PROFILE

The **PROFILE** statement defines profiles for impurities and other quantities to be used in the device structure.

```
PROFILE

   [REGION=<c>]
   [X.MIN=<n>] [ {WIDTH=<n> | X.MAX=<n>} ]
   [Y.MIN=<n>] [ {DEPTH=<n> | Y.MAX=<n>} ]

 Output Doping File
   [OUT.FILE=<c>]


 Uniform Profile
   {  ( UNIFORM {N-TYPE | P-TYPE | IMPURITY=<c> | OTHER=<c>} N.PEAK=<n> )

 Analytic Profiles
    | ( {N-TYPE | P-TYPE | IMPURITY=<c> | OTHER=<c>} {N.PEAK=<n> | DOSE=<n>}
        {Y.CHAR=<n> | Y.JUNCTI=<n>} {X.CHAR=<n> | XY.RATIO=<n>} [X.ERFC]
      )

 Analytic Polygonal Profiles
    | ( POLYGON {N-TYPE | P-TYPE | IMPURITY=<c> | OTHER=<c>} N.PEAK=<n>
        X.POLY=<a> Y.POLY=<a> N.CHAR=<n> [N.ERFC]
      )

 Analytic Rotated Profiles
    | ( ROTATE {N-TYPE | P-TYPE | IMPURITY=<c> | OTHER=<c>} N.PEAK=<n>
        X.CENTER=<n> Y.CENTER=<n> R.INNER=<n> R.OUTER=<n> R.CHAR=<n> [R.ERFC]
      )

 One-Dimensional Profiles from Data Files
    | ( IN.FILE=<c> [N.OFFSET=<n>] [Y.OFFSET=<n>]
        {  ( 1D.PROC [N-TYPE] [P-TYPE] )
         | ( SUPREM2 [N-TYPE] [P-TYPE] )
         | ( 1D.ASCII [Y.COLUMN=<n>]
             {  ( [N.COLUMN=<n>] [P.COLUMN=<n>] )
              | ( D.COLUMN=<n> {IMPURITY=<c> | OTHER=<c>} )
             }
           )
        }
        {X.CHAR=<n> | XY.RATIO=<n>} [X.ERFC]
      )
```

(**PROFILE** statement continued on next page)

(**PROFILE** statement continued from previous page)

```
Two-Dimensional Profiles from Data Files
   | ( IN.FILE=<c> [N.OFFSET=<n>] [X.OFFSET=<n>] [Y.OFFSET=<n>]
       {  ( 2D.PROC [N-TYPE] [P-TYPE] )
        | ( SUPRA [N-TYPE] [P-TYPE] )
        | ( TSUPREM4 [N-TYPE] [P-TYPE] )
        | ( 2D.ASCII [X.COLUMN=<n>] [Y.COLUMN=<n>]
            {  ( [N.COLUMN=<n>] [P.COLUMN=<n>] )
             | ( D.COLUMN=<n> {IMPURITY=<c> | OTHER=<c>} )
            }
          )
        | ( TIF [ {IMPURITY=<c> | ( [N-TYPE] [P-TYPE] )} ] [OTHER=<c>] )
        | ( MEDICI [ {IMPURITY=<c> | ( [N-TYPE] [P-TYPE] )} ] [OTHER=<c>] )
       }
       [X.CHAR=<n>] [X.ERFC] [Y.CHAR=<n>] [Y.ERFC]
     )
  }
```

Parameter	Type	Definition	Default	Units
REGION	char	The names of the regions to which the profile is to be added. If more than one name is given, they should be enclosed within parentheses and separated with commas (for example, "(silicon-1,silicon-2)").	All semiconductor regions.	
X.MIN	number	The minimum x location of the profile. **synonyms: X.LEFT, X.PEAK**	The minimum x location in the structure.	microns
WIDTH	number	The x extent of the profile.	The maximum x location in the structure minus **X.MIN**.	microns
X.MAX	number	The maximum x location of the profile. **synonym: X.RIGHT**	The maximum x location in the structure.	microns
Y.MIN	number	The minimum y location of the profile. **synonyms: Y.TOP, Y.PEAK**	The minimum y location in the structure for input from a file or if **UNIFORM** is specified; otherwise, 0.0.	microns
DEPTH	number	The y extent of the profile.	The maximum y location in the structure minus **Y.MIN** for input from a file or if **UNIFORM** is specified; else 0.0.	microns

