction.

`layoutfile`

Name of a layout file in DF-ISE layout format. All masks defined in the layout file will be read. By default, the origin of the layout file and the internal coordinate system coincide. The lateral coordinate of the layout file will be used as the Sentaurus Process y-coordinate, and the vertical coordinate of the layout file will be used as the Sentaurus Process '-z'-coordinate.

You can place the Sentaurus Process simulation domain anywhere in the layout file by specifying either the parameter name together with `layoutfile` or a `CutLine2D` in the `init` command. If `name` is specified, it must refer either to a mask that has been previously defined or to one of the masks in the layout file (SIM3D or SIM2D).

|                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|--------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| layoutfile               | <p>If a rectangle mask is used, either defined as SIM3D in the layout file or by referring to a previously defined mask, the minimum coordinates of the rectangle define the origin of the internal coordinate system. The layout <math>-x</math>-axis and <math>-y</math>-axis define the Sentaurus Process <math>z</math>-axis and <math>y</math>-axis, respectively.</p> <p>If a CutLine2D or a SIM2D or a polygon mask is used, the origin of the UCS is defined by the first point. The direction of the Sentaurus Process <math>y</math>-axis is aligned to the direction of the specified line. If a polygon mask is used, only the first two points are required for the placement of the simulation domain in the layout file.</p> <p>Default extensions of the 2D or 3D simulation domain in the <math>y</math>- and <math>z</math>-directions are defined from the specified mask. For a SIM2D or a two-point polygon, the default extension along the <math>y</math>-axis is defined for a rectangle, polygon, or SIM3D mask; default extensions are defined in both the <math>y</math>-direction and <math>z</math>-direction. If you did not specify the <code>line y</code> and <code>line z</code> commands, the default extensions are used.</p> |
| left, right, front, back | <p>Specify the corners of one rectangle. The rectangle is added to the current list for the mask. If several rectangles must be specified for a mask, several <code>mask</code> commands must be used with the same name. The default unit is <math>\mu\text{m}</math>.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| list                     | <p>Prints a list of all currently defined masks. If <code>name</code> is specified, it prints the information about that mask only.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| name                     | <p>Name of a mask. If used with <code>list</code> or <code>clear</code>, only the specified mask will be reported or removed. If defining a new mask, <code>name</code> must be given.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| negative                 | <p>Inverts the type of mask. By default, points inside the mask are considered masked. The commands <code>mask name=xyz negative</code> and <code>mask name=zyx !negative</code> can be used to invert an existing mask <code>xyz</code>.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| polygons                 | <p>Specifies a mask as a list of named polygons. The named polygons must have been defined using <code>polygon</code> commands (see <a href="#">polygon on page 1024</a>).</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| segments                 | <p>Specifies a list of coordinates of mask segments. The default unit is <math>\mu\text{m}</math>. Several mask segments can be specified at the same time. The first coordinate defines the beginning of a segment, the second coordinate defines the end of the segment, the third defines the beginning of the second segment, and so on. In a 3D simulation, mask segments are extended across the entire structure in the <math>z</math>-direction.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

## A: Sentaurus Process Commands

### mask

#### Examples:

```
mask name=field left=0.0 right=10.0
```

Defines a mask named `field`.

```
mask name=mgoals segments = {0.0 10.0}
```

The position of this mask is the same as in the previous example.

```
mask layoutfile=simple.lyt name=SIM3D
```

Reads the layout file and defines the position and default extensions of the Sentaurus Process simulation domain by one of the masks in the layout file. The default extensions of the simulation domain are `y: 0...length of SIM3D`  
`z: 0...width of SIM3D`. They are ignored if you defined the `line y` and `line z` commands.

```
polygon name=cutline segments= {1.65 0.15 1.95 0.6}
```

```
mask name=cutline polygons= {cutline}
```

```
mask layoutfile=simple.lyt name=cutline
```

Defines a mask as a two-point polygon, loads the layout file, and aligns the origin and y-axis of the default coordinate system with the specified mask. The default extension of the simulation domain along the y-axis is `0...length of the segment`.

```
init slice.angle= [CutLine2D 1.65 0.15 1.95 0.6]
```

```
mask layoutfile=simple.lyt
```

Loads a layout file. Aligns the origin and the y-axis of the default coordinate system with the specified `CutLine2D`.

**NOTE:** There are no default extensions defined in this case. You must specify `line y` explicitly.

```
# mask bbox example - return value in cm
```

```
mask name=m1 left=0.1<um> right=0.2<um> front=0.3<um> back=0.4<um>
```

```
set mlbbox [mask name= "m1" bbox]
```

```
# $mlbbox == {1.0e-05 3.0e-05} {2.0e-05 4.0e-05}
```

```
mask list
```

Returns information about all masks in array format.

```
array set maskinfo [mask list]
```

```
LogFile "Mask names: [array names maskInfo]"
```

Returns a list of mask names.

```
array set polyInfo $maskInfo(PolygonMask)
```

```
LogFile "Contents of PolygonMask: [array names polyInfo]"
```

Prints all information about a mask named `PolygonMask`.

**Examples:** LogFile "Number of polygons in PolygonMask: [length \$polyInfo(polygons)]"  
Prints the number of polygons in a mask named PolygonMask.

LogFile "polygon 0 in PolygonMask: [lindex \$polyInfo(polygons) 0]"  
Prints the first polygon in a mask named PolygonMask.

**See:** [deposit on page 870](#), [etch on page 889](#), [photo on page 1010](#),  
[point on page 1022](#), [polygon on page 1024](#)

---

## mater

**Function:** Returns a list of all materials in the current structure. Adds new materials to a global list.

**Syntax:**

```
mater
  [add] [name=<material>] [min= {<n> <n> <n>} max= {<n> <n> <n>}]
  [cropped.bbox] [new.like=<material>] [alt.matername=<c>]
  [list.all] [Interface] [like.interpolate]
  [bbox | bbox.cm | bbox.um]
  [syntax.check.value=<c>]
```

**Description:** Returns a list of all materials in the current structure. The format of the list is compatible with the material specification for the program. Bulk material names are returned if no options are given. Interface materials can be obtained with the `Interface` parameter. A new material is added to the global material list if the `add` parameter is given.

This command also computes the cropped bounding box of a material that lies within a user-specified bounding box defined by `min` and `max`. The `name` parameter is given as input.

### Options:

`add` Adds a material specified with the `name` option.

`alt.matername` Defines the alternative material to be used when saving a structure. When using the TDR format, regions that are converted using `alt.matername` will be converted back properly to the simulation material when the TDR file is read in from the `init` command. Although common materials such as SiGe and III–Vs are by default handled this way, special situations may require additional conversions when transferring to device simulation.

`bbox`, `bbox.cm`, `bbox.um`

If specified, the `mater` command returns the maximum extents of the material in two points in micrometer or centimeter.

`cropped.bbox` Returns the cropped bounding box of a material within a user-defined bounding box.

`Interface` Returns a list of interface materials in the current structure.

`like.interpolate`

Usually, the interpolation code interpolates data from and to materials that are ‘like’ each other (see [Like Materials: Material Parameter Inheritance on page 55](#)). Use this option to prevent such interpolation.



|                                 |                                                                                                                                                                                                                                                                                                                      |
|---------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>list.all</code>           | Lists all the materials defined.                                                                                                                                                                                                                                                                                     |
| <code>min, max</code>           | Specify the bounding box of a material. These parameters compute the cropped bounding box of a material.                                                                                                                                                                                                             |
| <code>name</code>               | Name of a material.                                                                                                                                                                                                                                                                                                  |
| <code>new.like</code>           | Name of the existing material from which all default values are inherited. For newly created materials, <code>pdb</code> parameters for this material are checked first and, if not found, the 'Like' material parameters are used (see <a href="#">Like Materials: Material Parameter Inheritance on page 55</a> ). |
| <code>syntax.check.value</code> | Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during normal run mode. Setting this value avoids such problems.                                      |

**Examples:** `mater add name=Germanium new.like=Silicon`

---

## math

**Function:** Sets the numeric and matrix parameters. Parameters set with the math command are stored in TDR files by default.

**Syntax:**

```

math
[coord.ucs] [coord.xyz] [coord.yxz] [coord.-zyx] [coord.dfise]
[coord.transform coord.translate (coord.read | coord.write)]

[numThreads=<i>]
[numThreadsAssembly=<i>]
[numThreadsBoxMethod=<i>]
[numThreadsDeatomize=<i>]
[numThreadsILS=<i>]
[numThreadsImp3d=<i>]
[numThreadsInterp=<i>]
[numThreadsKMC=<i>]
[numThreadsMC=<i>]
[numThreadsMGoals=<i>]
[numThreadsPardiso=<i>]
[numThreadsSano=<i>]
[numThreadsTopo=<i>]

[diffuse | flow]
[dimension = 1 | 2 | 3]
[pardiso | ils] [scale]

[fullNewton | modNewton]
[newtonSteps1=<i>] [newtonRate1=<n>] [newtonRate2=<n>]
[newtonTries1=<i>] [newtonStats=<i>] [newtonDeriv]

[NegErrCntrl] [FTS.NegErrCntrl] [AMS.NegErrCntrl] [LocTrnErrCntrl]

[maxNumberOfDomains=<i>]
[NumberOfElementsPerDomain=<i>]
[parallel.license= go.serial | go.wait | go.abort]
[threadStackSize=<i>]

[tr_bdf | euler] [milne | difference]

[limit.precision] [voronoitriangle] [use.interpolated.geom.coeff]

```

**Description:** This command is used to specify the:

- Different coordinate system types.
- Number of threads and parameters used for parallel processing on shared-memory computers.
- Default options on the matrix packages to be used for different equations.
- Parameters for the Newton method.
- Different time discretization schemes.

**Options:****Solver selection**

|                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>AMS.NegErrCntrl</code> | Allows stricter error control for each solve time step after an adaptive meshing step by calculating the error from negative updates instead of damped results.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| <code>diffuse, flow</code>   | Specifies the type of equation to which the command specification applies. If omitted, it applies to all equation types.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| <code>dimension</code>       | Specifies dimensionality to which the command specification applies. If omitted, it applies to all dimensions.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| <code>FTS.NegErrCntrl</code> | Allows stricter error control for the first solve time step by calculating the error from negative updates instead of damped results.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| <code>LocTrnErrCntrl</code>  | Allows stricter error control for each solve time step by modifying the handling of negative updates: <ul style="list-style-type: none"> <li>• 1 (<math> upd /org \leq abs</math>)</li> <li>• 0 (<math> upd /org \leq *abs</math>)</li> </ul> <code>LocTrnErrCntrl</code> can be switched on for individual solution variables in specific materials using:<br><pre>pdbSetBoolean &lt;mater&gt; &lt;solution&gt; LocTrnErrCntrl 1</pre>                                                                                                                                                                                                                                             |
| <code>NegErrCntrl</code>     | Allows stricter error control at each Newton iteration step by calculating the error from negative updates instead of damped results. <code>NegErrCntrl</code> can be switched on for individual solution variables in specific materials using:<br><pre>pdbSetBoolean &lt;mater&gt; &lt;solution&gt; NegErrCntrl 1</pre>                                                                                                                                                                                                                                                                                                                                                           |
| <code>pardiso, ils</code>    | Specifies the type of linear solver to apply to the system: <ul style="list-style-type: none"> <li>• <code>pardiso</code> selects the parallel direct solver PARDISO, which is based on the LU factorization with pivoting of the matrix. PARDISO decomposes the matrix.</li> <li>• <code>ils</code> selects the iterative linear solver ILS, including preconditioners, iterative methods, scaling, and convergence criteria. (You can change the default settings of ILS parameters by specifying <code>pdbSet Math</code> commands.) To set ILS parameters in the parameter database, see <a href="#">Setting Parameters of the Iterative Solver ILS on page 838</a>.</li> </ul> |
| <code>scale</code>           | Applies row/column scaling to the matrix in an attempt to make it better conditioned. This is a recommended option. No scaling is performed if the modified Newton scheme is used.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |

## A: Sentaurus Process Commands

math

### Newton method

`fullNewton`, `modNewton`

Specifies type of nonlinear equation solver to use:

- `fullNewton` performs a matrix factorization at each step.
- `modNewton` tries to reuse one matrix factorization for several solve steps. The full Newton method may be more robust, but it may use more solution time than the modified Newton method.
- `modNewton` is the default in 2D for both PARDISO and ILS.
- `modNewton` is the default for ILS in 3D.

`newtonDeriv` Allows the Jacobian computation to be switched on during the modified Newton step. The default is false.

`newtonRate1` For the modified Newton method, if the solution for any of the Newton steps 1 through `newtonSteps1` is `newtonRate1` or more times better than the previous step, the next step can be a solve-only step. Otherwise, the next step will perform a matrix factorization. The default value is 4.0.

`newtonRate2` For the modified Newton method, if the solution for any of the Newton steps `newtonSteps1+1` onwards is `newtonRate2` or more times better than the previous step, the next step can be a solve-only step. Otherwise, the next step will perform a matrix factorization. The default value is 32.0.

`newtonStats` Prints information on Newton iterations.

`newtonSteps1` For the modified Newton method, any of the Newton steps 1 through `newtonSteps1` must improve the solution by the factor `newtonRate1` over the previous step. Otherwise, the next step will be a full Newton step. For Newton steps `newtonSteps1+1` onwards, the solution at each step must improve by the factor `newtonRate2`. Otherwise, the next step will be a full Newton step. The default is 12.

`newtonTries1` Number of first modified Newton step breakdown allowed before switching to full Newton. The default is 2.

### Time discretization

`milne`, `difference`

Controls whether the next time step is estimated using the Milne's device or the divided difference method. The default is `milne`.

`tr_bdf`, `euler` Specifies the type of time discretization scheme to use. The options are TR-BDF(2) or the backward Euler method. The default is `tr_bdf`.

### Parallel processing

Sentaurus Process provides parallel processing for MC implantation, interpolation, 3D analytic implantation, the KMC charge model, the matrix assembly, the box method, and the linear solvers by generating multiple threads to accelerate simulations on multicore shared-memory computers. By default, only one processor (thread) is used.

**NOTE:** The number of threads must not exceed the number of actual CPUs (cores) of the computer.

**NOTE:** Observe the following general recommendations to obtain the best results from a parallel run: Speedup is only obtained for sufficiently large problems. As a general rule, the mesh should have at least 10000 nodes. Three-dimensional problems are good candidates for parallelization.

**NOTE:** You should run a parallel job on an unloaded computer. As soon as multiple jobs compete for processors, performance decreases significantly (a parallel job could run even longer than a serial one).

**NOTE:** The parallel execution of the matrix assembly on the linear solvers PARDISO and ILS produces different rounding errors. Therefore, the number of Newton iterations in particular may change.

**NOTE:** Parallel performance scalability of the different modules (such as implant, assembly, and linear solver) can vary dramatically.

**NOTE:** It is not necessary to set the OpenMP environment variable `OMP_NUM_THREADS`. You need only specify the number of threads required in the `math` command.

To use more than one thread, specify the following parameters of the `math` command in the command file:

`NumberOfElementsPerDomain`

Modifies the number of elements that should go to each domain (see [Partitioning and Parallel Matrix Assembly on page 840](#)).

`maxNumberOfDomains`

Modifies the maximum number of domains each level of partition can have (see [Partitioning and Parallel Matrix Assembly on page 840](#)).

## A: Sentaurus Process Commands

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`numThreads` Specifies the number of parallel threads for Sentaurus Process. Applies to Sentaurus MC implantation, interpolation, 3D analytic implantation, Sentaurus Process KMC, matrix assembly, the box method, and the linear solvers PARDISO and ILS.

To run MGOALS, Sentaurus Process KMC, matrix assembly, the box method, or the linear solvers with a different number of threads, specify the following parameters:

- `numThreadsAssembly`
- `numThreadsBoxMethod`
- `numThreadsDeatomize`
- `numThreadsILS`
- `numThreadsImp3d`
- `numThreadsInterp`
- `numThreadsKMC`
- `numThreadsMC`
- `numThreadsMGoals`
- `numThreadsPardiso`
- `numThreadsSano`
- `numThreadsTopo`

Separately, these parameters have priority over the generic parameter `numThreads`.

`numThreadsAssembly`

Number of threads used for the matrix assembly. Parallel assembly of the matrix applies only to inert anneals.

`numThreadsBoxMethod`

Number of threads used for the box method.

`numThreadsDeatomize`

Number of threads used when deatomizing KMC particles into continuum finite-element fields.

`numThreadsILS`

Number of threads for the ILS solver.

Some parallel implementations of a default diffusion iterative solver `gmres` can be activated by the command:

```
pdbSet Math diffuse <2D|3D> ILS.hpc.mode <0 | 1 | 2 | 3>
```

For the high-performance computing mode, the options are 0 (default), and the algorithmic parallel enhancements are activated by 1 for Version E-2010.12, by 2 for Versions F-2011.09 and G-2012.06, and by 3 for Version H-2013.03.

numThreadsImp3d

Number of threads used for 3D analytic implantation.

numThreadsInterp

Number of threads used for interpolation.

numThreadsKMC

Number of threads used for Sentaurus Process KMC diffusion.

**NOTE:** Parallelism for Sentaurus Process KMC only works for 1D or 2D Sentaurus Process simulations.

numThreadsMC

Number of threads used for Sentaurus MC implantation. This value is over written by numThreadsKMC when this last one is present.

numThreadsMGoals

Number of threads used for MGOALS level-set operations.

numThreadsPardiso

Number of threads when running PARDISO.

numThreadsSano

Number of threads used for the Sano method for KMC particle to finite element field smoothing computation.

numThreadsTopo

Number of threads used when calling Sentaurus Topography to perform etching and deposition steps.

parallel.license

If you run a simulation in parallel mode but the number of parallel licenses is insufficient, Sentaurus Process proceeds in serial mode (default behavior or if `parallel.license=go.serial` is specified), or waits for parallel licenses (`parallel.license=go.wait`), or aborts (`parallel.license=go.abort`).

threadStackSize

Stack size for each thread. Default stack size is  $2^{18} = 262144$  bytes (see [Partitioning and Parallel Matrix Assembly on page 840](#)).

## A: Sentaurus Process Commands

math

### Coordinate system input/output selection

When saving structures and meshes, a coordinate transformation is applied. By default, the transformation is to the TDR coordinate system (which is the same as DF-ISE and *visualization* coordinate systems discussed in more detail in [Understanding Coordinate Systems on page 64](#)).

**NOTE:** This coordinate system is different for 1D, 2D, and 3D structures. Options in this section can be used to change how files are written and read. Files written in alternative coordinate systems will be rotated when read by other tools. Nevertheless, it can be useful to write files in the Sentaurus Process native coordinate system to assist in writing command files. Even though the structure will appear rotated when it is displayed in Tecplot SV, the coordinates will match those in the Sentaurus Process command file, which can be helpful when setting up refinement boxes, masks, and so on.

`coord.dfise` Reads or writes files in DF-ISE coordinate system. This should be used only to revert coordinate systems. If the dimension of the structure changes, `math coord.dfise` must be recalled.

`coord.transform`, `coord.translate`, `coord.read`, `coord.write`

Both `coord.transform` and `coord.translate` allow a general coordinate transformation through specification of a rotation matrix defined as follows:

```
coord.transform= { a11 a12 a13 a21 a22 a23 a31 a32 a33 }
```

where  $a_{ij}$  ( $i$ =row,  $j$ =column) are the members of the rotation matrix, and:

```
coord.translate= { x y z }
```

specifies a translation vector (in the internal coordinate system).

Both `coord.transform` and `coord.translate` must be used with either `coord.write` or `coord.read` to indicate the transformation is specifying the transformation for writing or reading, respectively. When specifying `coord.write`, the inverse of the specified transformation is applied when reading. When `coord.read` is specified, the inverse transformation is applied when writing.

`coord.ucs`, `coord.xyz`

Reads and writes files in the unified coordinate system (UCS).

`coord.yxz` Same as `coord.dfise` in 2D.

`coord.-zyx` Same as `coord.dfise` in 3D.



### Generic options

`limit.precision`

For Intel x86 architecture, this option limits floating-point operations to 64 bits instead of the default 80 bits. This setting is applied by default to improve reproducibility among different platforms.

`use.interpolated.geom.coeff`

Switches on the method to be used for interpolating geometric coefficients for TRBDF, which reduces the number of box method calls by one third.

`voronoitriangle`

Switches on the internal box method calculation.

### Examples:

```
math flow dim=2 ils
```

The ILS solver is used for the mechanics in the 2D case.

```
math diffuse dim=2 pardiso numThreadsPardiso=2 scale  
pdbSetDouble Pardiso.Ordering 2
```

The PARDISO solver with two threads is used for the PDE equation system in the 2D case and specifies the nested dissection ordering for PARDISO.

**NOTE:** To run in parallel mode, the linear solvers PARDISO and ILS must be used with the nested dissection ordering ND for both the 2D and 3D cases. For example, to specify the ND ordering, use:

```
pdbSetDouble Pardiso.Ordering 2  
pdbSet Math diffuse 2D ILS.symmOrdering nd
```

```
math dim=2 ils newtonStats=1  
math dim=2 ils newtonStats=1 euler fullNewton
```

The solver ILS is selected for all equations in 2D. Newton statistics is printed at the end of each `diffuse` command:

- In the first case, the modified Newton method and TR-BFDF(2) methods are used.
- In the second case, Euler and full Newton methods are specified.

---

## mgoals

**Function:** Modify default parameters for geometric and meshing operations for the MGOALS library.

**Syntax:** `mgoals`

```
[resolution=<n>] [full.resolution=<n>]
[dx=<n> dy=<n> dz=<n>]
[reinitfrequency=<n>] [reinititerations=<n>]
[accuracy=<n>][<m>|<cm>|<um>|<nm>]
[maxangle=<n>][<degree>]
[nlayers=<i>]
[minedge=<n>][<m>|<cm>|<um>|<nm>]
[min.normal.size=<n>][<m>|<cm>|<um>|<nm>]
[min.levelset.size=<n>][<m>|<cm>|<um>|<nm>]
[normal.growth.ratio=<n>][<m>|<cm>|<um>|<nm>]
[max.lateral.size=<n>][<m>|<cm>|<um>|<nm>]
[max.neighbor.ratio=<n>]
[max.box.angle=<n>][<degree>]
[remove.floating.regions]
[aniso.etching.fragment.tol=<n>]
[aniso.etching.protect.materials]
[repair.2d] [repair.angle=<n>]
[print.params]
[min.gas.thickness=<n>][<m>|<cm>|<um>|<nm>]
[sliver.swap] [sliver.split] [sliver.smooth]
[force.analytic | force.full.levelset | force.full.levelset.etch |
  force.full.levelset.depo]
[fourier.local.diffusivity]
[fill.buried]
[analytic.thickness]
[offsetting.maxlevel=<i>]
[use.brep.2d]
[G-2012.06-SP2 | G-2012.06 | F-2011.09-SP1 | F-2011.09 | E-2010.12 |
  D-2010.03]
```

**Description:** Allows you to define parameters for MGOALS level-set and meshing operations.

**Options:**

`accuracy` Specifies the error that can be tolerated in transferring the new interface definition from the level-set grid to the simulation grid. There is a compromise between smoothness and the number of grid points. Smoother grids need more points on curved regions. The default value and unit is  $1.0 \times 10^{-5} \mu\text{m}$ .

`analytic.thickness`

For etching and deposition steps of layers of thickness of 1 nm or less, an analytic method is used to perform the etch because thin etches using the level-set method can be prohibitively CPU and memory intensive. For very large or very small structures, a 1-nm cutoff may not be appropriate, so this parameter can be used to modify the thickness where the analytic method is used.

`aniso.etching.fragment.tol`

Removes fragments remaining from 3D anisotropic etching. The tolerance measures the ratio of the volume and the surface of a region. The default value is 1.0e-6.

`aniso.etching.protect.materials`

When set to true, the 3D anisotropic algorithm attempts to protect areas shadowed by buried materials. The default is true.

`dx, dy, dz`

Explicitly set the level-set grid spacing in each direction. If set, these parameters override the automatic setting of `dx`, `dy`, and `dz`, which uses resolution.

`fill.buried`

For deposition, material is deposited on the surface exposed to the upper gas region. With `fill.buried` specified, deposition also occurs inside the buried gas bubbles that may exist.

`force.analytic`

When performing an isotropic etching or deposition, forces the use of an analytic algorithm instead of a level-set algorithm even when a boundary collision will occur. For very large structures or very small etch or deposition thicknesses, the level-set algorithm may consume too much memory and time.

`force.full.levelset, force.full.levelset.etch, force.full.levelset.depo`

Defines the general level-set time-stepping algorithm as the default algorithm for both etching and deposition, or etching only, or deposition only, respectively.

