Additional directives in MicroTec version for Photovoltaics applications

#DOP: Analytical doping data

This directive may include any number of **DOPA:** or **DOPF:** subdirectives.

The analytical doping profiles are described by a superposition of wells. For each well is defined by one **DOPA:** subdirective according to the following formula

$$N_{well} = N_0 S_{DOP}\left(Đ\left(\frac{f(x_l Đ x)}{L_x}\right)^{\alpha_x} Đ\left(\frac{f(x Đ x_r)}{L_x}\right)^{\alpha_x} Đ\left(\frac{f(y Đ y_b)}{L_y}\right)^{\alpha_y} Đ\left(\frac{f(y_t Đ y)}{L_y}\right)^{\alpha_y}\right)$$

$$N_{well} = N_0 S_{DOP}\left(Đ\left(\frac{f(x_l Đ x)}{L_x}\right)^{\alpha_x} Đ\left(\frac{f(x Đ x_r)}{L_x}\right)^{\alpha_x} Đ\left(\frac{f(y Đ y_b)}{L_y}\right)^{\alpha_y} Đ\left(\frac{f(y_t Đ y)}{L_y}\right)^{\alpha_y}\right)$$

$$f(x) = \frac{|x| + x}{2}$$

The concentration in every well is a constant equal to N_0 in the rectangle x_l, x_r, y_t, y_b (left, right, top, bottom coordinates) and decreases as a screening function beyond the rectangle. N_0 is the maximum concentration in the well, it is positive for donors and negative for acceptors.

Four choices of the screening functions are available according to the well type (IWEL variable in the parameters set)

DOPA: Doping well types

IWEL value	Screening function	Description
1	Step function	$S_{DOP} = 1$ if $x_l < x < x_r$, $y_t < y < y_b$ and $S_{DOP} = 0$ otherwise

IWEL value	Screening function	Description
2	Linear function	$S_{DOP} = 1$ if $x_l < x < x_r$, $y_t < y < y_b$ $S_{DOP} = 0$ if $x_l - L_x > x$ or $x > x_r + L_x$ or $y_t - L_y > y$ or $y > y_b + L_y$, everywhere else S_{DOP} changes from 1 to 0 linearly
3	Exponential function	$S_{DOP} = 1$ if $x_l < x < x_r$, $y_t < y < y_b$ Outside the rectangle S_{DOP} changes from 1 to 0 exponentially, for example $S_{DOP} = \exp(- ((x-x_l)/ALX)^{EXPX} - ((y-y_t)/ALY)^{EXPY})$
4	Complimentary error function	$S_{DOP} = 1$ if $x_l < x < x_r$, $y_t < y < y_b$ Outside the rectangle S_{DOP} changes from 1 to 0 as the error function, for example $S_{DOP} = \text{erf}((x-x_l)/ALX + (y-y_t)/ALY)$

DOPA: Doping well parameters

Name	Default	Units	Description
DOP	$1 \cdot 10^{18}$	cm^{-3}	Maximum concentration in the doping well.
ALX	0.05	none	Characteristic length in X direction.
ALY	0.07	none	Characteristic length in Y direction.
XLFT	0	um	Left edge of the doping well.
XRGT	1	um	Right edge of the doping well.
YTOP	0	um	Top of the doping well.
YBOT	1	um	Bottom of the doping well.
EXPX	2	um	Exponent in X direction.
EXPY	2	um	Exponent in Y direction.

DOPF: ASCII doping file input

This directive is analogous to the **DOPA:** directive. The only difference is that instead being constant within the defined rectangle the data is generated using one-dimensional ASCII file with doping data obtained from other sources, either measurements or simulation. The file

should contain two columns with the depth (microns) and doping concentration (cm^{-3}). Positive (negative) concentration values correspond to donor (acceptor) impurity.

#PHO: Phogeneration data

This directive may include any number of **PHOT:** or **PHOF:** subdirectives which are analogous to **DOPA:** and **DOPF:** subdirectives.

OXID: Oxide region

Name	Default	Units	Description
COMM	'Name'	none	Region description
PERM	3.8	none	Oxide permittivity
XOXL	0	um	Left edge of the oxide well.
XOXR	1	um	Right edge of the oxide well.
YOXT	0	um	Top of the oxide well.
YOXB	1	um	Bottom of the oxide well.
QOXL	0	cm^{-2}	Qss at the left edge of the oxide well.
QOXR	0	cm^{-2}	Qss at the right edge of the oxide well.
QOXT	0	cm^{-2}	Qss at the top of the oxide well.
QOXB	0	cm^{-2}	Qss at the bottom of the oxide well.

#REM: Remesh region

This directive may include up to 20 **REME** subdirectives. Each rectangular region is defined by one **REME** subdirective.

REME: Remesh region

Name	Default	Units	Description
COMM	'Name'	none	Region name
NXRM	10	no units	Number of extra X-nodes in the region

Name	Default	Units	Description
NYRM	10	no units	Number of extra Y-nodes in the region
XRML	0	um	Left edge of the remesh well.
XRMR	1	um	Right edge of the remesh well.
YRMT	0	um	Top of the remesh well.
YRMB	1	um	Bottom of the remesh well.

#REC: Additional recombination parameters

This directive may include up to 20 **RMCR:** subdirectives. Each rectangular region is defined by one **RMCR:** subdirective defining a rectangle with a modified SRH recombination rate that may be due to a grain boundary.

RMCR: Recombination region

Name	Default	Units	Description
XRML	0	um	Left edge of the recombination well.
XRMR	1	um	Right edge of the recombination well.
YRMT	0	um	Top of the recombination well.
YRMB	1	um	Bottom of the recombination well.
ETRR	0	e.V.	Trap energy
TNRR	10^{-7}	s	Electron life-time in the region
TPRR	10^{-7}	s	Hole life-time in the region