Parameter	Type	Definition	Default	Units
Y.MAX	number	The maximum y location of the profile. **synonym: Y.BOTTOM**	The maximum y location in the structure for input from a file or if **UNIFORM** is specified; otherwise, **Y.MIN**.	microns
N-TYPE	logical	Specifies that the impurity profile is n-type (donors). If the **1D.PROC**, **SUPREM2**, **2D.PROC**, **SUPRA**, **TIF**, or **MEDICI** parameter is specified, then the donor impurity profile is read from the data file. If the **TSUPREM4** parameter is specified, the donor impurity profile is reconstructed from the doping in the data file using N(donor)=[N(total)+N(net)]/2. **synonym: N.TYPE**	false	
P-TYPE	logical	Specifies that the impurity profile is p-type (acceptors). If the **1D.PROC**, **SUPREM2**, **2D.PROC**, **SUPRA**, **TIF**, or **MEDICI** parameter is specified, then the acceptor impurity profile is read from the data file. If the **TSUPREM4** parameter is specified, the acceptor impurity profile is reconstructed from the doping in the data file using N(acceptor)=[N(total)-N(net)]/2. **synonym: P.TYPE**	false	
IMPURITY	char	The name of an impurity for which a profile is being defined or read. The chemical name of the impurity should be specified here (such as "B" or "As"). Medici assumes all impurities specified with this parameter are electrically active. If the **TIF** or **MEDICI** parameter is specified, multiple impurities may be read (separate their names with commas and enclose the entire list with parentheses).	none	
OTHER	char	The name of an arbitrary quantity for which a profile is being defined or read. If the **TIF** or **MEDICI** parameter is specified, multiple **OTHER** quantities may be read (separate their names with commas and enclose the entire list with parentheses).	none	
Output Doping File				
OUT.FILE	char	The identifier for the data file to which the profile information is to be written. This file is used only in conjunction with the **REGRID** statement. **synonym: OUTFILE**	none	
Uniform Profile				
UNIFORM	logical	Specifies that the profile has a uniform distribution.	false	
N.PEAK	number	The peak impurity concentration for an impurity profile or the peak value for **OTHER** profiles. **synonym: CONCENTR**	none	$\#/cm^3$ for impurities
Analytic Profiles				
DOSE	number	The dose of the impurity profile assuming a full Gaussian distribution.	none	$\#/cm^2$
Y.CHAR	number	The y characteristic length of the profile outside the range of **Y.MIN** < y < **Y.MAX**. **synonym: CHAR**	0.0002 for data read from a file; otherwise, none	microns

Parameter	Type	Definition	Default	Units
Y.JUNCTI	number	The y location under the center of the profile where the magnitude of the profile being added equals the magnitude of the background profile. **synonym: JUNCTION**	none	microns
X.CHAR	number	The horizontal characteristic length of the profile outside the range **X.MIN** < x < **X.MAX**. **synonym: LAT.CHAR**	0.0002 for data read from a file; otherwise, **XY.RATIO***Y.CHAR,	microns
XY.RATIO	number	The ratio of the horizontal characteristic length to the vertical characteristic length for an analytic profile. If the vertical profile is input from a data file, **XY.RATIO** is the factor which multiplies the extent of the profile when the profile is rotated to the horizontal direction. **synonym: RATIO.LA**	1.0	none
X.ERFC	logical	Specifies that the x variation of the profile is described by a complementary error function. If this parameter is false, then the horizontal variation is uniform from **X.MIN** to **X.MAX** with Gaussian tails outside of this region. **synonym:ERFC.LAT**	false	
Analytic Polygonal Profiles				
POLYGON	logical	Specifies that the profile is a polygon. The polygon vertices are defined by a pair of arrays: **X.POLY** and **Y.POLY**.	false	
X.POLY	array	Specifies an array of x coordinates of the polygon vertices. The number of the vertices should not exceed 40.	none	microns
Y.POLY	array	Specifies an array of y coordinates of the polygon vertices. The number of the vertices should not exceed 40.	none	microns
N.CHAR	number	The characteristic length of the profile outside of the polygon. **synonym: R.CHAR**	none	microns
N.ERFC	logical	Specifies that the lateral variation of the polygonal profile outside of the polygon is described by a complimentary error function. **synonym: R.ERFC**	false	
Analytic Rotated Profiles				
ROTATE	logical	Specifies that the profile is rotated around a rotation center.	false	
X.CENTER	number	Specifies the x location of the rotation center.	none	microns
Y.CENTER	number	Specifies the y location of the rotation center.	none	microns
R.INNER	number	The inner radius (distance from the rotation center) of a circular profile.	none	microns
R.OUTER	number	The outer radius (distance from the rotation center) of a circular profile.	none	microns
R.CHAR	number	The characteristic length of the profile outside of the **R.INNER** to **R.OUTER** rotation range. **synonym: N.CHAR**	none	microns