`fourier.local.diffusivity`

Controls the artificial diffusion parameter. If the parameter is specified, the solution is more accurate but the corners are less sharp. For complex Fourier rates, switch off `fourier.local.diffusivity` to enhance stability.

## A: Sentaurus Process Commands

### mgoals

`full.resolution`

Usually, the full-time stepping level-set method is used in situations where more intricate boundaries will be generated. The full-time stepping level-set method is needed for Fourier, crystallographic, and multimaterial etching types, and for etching with shadowing on. This parameter allows a separate resolution setting for these cases. The default value is 0.025 compared to 0.1 for the `resolution` parameter.

`max.box.angle` Specifies maximum angle in the interior of any region where MGOALS can put locally an exact Cartesian grid. The default value and unit is  $120^\circ$ .

`max.lateral.size`

Specifies maximum lateral (parallel to the interface) spacing between elements. This is, however, also used to define an upper bound on the normal size. The default value and unit is  $10\ \mu\text{m}$ .

`max.neighbor.ratio`

Binary-tree smoothing is performed after refinements have been added to the binary tree. This prevents sudden changes in element size that can be especially detrimental to mechanics results. The ratio of neighboring collinear edges in the binary tree can be adjusted with this parameter. The default value is 3.0.

`maxangle` Maximum-allowed angle in the MGOALS-created grid. MGOALS tries to stay within this limit but may exceed it if meshing becomes very tough. The default value and unit is  $165^\circ$ .

`min.gas.thickness`

Minimum thickness of the gas layer at the top of the simulation structure. The default value and unit is  $0.1\ \mu\text{m}$ .

`min.levelset.size`

Specifies minimum size for the level-set mesh. Usually, the level-set mesh size scales with the operation according to the resolution factor and the etch or deposition thickness. However, for thin etch or deposition steps, this may lead to a small level-set mesh causing excessive memory use and simulation time. Often, it is not necessary (for thin layers, a mesh size between  $\text{thickness}/2.0$  and  $\text{thickness}/3.0$  is usually sufficient). This parameter limits the mesh size and, therefore, limits computational expense. The default value and unit is  $1.0 \times 10^{-4}\ \mu\text{m}$ .

`min.normal.size`

Specifies smallest normal (to the interface) mesh element size on either side of an interface. The default value and unit is  $8.0 \times 10^{-4}\ \mu\text{m}$ .

|                                      |                                                                                                                                                                                                                                                                                                                                                                                   |
|--------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>minedge</code>                 | Specifies minimum edge length allowed in MGOALS. The default value and unit is $2.0 \times 10^{-6} \mu\text{m}$ .                                                                                                                                                                                                                                                                 |
| <code>nlayers</code>                 | When using the MGOALS mesher, this parameter defines the number of layers of the original grid next to the interface that can be modified during an etching or a deposition. The default value is 2.                                                                                                                                                                              |
| <code>normal.growth.ratio</code>     | Used to increase the normal (to the interface) size of the element, moving away from the interface. For example, if <code>normal.growth.ratio=1.3</code> , this means that, one layer away from the interface, the maximum normal size of an element can be $1.3 * \text{min.normal.size}$ . The default value is 2.0.                                                            |
| <code>offsetting.maxlevel</code>     | Specifies the number of offsetting layers at an interface when Sentaurus Mesh offsetting is used at an interface.                                                                                                                                                                                                                                                                 |
| <code>print.params</code>            | Prints MGOALS current meshing constants.                                                                                                                                                                                                                                                                                                                                          |
| <code>reinitfrequency</code>         | Level-set reinitialization is performed every <code>reinitfrequency</code> time step in level-set operations. A reinitialization algorithm is run to condition the level-set distance function to reduce the effect of 'contour bunching,' which can cause etching distances to be less than expected. The default value is 0, which means that no reinitialization is performed. |
| <code>reinititerations</code>        | The internal reinitialization algorithm reinitializes first the 0 level set and works outwards from the front with higher numbers of iterations. The default value is 1. This option only comes into operation if <code>reinitfrequency</code> is nonzero.                                                                                                                        |
| <code>remove.floating.regions</code> | Determines whether MGOALS automatically removes regions that are not attached to the bottom of the structure. The default is true.                                                                                                                                                                                                                                                |
| <code>repair.2d</code>               | Controls the default behavior of the boundary repair operation in two dimensions. By default, boundary repairs are disabled in two dimensions.                                                                                                                                                                                                                                    |
| <code>repair.angle</code>            | Controls the dihedral angle at which repairs are performed. The algorithm attempts to repair any surface section with a dihedral angle less than <code>repair.angle</code> . The default is $1^\circ$ .                                                                                                                                                                           |

## A: Sentaurus Process Commands

### mgoals

|                            |                                                                                                                                                                                             |
|----------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>resolution</code>    | Specifies the minimum number of level-set cells across the thickness of a deposited or etched layer. For example, <code>resolution=0.2</code> implies five cells. The default value is 0.1. |
| <code>sliver.smooth</code> | Switches on element-smoothing in 3D to eliminate slivers. This operation may move the nodes on the boundary.                                                                                |
| <code>sliver.split</code>  | Switches on element-splitting in 3D to eliminate slivers. This operation will increase the number of non-Delaunay elements in the structure. This may adversely affect the simulation.      |
| <code>sliver.swap</code>   | Switches on element-swapping in 3D to eliminate slivers.                                                                                                                                    |
| <code>use.brep.2d</code>   | Switches on the <i>brep structure mode</i> for two dimensions when handling structural changes such as 2D etching and 2D deposition. The default is false.                                  |

The boundary representation (brep) structure mode in two dimensions handles structural changes similarly to how structural changes are handled by default in 3D. A brep of the structure is used and modified rather than the volume mesh.

Using brep reduces run-times by avoiding unnecessary meshing operations and increases stability and accuracy by eliminating both boundary simplification and variable interpolation associated with remeshing between structural modification operations.

G-2012.06-SP2, G-2012.06, F-2011.09-SP1, F-2011.09, E-2010.12, D-2010.03

Sets the backward compatibility of parameters and algorithms to the specified release. Support is available for Versions G-2012.06-SP2, G-2012.06, F-2011.09-SP1, F-2011.09, E-2010.12, and D-2010.03 (partial support).

#### Examples:

```
mgoals max.lateral.size=1.0 min.normal.size=2e-3
```

Sets parameters for meshing. The smallest normal mesh element size is 2 nm, and the maximum lateral spacing between elements is 1.0  $\mu\text{m}$ .

```
mgoals dx=0.01 dy=0.02 reinitfrequency=5 reinititerations=4
```

Explicitly sets the vertical level-set mesh spacing to 0.01  $\mu\text{m}$  and the horizontal level-set mesh spacing to 0.02  $\mu\text{m}$ . Reinitialization of the level-set distance function is performed every five time steps, and every reinitialization is performed to an internal iteration accuracy of four iterations.

## paste

**Function:** Assembles 3D simulations by incorporating fragments from a TDR file.

**Syntax:**

```
paste
  tdr = <filename>
  direction = (left | right | front | back)
  [Adaptive]
```

**Description:** Reads a TDR file containing a 3D valid geometry and appends it (pastes it) to the current 3D structure. The new structure is displaced automatically by the right amount to correctly fit at the specified side, but the structures are not stretched automatically. If the dimensions of nongas materials at the pasting sides are not the same, the command fails and quits. The `paste` command allows assembly of complex 3D structures by reading the different pieces from TDR files and putting all of them together.

**Options:**

`Adaptive` Specifies whether to use adaptive meshing.

`direction` Selects the side where to paste the incoming simulation. The new structure can be pasted on the `left`, `right`, `front`, or `back` side.

`tdr` Name of the file to be imported and pasted into the current simulation.

**Examples:** `paste tdr = "filename" direction = "right"`

**See:** [Inserting Polygons in Two Dimensions on page 762](#), [struct on page 1086](#)

---

## pdbDelayDouble

**Function:** Retrieves an expression for a double parameter that will be evaluated at each time step during diffusion.

**Syntax:** `pdbDelayDouble <c> <c> ...`

**Description:** This function is typically called from Alagator to retrieve a parameter expression. Since among other things, the temperature can change during a diffusion step, the evaluation of Arrhenius expressions must be delayed until the temperature is known. This command provides that functionality.

**Examples:** `pdbDelayDouble Si B D0`  
Returns an expression for D0 (not a value).



## **pdbdiff**

**Function:** Compare current structure with one from a TDR file.

**Syntax:** `pdbdiff <tdr file 1> <tdr file 2>`

**Description:** Compare parameters stored in two different TDR files. Report differences in which parameters are stored and any differences in value.

**Options:**

`<tdr file 1>, <tdr file 2>`

Give the full path or prefix for each TDR file. The prefix is the file name without `_fps.tdr`.

**Examples:** `pdbdiff n1 n2`  
Compares the pdb differences between `n1_fps.tdr` and `n2_fps.tdr`.

---

## pdbDopantLike

- Function:** Helps to create new dopants.
- Syntax:** `pdbDopantLike <c> <c>`
- Description:** Creates new dopants in materials. It takes two arguments. The first one must be the name of the material and the second must be the name of the new dopant. If dopants are not present in a material, an error message is displayed.
- Examples:** `pdbDopantLike Silicon MyDopant`  
Creates a new dopant called `MyDopant` in silicon. You can select dopant-related diffusion switches (such as `DiffModel` and `ActiveModel`) for `MyDopant`.

## **pdbExprDouble**

- Function:** Retrieves an expression for a double parameter without evaluating.
- Syntax:** `pdbExprDouble <c> <c> ...`
- Description:** This function is typically called from Alagator to retrieve a parameter expression. If the parameter depends on solution names, data fields, and so on, the evaluation of the expression must be delayed until the solution time. This command provides that functionality.
- Examples:** `pdbExprDouble Si Mechanics BulkModulus`  
Returns an expression for `Bulk` (not a value).

---

## pdbGet and Related Functions

**Function:** All of these functions retrieve database parameters:

- `pdbGet`
- `pdbGetArray`
- `pdbGetBoolean`
- `pdbGetDouble`
- `pdbDelayDouble`
- `pdbGetDoubleArray`
- `pdbGetElement`
- `pdbGetFunction`
- `pdbGetString`
- `pdbGetSwitch`
- `pdbGetSwitchString`

Only `pdbGet` has syntax checking.

**Syntax:** `pdbGet <c> <c> ...`

**Description:** These functions are used to obtain parameters that reside in the property database, which is hierarchical and is indicated by passing a series of strings to the command. In the command file, the command `pdbGet` should replace all other `pdbGet*` commands because the type of the parameter and the syntax are checked automatically. If a parameter does not exist in the directory, the tool exits and prints a list of parameters that can be found. The normal aliasing is applied to each string before the parameter is retrieved from the database.

The following commands all return 0 if the parameter is not found:

- `pdbGetArray`
- `pdbGetBoolean`
- `pdbGetDouble`
- `pdbDelayDouble`
- `pdbGetDoubleArray`
- `pdbGetElement`
- `pdbGetFunction`
- `pdbGetString`
- `pdbGetSwitch`

**Description:** The command `pdbGetSwitchString` returns nothing if the parameter is not found. These commands have a slight performance advantage and will not exit if a parameter has not been defined, so they are preferred for Alagator scripting.

The command `pdbGetSwitch` returns an integer value of a switch, and the command `pdbGetSwitchString` returns the string value. For example, if a switch has the choices a, b, or c, and a is chosen, `pdbGetSwitch` returns 0, and `pdbGetSwitchString` returns a.

**Examples:** `pdbGet Mechanics StressHistory`  
Retrieves the current value of `StressHistory`. The parameter `StressHistory` is known, but if it is spelled improperly, Setaurus Process exits and prints a list of known parameters at the `Mechanics` level.

`pdbGetBoolean Mechanics StressHistory`  
Retrieves `StressHistory` without syntax-checking and returns 0 if not found. It exits if there is a type mismatch between `StressHistory` and `Boolean` (which is not the case in this example).

---

## pdbsAvailable

- Function:** Checks if the given `pdb` command is available.
- Syntax:** `pdbsAvailable <c> ... <c>`
- Description:** Checks the availability of the given `pdb` command. If the command exists, it returns 1; otherwise, it returns 0.
- Examples:** `pdbsAvailable Silicon MyVacancy`  
Returns 1 if the command "Silicon MyVacancy" is available.

## **pdbSet and Related Functions**

**Function:** All of the following functions set database parameters:

- `pdbSet`
- `pdbSetArray`
- `pdbSetBoolean`
- `pdbSetDouble`
- `pdbSetDoubleArray`
- `pdbSetElement`
- `pdbSetFunction`
- `pdbSetString`
- `pdbSetSwitch`

Only `pdbSet` has syntax checking.

**Syntax:** `pdbSet <c> <c> ...<value>`

**Description:** These functions are used to set parameters that reside in the property database, which is hierarchical and is indicated by passing a series of strings to the command. In the command file, the command `pdbSet` should replace all other `pdbSet*` commands because the type of the parameter is checked automatically and syntax is checked as well. If a parameter does not exist in the directory, the tool exits and prints a list of parameters that can be found. The normal aliasing is applied to each string before the parameter is retrieved from the database for all these commands.

The following commands all create a new parameter if one does not already exist:

- `pdbSetArray`
- `pdbSetBoolean`
- `pdbSetDouble`
- `pdbSetDoubleArray`
- `pdbSetFunction`
- `pdbSetString`

These commands have a slight performance advantage and will not exit if a parameter has not been defined, so they are preferred for Alagator scripting. The units of the property database are cgs [s, cm, g, dyn/cm<sup>2</sup>, poise, cm<sup>2</sup>/s], except for activation energies [eV].

## A: Sentaurus Process Commands

### pdbSet and Related Functions

**Description:** The command `pdbSet` checks the type of variable trying to be set and checks that type against the `<value>` passed. The command `pdbSetDouble` takes a double for a value and, similarly, `pdbSetString` takes a string and `pdbSetBoolean` takes a Boolean (either 1 or 0). The command `pdbSetSwitch` will set a value for existing switches. If a switch is not found, a new one will be created.

The command `pdbSetArray` defines the array for string data.

The data type `DoubleArray` has a special format and can be modified in several different ways depending on the changes required.

This type is usually used for charge state-dependent parameters, in which case, the array index refers to the charge state. For example, the database entry for `Silicon Interstitial ChargeStates` is a list of length 10; the first entry is -2, the second entry is 0 (which means `ChargeStates[-2]=0`), the third entry is -1, and the fourth is `{[Arrhenius 5.68 0.48]}`, which means `ChargeStates[-1]=[Arrhenius 5.68 0.48]` and so on. There are also arrays that are intended for double sums. In this case, the array index entries have a comma-separated field. For example, with `Silicon Boron Interstitial kfKickOut`, the first entry (which corresponds to an array index) is `{-2,-2}`. The following examples show how to set and change these types.

The command `pdbSetElement` modifies the value of one element in an array.

**NOTE:** The arguments for `pdbSetDouble`, `pdbSetDoubleArray`, and `pdbSetBoolean` must evaluate to a numeric data. Calls to procedures or to the `pdbDelayDouble` command in the arguments may cause errors if they are not constructed correctly.



**Examples:**

```
pdbSet Si B Dstar 1e-7;
# Set the Dstar parameter for Boron in Silicon--quit with list if not found.
# Next line sets index 0 of ChargeStates to 0.1

pdbSet Si Int ChargeStates 0 0.1
#Next line sets all members of ChargeStates: index 0 = 0.1, and so on

pdbSet Si Int ChargeStates {0 0.1 1 0.2 3 0.3};
# Next sets one index of a double array meant for double charge state indexing

pdbSet Si B Int KfKickOut -2,1 {[expr 4.0*3.14159*([Arrhenius 0.1 0.2]+
[Arrhenius 0.3 0.4])]}

# Now for the non-syntax-checked versions:
pdbSetDouble Si B Dstar 1e-7
# Set Dstar , create Dstar if it does not already exist
# (in this example, Dstar would already exist)
pdbSetSwitch Si Dopant DiffModel Pair
# Set the DiffModel in Silicon to 'Pair'

pdbSetDoubleArray Si MyVar MyArray {0 0.1 1 0.2 3 0.3};
# Create a new DoubleArray,index 0 = 0.1, and so on

pdbSetArray MyArray { 0 abc 1 def 2 ghi }
pdbGetArray MyArray      ;# print "0 abc 1 def 2 ghi"
pdbGetElement MyArray 1  ;# print "def"
pdbSetElement MyArray 1 jkl ;# modifies A[1] data from "def" to "jkl"
```

---

## pdbUnSet-related Functions

- Function:** All of the following functions unset database parameters:
- `pdbUnSetBoolean`
  - `pdbUnSetDouble`
  - `pdbUnSetDoubleArray`
  - `pdbUnSetString`
- Syntax:**
- ```
pdbUnSetBoolean <c> <c> ...  
pdbUnSetDouble <c> <c> ...  
pdbUnSetDoubleArray <c> <c> ...  
pdbUnSetString <c> <c> ...
```
- Description:** Used to temporarily remove parameters from the parameter database during the simulation.
- Examples:**
- ```
pdbUnSetString Silicon Vac EquationProc  
  
pdbUnSetDouble Silicon Vac Cstar
```

## PDE2KMC

**Function:** Translates and transfers Sentaurus Process fields to Sentaurus Process KMC.

**Syntax:** PDE2KMC

**Description:** Called automatically when a switch from the PDE solver to the Sentaurus Process KMC solver is detected. It translates the continuum concentrations into suitable particle distributions to be used by Sentaurus Process KMC.

The atomization is performed using the `select` command with the appropriate KMC species names.

The translation between PDE fields and KMC species is performed with a mapping that translates the field names into their atomistic counterparts. This translation is made as accurately as possible, but sometimes a perfect one-to-one mapping is not possible. In that case, meaningful approximations are used. For example, `ICluster` is translated into `I4`. A complete list of these translations is available in the file `KMC.tcl`.

**Examples:** PDE2KMC

**See:** [SetAtomistic on page 1056](#)

---

## photo

|                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
|------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>       | Creates a photoresist layer.                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| <b>Syntax:</b>         | <pre>photo   [thickness=&lt;n&gt;][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]   [mask=&lt;c&gt;] [Adaptive] [sde] [repair]</pre>                                                                                                                                                                                                                                                                                                                                                     |
| <b>Description:</b>    | Creates photoresist layer of the specified thickness outside the mask. The mask must have been defined using a mask command. If the photoresist should be deposited inside of the mask, the parameter <code>negative</code> must be defined in the mask command.                                                                                                                                                                                                                      |
| <b>Options:</b>        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| <code>Adaptive</code>  | Specifies with or without adaptive meshing for the <code>photo</code> command. Parameters for adaptive meshing are described in <a href="#">Adaptive Refinement on page 679</a> . The default is the return value of <code>pdbGet Grid Adaptive</code> .                                                                                                                                                                                                                              |
| <code>mask</code>      | Specifies the name of the mask to be used to create the photoresist. The photoresist is deposited in the openings of the mask.                                                                                                                                                                                                                                                                                                                                                        |
| <code>repair</code>    | In MGOALS3D mode, small regions are removed automatically by default. Sometimes, this can cause small gas bubbles in the structure or other problems. Use <code>!repair</code> to switch off small region removal.                                                                                                                                                                                                                                                                    |
| <code>sde</code>       | String used to specify parameters and select algorithms for 3D Sentaurus Structure Editor. By default, the parameters <code>mask</code> and <code>thickness</code> are translated into appropriate Sentaurus Structure Editor commands. If an algorithm is specified in the <code>sde</code> parameter, it overwrites the algorithm used by default for isotropic or anisotropic etching. For example:<br><pre>photo thickness=2&lt;um&gt; mask=mask1 sde= {"algorithm" "lopx"}</pre> |
| <code>thickness</code> | Specifies the thickness of the photoresist. The default value is 2.0 $\mu\text{m}$ .                                                                                                                                                                                                                                                                                                                                                                                                  |
| <b>Examples:</b>       | <code>photo thickness=2&lt;um&gt; mask=mask1</code>                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| <b>See:</b>            | <a href="#">mask on page 977</a>                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

## plot.1d

**Function:** Plots a 1D cross section.

**Syntax:**

```
plot.1d
    [name=<c>] [fix.ratio]
    [x=<n>][<m>|<cm>|<um>|<nm>]
    [y=<n>][<m>|<cm>|<um>|<nm>]
    [z=<n>][<m>|<cm>|<um>|<nm>]
    [boundary] [clear]
    [max= <numeric list>] [min= <numeric list>]
    [color=<c>] [symb=<c>] [label=<c>] [title=<c>]
    [close] [rescale]
```

**Description:** Plots cross sections vertically or horizontally through the device with options to provide for initialization of the graphics device and plotting of axes. This command can optionally draw vertical lines whenever a material boundary is crossed.

**Options:**

|           |                                                                                                                                                                                                                                                              |
|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| boundary  | Specifies that any material boundaries that are crossed should be drawn in as vertical lines on the plot. The default is false.                                                                                                                              |
| clear     | Specifies whether the graphics screen should be cleared before the graph is drawn. If true (the default), the screen is cleared.                                                                                                                             |
| close     | Closes the plot window.                                                                                                                                                                                                                                      |
| color     | Specifies the line color for the plot. It can be any color supported by the X11 hardware and named in the color database.                                                                                                                                    |
| fix.ratio | Specifies the x-, y-axis ratio to be fixed. The default is false.                                                                                                                                                                                            |
| label     | Specifies the name of the line in the legend box of the plot window. The default is the name of the current dataset.                                                                                                                                         |
| max       | Takes a list of numeric values that will be the ends of the x- and y-axis. The first argument is the x-value and the second is the y-value. A single value is always interpreted as the x-value. The default is the maximum extent of the current structure. |
| min       | Takes a list of numeric values that will be the ends of the x- and y-axis. The first argument is the x-value and the second is the y-value. A single value is always interpreted as the x-value. The default is the minimum extent of the current structure. |
| name      | Specifies the name of a data field. This allows plots without using the select command. The default is Z_Plot_Var.                                                                                                                                           |

## A: Sentaurus Process Commands

plot.1d

|         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|---------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| rescale | Rescales the plot to fit the whole simulation domain.                                                                                                                                                                                                                                                                                                                                                                                                                                |
| symb    | Specifies a symbol type to be drawn on the cross-sectional line. Each point is drawn with the specified symbol. It defaults to no symbol. Whatever character is entered is placed at each data point on the plot.                                                                                                                                                                                                                                                                    |
| title   | Specifies the title of the plot window.                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| x, y, z | Specify the constant values of a line along which sectioning is performed. In 1D, these parameters are not necessary. In 2D, only one of x or y can be specified for a given device. Specifying x produces a horizontal slice through the device and y specifies a vertical slice. An easy way to remember is that the cross section is taken at the constant value specified. For a 3D simulation, two of these three values must be specified. The default unit is $\mu\text{m}$ . |

### Examples:

```
plot.1d x=1.0 symb=1 clear
```

Clears the screen, draws a set of axes, and draws the data along a horizontal cross section at  $x=1.0 \mu\text{m}$ . Each point is drawn with symbol 1.

```
plot.1d x=2.0 clear lab=Lateral
```

Draws a horizontal cross section at  $x = 2.0 \mu\text{m}$  on the previous set of axis. The line is labeled `Lateral` in the legend.

### See:

[select on page 1053](#), [slice on page 1073](#)

## plot.2d

**Function:** Plots a 2D xy graphic.

**Syntax:**

```
plot.2d
  [(x=<n>) | (y=<n>) | (z=<n>)] [<m> | <cm> | <um> | <nm>]
  [fix.ratio]
  [max= <numeric list>] [min= <numeric list>]
  [clear] [fill] [gas]
  [edges] [faces] [nodes]
  [boundary] [label.bound] [col.bound=<c>]
  [grid] [col.grid=<c>] [title=<c>]
  [kmc]
  [vector=<c>]
  [vlength=<n>] [<m> | <cm> | <um> | <nm>]
  [vmax=<n>] [<m> | <cm> | <um> | <nm>]
  [close] [rescale]
```

**Description:** Plots a 2D xy graphic. Usually, this command is used to look at material boundaries and grids; however, it also can be used to plot a flow field. This command can be executed immediately before a `contour` command to allow isoconcentration lines to be plotted in context with the structure.

