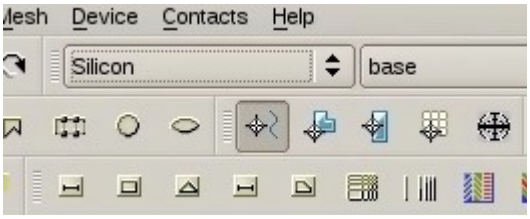
Sentaurus Structure Editor (sde)

1. Draw basic device structure

draw> overlap behavior> new replaces old (default)
select “Silicon” from menu



draw> exact coordinates > rectangle

(sdegeo:create-rectangle (position 0 0 0.0) (position 20 -100 0.0) "Silicon" "region_1")

2. Define and activate electrical contacts

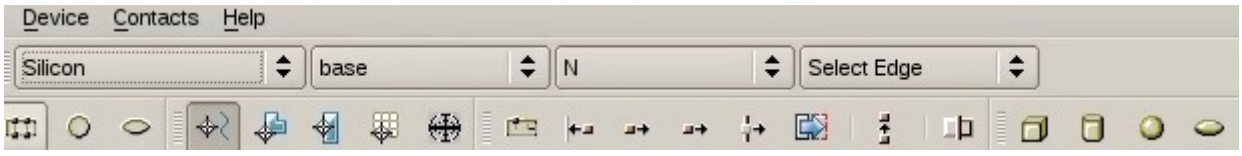
contacts> contact sets> … > set

(sdegeo:define-contact-set "P" 4 (color:rgb 1 0 0) "##")
(sdegeo:define-contact-set "N" 4 (color:rgb 0 1 0) "||")

activate
(sdegeo:set-current-contact-set "P")
(sdegeo:set-current-contact-set "P")

3. Set contact edges

select “select edges” from selection type menu, “N” from contact menu



contact> set contacts

(sdegeo:set-contact-edges (list (car (find-edge-id (position 10 -100 0)))) "N")

same for P

(sdegeo:set-contact-edges (list (car (find-edge-id (position 10 0 0)))) "P")

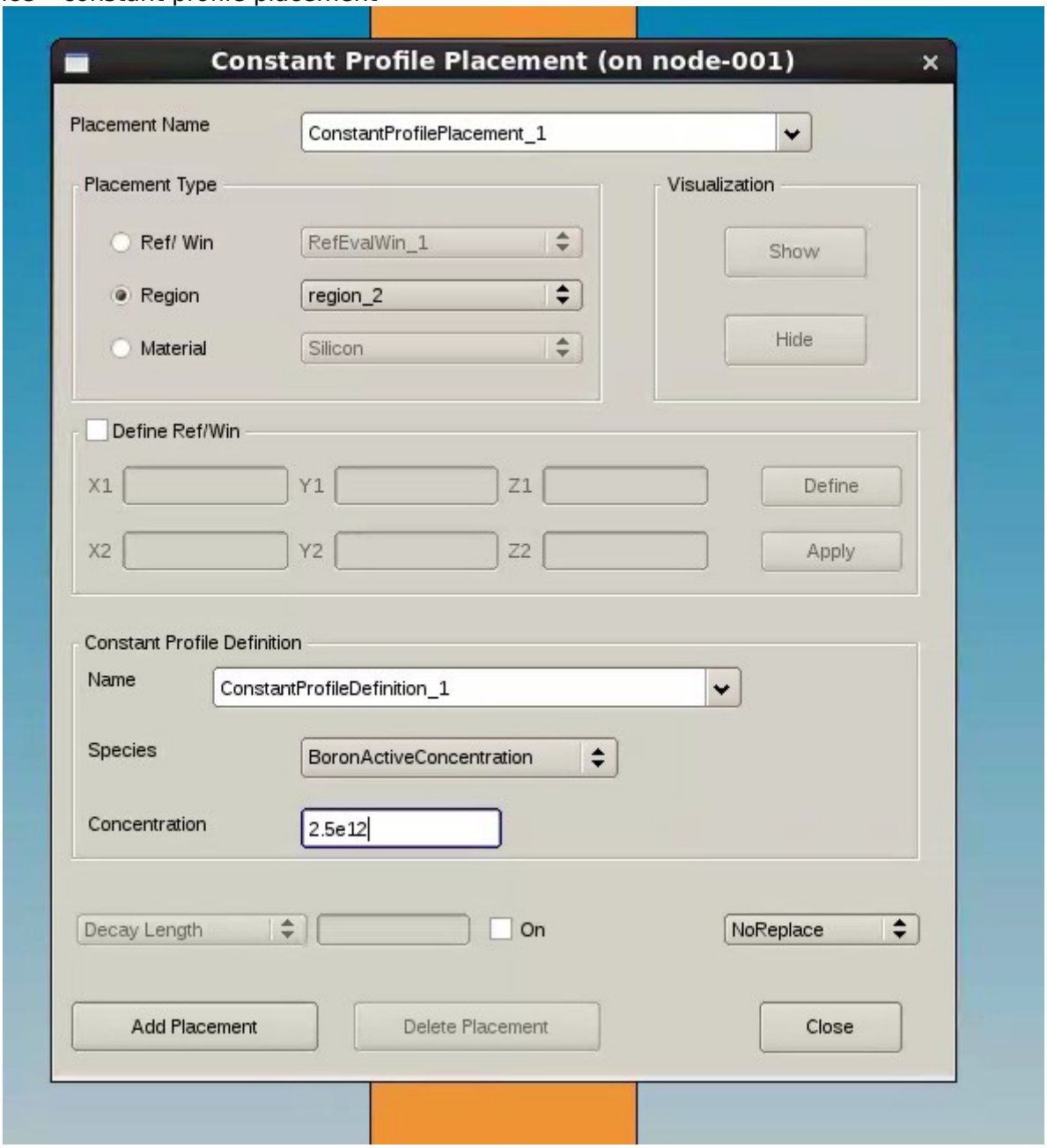
4. Doping profiles
a. Define ref-eval window
mesh> define refeval window> line
draw a random line and enter first electrode coordinate (N)