Parameter	Type	Definition	Default	Units
R.ERFC	logical	Specifies that the radial variation of the rotated profile outside of the **R.INNER** to **R.OUTER** range is described by a complimentary error function. **synonym: N.ERFC**	false	
One-Dimensional Profiles from Data Files				
IN.FILE	char	The identifier for the data file containing the profile. **synonyms: INFILE** and **FILE**	none	
N.OFFSET	number	The concentration to be subtracted from both the donor and acceptor impurity profiles obtained from a data file.	0.0	atoms/ cm^3
Y.OFFSET	number	The y direction shift of a profile obtained from a data file.	0.0	microns
1D.PROC	logical	Specifies that the data file containing an impurity profile was generated by TMA SUPREM-3.	false	
SUPREM2	logical	Specifies that the data file containing an impurity profile was generated by SUPREM-2.	false	
1D.ASCII	logical	Specifies that profile data is read from a formatted file. One column of the file should correspond to depth (in microns) and should be identified with **Y.COLUMN**. The file should also contain one or more columns of profile data that can be identified with the parameters **N.COLUMN**, **P.COLUMN**, or **D.COLUMN**.	false	
Y.COLUMN	number	The column of the formatted data file corresponding to the y coordinate.	1 if **1D.ASCII** is specified; 2 if **2D.ASCII** is specified.	none
N.COLUMN	number	The column of the formatted data file corresponding to net donor impurity concentration. Data with values less than zero are considered to correspond to net acceptor impurity concentration.	None if **P.COLUMN** is specified; otherwise, 2 if **1D.ASCII** is specified and 3 if **2D.ASCII** is specified.	none
P.COLUMN	number	The column of the formatted data file corresponding to net acceptor impurity concentration. Data with values less than zero are considered to correspond to net donor impurity concentration.	none	none
D.COLUMN	number	The column of the formatted data file corresponding to either **IMPURITY** or **OTHER** profile values.	none	none
Two-Dimensional Profiles from Data Files				
X.OFFSET	number	The x-direction shift of a two-dimensional profile obtained from a data file.	0.0	microns
2D.PROC	logical	Specifies that the data file is in a format generated by TMA SUPRA with a revision code of 8501 or later. This parameter is used to read a data that was saved by using TMA SUPRA's **SAVEFILE** statement with the **DEVICE** parameter specified.	false	
SUPRA	logical	Specifies that the data file is in a format generated by a version of TMA SUPRA with a revision code earlier than 8501.	false	

Parameter	Type	Definition	Default	Units
TSUPREM4	logical	Specifies that the data file is in a format generated by TSUPREM-4. This parameter is used to read a data that was saved by using TSUPREM-4's **SAVEFILE** statement with the **MEDICI** parameter specified.	false	
2D.ASCII	logical	Specifies that profile data is read from a formatted file. Two columns of the file should correspond to the x- and y coordinates (in microns) and should be identified with **X.COLUMN** and **Y.COLUMN**, respectively. The file should also contain one or more columns of profile data that can be identified with the parameters **N.COLUMN**, **P.COLUMN**, or **D.COLUMN**.	false	
X.COLUMN	number	The column of the formatted data file corresponding to the x coordinate.	1 if **2D.ASCII** is specified	none
TIF	logical	Specifies that the data file is in TIF.	false	
MEDICI	logical	Specifies that the data file is a standard Medici mesh file.	false	

Description

The **PROFILE** statement can be used to describe both impurity profiles and other arbitrary two-dimensional profiles for the structure. Profiles may be defined either analytically or through input from a data file. The data file can be a formatted file containing columns of data representing coordinates and values, the output generated by a process simulation program, or a Medici mesh file containing profile information.