To obtain standard color and other settings for the `plot.2d` window, use the following command from the UNIX command line:

```
unix:> xrdb -merge ${STROOT}/tcad/${STRELEASE}/lib/score/XFloops
```

**Options:**

|                        |                                                                                                                               |
|------------------------|-------------------------------------------------------------------------------------------------------------------------------|
| <code>boundary</code>  | Specifies that the device outline and material interfaces should be drawn. The default is false.                              |
| <code>clear</code>     | Specifies that the graphics screen should be cleared before the graph is drawn. If true (the default), the screen is cleared. |
| <code>close</code>     | Closes the plot window.                                                                                                       |
| <code>col.bound</code> | Specifies the color with which to draw the boundary. Any valid X11 color can be specified.                                    |
| <code>col.grid</code>  | Specifies the color with which to draw the grid. Any valid X11 color can be specified.                                        |
| <code>edges</code>     | Prints the edge indices on the plot. The default is false.                                                                    |
| <code>faces</code>     | Prints the face indices on the plot. The default is false.                                                                    |

## A: Sentaurus Process Commands

### plot.2d

|                          |                                                                                                                                                                                                                                                                                                                |
|--------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>fill</code>        | Specifies that the device should be drawn with the proper aspect ratio. If <code>fill</code> is false (the default), the device is drawn with the proper aspect ratio. When <code>true</code> , the device is expanded to fill the screen.                                                                     |
| <code>fix.ratio</code>   | By default, the x to y ratio is now fixed. This can be switched off with the <code>!fix.ratio</code> parameter.                                                                                                                                                                                                |
| <code>gas</code>         | Specifies that the grid in the gas should also be plotted. The default is false (so no gas grid is shown).                                                                                                                                                                                                     |
| <code>grid</code>        | Specifies that the numeric grid on which the problem was solved should be drawn. The default is false.                                                                                                                                                                                                         |
| <code>kmc</code>         | Plots particles in an atomistic KMC simulations as dots.                                                                                                                                                                                                                                                       |
| <code>label.bound</code> | Name of the material in the lower-left corner of the material region.                                                                                                                                                                                                                                          |
| <code>max</code>         | Takes a list of numeric values that will be the ends of the x- and y-axis, respectively. The first argument is the x-value and the second is the y-value. A single value is always interpreted as the x-value. The default is the maximum extent of the current structure. The default unit is $\mu\text{m}$ . |
| <code>min</code>         | Takes a list of numeric values that will be the ends of the x- and y-axis, respectively. The first argument is the x-value and the second is the y-value. A single value is always interpreted as the x-value. The default is the minimum extent of the current structure. The default unit is $\mu\text{m}$ . |
| <code>nodes</code>       | Prints the node indices on the plot. The default is false.                                                                                                                                                                                                                                                     |
| <code>rescale</code>     | Rescales the plot to fit the whole simulation domain.                                                                                                                                                                                                                                                          |
| <code>title</code>       | Specifies the plot window title.                                                                                                                                                                                                                                                                               |
| <code>vector</code>      | Takes a vector field name as an argument. This indicates arrows proportional to the size of the vector and in the direction of the vector at each node. Currently, this option does not work for 3D simulations.                                                                                               |
| <code>vlength</code>     | Scales the length of the vectors so that the maximum vector has length <code>vlength</code> . The default value and unit is $0.1 \mu\text{m}$ .                                                                                                                                                                |
| <code>vmax</code>        | Use this as the maximum velocity instead of searching for it. The default unit is $\mu\text{m}$ .                                                                                                                                                                                                              |
| <code>x, y, z</code>     | For a 2D simulation, these parameters are unnecessary. In three dimensions, one of these three must be specified to indicate the cutline through the structure. The default unit is $\mu\text{m}$ .                                                                                                            |



**Examples:** `plot.2d grid`  
Draws the triangular grid and axis. Each material is plotted in a different color.

`plot.2d bound min= {2 5}`  
Draws the material interfaces with the minimum x- and y-values of 2.0 and 5.0  $\mu\text{m}$ .

`plot.2d bound diamonds`  
Draws the material interfaces and places symbols at each coordinate in the mesh.

`plot.2d vector=Velocity vlength=0.1 !clear`  
Plots the `Velocity` vector field. The maximum arrow drawn will have a length of 0.1  $\mu\text{m}$ . The plot surface will not be cleared.

**See:** [bound on page 859](#), [Compatibility on page 860](#), [contour on page 865](#),  
[select on page 1053](#), [slice on page 1073](#)

---

## plot.tec

**Function:** Updates or initiates Sentaurus Process–Tecplot SV 1D, 2D, and 3D graphics.

**Syntax:** plot.tec

```

[autofit] [autorange]
[command=<c>]
[connect]
[contourvar=<c>]
[create.abs]
[data]
[data.bool] [data.int] [data.real] [data.symtensor] [data.vector]
[data.element] [data.face] [data.node]
[delete.frames] [detach] [display] [double_prec]
[framebg] [framebgname] [framecolor] [framecolorname] [frameheader]
[frameheight] [framewidth] [frameposx] [frameposy]
[frameshiftx] [frameshifty] [frametransparent]
[framezoom] [framezoomx] [framezoomy]
[Grid]
[host=<c>]
[interfaces]
[launch.timeout=<n>]
[legend]
[loadfile=<c>]
[macro=<c>]
[port=<n>]
[reset.display] [reset.xyaxes]
[scale = lin | log | ash]
[set.variables=<c>]
[start]
[suppressmat=<c>] [unsuppressmat=<c>]
[suppressvar=<c>] [unsuppressvar=<c>]
[terms]
[view.fit]
[x1auto] [x2auto] [x3auto] [x4auto] [x5auto] [xauto]
[y1auto] [y2auto] [y3auto] [y4auto] [y5auto] [yauto]
[x1log] [x2log] [x3log] [x4log] [x5log] [xlog]
[y1log] [y2log] [y3log] [y4log] [y5log] [ylog]
[x1max=<n>] [x1min=<n>] [x2max=<n>] [x2min=<n>] [x3max=<n>] [x3min=<n>]
[x4max=<n>] [x4min=<n>] [x5max=<n>] [x5min=<n>] [xmax=<n>] [xmin=<n>]
[xyautofit] [xyshow]
[y1axisvar=<n>] [y2axisvar=<n>] [y3axisvar=<n>] [y4axisvar=<n>]
[y5axisvar=<n>]
[y1max=<n>] [y1min=<n>] [y2max=<n>] [y2min=<n>] [y3max=<n>] [y3min=<n>]
[y4max=<n>] [y4min=<n>] [y5max=<n>] [y5min=<n>] [ymax=<n>] [ymin=<n>]

```

**Description:** Starts Tecplot SV, connects to a running Tecplot SV process, or sends commands or data to a running Tecplot SV process. After an instance of Tecplot SV with interprocess communication enabled (that is, the command-line option `tecplot_sv -s:ipc`) is running, subsequent Sentaurus Process runs will send graphics information to the same (already running) Tecplot SV to avoid a delay in Tecplot SV startup. The `plot.tec` command is called automatically by the `graphics` command.

**Options:**

- `autofit` Automatically fits the view for 2D and 3D modes after each update.
- `autorange` Automatically resets the minimum and maximum data range for contour plots after each update.
- `command` Specifies the command string used to launch the Tecplot SV process. The default is `"tecplot_sv -s:ipc"`.
- `connect` Permits connection to a running Tecplot SV process. The default is `true`.
- `contourvar` Selects the specified variable as the contour variable. By default, the first variable is selected as the contour variable.
- `create.abs` Automatically creates an `abs()` dataset for each vector variable.
- `data` Sends new values of all variables to Tecplot SV.
- `data.bool`, `data.int`, `data.real`, `data.syntensor`, `data.vector`  
Enables data of the corresponding value type. The default is `true` for `data.real`, `data.syntensor`, and `data.vector`.
- `data.element`, `data.face`, `data.node`  
Enables data of the corresponding location type. The default is `true` for all types.
- `delete.frames` Causes the old frame to be deleted when a new frame is created in Tecplot SV, due to switching from 1D to 2D, or from 2D to 3D mode. The default is `true`.
- `detach` Detaches display from a process.
- `display` Specifies the host name and sequence number for display.
- `double_prec` Uses double precision for all data transfers to Tecplot SV. This causes slower data transfer and higher memory consumption in Tecplot SV. This option must be specified before or together with the `start` option. The default is to use single precision.
- `framebg` Specifies the background color of the frame.

## A: Sentaurus Process Commands

plot.tec

|                                       |                                                                                                                                   |
|---------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|
| <code>framebgname</code>              | Specifies the background color name of the frame.                                                                                 |
| <code>framecolor</code>               | Specifies the header color of the frame.                                                                                          |
| <code>framecolorname</code>           | Specifies the header color name of the frame.                                                                                     |
| <code>frameheader</code>              | Enables display of frame header.                                                                                                  |
| <code>frameheight, framewidth</code>  | Specify the height and width of the frame.                                                                                        |
| <code>frameposx, frameposy</code>     | Specify the horizontal or vertical display position of the frame.                                                                 |
| <code>frameshiftx, frameshifty</code> | Specify the horizontal or vertical distance that the frame shifts.                                                                |
| <code>frametransparent</code>         | Sets transparency display mode of the frame.                                                                                      |
| <code>framezoom</code>                | Specifies scaling factor of the frame.                                                                                            |
| <code>framezoomx, framezoomy</code>   | Specify the horizontal or vertical scaling factor of the frame.                                                                   |
| <code>Grid</code>                     | Updates the grid (vertices and elements) in Tecplot SV.                                                                           |
| <code>host</code>                     | Specifies the name of the host where Tecplot SV should be started or connected to.                                                |
| <code>interfaces</code>               | Enables interface regions to be displayed. The default is false.                                                                  |
| <code>launch.timeout</code>           | Specifies how many seconds Sentaurus Process must wait for a Tecplot SV response after trying to start it. The default is 10 s.   |
| <code>legend</code>                   | Displays the contour legend.                                                                                                      |
| <code>loadfile</code>                 | Loads the specified file in Tecplot SV.                                                                                           |
| <code>macro</code>                    | Sends a macro command to Tecplot SV (see examples). The macro language is documented in the <i>Tecplot 360™ Scripting Guide</i> . |
| <code>port</code>                     | Specifies the port number for the Tecplot SV socket connection. The default is 2203.                                              |
| <code>reset.display</code>            | Resets to the default display mode.                                                                                               |

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>reset.xyaxes</code>                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Resets the axis scale and axis range for all axes.                                                                                                                                                                                                             |
| <code>scale</code>                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Sets the contouring scale to either <code>lin</code> , <code>log</code> , or <code>ash</code> for the variables specified with the option <code>set.variables</code> . The <code>set.variables</code> option must be specified with <code>scale</code> .       |
| <code>set.variables</code>                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Specifies a list of variables to be used with a second option such as <code>scale</code> . The variable names can contain wildcards, for example, <code>Stress*</code> .                                                                                       |
| <code>start</code>                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Tries to connect to a running Tecplot SV process or to launch a new process. See <a href="#">Tecplot SV User Guide, Chapter 5 on page 13</a> for detailed information on the behavior of the start procedure.                                                  |
| <code>suppressmat</code> , <code>unsuppressmat</code>                                                                                                                                                                                                                                                                                                                                                                                                                                          | Specifies the name of a material to be excluded or not excluded from the display.                                                                                                                                                                              |
| <code>suppressvar</code> , <code>unsuppressvar</code>                                                                                                                                                                                                                                                                                                                                                                                                                                          | Specifies the name of a variable to be excluded or not excluded from the display. A pattern can be specified to exclude a set of variables, for example, <code>*Interstitial*</code> . Patterns are matched using the <code>Tcl_StringMatch()</code> function. |
| <code>terms</code>                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Enables term fields.                                                                                                                                                                                                                                           |
| <code>view.fit</code>                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Fits the view.                                                                                                                                                                                                                                                 |
| <code>x1auto</code> , <code>x2auto</code> , <code>x3auto</code> , <code>x4auto</code> , <code>x5auto</code> , <code>xauto</code><br><code>y1auto</code> , <code>y2auto</code> , <code>y3auto</code> , <code>y4auto</code> , <code>y5auto</code> , <code>yauto</code>                                                                                                                                                                                                                           | Enables the automatic range reset for the specified axis. The default is true.                                                                                                                                                                                 |
| <code>x1log</code> , <code>x2log</code> , <code>x3log</code> , <code>x4log</code> , <code>x5log</code> , <code>xlog</code><br><code>y1log</code> , <code>y2log</code> , <code>y3log</code> , <code>y4log</code> , <code>y5log</code> , <code>ylog</code>                                                                                                                                                                                                                                       | Sets or unsets logarithmic mode for the specified axis. The default is true for y-axes.                                                                                                                                                                        |
| <code>x1max</code> , <code>x1min</code> , <code>x2max</code> , <code>x2min</code> , <code>x3max</code> , <code>x3min</code> , <code>x4max</code> , <code>x4min</code> , <code>x5max</code> , <code>x5min</code> , <code>xmax</code> , <code>xmin</code><br><code>y1max</code> , <code>y1min</code> , <code>y2max</code> , <code>y2min</code> , <code>y3max</code> , <code>y3min</code> , <code>y4max</code> , <code>y4min</code> , <code>y5max</code> , <code>y5min</code> , <code>ymin</code> | Sets the lower and upper range limits for the specified axis. This disables automatic range reset for the corresponding axis.                                                                                                                                  |
| <code>xyautofit</code>                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Resets all xy axes ranges to preset values after each update.                                                                                                                                                                                                  |
| <code>xyshow</code>                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Specifies variables that should be displayed as xy mappings. Wildcards can be used in the variable names.                                                                                                                                                      |

## A: Sentaurus Process Commands

plot.tec

ylaxisvar, y2axisvar, y3axisvar, y4axisvar, y5axisvar

Specifies the variable name to be displayed on the y-axis.

**Examples:**

```
# if a structure has already been created
plot.tec start      ;# start graphics
# Perform a process step here...
plot.tec grd data   ;# update graphics
```

Allows independent scaling of axes and fits the view:

```
plot.tec macro="TWODAXIS AXISMODE = INDEPENDENT"
plot.tec view.fit
```

Saves a Tecplot SV package file:

```
plot.tec macro="SAVE_LAYOUT 'example.lpk' INCLUDEDATA = YES"
```

Prepares for displaying boron and stress data on separate y-axes, with the legend enabled, with linear scaling for the stress variables, and with boron as the contouring variable for 2D mode:

```
plot.tec xyshow="Boron* Stress*" \
  ylaxisvar=Boron* y2axisvar=Stress*!y2log y2min=-1e-6 y2max=1e-5 \
  contourvar=Boron legend
plot.tec set.variables=Boron* scale=log
plot.tec set.variables=Stress* scale=lin
```

**See:** [Tecplot SV User Guide, Launching or Connecting to Tecplot SV on page 13](#)

## plot.xy

|                             |                                                                                                                                                                                                                                                                            |
|-----------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>            | Prepares an xy plot to draw on.                                                                                                                                                                                                                                            |
| <b>Syntax:</b>              | <pre>plot.xy   [clear]   [min= &lt;numeric list&gt;] [max= &lt;numeric list&gt;]   [x.axis=&lt;c&gt;] [y.axis=&lt;c&gt;] [x.log] [y.log]</pre>                                                                                                                             |
| <b>Description:</b>         | Configures a 2D plot surface for use with the <code>point.xy</code> command. This prepares axis scaling, labels, and controls log axes. (Using this command and the <code>point.xy</code> command could simulate all other commands in this section.)                      |
| <b>Options:</b>             |                                                                                                                                                                                                                                                                            |
| <code>clear</code>          | Clears the existing plot surface. The default is true.                                                                                                                                                                                                                     |
| <code>max</code>            | Takes a list of numeric values that will be the ends of the x- and y-axis, respectively. The first argument is the x-value and the second is the y-value. A single value is always interpreted as the x-value. The default is the maximum extent of the current structure. |
| <code>min</code>            | Takes a list of numeric values that will be the ends of the x- and y-axis, respectively. The first argument is the x-value and the second is the y-value. A single value is always interpreted as the x-value. The default is the minimum extent of the current structure. |
| <code>x.axis, y.axis</code> | Provide the labels for the x-axis and y-axis.                                                                                                                                                                                                                              |
| <code>x.log, y.log</code>   | Control whether there is a linear or log axis. If <code>log</code> is selected, the logarithm of the values on the <code>point.xy</code> command are taken. The axis also will have log scale form.                                                                        |
| <b>Examples:</b>            | <pre>plot.xy min = {1 0.0} max = {3600 0.75} x.axis=Time y.axis=Thickness</pre> Prepares a plot area.                                                                                                                                                                      |
| <b>See:</b>                 | <a href="#">point.xy on page 1023</a> , <a href="#">select on page 1053</a>                                                                                                                                                                                                |

---

## point

**Function:** Creates a point, for example, for a mask polygon.

**Syntax:** `point`  
[coord= {<n>[<m>|<cm>|<um>|<nm>]  
          <n>[<m>|<cm>|<um>|<nm>]  
          <n>[<m>|<cm>|<um>|<nm>]}]  
[name=<c>] [list] [clear]

**Description:** Defines a point in three dimensions or a 2D point in the yz plane. It can be used to construct polygons to define masks.

**Options:**

`clear` Clears the list of all points. If a name is specified, it clears only that point information.

`coord` Defines the coordinates of the point. For a 3D point, all three coordinates must be specified. If only two are defined, a 2D layout point in the yz plane is assumed. The default unit is  $\mu\text{m}$ .

`list` Returns the list of currently defined points. If a name is given, it prints the information for this point only.

`name` Specifies the name of the point.

**Examples:** `point name=p1 coord= {0 -1.5}`  
Defines a 2D point with the coordinates  $y = 0$  and  $z = -1.5$ .

`LogFile [point list]`  
Prints the list of defined points.

**See:** [mask on page 977](#), [polygon on page 1024](#)



---

## point.xy

- Function:** Adds a line segment to a plot.
- Syntax:** `point.xy`  
`x=<n> y=<n>`  
`[name=<c>] [color=<c>] [symb=<c>] [move]`
- Description:** Adds segments to a specified line on a plot surface using the X-windows-based plotting (`plot.1d` or `plot.2d`). The command is used to plot calculated values, data, or direct outputs from the simulation. The values can be added to any named line.
- Options:**
- `color` Specifies the color for the line. It can be any color supported by the X11 hardware and named in the color database.
- `move` Instead of drawing from the last point, the graphics pen is placed at this point without moving. This, combined with `symb`, can be used to draw scatter plots.
- `name` Specifies the name of a line, so that points can be added to the line at a later time. The name can be any valid character string and is used in the plot legend. If the named line does not exist, it is created.
- `symb` The first character of this string is used to mark the line. The default is `x`. If no symbol is specified, none will be used. If a symbol is specified once for a line, it is used for all lines.
- `x, y` Mandatory. Specify the values to be added to the plot.
- Examples:** `point.xy x=60.0 y=0.1 name=Thickness`  
The `x`- and `y`-values are added to the line named `Thickness`.
- See:** [interface on page 948](#), [interpolate on page 950](#), [plot.xy on page 1021](#), [select on page 1053](#)

---

## polygon

|                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>       | Creates a polygon, for example, for a mask.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <b>Syntax:</b>         | <pre> polygon   (list   clear       (name=&lt;c&gt;       (tdr=&lt;filename&gt; [regions= {reg_1 ... reg_n}]           [materials= {mat_1 ... mat_n}]           [points= {point_1 point_2 ... point_n}]           [segments= {           y_1[&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]           z_1[&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]           y_2[&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]           z_2[&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;] ...           y_n[&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]           z_n[&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]})           [rectangle]         [min= {           y[&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]           z[&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]})]         [max= {           y[&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]           z[&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]})]       )     )   [xy] </pre> |
| <b>Description:</b>    | <p>Defines a polygon. This command defines a mask or uses the polygon during an insertion. One of the following must be used to create a polygon:</p> <ul style="list-style-type: none"> <li>• <code>points</code></li> <li>• <code>segments</code></li> <li>• <code>rectangle</code></li> <li>• <code>tdr</code></li> </ul> <p>If named points are not given explicitly when forming polygons, they are generated automatically during the creation of the polygon.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| <b>Options:</b>        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| <code>clear</code>     | Clears the list of all polygons. If <code>name</code> is specified, it clears only the named polygon.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <code>list</code>      | Returns a list of all polygons. If <code>name</code> is given, it returns the information for this polygon only.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <code>materials</code> | Specifies a material or list of materials that will be read when using the <code>tdr</code> option.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

|                        |                                                                                                                                                                                                                                                                                                                                                                                                                                               |
|------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>max</code>       | Maximum point for a rectangular box. It should be used with the <code>rectangle</code> parameter to create a rectangular polygon. The default is the structure bounding box maximum.                                                                                                                                                                                                                                                          |
| <code>min</code>       | Minimum point for a rectangular box. It should be used with the <code>rectangle</code> parameter to create a rectangular polygon. The default is the structure bounding box minimum.                                                                                                                                                                                                                                                          |
| <code>name</code>      | Specifies the name of the polygon.                                                                                                                                                                                                                                                                                                                                                                                                            |
| <code>points</code>    | Lists the point names used to specify the polygon. A minimum of three must be specified. The points must have been specified using the <code>point</code> command. The polygon is closed implicitly by connecting the first and last points. This parameter also can be used with <code>rectangle</code> to specify a rectangular polygon. In this case, two points should be given: the minimum and maximum points of the rectangle.         |
| <code>rectangle</code> | Must be specified along with the parameters <code>min</code> and <code>max</code> to define a rectangular box. Alternatively, two named points can be given (using <code>points</code> ) corresponding to the minimum and maximum of the rectangle.                                                                                                                                                                                           |
| <code>regions</code>   | Specifies a region or list of regions to be used when reading the polygon by using the <code>tdr</code> option.                                                                                                                                                                                                                                                                                                                               |
| <code>segments</code>  | Lists the line segments in the <code>yz</code> plane (or <code>xy</code> when the option <code>xy</code> is specified) used to specify a polygon in 3D. The polygon is closed implicitly by connecting the first and last points. A minimum of three segments must be given.                                                                                                                                                                  |
| <code>tdr</code>       | Reads the polygon from the <code>filename</code> . If you use <code>tdr</code> , you must specify <code>xy</code> . It allows you to use materials and regions to further specify which polygon to be read from the TDR file.                                                                                                                                                                                                                 |
| <code>xy</code>        | Defines the polygon in the <code>xy</code> plane instead of the default <code>yz</code> plane. When using <code>xy</code> , the <code>segments</code> are defined as { <code>x_1 y_1 ... x_n y_n</code> }, and <code>min</code> and <code>max</code> as <code>x y</code> . This option is mandatory when using <code>tdr</code> . Specifying this option typically means that the polygon will be used for insertion rather than for masking. |

## A: Sentaurus Process Commands

### polygon

**Examples:**

```
point name=p1 coord= {0.0 0.0}
point name=p2 coord= {0.0 -0.5}
point name=p3 coord= {0.5 -0.5}
point name=p4 coord= {0.5 0.0}
```

```
polygon name=Box1 points= {p1 p2 p3 p4}
polygon name=Box2 points= {p2 p4} rectangle
polygon name=Box3 min= {0.0 -0.5} max= {0.5 0.0} rectangle
```

Creates three identical rectangles using points and coordinates.

```
polygon name=LShape segments= \
    {0.0 -1.5 0.0 -0.5 0.5 -0.5 0.5 1.5 1.5 1.5 1.5 -1.5}
```

Defines an L-shaped polygon using 1D line segments.

```
polygon name = "box" xy tdr="points_bnd.tdr" materials="Aluminum"
```

Reads the aluminum material structure in the file `points_bnd.tdr` as a polygon called `box`.

```
LogFile [polygon list]
```

Prints the list of polygons that have been defined.

```
polygon name=Box3 clear
```

Deletes `Box3`.

**See:** [Inserting Polygons in Two Dimensions on page 762](#), [insert on page 942](#), [mask on page 977](#), [point on page 1022](#)

---

## polyhedron

**Function:** Creates and stores 3D polyhedra, mainly for later insertion.

**Syntax:**

```
polyhedron
  clear | list |
  (name=<c>
    (external.sde
      (tdr=<filename> [regions= {reg_1 ... reg_n}] |
        [materials= {mat_1 ... mat_n}] [rotate]) |
      brick= {
        minx[<m>|<cm>|<um>|<nm>]
        miny[<m>|<cm>|<um>|<nm>]
        minz[<m>|<cm>|<um>|<nm>]
        maxx[<m>|<cm>|<um>|<nm>]
        maxy[<m>|<cm>|<um>|<nm>]
        maxz[<m>|<cm>|<um>|<nm>] } |
      polygons= {pol_1 ... pol_n} |
      (polygons= {pol}
        min=min_x[<m>|<cm>|<um>|<nm>]
        max=max_x[<m>|<cm>|<um>|<nm>])
    )
  )
```

**Description:** Creates a polyhedron and stores it under the name <c>. Different mechanisms can be used to create the polyhedron. It can be read from a TDR boundary file, defined as a brick, defined from the beginning using polygonal faces, or created as an extruded polygon. When a polyhedron is defined, it can be used to perform polyhedron insertion using the `insert` command.