(sdedr:define-refeval-window "RefEvalWin_1" "Line" (position 0 0 0) (position 20 0 0))

same for second electrode (P)

(sdedr:define-refeval-window "RefEvalWin_2" "Line" (position 0 -100 0) (position 20 -100 0))

b. bulk constant doping
device> constant profile placement

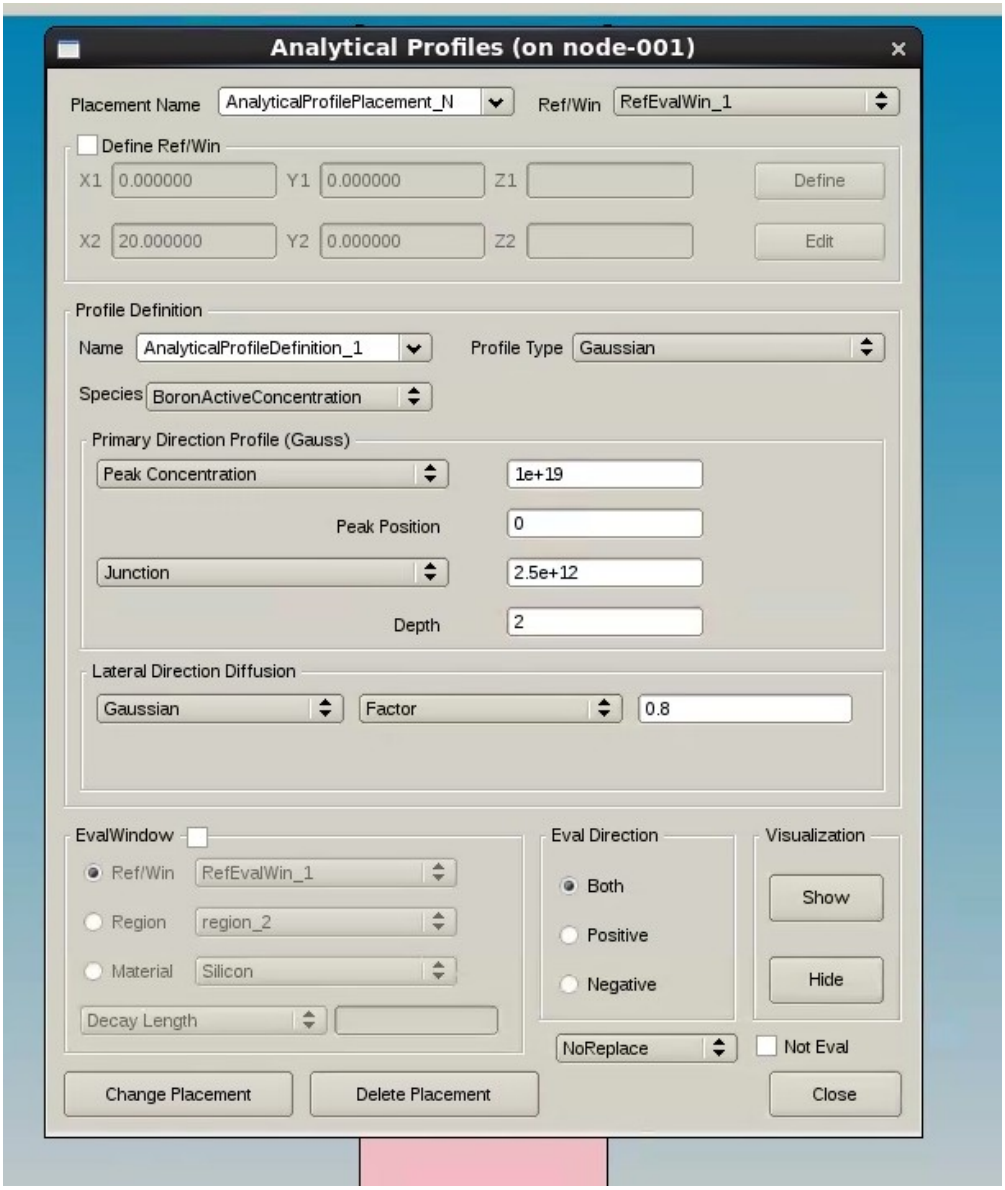


> add placement

(sdedr:define-constant-profile "ConstantProfileDefinition_1" "BoronActiveConcentration" 2.5e12)
(sdedr:define-constant-profile-region "ConstantProfilePlacement_1" "ConstantProfileDefinition_1" "region_2")

c. electrode doping
device> analytical profile placement
if refeval wind yet defined:
select refevalwin