See Also...

To further illustrate the **PROFILE** statement, refer to input file *mdex1* in N-Channel MOSFET Examples, Chapter 4, "Impurity Profiles" on page 4-5.

Profile Types

The profile type is specified with one of the parameters **N-TYPE**, **P-TYPE**, **IMPURITY**, or **OTHER**.

The parameters **N-TYPE** and **P-TYPE** are used with impurity profiles and merely classify them as either donors or acceptors.

Specifying Individual Impurity Profiles

The **IMPURITY** parameter is used to specify individual impurities for the structure (such as B or As). This parameter can be used to specify the name of an impurity that is being defined analytically or the names of the impurities to be read from ASCII, Medici, or TIF files. The use of the **IMPURITY** parameter is illustrated in the following examples.

Define an analytic boron profile:

```
PROFILE  IMPURITY=B N.PEAK=1E18 Y.MIN=0 Y.MAX=0
+        Y.CHAR=.2 X.MIN=0 X.MAX=0.5 X.CHAR=0.2
```

Read an arsenic profile from a 2D ASCII file:

```
PROFILE  IMPURITY=As IN.FILE=cool_data 2D.ASCII
+        X.COLUMN=1 Y.COLUMN=2 D.COLUMN=3
```

Read multiple profiles from a TIF file:

```
PROFILE  IMPURITY=(B,As,P,In) IN.FILE=cool.tif TIF
```

Note:

When using the* `IMPURITY` *parameter, impurities should be specified with their chemical name. All impurities specified with* `IMPURITY` *are assumed to be electrically active and their names are stored internally with the letter "a" appended to their chemical name. When reading impurities from TIF files, specifying* `IMPURITY=(B,As,P,...)` *will cause the program to look for* `Ba`, `Asa`, `Pa`,*... in the TIF file.

Specifying Profiles for Other Quantities

The **`OTHER`** parameter is used to specify spatial distributions of arbitrary quantities other than electrically active impurities. As with impurities, **`OTHER`** quantities can be defined analytically or read from ASCII, Medici, or TIF files. Some uses of the **`OTHER`** parameter are illustrated in the following examples.

Define an analytic density of states for use with the **`TRAP`** statement:

```
PROFILE  OTHER=DOS N.PEAK=1E19 Y.MIN=0 Y.MAX=0
+        Y.CHAR=.1
```

Read a lifetime profile from a 2D ASCII file for use on **`EXTRACT`** or **`TRAP`** statements:

```
PROFILE  OTHER=Lifetime IN.FILE=life.dat 2D.ASCII
+        X.COLUMN=1 Y.COLUMN=2 D.COLUMN=3
```

Read the chemical boron concentration from a TIF file:

```
PROFILE  OTHER=B IN.FILE=stuff.tif TIF
```

Read the stress components from a TIF file:

```
PROFILE  OTHER=(Sxx,Syy,Sxy) IN.FILE=stuff.tif TIF
```

Analytic Profiles

Specifying **`UNIFORM`** creates a uniform profile of concentration **`N.PEAK`**. Otherwise, the profile has a constant concentration of **`N.PEAK`** only in the region **`X.MIN`** < x < **`X.MAX`** and **`Y.MIN`** < y < **`Y.MAX`**. Outside this region, the profile varies vertically as a Gaussian with a characteristic length of **`Y.CHAR`**.

The horizontal profile outside this region can either vary as a Gaussian (the default) or as the difference of two complementary error functions (if **`X.ERFC`** is specified). In either case, a characteristic length of **`X.CHAR`** or **`XY.RATIO`***__`Y.CHAR`__ is used in the x direction.