### Options:

|                           |                                                                                                                                                                                                                                                                  |
|---------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>brick</code>        | Creates a rectangular prism, given its two corners as <code>minx miny minz</code> and <code>maxx maxy maxz</code> .                                                                                                                                              |
| <code>clear</code>        | Erases all the previously defined polyhedra from memory.                                                                                                                                                                                                         |
| <code>external.sde</code> | Creates a polyhedron from the external Sentaurus Structure Editor structure. For more information, see <a href="#">Sentaurus Structure Editor Interface on page 767</a> .                                                                                        |
| <code>list</code>         | Displays a list of the currently defined polyhedra.                                                                                                                                                                                                              |
| <code>materials</code>    | Optional. It can be used with the <code>tdr</code> option only and is used to choose which materials will be included in the file. In addition to explicit material names, the keyword <code>bulk.materials</code> is available to specify all nongas materials. |
| <code>max</code>          | Maximum x-coordinate for extrusion (see <code>polygon</code> below).                                                                                                                                                                                             |
| <code>min</code>          | Minimum x-coordinate for extrusion (see <code>polygon</code> below).                                                                                                                                                                                             |

## A: Sentaurus Process Commands

### polyhedron

|          |                                                                                                                                                                                                                                                                                                                                                                         |
|----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| name     | Mandatory. Specifies the name of the polyhedron to be created.                                                                                                                                                                                                                                                                                                          |
| polygons | Parameter polygons can be used in two contexts: <ul style="list-style-type: none"><li>• When specifying a whole list of polygons that form a polyhedron, it will build such a polyhedron.</li><li>• When specifying one planar axis-oriented polyhedron, it will (with the help of min and max) extrude that polygon in the x-direction to form a polyhedron.</li></ul> |
| regions  | Optional. It must be used together with tdr. It is used to choose which regions of the TDR boundary file are included.                                                                                                                                                                                                                                                  |
| rotate   | Used to avoid the automatic rotation that Sentaurus Process performs when reading polyhedra to transfer them from the TDR boundary file (assumed to be in DF-ISE coordinates) to the Sentaurus Process structure in Sentaurus Process coordinates. It requires the use of the tdr option.                                                                               |
| tdr      | Reads all the polyhedra included in the specified TDR boundary file.                                                                                                                                                                                                                                                                                                    |

**Examples:**

```
polyhedron name=sphere tdr=sphere_bnd.tdr materials= { Silicon Gas }
Loads the polyhedra containing silicon and gas from a boundary file
sphere_bnd.tdr with the name sphere.
```

```
polyhedron name=prism polygons= { triangle } min=-6 max = 2
Creates a polyhedron named prism, extruding from x = -6 μm to
x = 2 μm an already existing polygon called triangle.
```

```
polyhedron name=tetrahedron polygons = { face1 face2 face 3 face4 }
Using the polygons face1, face2, face3, and face4 (that must be
correctly defined), builds a polyhedron called tetrahedron.
```

```
polyhedron name=smallPrism brick= { -6 -4 -2 -1 4.5 1 }
Defines a rectangular prism (brick shape) called smallPrism by using its
two corners, that is, minx = -6 μm, miny = -4 μm, minz = -2 μm, and
maxx = -1 μm, maxy = 4.5 μm, maxz = 1 μm.
```

**See:** [Inserting Polyhedra on page 765](#), [insert on page 942](#)

---

## PowerDeviceMode

**Function:** Sets diffusion models to match the `pd.fermi` model of TSUPREM-4 for power-device applications. It also relaxes time-step controls and reduces mesh refinement around the interfaces.

**Syntax:** `PowerDeviceMode`

**Description:** Sentaurus Process and TSUPREM-4 use different code and, sometimes, have different assumptions or algorithms for diffusion. This command tries to minimize these differences by setting appropriate switches that make the results of a Sentaurus Process simulation as close as possible to those produced by TSUPREM-4 with the `pd.fermi` model for boron, phosphorus, arsenic, antimony, and indium in silicon. This includes:

- Switch on Fermi model.
- Switch on solid solubility model.
- Switch on `DopantOnly` charge model.
- Switch on equilibrium activation model for arsenic.
- Switch on segregation model at oxide–silicon interface.
- Switch off dopant and defect clusters.
- Switch off point-defect equations.
- Relax time-step controls by modifying `InitTimeStep`, `delT`, `delTox`, `delNT`, `IncreaseRatio`, `ReduceRatio`, and `MaxGrowthStep`.
- Switch on TSUPREM-4-style time-step controls.
- Reduce mesh refinement around the interfaces.
- Relax meshing criteria during boundary movement.

---

## print.1d

**Function:** Prints values along a 1D cross section.

**Syntax:**

```
print.1d
  [x=<n>][<m>|<cm>|<um>|<nm>]
  [y=<n>][<m>|<cm>|<um>|<nm>]
  [z=<n>][<m>|<cm>|<um>|<nm>]
  [<material>] [region=<c>] [name=<c>]
  [gas] [interfaces]
  [syntax.check.value=<c>]
```

**Description:** Prints the values along cross sections through the device. This command is particularly useful for creating input for another xy plot. A Tcl list is returned for all values. This allows subsequent processing (for example, integration) of the resulting profile.

**Options:**

`gas` By default, gas values are not reported. This option allows the gas mesh to be included in the extracted data.

`interfaces` Prints interface data from the field specified with the `name` parameter. Values from all interfaces are displayed on the screen and are organized by interface. For each point on the interface, a set of numbers is displayed as follows:

- {x value} in 1D
- {x y value} in 2D
- {x y z value} in 3D

where x, y, and z are the coordinates of the interface point, and `value` is the value of the specified field.

`<material>` Name of the material for which the data fields are printed.

`name` Specifies the name of a data field. This allows printing without using the `select` command. The default is to use the field specified in the most recent `select` command.

`region` Name of the region for which the data fields are printed.

`syntax.check.value`

Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during normal run mode. Setting this value avoids such problems.



*x, y, z*

Specify the constant values of a line along which sectioning is performed. In one dimension, these parameters are not necessary. In two dimensions, only one of *x* or *y* can be specified for a given device. Specifying *x* produces a horizontal slice through the device and *y* specifies a vertical slice. An easy way to remember this is that the cross section is taken at the constant value specified. For a 3D simulation, two of these three parameters must be specified. The default unit is  $\mu\text{m}$ .

**Examples:**

```
print.1d x=1.0
```

Prints the selected value at *x* equal to 1.0  $\mu\text{m}$ .

```
print.1d y=1.0 name=Arsenic
```

Prints the data field named *Arsenic* along a vertical line at a lateral position of 1.0  $\mu\text{m}$ .

**See:**

[plot.1d on page 1011](#), [select on page 1053](#), [tclsel on page 1091](#)

---

## print.data

**Function:** Writes data in x-, y-, and z-format.

**Syntax:** `print.data`  
`[name=<c>] [outfile=<c>]`  
`[xlo=<n>][<m>|<cm>|<um>|<nm>] [xhi=<n>][<m>|<cm>|<um>|<nm>]`  
`[ylo=<n>][<m>|<cm>|<um>|<nm>] [yhi=<n>][<m>|<cm>|<um>|<nm>]`  
`[zlo=<n>][<m>|<cm>|<um>|<nm>] [zhi=<n>][<m>|<cm>|<um>|<nm>]`  
`[NODE | EDGE]`

**Description:** Displays the selected data field. The file format is the x-position, y-position, and z-position. This command is used primarily to write a data field for use with more sophisticated 3D plotting tools.

**Options:**

`name` Specifies the name of a data field. This allows printing without using the `select` command. The default is `Z_Plot_Var`.

`NODE, EDGE` These Booleans specify either a node-based field or an edge-based field. The default is `NODE`.

`outfile` Name of output file. The file is opened for writing, and any previous content is destroyed.

`xlo, ylo, zlo, xhi, yhi, zhi`

Specify a 3D bounding box. Only data within these limits is printed. The default value and unit is 0  $\mu\text{m}$ .

**Examples:** `print.data outfile=foo name=Boron`  
 Prints the data field named `Boron`.

**See:** [select on page 1053](#)

## profile

|                                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|----------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>                 | Reads a data file and constructs a data field.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| <b>Syntax:</b>                   | <pre>profile   infile=&lt;c&gt; name=&lt;c&gt; concentration=&lt;n&gt; region=&lt;c&gt; [&lt;material&gt;]   xcoord=&lt;n&gt;   [offset= {&lt;n&gt; &lt;n&gt; &lt;n&gt;}][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]   [xscale=&lt;n&gt;] [ymin=&lt;n&gt;]   [(logarithmic   linear)]   [min= {&lt;n&gt; &lt;n&gt; &lt;n&gt;}] [max= {&lt;n&gt; &lt;n&gt; &lt;n&gt;}]   [x.sigma=&lt;n&gt;] [y.sigma=&lt;n&gt;] [z.sigma=&lt;n&gt;]</pre>                                                                                                                                                                                                                                                                                                                                                         |
| <b>Description:</b>              | Reads data fields from an ASCII data file or a TDR file and adds them to the structure. This command allows reading a doping profile from a SIMS measurement. In this case, if the simulated structure is 2D or 3D, the data field is created uniformly in the lateral direction. This command also allows reading a field from a TDR file with the same dimension as the simulated structure. You also can limit the extent of the imported profile within a rectangular box by specifying <code>min</code> or <code>max</code> , or both. Outside this box, the profile falls off with complementary error function ( <code>erfc</code> ) with standard deviations given by <code>x.sigma</code> , <code>y.sigma</code> , and <code>z.sigma</code> in the x-, y-, and z-direction, respectively. |
| <b>Options:</b>                  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <code>concentration</code>       | Specifies concentration of the field at the specified <code>xcoord</code> .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <code>infile</code>              | Name of the file to be read. If it is an ASCII data file, the file should be in a two-column format with depth (in $\mu\text{m}$ ) in Column 1 and the variable in Column 2. It also will read the output of the <code>print.ltd</code> command, which includes Tcl braces for list processing and the material name. If it is a TDR file, it must be in the same dimension as the simulated device structure and requires <code>.tdr</code> as the file extension.                                                                                                                                                                                                                                                                                                                                |
| <code>logarithmic, linear</code> | Interpolates data using logarithmic or linear interpolation. The default value is <code>logarithmic</code> , which is usually more accurate for concentration profiles.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| <code>&lt;material&gt;</code>    | Name of the material to which the field profile is applied. For information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| <code>max</code>                 | Takes a list of numbers defining the x-, y-, and z- coordinates of the lower-right front corner of the 1D, 2D, or 3D rectangular box in the internal coordinate system into which the profile is imported. For 1D, 2D, and 3D structures, a list of one, two, or three numbers is required, respectively. The possible maximum number is used for missing numbers.                                                                                                                                                                                                                                                                                                                                                                                                                                 |

## A: Sentaurus Process Commands

### profile

|         |                                                                                                                                                                                                                                                                                                                                                                     |
|---------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| min     | Takes a list of numbers defining the x-, y-, and z- coordinates of the upper-left back corner of the 1D, 2D, or 3D rectangular box in the internal coordinate system into which the profile is imported. For 1D, 2D, and 3D structures, a list of one, two, or three numbers is required, respectively. The possible minimum number is used for missing numbers.    |
| name    | Mandatory. Specifies name of data field. This parameter allows the creation of arbitrary fields, for example, a field called <code>Measured</code> .                                                                                                                                                                                                                |
| offset  | A list of numbers that specify the offsets in the x-, y-, and z-direction, respectively. The missing values are treated as 0. These values will be subtracted from the x-, y-, and z-coordinate, respectively, when creating the data field from the imported field. This parameter allows a profile to be shifted. The default value and unit is 0 $\mu\text{m}$ . |
| region  | Name of the region to which the profile is applied.                                                                                                                                                                                                                                                                                                                 |
| x.sigma | Standard deviation of erfc falloff from a rectangular box in the x-direction. This parameter must be specified if a rectangular box is specified.                                                                                                                                                                                                                   |
| xcoord  | Coordinate in x-direction where the concentration will be defined.                                                                                                                                                                                                                                                                                                  |
| xscale  | The <code>profile</code> command assumes the x-dimension is in micrometers. This command allows you to scale the depth dimension if necessary. For example, if the depth is in ångströms, $1 \times 10^{-4}$ should be specified. The default value is 1.0.                                                                                                         |
| y.sigma | Standard deviation of erfc falloff from a rectangular box in the y-direction. If it is not specified, it takes the value of <code>x.sigma</code> .                                                                                                                                                                                                                  |
| ymin    | Minimum-acceptable value of the data field. Values less than <code>ymin</code> in the data field are set to <code>ymin</code> . This is useful for data that may approach zero when using logarithmic interpolation.                                                                                                                                                |
| z.sigma | Standard deviation of erfc falloff from a rectangular box in the z-direction. If it is not specified, it takes the value of <code>y.sigma</code> .                                                                                                                                                                                                                  |

**Examples:**

```
profile name=Boron infile=utmar.bor xscale=1.0e-4 ymin=1.0e14
```

Reads a boron profile into the program. This could be from a Monte Carlo implant code – UT MARLOWE. Scales the depth by  $1 \times 10^{-4}$  to convert the ångström of MARLOWE to micrometer. Since the output of MARLOWE is sometimes zero, a minimum value of  $1 \times 10^{14}$  is specified.

```
profile name=Data inf=SIMS
```

Reads a file named SIMS into a data field called Data. This can be performed to initialize a device doping profile or to read in a measured profile that is the target of a diffusion extraction.

## RangeRefineboxes

**Function:** Creates a set of refinement boxes based on a mask and a set of range and extent parameters. All boxes share a set of global refinement settings, but each box can have additional local refinement settings.

**Syntax:**

```
RangeRefineboxes
  name= <root>
  mask= <mask>
  range= <range>
  [<default parameters>]
  boxes= {
    {drange= <drange_1> [<box_1-specific parameters>]}
    [{drange= <drange_2> [<box_2-specific parameters>]]}
    ...
  }
```

**Description:** Creates a set of refinement boxes with a single command. The refinement is applied to the area under the specified mask. The lateral extent is controlled by the same parameters as in the `refinebox` command, for example, `mask.edge.refine.extent` and `mask.edge.mns`.

The primary extent is defined by the parameters `range` and `drange`. The `range` parameter is common to all refinement boxes and may be taken as the `range` parameter for a given implantation. The `drange` parameter can be set for each related refinement box separately.

As optional global default parameters, any parameter from the `refinebox` command is allowed. These parameters are applied to all refinement boxes of the set. For each individual refinement box, an additional `refinebox` command can be set, which can overwrite globally defined parameters or add new parameters. There are no limits on how many refinement boxes can be in the set. The individual refinement boxes inherit the `<root>` name with a numeric post-fix counter.

**NOTE:** This command makes one call to the `refinebox` command per individual refinement box.

**NOTE:** You can use the `DeleteRefinementboxes` command to remove the entire set of refinement boxes created with the `RangeRefineboxes` command.

**Options:**

<box-specific parameters>

Any parameter of the `refinebox` command. These parameters are applied only to the individual refinement box. They can overwrite global parameters defined in the <default parameters> section.

- boxes      A Tcl list containing a set of Tcl lists. Each Tcl list contains specific parameter settings for one individual refinement box.
- drange     Specifies the primary extent of an individual refinement box, which extends from  $x_{min} = range - drange$  to  $x_{max} = range + drange$ .
- mask       Specifies the mask under which the refinement is to be applied.
- name       Specifies the root name for the set of refinement boxes. Each individual refinement box inherits a name of the form <root>\_<n>, where <root> is the argument of the name parameter and <n> is a counter.
- range      Specifies the center of the primary extent for all refinement boxes in the set. For example, you can use the range parameter from an implant table to define a set of refinement boxes to resolve the area that dopants penetrate in a subsequent implantation step.

**Examples:**

```
mask name= M1_p segments= { 6 10 }
array set moments [implant Arsenic dose= 5e13<cm-2> energy= 1000<keV> \
  tilt= 0 rotation= 0 get.moments]
set range $moments(rp)
set sigma $moments(stdev)
eval RangeRefineboxes name= "RM1" mask= "M1_p" range= $range \
  boxes= \{ \
    { drange= $sigma xrefine= [expr $sigma/4.0] yrefine= [expr $sigma/4.0] \
      extend= 0 } \
    { drange= [expr 4*$sigma] xrefine= $sigma yrefine= $sigma \
      extend= [expr 2*$sigma] } \
    { drange= [expr 2*$sigma] mask.edge.mns= [expr $sigma/8.0] \
      mask.edge.refine.extent= [expr 2*$sigma] mask.edge.ngr= 1 } \
  extend=1.0 xrefine=0.5 yrefine=0.5 info=3
```

**See:**            [refinebox on page 1040](#)

---

## reaction

**Function:** Defines the reacting materials.

**Syntax:**

```
reaction
  (list | (name=<c> mat.l=<c> mat.r=<c> mat.new=<c>))
  [new.like=<c> mat.final=<c>]
  [diffusing.species= <string list>]
  [ambient.name] [clear] [delete]
```

**Description:** Defines reacting materials and the new material that forms as the product of the reaction. The convention for interface materials is `mat1_mat2` where the materials are ordered alphabetically. For the purpose of this command, left refers to `mat1` and right refers to `mat2`. Both materials must be specified when using this command. Silicidation and oxidation rely on this information.

**Options:**

`ambient.name` Specifies an ambient-type reaction and which ambient must be present for this reaction to occur.

`clear` If a reaction is named, this parameter clears the diffusing species list from that reaction. If no reaction is named, it deletes all reactions (may only be useful for special situations).

`delete` Deletes the named reaction.

`diffusing.species`

List of reactants for material growth reactions either ambient type or nonambient type. For ambient type reactions, the (one only) default diffusing species name is the ambient name, but it can be changed using this parameter. For nonambient reactions (such as silicidation), multiple diffusing species can be listed. Reactants are added automatically to the global solution list in the `SetReactantSolutions` procedure.

`list` Lists the names of the already defined reactions.

`mat.final` For reactions that use a temporary material during growth, this parameter can be set to convert the temporary material to a final material after the diffuse step is finished. This is usually used with epitaxial reactions to keep regions separated during growth and only merged afterwards.

`mat.l, mat.r` Specify the material names for each side of the interface before the reaction.

`mat.new` A valid material name as the product of the reaction.



**name** A reaction name must be specified. The parameter name is used to identify the reactions during growth process.

**new.like** Name of the existing material that the new material is behaving like. This includes the existing material and other material interfaces. It is performed in the `ReactantLike` procedure.

**Examples:**

```
reaction name=MyDryOx mat.l=Silicon mat.r=Gas mat.new=oxide \  
diffusing.species = O2
```

Defines a reaction named `MyDryOx`. The reaction will occur at the gas-silicon interface and the new material will be oxide. For the reaction to occur,  $O_2$  must be present in the structure. It is expected that you will provide the actual reaction equation for the interface using the Alagator language (see [Alagator for Generic Growth on page 584](#)).

```
reaction name=silicidation mat.l=Silicon mat.r=Titanium \  
mat.new=TiSilicide diffusing.species = {Silicon Titanium} \  
new.like=oxide
```

In this example, silicon and titanium are the reacting materials. The product of the reaction is titanium silicide. Two species, silicon and titanium, are needed for the reaction. It is expected that you will provide the actual reaction equations for the interface using Alagator language.

**See:** [Alagator for Generic Growth on page 584](#)

---

## refinebox

**Function:** Sets the local grid parameters and performs a grid refinement using the MGOALS library.

**Syntax:**

```
refinebox
  [name=<c>] [clear] [list] [print]
  [<material>] [materials= {string list}] [regions= {string list}]
  [min= <numeric list>] [max= <numeric list>]
  [xrefine= <numeric list>]
  [yrefine= <numeric list>]
  [zrefine= <numeric list>]
  [interface.materials= {<string list>}]
  [interface.regions= {<string list>}]
  [offsetting] [double.side]
  [offsetting.maxlevel=<i>]
  [interface.mat.pairs= {string list}]
  [interface.region.pairs= {string list}]
  [min.normal.size=<n>][<um>]
  [Adaptive] [kmc]
  [normal.growth.ratio=<n>]
  [max.lateral.size=<n>][<um>]
  [def.rel.error=<n>] [def.abs.error=<n>]
  [def.max.difference=<n>]
  [def.max.logdiff=<n>]
  [def.max.asinhdiff=<n>]
  [def.max.gradient=<n>]
  [def.max.dose.error= n]
  [rel.error= {field1 = <n> field2 = <n> ...}]
  [abs.error= {field1 = <n> field2 = <n> ...}]
  [max.difference= {field1 = <n> field2 = <n> ...}]
  [max.logdiff= {field1 = <n> field2 = <n> ...}]
  [max.asinhdiff= {field1 = <n> field2 = <n> ...}]
  [max.gradient= {field1 = <n> field2 = <n> ...}]
  [max.dose.error= {field1 = <n> field2 = <n> ...}]
  [refine.add.fields= {string list}]
  [refine.rm.fields= {string list}]
  [refine.fields= {string list}]
  [refine.expr= string]
  [refine.field.expr= {field1= <string> field2= <string> ...}]
  [refine.type= <string>]
  [refine.min.edge= <numeric list>] [refine.max.edge= <numeric list>]
  [refine.dir.factor= <numeric list>]
  [min.value=<n>] [max.value=<n>]
  [target.length=<n>] [target.length.scaling=<scaling>]
  [3d]
  [(mask=<maskname> extrusion.min=<n> extrusion.max=<n>) [extend=<n>]
  [mask.edge.mns] [mask.edge.ngr] [mask.edge.refine.extent]]
```

|                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
|----------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Description:</b>                                      | <p>Specifies mesh refinement. The following types of refinement box are available:</p> <ul style="list-style-type: none"> <li>• Standard: Independent <code>xrefine</code>, <code>yrefine</code>, <code>zrefine</code> settings.</li> <li>• Interface: Refinement near one or more interfaces.</li> <li>• Adaptive: Adaptive refinement on fields.</li> <li>• Plane: Planar refinement for crystal boundaries.</li> <li>• Bulk mask: Confine refinement to an extruded boundary defined by a mask.</li> <li>• Mask edge: Confine refinement to a specified distance from a specified mask.</li> </ul> <p>All refinement boxes can be limited by material or spatially by specifying x-, y-, or z- minimum or maximum limits.</p> |
| <b>Options:</b>                                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| <code>3d</code>                                          | Specifies the refinement box for only 3D, or for only 1D and 2D. The default behavior is to always apply the refinement box. If <code>3d</code> is specified, the refinement box only applies to 3D. If <code>!3d</code> is specified, the refinement box only applies to 1D and 2D.                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>Adaptive</code>                                    | Specifies an adaptive refinement box. Adaptive refinement boxes are used during all MGOALS remeshing operations ( <code>etch</code> , <code>depo</code> , <code>photo</code> , <code>transform</code> , and so on) but will not be used during solve unless adaptive meshing is switched on (which can be accomplished using <code>pdbSet Grid Adaptive 1</code> ).                                                                                                                                                                                                                                                                                                                                                              |
| <code>clear</code>                                       | When used alone, this parameter clears all previously defined refinement boxes. When used with the <code>name</code> parameter, only the named refinement box is deleted.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <code>double.side</code>                                 | If <code>!double.side</code> is specified with the <code>offsetting</code> keyword, <code>interface.mat.pairs</code> and <code>interface.region.pairs</code> are interpreted in a nonsymmetric fashion by Sentaurus Mesh. The default is <code>double.side</code> , that is, the specification of a material or region pair $x_1/x_2$ is interpreted by Sentaurus Mesh as if the parameters were defined symmetrically for both $x_1/x_2$ and $x_2/x_1$ .                                                                                                                                                                                                                                                                        |
| <code>extend</code>                                      | Optional extension when using a mask driven refinement. This value can be positive (or negative) and extends (shrinks) the refinement isotropically in y and z. The original mask is left unchanged.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>extrusion.max</code><br><code>extrusion.min</code> | Minimum and maximum lengths in the x-axis where the refinement will be applied when using the <code>mask</code> option.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| <code>kmc</code>                                         | Refines the internal KMC boxes only.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>list</code>                                        | Lists the defined refinement boxes.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |

## A: Sentaurus Process Commands

### refinebox

|                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|-------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| mask                    | Uses an existing mask name as an extra constrain to where the refinement will be applied. If the refinement contains another spatial constrain (for example, using <code>min</code> and <code>max</code> parameters), the final application region is the intersection of the other constrains and the specified extruded mask. This parameter requires specifying the box length in x (lacked by the mask) using <code>extrusion.min</code> and <code>extrusion.max</code> , and optionally allows the use of the parameter <code>extend</code> . This option allows the definition of layout (mask) driven refinements. |
| mask.edge.mns           | Specifies minimum mesh size near mask edge (actual edge length may be up to 2 times smaller than this setting. This parameter must be used with <code>mask.edge.refine.extent</code> to have an effect.                                                                                                                                                                                                                                                                                                                                                                                                                   |
| mask.edge.ngr           | Specifies the growth rate of refinement away from the mask edge (default is 1.0, == no growth). This parameter must be used with <code>mask.edge.refine.extent</code> to have an effect.                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| mask.edge.refine.extent | Specifies the distance from the mask edge over which edge-based refinement occurs. It must be specified to obtain mask edge-based refinement.                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <material>              | Limits the refinement box to a particular material. By default, the refinement box applies to all materials. For more information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                                                                                                                                                                                                                                                                                                                                                     |
| materials               | Limits the refinement box to a list of materials. By default, the refinement box applies to all materials. For more information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                                                                                                                                                                                                                                                                                                                                                       |
| max, min                | Limits the extent of the refinement box. Both parameters take a Tcl list of numbers defining the refinement box extent in the x-, y-, and z-axes (in the internal coordinate system). You may specify either one or both <code>min</code> and <code>max</code> with a Tcl list of one, two, or three numbers for each parameter. If one number is specified, it is taken to be the limit in the x-axis. If two numbers are specified, they set limits for the x-axis and y-axis. Similarly, three numbers specify a limit in all three axes. The default unit is $\mu\text{m}$ .                                          |
| name                    | Name of the refinement box.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| print                   | Prints information for all refinement boxes unless <code>name</code> is specified; in which case, only the named refinement box information is printed.                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| regions                 | Limits the refinement box to a list of regions. By default, the refinement box applies to all regions.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |

- `xrefine` Sentaurus Process list of three numbers defining the element sizes in the x-direction at the top, middle, and bottom (in Sentaurus Process coordinates) of the box. The default unit is  $\mu\text{m}$ .
- `yrefine` Sentaurus Process list of three numbers defining the element sizes in the y-direction at the left, middle, and right (in Sentaurus Process coordinates) of the box. The default unit is  $\mu\text{m}$ .
- `zrefine` Sentaurus Process list of three numbers defining the element sizes in the z-direction at the front, middle, and back (in Sentaurus Process coordinates) of the box. The default unit is  $\mu\text{m}$ .

**Interface refinement control**

`interface.materials`

All interfaces that contain any of the materials listed here are refined using the `min.normal.size` criterion. By default, in 2D, interface refinement is applied to all interfaces of Silicon, Polysilicon, or Oxide. In 3D, interface refinement is only by default applied to interfaces of Silicon.

`interface.regions`

Used only in conjunction with `offsetting` or `offsetting.maxlevel` to switch on Sentaurus Mesh offsetting or to specify `offsetting.maxlevel` on a regionwise basis for Sentaurus Mesh offsetting.

`interface.mat.pairs`

A set of pairs of materials where interface meshing will be switched on (1st and 2nd, 3rd and 4th, and so on).

`interface.region.pairs`

A set of pairs of regions where interface meshing will be switched on (1st and 2nd, 3rd, 4th, and so on). This region-based interface specification is supported only for Sentaurus Mesh offsetting, in other words, when the `offsetting` keyword is also given.

`max.lateral.size`

Specifies maximum lateral spacing at the interface.

`min.normal.size`

Specifies minimum edge spacing at interfaces for this box.

`normal.growth.ratio`

Specifies edge-to-edge growth ratio moving away from an interface.

## A: Sentaurus Process Commands

### refinebox

`offsetting` When this keyword is given, along with `interface.materials`, `interface.mat.pairs`, `interface.regions`, or `interface.region.pairs`, causes the Sentaurus Mesh offsetting algorithm to be used to generate offsetting layers at the given interface.

`offsetting.maxlevel`

Specifies number of offsetting layers at the interface when Sentaurus Mesh offsetting is used, specified by material or region with the `interface.materials` or `interface.regions` keywords.

#### Adaptive meshing

`abs.error` Sets a field-dependent value of minimum significant field value.

`def.abs.error` Sets the field-independent default value of minimum significant field value.

`def.max.asinhdiff`

Sets the field-independent default value of maximum inverse hyperbolic sine (asinh) difference criteria.

`def.max.difference`

Sets the field-independent default value of maximum absolute difference criteria.

`def.max.dose.error`

Sets the field-independent default value of maximum local dose error criteria.

`def.max.gradient`

Sets the field-independent default value of maximum gradient criteria.

`def.max.logdiff`

Sets the field-independent default value of maximum logarithmic difference criteria.

`def.rel.error` Sets the field-independent default value of the required relative change of a field across an edge.

`max.value` Maximum interval value for interval refinement.

`max.asinhdiff` Sets a field-dependent value of inverse hyperbolic sine difference criteria.

`max.difference`

Sets a field-dependent value of maximum absolute difference criteria.

|                                |                                                                                                                                                                                                                                                                                                                                                                              |
|--------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>max.dose.error</code>    | Sets a field-dependent value of the maximum local dose error criteria.                                                                                                                                                                                                                                                                                                       |
| <code>max.logdiff</code>       | Sets a field-dependent value of maximum logarithmic difference criteria.                                                                                                                                                                                                                                                                                                     |
| <code>max.gradient</code>      | Sets a field-dependent value of maximum gradient criteria.                                                                                                                                                                                                                                                                                                                   |
| <code>min.value</code>         | Minimum interval value for interval refinement.                                                                                                                                                                                                                                                                                                                              |
| <code>rel.error</code>         | Sets a field-dependent value of the required relative change of the refined field across an edge.                                                                                                                                                                                                                                                                            |
| <code>refine.add.fields</code> | Adds fields to the default list of fields considered for adaptive refinement.                                                                                                                                                                                                                                                                                                |
| <code>refine.dir.factor</code> | Applies adaptive refinement more strongly in one direction than another. A factor of 1 will have no effect: A factor less than 1 causes smaller edges in that direction. For example, <code>refine.dir.factor= {0.1 1.0}</code> requests that, for a given adaptive refinement expression value, edges in the x-direction be 10 times smaller than edges in the y-direction. |
| <code>refine.expr</code>       | Sets a refinement expression. This takes any valid Alagator expression that produces a node-based result. Earlier releases required the <code>diff()</code> operator, but now, the <code>diff</code> operator must not be used. Similar results can be obtained for earlier releases by removing the <code>diff</code> operator.                                             |
| <code>refine.fields</code>     | Replaces the default list of fields considered for adaptive refinement. Solution variables and terms can appear in the <code>refine.fields</code> list. (For a description of a term, see <a href="#">Chapter 6 on page 559</a> .) The default list includes all dopants and point defects.                                                                                  |
| <code>refine.field.expr</code> | Sets a field-dependent refinement expression.                                                                                                                                                                                                                                                                                                                                |
| <code>refine.max.edge</code>   | Sets the direction-dependent maximum edge length.                                                                                                                                                                                                                                                                                                                            |
| <code>refine.min.edge</code>   | Sets the direction-dependent minimum edge length.                                                                                                                                                                                                                                                                                                                            |
| <code>refine.rm.fields</code>  | Removes specified fields from the default list of fields considered for adaptive meshing.                                                                                                                                                                                                                                                                                    |

## A: Sentaurus Process Commands

### refinebox

`refine.type` Specifies the type of criteria to apply for adaptive refinement. Allowed values are `interval` and `error` (the default).

`target.length` Target length (in micrometers) for interval refinement.

`target.length.scaling`

Scaling factor used in the calculation of the effective target length for interval refinement.

#### Examples:

```
refinebox min= {-0.25 0.4} max= {0.4 0.6} xrefine= {0.1 0.06 0.1} \  
  yrefine= {0.1 0.01 0.1} oxide  
refinebox min= {0.6 0.6} max= {0.8 0.8} xrefine= {0.1 0.03 0.1} \  
  yrefine= {0.1 0.03 0.1} silicon
```

Defines two refinement boxes.

```
refinebox adaptive def.rel.error = 100 def.max.dose.error=5e9
```

Creates an adaptive box that applies maximum dose error criteria to the default list of adaptive species, and effectively switches off relative error criteria which is on by default.

```
polygon name=pol segments = { -.5 -.5 .5 -.5 .5 .5 0 .5 0 0 -.5 0 }  
mask name=Mask1 polygons = { pol }  
refinebox name="ref1" mask=Mask1 yrefine = { 0.05 0.075 0.075 } \  
  extrusion.min = 0 extrusion.max = 0.05 extend = 0.2
```

The boundary for the refinement will be formed by the extension (by 0.2  $\mu\text{m}$ ) of the existing mask called `Mask1` extruded from 0 to 0.05  $\mu\text{m}$ .

#### See:

[Mesh Refinement on page 674](#), [mask on page 977](#), [mgoals on page 992](#)



## region

**Function:** Creates regions, marks substrates, and changes region materials.

**Syntax:**

```
region
  <material>
  xlo=<c> [ylo=<c>] [zlo=<c>]
  xhi=<c> [yhi=<c>] [zhi=<c>]
  [substrate] [name=<c>] [min= {<n> <n> <n>} max= {<n> <n> <n>}]
  [cropped.bbox] [alt.matername] [change.material]
  [zero.data]
  [field=<c> & (resistivity=<n>[<ohm-cm>] | concentration=<n>)]
  [list | list.bulk | list.gas | list.interface]
  [exact.name]
  [material]
  [bbox | bbox.cm | bbox.um]
  [new.name=<c> point= {<n> <n> <n>}]
  [volume]
  [syntax.check.value=<c>]
```

**Description:** The `region` command has different uses:

- At the beginning of a simulation, the initial regions are created with the `region` command in concert with the `line` command and the `init` command. The `line` command defines where mesh lines go.
- The `region` command specifies between which mesh lines the regions are created and what material the regions will be, and whether this region will be a substrate. It is used to change the material of a region at any point in the simulation after the structure has been initialized.
- The `region` command also can be used to return a cropped bounding box of a region, specified within a user-specified bounding box, defined by `min` and `max` along with a region name.

**Options:**

`alt.matername` Specifies an alternative material to be used when saving a structure. When using the TDR format, regions that are converted using `alt.matername` are properly converted back to the simulation material when the TDR file is read in from the `init` command. Although common materials such as SiGe and III-Vs are by default handled this way, special situations may require additional conversions when transferring to device simulation.

`bbox`, `bbox.cm`, `bbox.um`

If specified, the `region` command returns the maximum extents of the region in two points. If `bbox.cm` is specified, it returns the maximum extents of the region in centimeter. If `bbox.um` is specified, it returns the maximum extents of the region in micrometer.

## A: Sentaurus Process Commands

### region

`change.material`

Changes the material of an existing region (must be used with the `name` parameter). Changing the material of selected regions (to and from gas) can be used to change the structure without remeshing. Meshes of material gas are ignored in most process steps: implantation and oxidation.

`concentration` Specifies the value of the field directly.

`cropped.bbox` If specified, returns the cropped bounding box of a region that lies within a user-specified bounding box.

`exact.name` Normally when changing the material of a region, all ancestors of the named region (if there are any) are converted as well as the named region if it exists. For more information on region naming, see [Regionwise Parameters and Region Name-handling on page 56](#). If `exact.name` is switched on (it is switched off by default), only a region whose name exactly matches the `name` parameter will have its material changed.

`field` Name of a field to be initialized within this region.

`list`, `list.bulk`, `list.gas`, `list.interface`

Used to obtain a Tcl list of regions:

- `list` returns a list of all regions.
- `list.bulk` returns a list of nongas, noninterface regions (that is, all bulk regions).
- `list.gas` returns a list of gas regions.
- `list.interface` returns a list of interface regions.

`<material>` Material of the region. For more information about specifying materials, see [Material Specification on page 50](#).

`material` This Boolean flag returns the material name for the named region.

`min`, `max` User-specified bounding box.

`name` Specifies a name for the region. The name should not contain an underscore (`_`) or a period (`.`) because these characters have special meaning.

`new.name`, `point`

Used together to change the name of a region. The parameter `point` must specify a point (a list of doubles) within a region. The point should not be on or very near a border. The parameter `new.name` specifies the new name of the region.

`resistivity` Sets the value of the field by requesting a resistivity. This parameter only works for fields that have the resistivity parameters in the PDB (which by default is only As, B, P, Sb, and In in silicon).

`substrate` Tags a named region as the substrate for subsequent analysis. This Boolean flag allows the `update_substrate` command (see [update\\_substrate on page 1112](#)) to apply the lattice mismatch strain due to impurities. Setting `!substrate` clears the substrate tag. If no region name is specified and `!substrate` is set, all substrate tags are cleared.

`syntax.check.value`

Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during normal run mode. Setting this value avoids such problems.

`xlo, ylo, zlo, xhi, yhi, zhi`

Specify the bounds of the region. The `<c>` value should be one of the tags created in a preceding `line` statement.

`volume`

If specified, the command returns the volume of the named region. The units will be in  $\text{cm}^{\langle\text{dim}\rangle}$ , where `<dim>` is the simulation dimension.

`zero.data`

Usually when the material of a region is changed using the `change.material` parameter, all data in that region is set to 0. Setting `!zero.data` leaves the data untouched. The default value for this parameter is taken from `pdbGet Grid default.zero.data`, which allows a global setting for this parameter.

**Examples:**

```
mater name=MySilicon new.like=Silicon add
region name=bulk MySilicon change.material !zero.data
```

Creates a new material `MySilicon`, and then changes the material of a region named `bulk` to `MySilicon` without changing the data.

```
region name=Gate Gas change.material
```

Changes the region `Gate` to `Gas` before setting all fields to zero in `Gate` (`zero.data` defaults to true).

```
region silicon ylo=left yhi=right xlo=surf xhi=back
```

Creates a 2D silicon region using the statements from the example for the `line` command (see [line on page 969](#)).

```
region name=bulk min= {-5.0 0.0 0.0} max= {5.0 1.0 1.0} cropped.bbox
```

Returns a cropped bounding box of the region `bulk` that lies within the specified bounding box defined by the `min` and `max` parameters.

**See:** [integrate on page 945](#), [line on page 969](#)

---

## sde

**Function:** Dispatches commands to Sentaurus Structure Editor (only available in 3D).

**Syntax:**

```
sde
  {<Sentaurus Structure Editor commands>}
  [Adaptive] [remesh]
  [on] [off] [external]
  [polyhedron=<c>] [polyhedron.material=<c>]
  [SdeCheck]
  [logfile=<c>]
```

**Description:** Enables and configures the interface between Sentaurus Process and Sentaurus Structure Editor. When `sde on` is specified, all 3D geometry modeling is performed using Sentaurus Structure Editor. Sentaurus Process will translate geometry-modifying commands to the Sentaurus Structure Editor language and retrieve the resulting modified structure when necessary. The following commands are supported: `etch`, `deposit`, `photo`, `strip`, `transform`.

**NOTE:** Scheme commands may be sent directly Sentaurus Structure Editor using this command, but they must be enclosed in a pair of braces to prevent syntax errors in the Tcl interpreter. Several Scheme commands can be specified inside one `sde` command; each of them must start on a new input line.

**Options:**

**Adaptive** If `remesh` is selected, this parameter determines if adaptive meshing is used. The default value is read from the Boolean `pdb` parameter `Grid Adaptive`.

<Sentaurus Structure Editor commands>

Any number of `sde` commands in the Scheme language. You must enclose the Scheme commands in a pair of braces to protect them from the Tcl command interpreter. The opening brace must be on the same line as the `sde` command, for example:

```
sde {
  (sdepe:depo "thickness" 0.01 "type" "iso" "algorithm" "pt"
    "max-chamfer-angle" 30 "steps" 1 "material" "Oxide")
  (sdeio:save-dfise-bnd "all" "out1_sde.bnd")
}
```

|                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
|---------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| external            | Puts Sentaurus Structure Editor interface in external mode. This mode can be used to create polyhedra that can be inserted into a Sentaurus Process structure using MGOALS3D. When the external mode is switched on, all geometry transformations such as <code>etch</code> , <code>deposit</code> , and <code>transform</code> are applied to the external Sentaurus Structure Editor structure. See <a href="#">Sentaurus Structure Editor Interface: External Mode on page 764</a> .                                                                                                                    |
| logfile             | Specifies name of a file to log all of the Scheme commands dispatched to Sentaurus Structure Editor. The recommended file extension is <code>.scm</code> . The file will contain both the Scheme commands translated from Sentaurus Process <code>etch</code> , <code>deposit</code> , <code>strip</code> , <code>photo</code> , and <code>transform</code> commands, and the Scheme commands specified by users inside the <code>sde</code> command. The log file can be used for fine-tuning and debugging in a stand-alone run of Sentaurus Structure Editor such as: <code>sde -l mylogfile.scm</code> |
| off                 | Switches off Sentaurus Structure Editor mode. Operations will be performed by the MGOALS library instead.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| on                  | Enables use of Sentaurus Structure Editor for 3D geometry modeling. Even when Sentaurus Structure Editor is the default engine for 3D etching and deposition, the command <code>sde on</code> must always be specified to ensure that future simulations are performed using the same algorithms.                                                                                                                                                                                                                                                                                                          |
| polyhedron          | Used for external mode only (see the <code>external</code> parameter definition). This polyhedron is used to initialize the external Sentaurus Structure Editor interface. The material to be used for this polygon is chosen with the <code>polyhedron.material</code> parameter, which has a default value of <code>Silicon</code> .                                                                                                                                                                                                                                                                     |
| polyhedron.material | Selects the material of the polyhedron that is used to initialize the external mode. See <code>polyhedron</code> and <code>external</code> parameters.                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| remesh              | Enforces a remesh at the end of the <code>sde</code> command.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| SdeCheck            | Performs a geometry check for every boundary file that is created by Sentaurus Structure Editor. This helps to detect failures in the geometry-modeling part and prevents the Sentaurus Process simulation from continuing after an incorrect boundary representation is found.                                                                                                                                                                                                                                                                                                                            |

## A: Sentaurus Process Commands

sde

### Examples:

```
sde logfile=depo.scm on SdeCheck
pdbSet InfoDefault 1
```

Enables the use of Sentaurus Structure Editor or geometry modeling, specifies the log file for the Scheme commands, and checks all boundary files written by Sentaurus Structure Editor.

```
sde {
  (sdegeo:set-default-boolean "ABA")
  (define r1 (sdegeo:create-cuboid (position 0 0.6 0)
    (position 0.2 0.3 0.5) "Silicon" "Silicon_2"))
  (define facelist (list (car (find-face-id (position 0.1 0.3 0.25)))
    (car (find-face-id (position 0.2 0.5 0.25)))))
  (sdegeo:taper-faces facelist (position 0.2 0.3 0.5) (gvector 0 0 1) 5)
  (sdeio:save-dfise-bnd "all" "out1_sde.bnd")
}
```

Creates a cuboid in Sentaurus Structure Editor with tapered sidewalls and saves the structure to a .bnd file.

**NOTE:** The coordinates in the position vectors must be specified in DF-ISE coordinates: x, y, z in the position vectors correspond to Sentaurus Process z-, y-, and -x-coordinates.

### See:

For details about the Scheme commands, refer to the *Sentaurus Structure Editor User Guide*.

## select

**Function:** Selects the plot variable for the postprocessing routines.

**Syntax:**

```
select
  [<material>] [region=<c>]
  [z=<c>] [value=<c>]
  [name=<c>]
  [list] [list.all]
  [store] [present] [permanent] [delete]
  [min | max] | [report.location]
  [element] [edge.vector] [interfaces] [node.evaluate]
  [syntax.check.value=<c>]
```

**Description:** Specifies the variable for display in all postprocessing commands. Data can be selected directly in most commands, but it is usually more effective to specify it with the `select` command, which allows for manipulation of data fields and also will list all currently defined data fields. The quantity can be computed on nodes (default) or on elements using the `element` parameter. In either case, if necessary, interpolation will be performed to obtain the proper value type (to obtain element values from nodal ones or vice versa).

**NOTE:** The `select` command can be abbreviated to `sel`.

**NOTE:** The `select` command always sets or retrieves data in internal units. Internal units are cgs, for example, pressure is  $\text{dyn/cm}^2$ .

**Options:**

|                          |                                                                                                                                                                                                                           |
|--------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>delete</code>      | Deletes the data field with the name defined by the <code>name</code> parameter.                                                                                                                                          |
| <code>edge.vector</code> | Computes the weighted field with respect to edge orientation strongly favoring axis-oriented edges. Used with adaptive meshing.                                                                                           |
| <code>element</code>     | Computes the field on elements interpolating fields in the <code>z</code> expression if necessary. If false and element fields appear in the <code>z</code> expression, those values are interpolated to the nodes first. |
| <code>interfaces</code>  | Computes the field or minimum/maximum on interfaces as well as bulk. The default is on, that is, include interfaces.                                                                                                      |
| <code>list</code>        | Returns a list of currently defined and named real data fields. This returns a full Tcl list, for use with those commands that require list variables.                                                                    |
| <code>list.all</code>    | Returns a list of currently defined and named data fields (for example, real data, vector data, and so on). This returns a full Tcl list for use with commands that require list variables.                               |

## A: Sentaurus Process Commands

### select

|                                 |                                                                                                                                                                                                                                                                                                                              |
|---------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>&lt;material&gt;</code>   | Specifies the material to which the command applies. Different expressions for the data field initialization in different materials can be used. For information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                         |
| <code>min, max</code>           | These parameters must be used with the <code>name</code> parameter. When specified, the <code>select</code> command returns the minimum or maximum of the field name. You can limit the query to a specific material using the <code>material</code> parameter or a specific region using the <code>region</code> parameter. |
| <code>name</code>               | Name of the new data field. The default is the name is <code>Z_Plot_Var</code> . This is used by all of the commands when a plot name is not specified. This is a powerful feature, as solution fields also can be created.                                                                                                  |
| <code>node.evaluate</code>      | Computes the divergence of a vector field at a node.                                                                                                                                                                                                                                                                         |
| <code>permanent</code>          | Returns 1 if the data field is written into permanent storage. If not, it returns 0.                                                                                                                                                                                                                                         |
| <code>present</code>            | Returns 1 if the data field with the name defined by the <code>name</code> parameter exists. If it does not exist, it returns 0.                                                                                                                                                                                             |
| <code>region</code>             | Name of the region. This parameter specifies the region to which the command applies. Different expressions for the data field initialization in different regions can be used.                                                                                                                                              |
| <code>report.location</code>    | Works with the <code>min</code> and <code>max</code> parameters, Reports the coordinate of the minimum or maximum value of the selected field.                                                                                                                                                                               |
| <code>store</code>              | Sets the data field with the name defined by the <code>name</code> parameter to be written into permanent storage when a structure file is output. The default is false.                                                                                                                                                     |
| <code>syntax.check.value</code> | Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during normal run mode. Setting this value avoids such problems.                                              |



`z, value` Accepts an expression of data fields that are used to build a new data field. The operators `*`, `/`, `+`, `-`, and `^` all work as expected. The vector variables are listed below. The data fields available can be listed with the `list` parameter. In addition to the listed data fields, the `x`- and `y`-coordinates can be specified. Several functions also are available to operate on data fields:

- `abs` Absolute value.
- `erf` Error function.
- `erfc` Complementary error function.
- `exp` Exponential.
- `log` Logarithm.
- `log10` Logarithm base 10.
- `sqrt` Square root.

**Examples:**

```
select z=log10(Vacancy)
```

Selects as the plot variable the base 10 logarithm of the vacancy concentration.

```
sel z=(Vacancy - 5.0e14)
```

Selects as the plot variable the `Vacancy` concentration minus a constant value of  $5 \times 10^{14}$ .

```
sel z=(MyData - 1.0e18 * exp ( y * y / 1.0e-8 )) name=MyField store
```

Selects as the plot variable the difference between the `MyData` and an analytic profile. This data field will be named `MyField`. The `store` flag indicates that the doping field must be written into any saved structure files.

```
sel z=1.0e9 name=Pressure store
```

Sets the value of the data field `Pressure` to  $10^9$  dyn/cm<sup>2</sup>. The CGS unit is used internally for mechanics.

```
select name=MyField delete
```

Deletes the `MyField` data field.

```
select z= "-diff(Potential)" edge.vector store name=ElectricField
```

Calculates the electric field in a new data field called `ElectricField`. The `store` option ensures that the new data field is stored to disk in subsequent calls of the `struct` command.

```
select list
```

Lists all available real data fields.

```
select z= "grad(Temperature)" node.evaluate store name=TotalHeat
```

Calculates the total heat field in a new data field called `TotalHeat`.