The mathematical description of an analytic profile is given by

$$N(x,y) = \mathbf{N.PEAK} \cdot a(x) \cdot b(y) \qquad \text{Equation 3-3}$$

Vertical Variation

The function $b(y)$ describes the vertical variation of the profile and is given by

$$b(y) = \begin{cases} \exp\left[-\left(\dfrac{y-\mathbf{Y.MIN}}{\mathbf{Y.CHAR}}\right)^2\right] & y < \mathbf{Y.MIN} \\ 1 & \mathbf{Y.MIN} \le y \le \mathbf{Y.MAX} \\ \exp\left[-\left(\dfrac{y-\mathbf{Y.MAX}}{\mathbf{Y.CHAR}}\right)^2\right] & y > \mathbf{Y.MAX} \end{cases} \qquad \text{Equation 3-4}$$

Lateral Direction Variation

The function $a(x)$ describes the lateral variation of the profile and is given by

$$a(x) = \begin{cases} a_1(x) & \mathbf{X.ERFC} \text{ not specified} \\ a_2(x) & \mathbf{X.ERFC} \text{ specified} \end{cases} \qquad \text{Equation 3-5}$$

where

$$a_1(x) = \begin{cases} \exp\left[-\left(\dfrac{x-\mathbf{X.MIN}}{\mathbf{X.CHAR}}\right)^2\right] & x < \mathbf{X.MIN} \\ 1 & \mathbf{X.MIN} \le x \le \mathbf{X.MAX} \\ \exp\left[-\left(\dfrac{x-\mathbf{X.MAX}}{\mathbf{X.CHAR}}\right)^2\right] & x > \mathbf{X.MAX} \end{cases} \qquad \text{Equation 3-6}$$

and

$$a_2(x) = \frac{\operatorname{erfc}\left(\dfrac{x-\mathbf{X.MAX}}{\mathbf{X.CHAR}}\right) - \operatorname{erfc}\left(\dfrac{x-\mathbf{X.MIN}}{\mathbf{X.CHAR}}\right)}{2} \qquad \text{Equation 3-7}$$

Junction Depth

The **Y.JUNCTI** parameter may be used to specify the p-n junction depth as a y location where the magnitude of the impurity profile equals the magnitude of the current background impurity concentration.

Y.JUNCTI is used to define the vertical characteristic length which otherwise must be specified with the **Y.CHAR** parameter.

Impurity Dose

The **DOSE** parameter may be used to specify the integral amount of doping atoms which relates to the peak concentration in terms of the vertical characteristic length as **N.PEAK** = **DOSE**/($\sqrt{\pi}$ · **Y.CHAR**).

Polygonal Profiles

A polygon can be defined in the XY plane for describing an area where the profile has a constant value of **N.PEAK**. The polygon is defined by a pair of coordinate arrays **X.POLY** and **Y.POLY** representing the location of vertices of the polygon. The polygon can be arbitrary as long as it is non-self-intersecting. The last vertex may or may not coincide with the first one, either way will do.

Lateral profile extension outside of the polygon is determined by the parameters **N.CHAR** and **N.ERFC**. These parameters are applied to the lateral profile extension in the direction, normal to the nearest polygon edge.

Outside of the profile bounding box (**X.MIN**, **X.MAX**, **Y.MIN**, and **Y.MAX**) there is no lateral profile extension for a polygonal profile.

Profile Rotation

A profile can also be described by a rotation in the XY plane around a rotation center, defined by the center location coordinates **X.CENTER** and **Y.CENTER**. When using a rotated profile, the profile has a constant value of **N.PEAK** within the range **R.INNER** to **R.OUTER**. If **R.INNER** is zero, then a circular profile is created, otherwise, a donut-shaped profile is created.

Lateral profile extension outside of the range **R.INNER** to **R.OUTER** is determined by the parameters **R.CHAR** and **R.ERFC**. These parameters are applied to the lateral profile extension in the radial direction.

Outside of the profile bounding box the lateral profile extension is defined by the conventional parameters **X.CHAR**, **X.ERFC**, and **Y.CHAR**.

A combination of the profile rotation and profile bounding box (**X.MIN**, **X.MAX**, **Y.MIN**, and **Y.MAX**) can be used in order to form segments of a circular profile.

One-Dimensional Profiles from Data Files

The vertical impurity profile may be input from a data file by specifying the **IN.FILE** parameter and one parameter from the set **1D.PROC**, **SUPREM2**, or **1D.ASCII**. By default, the origin for the impurity profile is aligned with the vertical origin in Medici.

For one-dimensional impurity profiles input from data files created by a process simulation program, the origin occurs at the first point of the bottom semiconductor material (polysilicon and silicon are treated as the same material). The **Y.OFFSET** parameter may be used to shift the vertical profile relative to the Medici structure.

Vertical Range

The **Y.MIN** and **Y.MAX** parameters define the y interval within which the impurity profiles contribute to the total impurity distribution for the structure. The