**See:** All postprocessing commands

---

## SetAtomistic

**Function:** Sets the atomistic mode as the simulation mode.

**Syntax:** `SetAtomistic`

**Description:** Switches the simulation domain to the atomistic mode. The following commands are affected in this mode:

- `deposit`
- `diffuse`
- `etch`
- `implant`
- `profile`
- `region`
- `select`
- `strip`
- `struct`

If there are continuum fields, `SetAtomistic` automatically calls `PDE2KMC` to atomize the fields and to make them available as an initial state for the KMC simulation.

**Examples:** `SetAtomistic`

**See:** [Chapter 5 on page 369](#)

---

## SetDFISEList

**Function:** Sets a list of solution or term names to be included when saving DF-ISE format files.

**Syntax:** SetDFISEList  
[solution/term names]  
[Solutions] [Dopants]

**Description:** Creates a solution or term name list that is passed to the `struct` command. Depending on the flags provided by users, solution names or dopant names can be included or excluded from the fields that need to be written to the DF-ISE files. If the command is executed without arguments, the default saving is used, which includes all solutions, total and active dopant fields, and `NetActive` (`DopingConcentration`). If DF-ISE or TDR files are saved in the `struct` command with the `smesh` parameter, the selection of fields does not depend on the `SetDFISEList` specifications.

**Options:**

**Dopants** Dopants include the total and active dopant concentrations. Specifying `!Dopants` does not save total and active dopant concentrations, but still saves `NetActive` (`DopingConcentration`). The default is `true`.

solution/term names

Any known fields listed on the command line are added to files saved with `struct dfise=<filename>`.

**Solutions** Stores all solution variables (necessary for restarting a simulation). Using `!Solutions` switches off all default savings (only fields specified by name will be saved to DF-ISE files). The default is `true`.

**Examples:** SetDFISEList VTotal !Solutions  
Allows only the `VTotal` field to be written to the DF-ISE file.

SetDFISEList Vac Temperature  
Adds the `Vac` and `Temperature` fields to those usually saved in DF-ISE files.

SetDFISEList Int0 Intm Vac0 Vacpp  
Adds the `Int0`, `Intm`, `Vac0`, and `Vacpp` fields to those usually saved in DF-ISE files.

SetDFISEList !Solutions Dopants  
Saves only `NetActive`, and the total and active dopants.

---

## SetDielectricOxidationMode

**Function:** Sets the oxidation mode to grow oxide with dielectric on top.

**Syntax:** `SetDielectricOxidationMode  
<Dielectric> <Oxidant>  
[Dirichlet | MassTransfer] [Continuous | Segregation]`

**Description:** Sets the related parameters and models for oxidation with a dielectric on top. Boundary conditions at the gas–dielectric interface and the dielectric–oxide interface default to `Dirichlet` and `Continuous`, respectively.

In addition, these settings can be changed with:

```
pdbSetString <Dielectric> <Oxidant> DielectricOxTransportBC MassTransfer  
pdbSetString <Dielectric> <Oxidant> DielectricOxInterfaceBC Segregation
```

**Options:**

`Continuous` Sets continuous boundary condition at the dielectric-oxide interface.

`<Dielectric>` Specifies name of dielectric material to grow oxide underneath.

`Dirichlet` Sets Dirichlet boundary condition at the gas–dielectric interface.

`<Oxidant>` Specifies name of oxidant.

`MassTransfer` Sets mass transfer boundary condition at the gas–electric interface.

`Segregation` Sets segregation boundary condition at the dielectric–oxide interface.

**Examples:** `SetDielectricOxidationMode Nitride O2 MassTransfer Segregation`

**See:** [UnsetDielectricOxidationMode on page 1111](#)

## SetFastMode

**Function:** Omits diffusion and Monte Carlo implantation to simulate the device geometry quickly.

**Syntax:** SetFastMode

**Description:** Runs the simulation quickly without simulating dopants and defects. This can be useful when setting up a command file to confirm quickly that the geometry is satisfactory before simulating more computationally expensive steps.

To switch off implantation, use:

```
pdbSet ImplantData NoImplant 1
```

To switch off oxidation/reaction, use:

```
pdbSet Diffuse NoDiffusionReaction 1
```

This may be useful for 3D geometry simulation.

**Examples:** SetFastMode

## SetPlxList

**Function:** Sets a list of solution and term names to be passed to the `WritePlx` command.

**Syntax:** `SetPlxList [solution/term names]`

**Description:** Sets the list of fields to be saved in the next call to `WritePlx`. The list can contain solutions or term names.

**Options:**

`solution/term names`

Defines the name list to be passed to the `WritePlx` command.

**Examples:** `SetPlxList { Vacancy Potential }`  
`WritePlx V_and_P.plx`  
Write a `.plx` file with the data fields `Vacancy` and `Potential`.

**See:** [WritePlx on page 1113](#)

---

## SetTDRList

- Function:** Sets a list of solution or term names to be included when saving TDR format files.
- Syntax**            `SetTDRList`  
                      `[solution/term names]`  
                      `[Solutions] [Dopants]`
- Description:** This command has the same syntax as `SetDFISEList`. Currently, there is only one list of fields to be stored when using either TDR or DF-ISE format files (that is, `SetTDRList` and `SetDFISEList` perform exactly the same function).
- Options:**
- `Dopants`            `Dopants` include total and active dopant concentrations. `!Dopants` does not save total and active dopant concentrations, but still saves `NetActive` (`DopingConcentration`). The default is true.
- `solution/term names`
- Any known fields listed on the command line are added to files saved with `struct dfise=<filename>`.
- `Solutions`            Stores all solution variables (necessary for restarting a simulation). Using `!Solutions` switches off all default savings (only fields specified by name will be saved to DF-ISE files). The default is true.
- See:**                [SetDFISEList on page 1057](#)

## SetTemp

- Function:** Sets the temperature value.
- Syntax:** SetTemp <n>[<C>|<K>]
- Description:** Sets the temperature value. The default unit is degree Celsius.
- Examples:** SetTemp 1000.0  
Sets the temperature to 1000°C .



## SetTS4ImplantMode

**Function:** Sets implant-related parameters and models to match those of TSUPREM-4.

**Syntax:** SetTS4ImplantMode [Taurus | Native]

**Description:** Sentaurus Process and TSUPREM-4 use different codes and, sometimes, have different assumptions or algorithms for analytic implantations. This command tries to minimize this difference by setting appropriate switches that make Sentaurus Process simulation results as close as possible to those produced by TSUPREM-4. This includes:

- Use beam dose.
- Switch on `ts4.backscattering` model.
- Switch off Sentaurus Process `backscattering` model.
- In Taurus mode, also switch on PAI model with TSUPREM-4-compatible PAI mode.

The results may not be exactly the same due to differences in numeric methods for some cases.

**Options:**

Native            Makes simulation results close to those of TSUPREM-4 native implanter.

Taurus            Makes simulation results close to those of TSUPREM-4 Taurus implanter.

---

## SetTS4MechanicsMode

**Function:** Sets mechanics-related parameters and models to match those of TSUPREM-4.

**Syntax:** SetTS4MechanicsMode [advanced | 2008.09]

**Description:** Sets mechanics-related parameters and models in Sentaurus Process to match TSUPREM-4 settings. This includes the:

- Viscoelastic model and parameters.
- Elastic moduli.
- Stress relaxation factor setting.
- Stress smoothing setting.
- Thermal mismatch coefficients.
- Some settings for oxidation used for backward compatibility (these settings are the same as the defaults in the PDB).

The parameters above are set to match TSUPREM-4 defaults. The results may differ due to different numeric methods.

**Options:**

2008.09 Used for backward compatibility.

advanced Sets TSUPREM-4 advanced settings.

---

## SetTS4OxidationMode

**Function:** Sets oxidation-related parameters and models to match those of TSUPREM-4.

**Syntax:** SetTS4OxidationMode [advanced | 2008.09]

**Description:** Sets oxidation-related parameters and models in Sentaurus Process to match TSUPREM-4 settings. This includes:

- Settings from SetTS4MechanicsMode
- Activation volumes of SDO reaction rate and diffusivity
- Activation volumes of stress-dependent viscosity
- Native layer thickness
- Stress-dependent oxidation flag

Because TSUPREM-4 has different values for the activation volume of stress-dependent viscosity during oxidation and nonoxidation steps, it is recommended to call SetTS4OxidationMode immediately before the oxidation step and call SetTS4MechanicsMode after it.

The parameters above are set to match TSUPREM-4 defaults. The results may not be very close due to differences in numeric methods for some cases.

**Options:**

2008.09 Sets oxidation and mechanics parameters to Version A-2008.09 default values.

advanced Sets parameters to TSUPREM-4 advanced settings.

---

## SetTS4PolyMode

- Function:** Sets the polycrystalline model to match those of TSUPREM-4.
- Syntax:** SetTS4PolyMode
- Description:** Sets the related parameters and models for the polycrystalline model in Sentaurus Process to match TSUPREM-4 settings.

## SheetResistance

- Function:** Calculates the sheet resistance and p-n junction depth.
- Syntax:** `SheetResistance`  
`[x=<n>] [y=<n>] [z=<n>]`
- Description:** Calculates the sheet resistance and p-n junction depth of a semiconductor layer in the vertical direction. It can only be used after a diffusion step.
- Options:**
- `x, y, z` Specify the cut position. For 1D simulations, no cut specification is necessary. In 2D, either `x` or `y` should be specified and, for 3D simulations, two axes must be specified. The unit for `x`, `y`, and `z` is  $\mu\text{m}$ .
- Examples:** `SheetResistance y=0.4 z=-0.1`  
Calculates the sheet resistance and p-n junction depth of a 3D structure using the cut plane `y = 0.5  $\mu\text{m}$`  and `z = (-0.1)  $\mu\text{m}$` .
- See:** [Chapter 13 on page 825](#)

---

## simDelayDouble

**Function:** Retrieves the Tcl expression used to evaluate a double-precision simulator state variable.

**Syntax:** `simDelayDouble <c> [<c>]`

**Description:** This command is very similar to the `simGetDouble` command except that the evaluation of the return expression is delayed.

**Examples:** `simDelayDouble Diffuse tempC`  
Returns `[simGetDouble Diffuse tempC]`, which is the unevaluated expression itself.

**See:** [simGetDouble on page 1070](#)

## simGetBoolean

- Function:** Reads a global simulator state variable.
- Syntax:** `simGetBoolean <c> [<c>]`
- Description:** Collects the one of the following global simulator state variables:
- AmbientReactions
  - IsEpi
  - IsGrowing
  - laser
  - MaterialReactions
- Examples:** `simGetBoolean Diffuse laser`  
Returns true if laser annealing is switched on.

---

## simGetDouble

**Function:** Reads a double-precision simulator state variable.

**Syntax:** `simGetDouble <c> [<c>]`

**Description:** Collects a simulator set global variable. These variables are:

- `EpiThick`
- `PH2O`
- `pO2`
- `pressure`
- `ramprate`
- `temp`
- `tempC`
- `tempK`
- `time`
- `Vt`
- `Vti`

If the variable is not defined, it returns zero.

**Examples:** `simGetDouble Diffuse tempK`

Returns the last diffusion temperature [K].

`simGetDouble Diffuse pO2`

Returns the oxygen partial pressure used during simulation.



## simSetBoolean

**Function:** Sets a global simulator state variable.

**Syntax:** `simSetBoolean <c> [<c>] <n>`

**Description:** Sets one of the following global simulator state variables:

- AmbientReactions
- IsEpi
- IsGrowing
- laser
- MaterialReactions

**NOTE:** Modifying global simulator state variables may cause errors in the simulation.

**Examples:** `simSetBoolean Diffuse laser 1`  
Sets the value of the global simulator state variable `laser` to true.

---

## simSetDouble

**Function:** Sets a double-precision simulator state variable.

**Syntax:** `simSetDouble <c> [<c>] <n>`

**Description:** Sets one of the following global double-precision simulator state variables:

- PH2O
- pO2
- temp
- tempC
- tempK
- Vti

**NOTE:** Modifying global simulator state variables may cause errors in the simulation.

**Examples:** `simSetDouble Diffuse temp 900`  
Sets the last diffusion temperature to 900°C .

---

## slice

**Function:** Extracts a 1D data slice through the 2D to 3D simulation object.

**Syntax:**

```
slice
  [name=<c>] [<material>]
  [value=<n>] [side=<c>]
  [mx] [my] [mz] [mdist]
  [x=<n>][<m>|<cm>|<um>|<nm>]
  [y=<n>][<m>|<cm>|<um>|<nm>]
  [z=<n>][<m>|<cm>|<um>|<nm>]
  [p1= <numeric list>]
  [p2= <numeric list>]
  [syntax.check.value=<c>]
```

**Description:** This is an extremely powerful data analysis command. It extracts xy data along a slice through a specified material. It returns a Tcl list of coordinate–value pairs, where the coordinate is the distance [ $\mu\text{m}$ ] along the reference segment, and the value is the local value of the parameter specified either with the `-name` option or, if that is not provided, in the most recent `select` command. For example:

```
select z=Boron
set sliceRet [slice y=0.5]
foreach { x value } $sliceRet {
  LogFile "$x\t$value\n"
}
```

This will print and send to the log file the boron profile in x-coordinate value pairs at  $y=0.5$ .

This command extracts the selected variables as a function of position along a constant line. In one dimension, the command returns the concentration versus depth, for example. It also can extract a constant contour of the data selected and returns the coordinates of the isoconcentration line.

**Options:**

`<material>` For information about specifying materials, see [Material Specification on page 50](#).

`mx, my, mz, mdist`

These Booleans change the reporting information when interface materials are selected. The interface distance can be reported as projected along one of the three primary axes (`mx`, `my`, `mz`). Alternately, it can be reported as the distance along the extracted line (`mdist`).

`name` Specifies the name of the data field. The default is `Z_Plot_Var`.

## A: Sentaurus Process Commands

### slice

`p1, p2` Specify the start point and endpoint for the cutline, and each parameter takes a list of numeric values. The first, second, and third values in the list are taken as the x-, y-, and z-value, respectively. The missing value will be treated as zero. These parameters allow the `slice` command to extract data along an arbitrary line. The output from the `slice` command is a list of (distance, value) pairs, where distance is measured from `p1` point, and value is the extracted value of the selected quantity along the line. Error messages will given if `p1` and `p2` are mixed with `x`, `y`, `z`, or `value` parameters.

`side` Takes the value from one of the two bulk materials consisting of the interface or 'interface' (literally) itself. If `side` is not specified, 'interface' itself is assumed. If `side` is specified as one of the bulk materials, the value of the selected quantity for the bulk material at the interface is returned. This parameter is effective only if an interface material is specified.

`syntax.check.value`

Sets a value to be returned only during syntax-checking mode. Sometimes, the value returned by a command can cause a false syntax-check error because the value returned by the command would not be the value during normal run mode. Setting this value avoids such problems.

`x, y, z, value`

Specify a cutline for up to a four-dimensional solid, so that a 2D return is provided. For 1D simulations, none of these parameters is required. For 2D simulations, one is required. For 3D simulations, two are required. These requirements are reduced by one if an interface material has been specified. The default unit for `x`, `y`, and `z` is  $\mu\text{m}$ .

#### Examples:

```
slice silicon y=0.01
```

Returns the selected variable as a function of depth at a constant lateral position of 0.01  $\mu\text{m}$ .

```
slice silicon val=16.0
```

Returns the x- and y-positions of a contour of the selected variable at 16.0.

```
slice silicon /oxide mdist side=silicon
```

Returns the value of the selected quantity at the silicon side of the interface as a function of distance from the start of the interface.

```
slice name=Boron p1= {0 0} p2= {1. 2}
```

Returns the boron concentration along a line passing through points (0, 0) and (1, 2).

#### See:

[select on page 1053](#), [tclsel on page 1091](#)

---

## smooth

**Function:** Smooths a set of fields.

**Syntax:** `smooth`  
`smooth.field= {list of fields}`  
`[smooth.distance= {double array}]`  
`[init=<n>][<hr>|<min>|<s>]`

**Description:** Smooths a set of fields with specified smooth distances.

**Options:**

`init` Specifies the first time step for solving the smoothing equations. The default value is 0.0001 s, which is sometimes inappropriate for defect simulations, particularly in cases of damage. The default unit is minute.

`smooth.field` Specifies a set of fields to be smoothed. Any existing field can be specified.

`smooth.distance` Specifies the smoothing distance for each field as specified in the `smooth.field` parameter. The default is 2.0 nm.

**Examples:** `smooth smooth.field= {Int_Implant Vac_Implant} \  
smooth.distance= {2<nm> 3<nm>}`  
Smooths the interstitial and vacancy implantation profiles with smooth distances of 2 nm and 3 nm, respectively.

---

## solution

**Function:** Obtains and sets solution parameters for generic solutions using Alagator.

**Syntax:**

```
solution
  [add] [list] [present] [needsolution]
  [nosolve | solve | ifpresent=<c>] [smooth]
  [damp] [negative] [DiffStep] [GrowthStep] [InitStep] [Heat]
  [name=<c>] [reset] [store]
  [material.list= {<string list>}]
  [unit=<c>]
```

**Description:** Creates and modifies solution names, and sets conditions for their inclusion in the assembly. Solutions also can be listed and checked.

**Options:**

**add** Creates a new solution.

**damp** Damps the Newton iteration updates for this solution.

DiffStep, GrowthStep, InitStep, Heat, smooth

Determines in which solver the solution variable will be solved:

- DiffStep variables are solved with the diffusion solver such as dopants and defects.
- GrowthStep variables are solved in the reaction step and are usually oxidants.
- InitStep variables are solved during initialization step.
- Heat variables are solved during laser annealing step.
- smooth variables are solved during smoothing steps (such as occurs when using the smooth command).

**list** Lists all of the currently defined solutions.

**material.list** List of materials where the solution variable will be solved. If the list is empty, the solution variable will be solved only if the equations are set for a specific material.

**name** The character string used for the solution. Capitalization is not ignored, for example, vacancy and Vacancy are different. Abbreviations of names are not accepted.

**needsolution** Returns true if the solution must be solved.

**negative** Allows the solution specified to have negative values.

`nosolve, solve, ifpresent`

Only one of these options can be used at a time. They control the solution status for the next command:

- `nosolve` means do not solve.
- `solve` switches on the solution status for the next command.
- `ifpresent` sets up a conditional solve.

If all the solutions in the specified list are also being solved, this solution is solved.

`present` Returns true if the solution is defined and a data field matches the name.

`reset` Allows reaction solution variables to be reset before the diffusion starts. The default is on.

`store` Allows the `solution` command to be stored in a TDR file.

`unit` Unit of the solution variable. The default is  $\text{cm}^{-3}$ .

**Examples:**

```
solution name=Potential damp negative solve add
```

Creates a solution named `Potential` and always solves for it. Allows the solution to have negative values and uses damping on the Newton iteration updates.

```
solution name=Vac !damp !negative solve add
```

Creates a solution name `Vac` and always solves for it. Does not use damping and does not allow values to become negative.

```
solution name=I2 !damp !negative ifpresent = {Int Vac} add
```

Creates a solution named `I2` and solves for it if `Int` and `Vac` are also present and being solved.

```
solution list
```

Returns a list of all solutions.

```
solution name=Vac present
```

Returns a Boolean true if `Vac` has been defined and if there is a data field with the name `Vac`.

**See:** [term on page 1099](#)

---

## sptopo

**Function:** Exchanges structure and dispatches commands to the 2D etch and deposit simulator Sentaurus Topography.

**Syntax:** `sptopo { <commands> }`

**Description:** Transfers the boundary representation of the current structure to Sentaurus Topography and dispatches the commands to Sentaurus Topography. After executing the commands in Sentaurus Topography, the modified structure is retrieved and remeshed in Sentaurus Process.

**NOTE:** A license for Sentaurus Topography must be available, and a version of the Sentaurus Process binary with Sentaurus Topography included must be installed.

**Options:**

<commands> Any number of Sentaurus Topography commands. It is recommended to enclose the commands in a pair of braces to protect them from interpretation by the Tcl interpreter.

**Examples:**

```
sptopo {
    deposit material=Oxide thickness = 0.005
    deposit material=PolySilicon thickness = 0.180
}
```

**See:** Refer to the *Sentaurus Topography User Guide*.  
For 3D operations, see [topo on page 1101](#).



## stdiff

**Function:** Compares current structure with one from a TDR file.

**Syntax:** `stdiff <tdr file>`

**Description:** Reads the external TDR file, interpolates the data onto the current structure, compares data, and reports if data exceeds relative error criteria (subject to absolute error minimum value).

**Options:**

`<tdr file>` Gives the full path or prefix of a TDR file. The prefix is the file name without `_fps.tdr`.

**Examples:** `stdiff n1_fps.tdr`

---

## strain\_profile

**Function:** Defines the strain introduced by a impurity as a piecewise linear function of the mole fraction in a given substrate.

**Syntax:**

```
strain_profile
  <material>
  species=<c>
  ratio= <numeric list>
  strain= <numeric list>
```

**Description:** The presence of certain materials such as germanium in silicon can modify the lattice spacing. This command allows Sentaurus Process to compute strains using the impurity mole fraction.

**Options:**

<material> Substrate material where the strains are defined.

ratio Mole fraction of the species; ranges from 0 to 1.

species Species in the substrate that cause the strain.

strain Strain caused by the specified mole fraction; ranges from 0 to 1.

**Examples:** strain\_profile silicon species=Germanium ratio= {0 1} strain= {0 0.0425}

**See:** [transform on page 1102](#)

## stressdata

- Function:**
- Defines intrinsic stress of materials for use in stress calculations.
  - Defines boundary conditions for stress analysis.
  - Reports the maximum stress values and their locations.
  - Defines edge dislocation settings.

**Syntax:**

```
stressdata
  [<material> | region=<c>]
  [sxxi=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [syyi=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [szz1=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [sxyi=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [syzi=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [szxi=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [sxx1=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [syy1=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [szz2=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [sxx2=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [syy2=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [szz2=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
  [base=<n>][<m>|<cm>|<um>|<nm>]
  [bc.location=Left | Right | Front | Back | Bottom]
  [bc.rotation.axis= { [xa=<n>] | [ya=<n>] | [za=<n>] }]
  [bc.value= { [dx=<n>] | [dy=<n>] | [dz=<n>] | [pressure=<n>] |
    [pfx=<n>] | [pfy=<n>] | [pfz=<n>] |
    [rx=<n>] | [ry=<n>] | [rz=<n>]
  }]
  [point.coord= {<n> <n> <n>}]
  [apply.dislocation]
  [dislocation.origin= {<n> <n> <n>}]
  [para.orient= {<n> <n> <n>}]
  [perp.orient= {<n> <n> <n>}]
  { [optimize.dislocation]
    [origin.min= {<n> <n> <n>}] [origin.max= {<n> <n> <n>}]
    [opt.mindssq=<n>] [opt.mindnrm=<n>]
    [opt.maxiter=<n>] [opt.tolerance=<n>] }
  [number=<n>] [sxx] [syy] [szz] [sxy] [syz] [szx] [vms] [ps] [hs] [pr]
```

**Description:** Provides stress analysis parameters for input and output. Zero is the default value for all intrinsic stress parameters. Wherever possible, you should use the `deposit` command with specified stresses to apply intrinsic stresses.

**Options:**

`<material>` Material in which the stress parameters are to be set.

`region` Region where the stresses are to be applied.

## A: Sentaurus Process Commands

### stressdata

`sxxi, syyi, szzi, sxyi, syzi, szxi`

Intrinsic stresses. The default unit is  $\text{dyn/cm}^2$ .

#### Width-dependent intrinsic stress

`base` Base width. The default unit is  $\mu\text{m}$ .

`sxx1, syy1, szz1`

Scale factors in linear width-dependent intrinsic stress.

`sxx2, syy2, szz2`

Scale factors in natural logarithmic width-dependent intrinsic stress.

#### Boundary conditions

`bc.location` Specifies the area where the boundary conditions are applied. The value can be `Left` | `Right` | `Front` | `Back` | `Bottom`.  
`Left` | `Right` | `Front` | `Back` | `Bottom` refer to the outer boundary surfaces of the simulation domain.

`bc.rotation.axis`

Specifies the coordinates of the point around which rotational boundary conditions are applied. The default unit is centimeter (cm).

`bc.value` Specifies the boundary condition types and values. The type can be:

- `dx/dy/dz` for displacement rate (default unit: cm/s).
- `pressure` for pressure (default unit:  $\text{dyn/cm}^2$ ).
- `pfx/pfy/pfz` for point force (default unit: dyne).
- `rx/ry/rz` for rotational velocity (default unit: rad/s).

`point.coord` Specifies the location where the point force is applied.

#### Maximum stress list

`number` Specifies the number of the largest stress values to report.

`sxx, syy, szz, sxy, syz, szx, vms, ps, hs, pr`

Specifies from which stress component (`sxx`, `syx`, `szz`, `sxy`, `syz`, `szx`) or which derived stress (`vms` is the von Mises stress, `ps` is the principal stress, `hs` is the hydrostatic stress, and `pr` is the pressure) to extract the maximum stress values. Values for stress components and principal stresses are computed at element centroid, while values for von Mises stresses, hydrostatic stresses, and pressures are computed at nodes.

**NOTE:** To extract maximum principal stresses, use:

```
pdbSet Mechanics Calculate.Principal.Stress 1
```

### Edge dislocation settings

`apply.dislocation`

Indicates that an edge dislocation will be defined.

`dislocation.origin`

Specifies the location of dislocation core.

`para.orient`

Specifies the direction of edge dislocation.

`perp.orient`

Specifies the Burger's vector in the perpendicular direction to the half plane. The magnitude is the slip distance.

### Edge dislocation-induced strain energy minimization settings

`opt.maxiter`

Specifies the maximum number of iterations allowed in the optimization loop. The default value is 500.

`opt.mindnrm`

Specifies the change in norm of the parameter vector for convergence. The default value is 5e-3.

`opt.mindssq`

Specifies the relative change in the sum of the squares for convergence. The default value is 1e-5.

`opt.tolerance`

Specifies the tolerance of target errors. The default value is 1e-3.

`optimize.dislocation`

Switches on the elastic strain energy minimization of edge dislocations defined with the option `!apply.dislocation`.

`origin.max`

List of numbers defining the x-, y-, and z-coordinates of the lower-right front corner of the bounding box for the location of the edge dislocation core.

`origin.min`

List of numbers defining the x-, y-, and z-coordinates of the upper-left back corner of the bounding box for the location of the edge dislocation core.

### Examples:

`stressdata nitride syyi=1.4e10`

Sets the yy component of the intrinsic stress in nitride to  $1.4 \times 10^{10}$  dyn/cm<sup>2</sup>.

## StressDependentSilicidation

- Function:** Enables stress-dependent silicidation for a particular silicide.
- Syntax:** `StressDependentSilicidation <silicide>`
- Description:** Switches on stress-dependent silicidation in the material `<silicide>`. In the model, reaction rates are normal stress dependent; the diffusivity of the reactant species, silicon, (represented by the field `iSilicon`) is pressure dependent; and the silicide is allowed to relax.
- Options:**
- `<silicide>` Specifies the name of the silicide that will use the pressure-dependent model.
- Examples:** `StressDependentSilicidation NickelSilicide`
- See:** [Stress-dependent Silicidation on page 623](#)

## strip

- Function:** Completely removes a layer exposed to the top gas region.
- Syntax:** `strip <material> [remesh]`
- Description:** Completely removes a layer exposed to the top gas region. In 2D, the mesh is regenerated immediately. In 3D, only the boundary is modified and the mesh is regenerated later when necessary.
- Options:**
- `<material>` The specified material, if exposed, is completely removed. For information about specifying materials, see [Material Specification on page 50](#).
- `remesh` By default, the structure is remeshed in 2D after strip. Setting `!remesh` prevents remeshing. In 3D, the boundary is changed without generating a mesh, so this parameter has no effect in 3D. Preventing remeshing can save time for very large structures.
- Examples:** `strip oxide`  
Removes all oxide regions exposed to the top gas region.

---

## struct

|                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
|---------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>          | Writes files containing the structure or the mesh and solutions.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <b>Syntax:</b>            | <pre> struct   [dfise=&lt;c&gt;   tdr=&lt;c&gt;   smesh=&lt;c&gt;]   [pdb] [pdb.only] [bnd] [sat]   [contacts] [interfaces]   [bndfile=&lt;c&gt;] [datfile=&lt;c&gt;] [grdfile=&lt;c&gt;] [satfile=&lt;c&gt;] [tdr.bnd]   [compress] [alt.maternames]   [Gas]   [mshcmd]   scale=&lt;n&gt; [binary] [FullD] [simplify=&lt;n&gt;]   {[x=&lt;n&gt;][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]    [y=&lt;n&gt;][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]    [z=&lt;n&gt;][&lt;m&gt; &lt;cm&gt; &lt;um&gt; &lt;nm&gt;]}   [visual.1D] [Adaptive] </pre> |
| <b>Description:</b>       | Writes the structure and the simulation mesh and field data to one or several files. The data saved is from the current set of solution values.                                                                                                                                                                                                                                                                                                                                                                                                          |
| <b>Options:</b>           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Adaptive                  | In 3D, meshing is delayed until it is needed; to save a file, a mesh may need to be created. This parameter controls whether adaptive meshing is used. The default is taken from the <code>pdb</code> parameter <code>Grid Adaptive</code> .                                                                                                                                                                                                                                                                                                             |
| alt.maternames            | Saves alternative material names to DF-ISE or TDR format files. If you choose an alternative name for a material using <code>mater alt.matername</code> or <code>region alt.matername</code> , the alternative material name is used in the file when this parameter is specified. When writing DF-ISE files, the original material name is not available upon loading. In TDR files, the Sentaurus Process material name also is stored in the file, so both the proper material names and the alternative names are restored when loading a TDR file.  |
| binary                    | Uses binary (not the default compressed ASCII) format when writing DF-ISE files.                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| bnd                       | Saves a boundary file in 2D and 3D along with the DF-ISE or TDR file. The default is false.                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| bndfile, datfile, grdfile | Specify the corresponding file names separately.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| compress                  | Writes compressed or uncompressed DF-ISE format files. The default is true.                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |



|                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|-------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>contacts</code>   | Writes contacts defined in the <code>contact</code> command into the boundary file. The default is true.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>dfise</code>      | Saves files in DF-ISE format. The extensions <code>_fps.grd</code> and <code>_fps.dat</code> are added automatically. Therefore, if <code>dfise=filename</code> is specified, Sentaurus Process saves the files <code>filename_fps.grd</code> and <code>filename_fps.dat</code> .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|                         | The coordinate system for Sentaurus Process differs from the coordinate system in the DF-ISE files. In Sentaurus Process, the x-direction is always perpendicular to the substrate surface and the positive direction increases with depth into the substrate (the negative direction is up). The y-direction and z-direction are parallel to the initial substrate surface in 2D and 3D, respectively. In DF-ISE, different coordinate systems are used for 1D, 2D, and 3D. In 2D, x is parallel to the initial substrate surface and negative-y points up. In the 3D DF-ISE coordinate system, positive-z is up, and x and y are parallel to the initial substrate surface. The appropriate coordinate transformation is applied by default. To change the coordinate rotation, use the <code>math</code> command. |
| <code>FullD</code>      | If this Boolean parameter is specified, the mesh is extruded to the maximum dimension allowed in the simulation temporarily before saving the file. After saving the file, the simulation is continued in the same dimension as before.<br>If <code>!FullD</code> is specified in a <code>struct</code> command, the saved files contain mesh and data in the dimension currently used in the simulation.                                                                                                                                                                                                                                                                                                                                                                                                            |
|                         | <b>NOTE:</b> When TDR restart files are saved, by default, no extrusion is performed.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| <code>Gas</code>        | By default, Sentaurus Process writes regions of material gas to DF-ISE, <code>.bnd</code> , and TDR files. If <code>!Gas</code> is specified, regions of material gas are not saved.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| <code>interfaces</code> | Saves interface data in DF-ISE and TDR format files. Specify <code>!interfaces</code> to prevent storing interface data. The default is true.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <code>mshcmd</code>     | When specified with the <code>smesh</code> keyword, <code>mshcmd</code> writes a <code>.cmd</code> file with refinement information readable by Sentaurus Mesh.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| <code>pdb</code>        | Saves <code>pdb</code> parameters along with the geometry and data in TDR format file.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| <code>pdb.only</code>   | Saves only <code>pdb</code> parameters (without geometry and data) in TDR format file.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| <code>sat</code>        | This Boolean parameter is used to enforce or prevent the saving of a Sentaurus Structure Editor restart file.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

## A: Sentaurus Process Commands

struct

|          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
|----------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| satfile  | <p>When using Sentaurus Structure Editor for 3D geometry-modeling steps, a Sentaurus Structure Editor restart file is saved by default. The parameter <code>satfile</code> defines the file name. The default file extension is <code>.sat</code>.</p> <p>When saving a 2D or 3D boundary file in <code>.bnd</code> or <code>.tdr</code> files, the extracted geometry is simplified before saving to file. The double parameter <code>simplify</code> defines the maximum deviation of the simplified boundary from the extracted geometry.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| scale    | <p>The coordinates are multiplied by the specified value before writing them to the file. The default is <code>1.0e4</code>, which converts from Sentaurus Process internal standard units (centimeter) to DF-ISE units (micrometer).</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| simplify | <p>When saving a 2D or 3D boundary file in <code>.bnd</code> or <code>.tdr</code> files, the extracted geometry is simplified before saving to file. The double parameter <code>simplify</code> defines the maximum deviation of the simplified boundary from the extracted geometry.</p>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| smesh    | <p>Selects regions and fields, and saves a set of files to be transferred to Sentaurus Mesh. If <code>smesh=&lt;filename&gt;</code> is specified, a TDR file with the boundary description <code>&lt;filename&gt;.bnd.tdr</code>, a TDR file <code>&lt;filename&gt;.fps.tdr</code> with the simulation mesh, and the field data are saved. Regions of material gas and interface meshes are omitted. Only total and active dopant concentrations, stress fields, and <code>NetActive</code> (<code>DopingConcentration</code>) are stored. If contacts have been defined, they are included in both files.</p> <p>If the <code>mshcmd</code> keyword is also given, a text file <code>&lt;filename&gt;.msh.cmd</code> is written which contains refinement information readable by Sentaurus Mesh.</p> <p>If the parameter <code>StoreDelaunayWeight</code> is set (<code>pdbSet Grid SnMesh StoreDelaunayWeight 1</code>), the TDR file will have the field variable <code>Delaunay-Voronoi weight</code> (<code>DelVorWeight</code>) in the unit of <math>\mu\text{m}^2</math>. This variable is used in the weighted box method in Sentaurus Device.</p> |

**NOTE:** Files written using the `smesh` parameter cannot be used to restart a Sentaurus Process simulation.

- tdr** Saves a file in TDR format. The extension `_fps.tdr` is added automatically. By default, all modifications to the parameter database are written to the TDR file to support splitting and restarting simulations. The coordinate system in TDR files is the same as DF-ISE files. By default, TDR files can be used for splitting and restarting simulations. Coordinates and field values are stored with their unscaled internal values. If `!Gas` or `!interfaces` is specified, coordinates and field values are scaled to the DF-ISE units and information required for restart is omitted. For information about the TDR format, refer to the *Sentaurus Data Explorer User Guide*.
- tdr.bnd** Writes a TDR file that contains just the boundary representation.
- visual.1D** Applies only to 1D simulations. If specified, Sentaurus Process orders the nodes when writing them in a TDR file, so that the file can be easily visualized with Tecplot SV.
- x, y, z** Specify a cutline for up to a 3D solid, so that a 1D TDR file is stored. For 1D simulations, none of these parameters is required. For 2D simulations, one is required. For 3D simulations, two are needed. Since the file is stored in TDR format, the `tdr` parameter must be used together with these parameters.

**Examples:**

```
struct dfise=output
```

Saves the DF-ISE files `output_fps.grd.gz` and `output_fps.dat.gz`.

```
struct smesh=output
```

Writes two files: `output_fps.tdr` and `output_bnd.tdr`.

```
struct tdr=output
```

Writes a TDR file with the current simulation mesh and data. By default, a restart file is written.

```
struct tdr=output bnd
```

Writes two files: `output_fps.tdr` and `output_bnd.tdr`.

```
struct bndfile=output
```

Writes one file `output_fps.bnd` with the boundary representation in DF-ISE format.

**See:** [contact on page 861](#), [integrate on page 945](#)

---

## substrate\_profile

**Function:** Defines the impurity profile in the substrate.

**Syntax:**

```
substrate_profile  
  <material>  
  species=<c>  
  xcoord= <numeric list>  
  concentration= <numeric list>
```

**Description:** Defines the profile of a species in a substrate in a piecewise linear manner. The piecewise linear function is given by the concentration corresponding to xcoord.

**Options:**

concentration Concentration of the impurity at the specified xcoord.

<material> Substrate material where the impurities are to be defined.

species Name of the impurity.

xcoord Coordinate in x-direction where the concentration will be defined.

**Examples:**

```
substrate_profile Silicon species=Germanium \  
  xcoord= {0 0.01 0.011 0.5 0.7 10} \  
  concentration= {1e10 1e10 2e22 2e22 1e10 1e10}
```

**See:** [transform on page 1102](#)

## tclsel

|                               |                                                                                                                                                                                                                                                                                                                                                                                             |
|-------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Function:</b>              | Selects the plot variable for the postprocessing routines.                                                                                                                                                                                                                                                                                                                                  |
| <b>Syntax:</b>                | <pre>tclsel   [&lt;material&gt;] [z=&lt;c&gt;] [name=&lt;c&gt;]   [store] [list] [vec]</pre>                                                                                                                                                                                                                                                                                                |
| <b>Description:</b>           | Specifies the plot variable for almost all other <code>plot</code> commands. This command is a companion to the <code>select</code> command, and it differs from the <code>select</code> command in that it accepts any general Tcl expression. Data fields are made into Tcl variables and can be accessed with standard Tcl variable methods.                                             |
| <b>Options:</b>               |                                                                                                                                                                                                                                                                                                                                                                                             |
| <code>list</code>             | Returns a list of currently defined and named data fields. The real data fields are listed by default. Vector data fields can be listed using the <code>vec</code> parameter. This returns a Tcl list for use with those commands that require list variables.                                                                                                                              |
| <code>&lt;material&gt;</code> | Specifies the material to which the command applies. Different expressions for the data field initialization in different materials can be used. For information about specifying materials, see <a href="#">Material Specification on page 50</a> .                                                                                                                                        |
| <code>name</code>             | Name of the new data field. The default is <code>Z_Plot_Var</code> . This is used by all commands when a plot name is not specified. This is a powerful feature, as solution fields also can be created.                                                                                                                                                                                    |
| <code>store</code>            | Controls whether the data field is written into permanent storage when a structure file is output. The default is <code>false</code> .                                                                                                                                                                                                                                                      |
| <code>vec</code>              | Lists the vector data fields. The default is <code>false</code> .                                                                                                                                                                                                                                                                                                                           |
| <code>z</code>                | Accepts a Tcl expression that are used to build a new data field. All valid Tcl expressions can be used in the string. Existing data fields are defined as Tcl variables, and the expression is evaluated node-by-node with the updated value of the variable. In general, this parameter must be enclosed in braces, so that variable substitution is performed when the string is parsed. |

## A: Sentaurus Process Commands

tclsel

**Examples:**

```
tclsel z = {log10($Arsenic)}
```

Selects as the plot variable the base 10 logarithm of the arsenic concentration.

```
tclsel z= {($Phosphorus - 5.0e14)}
```

Selects as the plot variable the phosphorus concentration minus a constant value of  $5 \times 10^{14}$ .

```
tclsel z= {($Phosphorus - 1.0e18 * exp ( $y * $y / 1.0e-8 ))} \  
name=Doping store
```

Selects as the plot variable the difference between the phosphorus and an analytic profile. This data field will be named `Doping`. The `store` flag indicates that the doping field should be written into any saved structure files.

```
tclsel list vec
```

Lists all available real and vector data fields.

**See:**

All postprocessing commands

## temp\_ramp

**Function:** Defines a temperature profile for use with the diffuse command.

**Syntax:**

```
temp_ramp
(list | clear | name=<c>)
[time=<n>][<hr>|<min>|<s>]
[temperature=<n>][<C>|<K>] |
[rampate=<n>][<C/s>|<K/s>|<C/min>|<K/min>]
[t.final=<n>][<C>|<K>]
[reset.init.time] [read.temp.file=<c>]
[current.time=<n>][<hr>|<min>|<s>]
[density.increase= [<regionName>=<n> | <material>=<n>]]
[delNT=<n>][<C>|<K>] | [delT=<n>][<C>|<K>]
[last] [hold]
[gas.flow=<c>]
[<ambient>]
[flow<ambient>=<n>][<l/min>]
[flows= {
    [<ambient1>=<n>][<l/min>]
    [<ambient2>=<n>][<l/min>]
}]
[ISSG]
[p<ambient>=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
[partial.pressure= {
    [<ambient1>=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa> |<dyn/cm2>]
    [<ambient2>=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa> |<dyn/cm2>]
    ...}]
[pressure=<n>][<atm>|<GPa>|<MPa>|<KPa>|<Pa>|<dyn/cm2>]
[epi.layers=<i>] [epi.model=<i>]
[epi.resist= { [<dopant1>=<n>[<ohm-cm>]] [<dopant2>=<n>[<ohm-cm>]]... }]
[epi.thickness=<n>][<m>|<cm>|<um>|<nm>]
[epi.doping= <parameter list>] [epi.doping.final= <parameter list>]
[sources= {<beam1> <beam2> ... <beamn>}]
[repair]
[deposit.type=<c>]
[crystal.rate= {"<100>"=<n> "<110>"=<n> "<111>"=<n>}]
[coeffs= {<A0> <A1> <A2> ... <An>}]
[mat.coeffs= {
    <material1>= {<A0> <A1> <A2> ... <An>}
    <material2>= {<A0> <A1> <A2> ... <An>}
    ...
    <materialn>= {<A0> <A1> <A2> ... <An>} }]
[angles.factors= {
    [<interface_mat1>= <numeric list>]
    [<interface_mat2>= <numeric list>]
}]
[auto.doping= <string list>]
```

## A: Sentaurus Process Commands

### temp\_ramp

**Description:** Specifies multiple-step temperature ramps and holds. This command can be used to construct a complex temperature sequence to be simulated with the `diffuse` command (by specifying the `temp.ramp` parameter of the `diffuse` command).

All `gas_flow` command parameters are available with the `temp_ramp` command (see [gas\\_flow on page 901](#)). The list of ambients is given in [Table 63 on page 605](#) and includes O<sub>2</sub>, H<sub>2</sub>O, HCl, N<sub>2</sub>, H<sub>2</sub>, and N<sub>2</sub>O. To specify epi, an epi-type ambient should be used. By default, two are available: `Epi` and `LTE`. For more information about epitaxy, see [Epitaxy on page 270](#).

#### Options:

`<ambient>` Shorthand specification to set the ambient partial pressure the same as the total pressure. If an ambient is specified this way, it should be the only ambient set in the `temp_ramp` command.

#### `angles.factors`

Specifies interface-specific anisotropic epi growth rate factors. This parameter specifies a piecewise linear growth rate factor versus angle for each growing interface (the factors should be between 0 and 1). For example, to create a 30° silicon facet and a 40° polysilicon facet, specify:

```
angles.factors= {  
  EpiOnSilicon_Gas= {0.0 1.0 25.0 1.0 30 0.0}  
  EpiOnPolySilicon_Gas= {0.0 1.0 35.0 1.0 40 0.0} }
```

`auto.doping` List of species for which the auto-doping model will be switched on during epitaxial growth.

`clear` Clears the global list of temperature ramps. When defining profiles, the action is to unite the new definition with any prior profiles of the same name.

`current.time` Returns the value of the ramp for the given time.

`coeffs` List of single-material coefficients  $A_0, A_1, \dots, A_n$  used in Fourier deposition when `epi.model=1` and `deposit.type=fourier`.

`crystal.rate` List of etching rates defined per crystallographic direction in the format: `{"<100>"=<dep rate> "<110>"=<dep rate> "<111>"=<dep rate>}` used for crystallographic deposition when `epi.model=1` and `deposit.type=crystal`.

`delNT` Defines the maximum temperature step during a temperature ramp-down if specified. The default unit is degree Celsius. It also can be defined globally with the command: `pdbSet Diffuse delNT {<n>}`.



|                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
|-------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>delT</code>             | Defines the maximum temperature step during a temperature ramp-up if specified. The default unit is degree Celsius. It also can be defined globally with the command: <code>pdbSet Diffuse delT {&lt;n&gt;}</code> .                                                                                                                                                                                                                                                                                           |
| <code>density.increase</code> | Applies densification model where the density increases in percentage. The increase value can be specified per region <code>&lt;regionName&gt;=&lt;n&gt;</code> (where <code>regionName</code> is the name of an existing region in the current structure) or per material <code>&lt;material&gt;=&lt;n&gt;</code> (where <code>material</code> is the name of a material in the current structure).                                                                                                           |
| <code>deposit.type</code>     | When using <code>epi.model=1</code> , epitaxy is solved as a series of alternating deposit and diffuse steps. This parameter specifies the deposit type, and allowed values are: <ul style="list-style-type: none"> <li>• <code>isotropic</code> (default).</li> <li>• <code>fourier</code> (in which case, either <code>coeffs</code> or <code>mat.coeffs</code> must be specified as well).</li> <li>• <code>crystal</code> (in which case, <code>crystal.rate</code> must be specified as well).</li> </ul> |
| <code>epi.doping</code>       | Takes a list of parameters where the parameter name is the name of the species to be initialized, and the value is the initial value. A list of fields of any name can be initialized with this parameter and, for solution variables, units are accepted, for example:<br><code>epi.doping= {boron=1e18&lt;cm-3&gt; GSize=1&lt;nm&gt; myfield=1}</code>                                                                                                                                                       |
| <code>epi.doping.final</code> | Takes a list of parameters where the parameter name is the name of the species to be initialized, and the value is the final value. A list of fields of any name can be initialized with this parameter and, for solution variables, units are accepted, for example:<br><code>epi.doping.final= {boron=1e18&lt;cm-3&gt; GSize=1&lt;nm&gt; myfield=1}</code>                                                                                                                                                   |
| <code>epi.layers</code>       | Number of layers of mesh lines required during epitaxial growth (for <code>epi.model=0</code> ). The default is 40. You also can set globally a distance between mesh lines using:<br><code>pdbSet Silicon Grid epi.perp.add.dist &lt;n&gt;</code><br>If <code>epi.perp.add.dist</code> is set to a positive number, <code>epi.layers</code> is ignored.                                                                                                                                                       |
| <code>epi.model</code>        | The two methods described above can be chosen using this parameter: <ul style="list-style-type: none"> <li>• <code>epi.model=0</code> (default) applies a boundary-moving algorithm similar to oxidation.</li> <li>• <code>epi.model=1</code> uses alternating doped deposition and inert annealing steps.</li> </ul>                                                                                                                                                                                          |

## A: Sentaurus Process Commands

### temp\_ramp

- `epi.resist` List of parameters with dopant name and resistivity to calculate the background dopant concentration. If more than one dopant name appears in the list, the doping concentration is calculated individually for each dopant by ignoring the other ones.
- `epi.thickness` Sets the epitaxial layer thickness to be deposited. The default unit is  $\mu\text{m}$ .
- `flow<ambient>, flows`
- List of gas flows in the reaction chamber. The gas flows are used to compute the partial pressures of the active ambients (those causing material growth). You can specify flows using either a parameter name composed of `flow + <ambient>` (for example, `flowO2` and `flowHCl` where `O2` and `HCl` are ambient names) or the `flows` parameter that takes a list of parameters with names of the ambients, for example:
- ```
flows= { O2 = 1.0<l/min> HCl = 1.0<l/min> }
```
- The list of default ambients is given in [Table 63 on page 605](#), but this list can be extended by using the `ambient` command. When a gas flow is specified as a combination of flows (and not when using partial pressures), a complete reaction of the ambients is assumed to occur, for example,  $\text{O}_2 + 2\text{H}_2 \rightarrow 2\text{H}_2\text{O}$ . Besides gas reactions, the addition of inert gases also will change the partial pressure of the material growing ambients. For example, if the flows of only  $\text{N}_2$  and  $\text{O}_2$  are specified and are equal, then the partial pressure of  $\text{O}_2$  will be  $\text{<total pressure>/2.0}$  where `<total pressure>` is given by the `pressure` parameter (see below).
- NOTE:** Flows and partial pressures must not be specified in the same `temp_ramp` together.
- `gas.flow` Specifies a gas flow to be used for this `temp_ramp` (should not be used with other `gas_flow` parameters).
- `hold` During this segment, allows the `diffuse` command time to specify the time of the segment.
- `ISSG` Switches on *in situ* steam-generated (ISSG) oxidation.
- `last` Defines the final component of the temperature profile. There will be no more additions to the ramp.
- `list` This Boolean parameter generates a list of temperature profiles. It returns a Tcl list and can be operated on as such. The default action for commands is to print the return, so if no handling is required, this prints a list of names of defined temperature profiles. If a name is specified, then `temp_ramp` only is listed along with details about the ramps.
- `mat.coeffs` List of multimaterial coefficients  $A_0, A_1, \dots, A_n$  used in Fourier deposition when `epi.model=1` and `deposit.type=fourier`.

`name` Name used to identify the temperature ramp. Use this name in a subsequent `diffuse` command.

`p<ambient>`, `partial.pressure`

List of the partial pressures of active ambients. Partial pressure specifications must not be used with `flows`, `flow<ambient>`, or `pressure` specifications. Partial pressures can be specified using either a parameter name composed of `p + <ambient>` (for example, `pO2` and `pN2O` where `O2` and `N2O` are active ambient names) or with the parameter `partial.pressure` that takes a list of parameters with names of the ambients, for example:

```
partial.pressure= {O2 = 1.0<atm> N2O= 1.0<atm>}
```

The list of default ambients is given in [Table 63 on page 605](#), but this list can be extended by using the `ambient` command. These partial pressures are assumed to contribute to the oxidation or user-defined reaction processes. No reaction between the species is assumed. The default unit is atm.

**NOTE:** Only the partial pressures of the active ambients are used directly in the oxidation reaction equations. Therefore, setting the partial pressure of inactive (in the sense that they cause a material growth reaction) ambients, such as  $N_2$  and  $HCl$ , has no effect.

`pressure` The (total) pressure of the ambient gas. The default value and unit is 1.0 atm. This setting takes effect only if `flows` or `flow<ambient>` is defined explicitly. If `gas.flow` is specified, the pressure is set in the corresponding `gas_flow` command.

`ramprate` Temperature change during anneal. The default value and unit is  $0.0^\circ C/s$ .

`read.temp.file`

Reads a thermal profile from a file. It must not be used with any other thermal specification. To create this profile file during laser annealing, use the `write.temp.file` parameter of the `diffuse` command. The format of the file is two columns: time (in seconds) and temperature (in degree Celsius). Lines beginning with a '#' are ignored.

`repair` In MGOALS3D mode, small regions are removed automatically by default. Sometimes, this can cause small gas bubbles in the structure or other problems. Use `!repair` to switch off removal of small regions.

`reset.init.time`

Starts each annealing step with the same initial time step.

## A: Sentaurus Process Commands

### temp\_ramp

<code>sources</code>	Defines deposition sources used in Fourier deposition when <code>epi.model=1</code> and <code>deposit.type=fourier</code> .
<code>t.final</code>	Final temperature for a temperature ramp-up or ramp-down. It is used if <code>ramprate</code> is not given. The ramp time is calculated automatically.
<code>temperature</code>	Annealing temperature. The default unit is degree Celsius.
<code>time</code>	Annealing time. The default unit is minute.

**Examples:** `temp_ramp name=tr1 temp=20 ramprate=10<K/s> time=100<s>`  
Defines the temperature profile named `tr1`. Temperature rate is 10 K/s.

**See:** [diffuse on page 875](#), [gas\\_flow on page 901](#)

---

## term

**Function:** Defines a new subexpression for use in the equation specification of the Alagator language.

**Syntax:**

```
term
  [<material>]
  [add] [list] [delete] [clear]
  [name=<c>] [eqn=<c>] [print] [store]
```

**Description:** Creates subexpressions for use with the Alagator scripting language. Terms are never required but can offer substantial computational benefit. Each term is evaluated only once during assembly, and the results are cached. If multiple equations refer to a term, the first equation to use it evaluates the expression and the remainder use the cached values. Terms are usually used for expressions that need to appear in several partial differential equations. For example, a recombination term between vacancies and interstitials needs to appear in both the vacancy and interstitial equation. A term can be used for the recombination and can be placed in both partial differential equations. The recombination is then evaluated only once during the assembly process.

Terms can be created, searched, and printed. That allows inquiries about terms to be made in the various callback procedures. This allows intelligent decisions to be made. For example, the charge term in the Poisson equation can be accumulated by obtaining the current charge and adding new pieces to the term.

### Options:

**add** Creates a new term. A term with that name will be overwritten.

**clear** Removes a term from the current set if the term exists otherwise it clears the content of all terms.

**delete** Removes a term from the current set.

**eqn** The string defines the equation part of the term. The equation must conform to all the standard constraints of the Alagator language. Terms can be nested; the equation specified here can refer to other terms. Parsing of the equation is performed during diffusion, so there is no need for everything to be predefined.

**list** List of all of the names of the current terms. This is returned as a Tcl list, so it can be used in conjunction with all of the list functionality.

## A: Sentaurus Process Commands

term

<code>&lt;material&gt;</code>	If a material is specified, the term becomes specific for this material only. This allows the same name to have different equations in different materials. For information about specifying materials, see <a href="#">Material Specification on page 50</a> .
<code>name</code>	Reference name for the term. This name is defined and is compared to strings found in the equation parsing. Capitalization is important, and only exact matches are allowed.
<code>print</code>	Prints the equation for the term matching the name specified. If no term matches, 0.0 is returned. If the material name is not given, the first term with the matching name is returned (for example, you may obtain <code>vTotal</code> in oxide instead of silicon).
<code>store</code>	Allows the <code>term</code> command to be stored in a TDR file.

**Examples:**

```
term name=vTotal add silicon eqn="Vacancy+VacancyGbc"
```

Creates a term named `vTotal` in silicon only. The keyword `vTotal` will be replaced with the subexpression `Vacancy+VacancyGbc`.

```
term name=Noni add silicon eqn = exp(Potential*$Vti)
```

Creates a term named `Noni` in silicon only. The equation will be the exponential of `Potential` multiplied by `$Vti`. The normal rules for Tcl string variables and executions apply, so that `Vti` must be a currently defined variable. The value will be replaced when the `term` command is executed.

```
term name=Noni add silicon eqn= {exp(Potential*$Vti)}
```

This is the same as the previous command. The difference is the braces around the equation, which delay variable expansion. The variable will not be expanded until the `diffuse` command is executed. This is the more normal form. You want the `vti` variable to be replaced with the value of the current temperature of the `diffuse` command, not the temperature at the time of the `term` command execution.

```
term list
```

Returns a list of all the current term names defined.

```
term name=Charge print
```

Returns the currently defined equation corresponding to the name `Charge`.

**See:** [solution on page 1076](#)

## topo

**Function:** Performs 3D etch and deposition using Sentaurus Topography 3D.

**Syntax:** topo <Sentaurus Topography 3D commands>

**Description:** Physical etch and deposition is available through the interface to Sentaurus Topography 3D and is executed using the `topo` command. Commands entered into the `topo` command are passed directly to the Sentaurus Topography 3D library. The exchange of the boundary between Sentaurus Process and Sentaurus Topography 3D is handled automatically and only when required.

**NOTE:** A licence for Sentaurus Topography 3D must be available, and a version of the Sentaurus Process binary with Sentaurus Topography 3D included must be installed.

**Options:** All options to the `topo` commands are described in the *Sentaurus Topography 3D User Guide*.

**See:** Refer to the *Sentaurus Topography 3D User Guide*.

---

## transform

**Function:** Performs a transformation step.

**Syntax:**

```
transform
  (reflect | stretch | cut | flip | rotate)
  ([location=<n>][<m>|<cm>|<um>|<nm>] &
   left | right | front | back | up | down &
   ymin | ymax | zmin | zmax)
  (min= {
    <n>[<m>|<cm>|<um>|<nm>]
    <n>[<m>|<cm>|<um>|<nm>]
    <n>[<m>|<cm>|<um>|<nm>]} &
   max= {
    <n>[<m>|<cm>|<um>|<nm>]
    <n>[<m>|<cm>|<um>|<nm>]
    <n>[<m>|<cm>|<um>|<nm>]} )
  [length=<n>][<m>|<cm>|<um>|<nm>]
  (translate= {
    <n>[<m>|<cm>|<um>|<nm>]
    <n>[<m>|<cm>|<um>|<nm>]
    <n>[<m>|<cm>|<um>|<nm>]} )
  ([angle=<n> & axis= "X" | "Y" | "Z"])
  [keep.original] [mesh.align] [remesh] [Adaptive]
```

**Description:** Reflects, stretches, cuts, flips, rotates, or translates the structure. Previously, cut and clip had slightly different behavior. Now, they are the same and are referred to as cut. All operations work in 2D and 3D. All these operations, except flip and stretch, are also available in the KMC mode.

**Options:**

**The cut options**

**Adaptive** If the remesh parameter is set, Adaptive specifies with or without adaptive meshing. Parameters for adaptive meshing are described in [Adaptive Refinement on page 679](#). The default is the return value of `pdbGet Grid Adaptive`.

**cut** Crops the structure to a new bounding box (using the min and max parameters) or crops half the structure (using the left, right, front, back, up, or down parameters).

left, right, front, back, up, down

Indicates a cut at a location given by the `location` parameter, and specifies which half is to be removed. These parameters should not be used with either the min or max parameter.



location	The x-, y-, or z-coordinate (in internal coordinate system) where the cut is to be performed. The default is 0.0 $\mu\text{m}$ . The <code>location</code> parameter is used with <code>left</code> , <code>right</code> , <code>front</code> , <code>back</code> , <code>up</code> , or <code>down</code> to indicate which direction and side to cut.
max, min	The cut box can either be specified by the <code>min</code> and <code>max</code> parameters: <code>min= {minx miny minz}</code> and <code>max= {maxx maxy maxz}</code> , or there are shortcut parameters ( <code>left</code> , <code>right</code> , <code>front</code> , <code>back</code> , <code>up</code> , <code>down</code> ) to specify an axis-aligned cut at the coordinate given by the <code>location</code> parameter. The parameters <code>min</code> and <code>max</code> must be used together and cannot appear with any of the <code>left</code> , <code>right</code> , <code>front</code> , <code>back</code> , <code>up</code> , or <code>down</code> parameters.
mesh.align	By default, <code>mgoals</code> cuts the structure at the nearest mesh line and does not perform a remesh. If <code>!mesh.align</code> is specified, <code>mgoals</code> cuts precisely at the specified coordinates and remeshes the structure.
remesh	Optional Boolean only for two dimensions, which forces a remesh after the transform. However, remeshing is always possible using the <code>grid remesh</code> command if required.

#### The translate options

translate	Translates the entire structure by specifying a translation vector: {translate_x translate_y translate_z}
-----------	--

#### The flip options

Adaptive	Specifies whether to use adaptive meshing.
flip	Selects the flip operation (flip from top to bottom). For more details, see <a href="#">The transform flip Command and Backside Processing on page 752</a> .
location	Selects the x-coordinate about which the structure will be flipped. By default, the middle of the structure is chosen. Subsequent <code>transform flip</code> commands will, by default, use the same location for flipping whether the default is used or a chosen <code>location</code> is used. In 3D, the z-coordinate of the rotation is the middle of the structure in the z-direction. The location of the flip is also the fixed coordinate for mechanics simulations, which is otherwise at the bottom of the structure when no flip has occurred.

#### The reflect options

Adaptive	Specifies whether to use adaptive meshing.
keep.original	Keeps the original structure after reflection (having both the original and the reflected) or stores only the reflected structure when disabled with <code>!keep.original</code> . It is enabled by default.

## A: Sentaurus Process Commands

### transform

left, right, front, back

Selects the side of the simulation domain at which the reflection is performed.

reflect Indicates that a reflection will be performed.

ymin, ymax, zmin, zmax

Specify the location where the reflection is performed. ymin is the same as left, ymax is the same as right, zmin is the same as back, and zmax is the same as front.

#### The rotate options

Adaptive Specifies whether to use adaptive meshing.

angle Rotation angle. It must be one of 90, 180, or 270. Angles leading to structures having gas in a side are not allowed. This means that only 180° is allowed for y- and z-axes. Two-dimensional simulations are extruded into three dimensions and are then rotated.

axis Rotation axis. It must be x, y, or z.

rotate Indicates that a rotation will be performed.

#### The stretch options

Adaptive Specifies whether to use adaptive meshing if remeshing.

left, right, front, back

Indicates which side of the structure will be moved.

length Length of stretching. The default value and unit is 0  $\mu\text{m}$ .

location The y- or z-coordinate (in internal coordinate system) where the structure will be stretched. The default value and unit is 0  $\mu\text{m}$ .

remesh Optional Boolean that indicates whether a remesh will be performed. The default is on.

stretch Indicates that a stretching action will be performed.

**Examples:**

```
transform reflect right  
transform reflect ymax
```

Both commands reflect the structure to the right side.

```
transform reflect right !keep.original
```

Reflects the structure to the right side and keeps the reflected part only.

```
transform stretch location=0.7 length=0.02 right remesh
```

Stretches the structure to the right side. The structure left of 0.7 remains unchanged; the structure to the right of 0.7 will be moved by 20 nm.

```
transform cut location=0.7 left !remesh
```

Cuts the structure at  $y=0.7$ . The left part will be removed without remeshing.

```
transform cut min= {0<um> 0<um>} max= {1<um> 3<um>}
```

Cuts the structure at  $x$  between 0 and 1  $\mu\text{m}$ , and  $y$  between 0 and 3  $\mu\text{m}$ .

```
transform translate = {-1 0 0}
```

Shifts the structure up in the  $x$ -direction by 1  $\mu\text{m}$ .

```
transform flip
```

Flips the structure from top to bottom about its midpoint if it is the first flip, or stores the flip location for subsequent flips.

```
transform rotate axis=X angle=90
```

Rotates the structure  $90^\circ$  in the  $x$ -axis.

**See:**

[mgoals on page 992](#), [Stress Handling on page 734](#)

---

## transform.refinement

**Function:** Transforms a refinement box and optionally preserves the original.

**Syntax:**

```
transform.refinement
(reflect | stretch | cut | flip | rotate)
([[location=<n>][<m>|<cm>|<um>|<nm>] &
left | right | front | back | up | down | ymin | ymax | zmin | zmax)
(min= {
  <n>[<m>|<cm>|<um>|<nm>]
  <n>[<m>|<cm>|<um>|<nm>]
  <n>[<m>|<cm>|<um>|<nm>]} &
max= {
  <n>[<m>|<cm>|<um>|<nm>]
  <n>[<m>|<cm>|<um>|<nm>]
  <n>[<m>|<cm>|<um>|<nm>]} )
[length=<n>][<m>|<cm>|<um>|<nm>]
(translate=
  <n>[<m>|<cm>|<um>|<nm>]
  <n>[<m>|<cm>|<um>|<nm>]
  <n>[<m>|<cm>|<um>|<nm>]} )
([angle=<n> & axis= "X" | "Y" | "Z"])
[keep.original]
[name=<oldName>] [name.new=<newName>]
```

**Description:** Reflects, stretches, cuts, flips, rotates, or translates a given refinement box or all refinement boxes. A new transformed refinement box is created by default, while the old one is kept. This can be overridden with `!keep.original`. The transformation applies to all existing refinements, except if a name is specified. In this case, a transformed refinement name also can be specified by using `name.new`.

### Options:

#### General

`keep.original` Specifies whether to keep the original after the transformation. When keeping the original refinement, the original is untouched, and a new one is created by transforming the original refinement. Otherwise, the refinement itself is transformed.

`name` Name of refinement to apply the transformation.

`name.new` Name of the transformed refinement. If not specified, a default name is given.

### The cut options

`cut` Crops the refinement to a new bounding box (using the `min` and `max` parameters) or crops half of it (using the `left`, `right`, `front`, `back`, `up`, or `down` parameters).

`left`, `right`, `front`, `back`, `up`, `down`

Indicates a cut at a location given by the `location` parameter, and specifies which half is to be removed. These parameters must not be used with either the `min` or `max` parameter.

`location` The x-, y-, or z-coordinate (in internal coordinate system) where the cut is to be performed. The default is 0.0  $\mu\text{m}$ . The `location` parameter is used with `left`, `right`, `front`, or `back` to indicate which direction and side to cut.

`max`, `min` The cut box can be specified by either the `min` and `max` parameters `min= {minx miny minz}` and `max= {maxx maxy maxz}`, or there are shortcut parameters (`left`, `right`, `front`, `back`) to specify an axis-aligned cut at the coordinate given by the `location` parameter. The parameters `min` and `max` must be used together and cannot appear with any of the `left`, `right`, `front`, or `back` parameters.

`ymin`, `ymax`, `zmin`, `zmax`

Specify the location where the refinement reflection is performed. `ymin` is the same as `left`, `ymax` is the same as `right`, `zmin` is the same as `back`, and `zmin` is the same as `front`.

### The translate options

`translate` Translates the refinement by specifying a translation vector:  
{`translate_x` `translate_y` `translate_z`}

### The flip options

`flip` Flips a refinement (top to bottom).

`location` Selects the x-coordinate about which the refinement will be flipped. By default, the middle of the structure is chosen. Subsequent `transform flip` commands will, by default, use the same location for flipping whether the default is used or a chosen `location` is used. In 3D, the z-coordinate of the rotation is the middle of the structure in the z-direction.

### The reflect options

`left`, `right`, `front`, `back`

Selects the side of the simulation domain at which the reflection is performed.

`reflect` Indicates that a reflection will be performed.

## A: Sentaurus Process Commands

### transform.refinement

#### The stretch options

left, right, front, back

Indicates which side of the refinement will be moved.

length Length of stretching. The default value and unit is 0  $\mu\text{m}$ .

location The y- or z-coordinate (in internal coordinate system) where the refinement will be stretched. The default value and unit is 0  $\mu\text{m}$ .

stretch Indicates that a stretching action will be performed.

#### The rotate options

angle Rotation angle. It must be 90, 180, or 270.

axis Rotation axis. It must be x, y, or z.

rotate Indicates that a rotation will be performed.

#### Examples:

```
transform.refinement reflect right
```

Creates a set of new refinements as reflections of all the current refinements to the right side.

```
transform stretch location=0.7 length=0.02 right name=box1 name.new=sbox1
```

Creates a new refinement called `sbox1` by stretching the existing refinement `box1` to the right side. The area left of 0.7 remains unchanged; the structure to the right of 0.7 will be moved by 20 nm.

```
transform cut location=0.7 !keep.original
```

Cuts all the existing refinements at  $y = 0.7$ . The left part will be removed.

```
transform translate = {-1 0 0} name=r1 name.new=new2
```

Creates a new refinement `new2` by coping and shifting `r1` up in the x-direction by 1  $\mu\text{m}$ .

```
transform rotate axis=Y angle=270 name=refbox name.new=refbox \  
!keep.original
```

Rotates the refinement `refbox`  $270^\circ$  around the y-axis without changing its name.

#### See:

[Mesh Refinement on page 674](#), [Stress Handling on page 734](#), [refinebox on page 1040](#), [transform on page 1102](#)

## translate

**Function:** Translates a named dataset with the specified offset.

**Syntax:**

```
translate
  <material>
  [name=<c>]
  [offset= {<n> <n> <n>}]
  [min=<n>]
```

**Description:** Spatially shifts a profile (dataset) with the specified offset. If a material is specified, the profile is shifted in the specified material only. Otherwise, the profile is shifted in all materials. When a profile is shifted, the value at some points may become undefined, in which case, these points are filled with a minimum value as specified by the `min` parameter.

**Options:**

`<material>` If a material is specified, the dataset is translated in the specified material only. Otherwise, the dataset is translated in all materials. For information about specifying materials, see [Material Specification on page 50](#).

`min` Minimum value to fill the points with undefined value. The default value is 0.0.

`name` Specifies the name of a dataset. The default is `Z_Plot_Var`.

`offset` Takes a list of numeric values. The first, second, and third values in the list are taken as the x-, y-, and z-value, respectively. The missing value is treated as zero.

**Examples:**

```
translate name=Boron offset= {0.01 0.02}
```

Shifts the `Boron` data field with a shifting vector (0.01  $\mu\text{m}$ , 0.02  $\mu\text{m}$ , 0.0  $\mu\text{m}$ ).

---

## UnsetAtomistic

**Function:** Disables the atomistic KMC diffusion model and continues the simulation using the PDE solver.

**Syntax:** `UnsetAtomistic`  
`[sano] [sano.list] [sano.materials]`

**Description:** Disables the KMC diffusion module. It transfers all the information into the Sentaurus Process standard mesh (by calling `KMC2PDE`), sets the atomistic mode to false, and deletes all the atomistic related information.

**Options:**

`sano` Remeshes the Sentaurus Process finite-element mesh and converts KMC particles to finite-element fields. To adaptively remesh on Sano fields and Sano smoothed `NetActive` (`DopingConcentration`), it is necessary to specify adaptive meshing parameters *before* `UnsetAtomistic`.

Any adaptive criteria specified for a field that is in the Sano list will be applied to the Sano smoothed value of the field, and any criteria specified for `NetActive` will be applied by default to `NetActive` computed from Sano-smoothed active fields. To set the list of Sano fields, use the `sano.list` parameter, but by default the list contains the active dopants. The field `NetActive` is updated automatically using Sano fields and does not need to be included explicitly.

`sano.list` Sets the list of Sano fields. These fields are converted from KMC particle distributions using the Sano method and are used for adaptive remeshing, and subsequently converted to finite-element fields on the newly created mesh. By default, the Sano list includes all active dopants that are present. The field `NetActive` is updated automatically using Sano fields and does not need to be included explicitly.

`sano.materials`

Sets the list of materials in which the Sano method is applied. By default, the list contains only `Silicon` because that is the only material that by default has nontrivial KMC diffusion models.

**Examples:** `UnsetAtomistic`  
`UnsetAtomistic sano sano.list= {PActive AsActive BActive}`



## UnsetDielectricOxidationMode

- Function:** Disables the oxidation mode to grow oxide with dielectric on top.
- Syntax:** UnsetDielectricOxidationMode <Dielectric> <Oxidant>
- Description:** Disables the dielectric oxidation mode of material <Dielectric> and ambient <Oxidant>. It deletes all the dielectric oxidation-related callback settings, the boundary conditions, and the parameter settings.
- Options:**
- <Dielectric> Specifies name of dielectric material to grow oxide underneath.
- <Oxidant> Specifies name of oxidant.
- Examples:** UnsetDielectricOxidationMode Nitride O2
- See:** [SetDielectricOxidationMode on page 1058](#)

---

## update\_substrate

**Function:** Sets up the substrate with impurities, strains, and modified lattice constants for analyses that involve strained silicon layers.

**Syntax:** `update_substrate top.relaxed.coord=<n>`

**Description:** Takes into account the strains that certain impurities introduce to the wafer as defined by the `strain_profile` command or in the PDB and sets up the lattice constants and strains in the substrate as defined in the `region` command. This command applies to the impurity profile to the substrate as defined by the `profile` command or the `substrate_profile` command. The `top.relaxed.coord` is the lowest x-coordinate below which the wafer is totally relaxed from the impurity-related strains.

This command should be called only once for initialization. It is recommended to replace it with a short solve step and set:

```
pdbSet Silicon Mechanics UpdateStrain 1
```

**Options:**

`top.relaxed.coord`

Top of the region that is totally relaxed from the lattice strains. It can be thought of as the top point above which no dislocations can be found.

**Examples:** `update_substrate top.relaxed.coord=0.3`

**See:** [region on page 1047](#), [strain\\_profile on page 1080](#),  
[substrate\\_profile on page 1090](#)

---

## WritePlx

**Function:** Writes a 1D .plx file.

**Syntax:** WritePlx  
    <filename>  
    [x=<n>] [y=<n>] [z=<n>]  
    [<material>]

**Description:** Makes a 1D profile along a given cutline and writes a .plx file of the solutions and terms given in the list provided by the SetPlxList command. If the list is not provided, only present solution names are written. If a material is specified, only data from the given material is used to create the plot.

**NOTE:** The <filename> parameter must be the first one on the WritePlx command line.

**Options:**

<filename> Name of the output file.

<material> If a material is specified, only the plot from the given material is created. For information about specifying materials, see [Material Specification on page 50](#).

x, y, z Specify the cut position. For 1D simulations, no cut specification is necessary. In 2D, either x or y should be specified and, for 3D simulations, two axes must be specified. It is also possible to shift .plx output files by specifying PlxShift variables. The unit for x, y, and z is  $\mu\text{m}$ .

**Examples:** WritePlx 1.5.plx y=1.5  
Writes a 1D .plx file at the  $y = 1.5 \mu\text{m}$  cutline.

```
set PlxShift 0.2
WritePlx test.plx
```

Shifts the axis by  $0.2 \mu\text{m}$  and writes a 1D .plx file.

**See:** [SetPlxList on page 1060](#)

**A: Sentaurus Process Commands**  
WritePlx