N electrode
placement name: add placement name
ref/win = RefEvalWin_1
select species BoronActiveConcentration
junction = bulk doping concentration, depth = where the gaussian profile merges the bulk

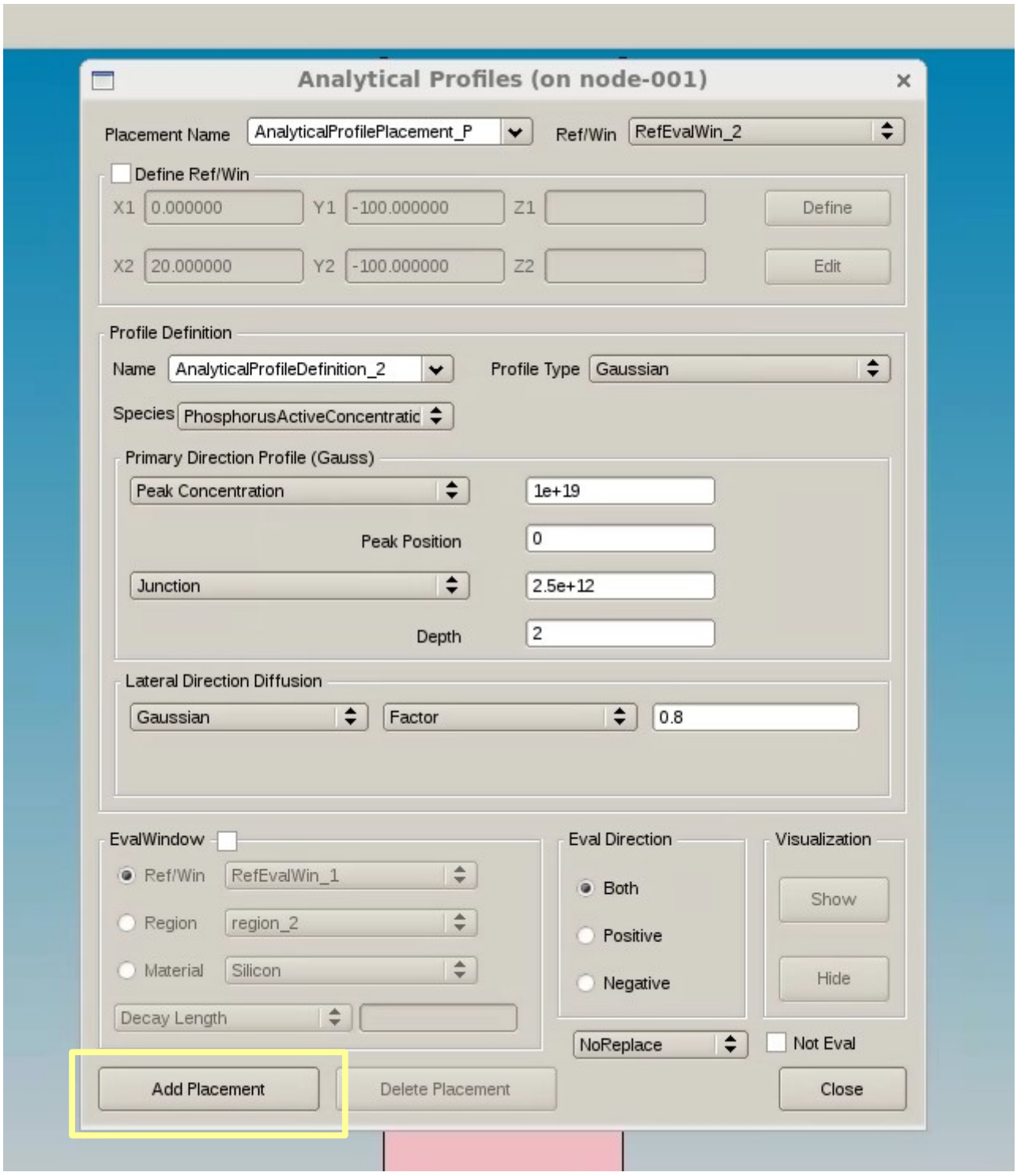


> add placement

P electrode
device> analytical profile placement
placement name: add placement name (different from the previous!)
ref/win = RefEvalWin_2
select species Phosphorus/Arsenic ActiveConcentration
> add placement

(sdedr:define-analytical-profile-placement "AnalyticalProfilePlacement_N"
"AnalyticalProfileDefinition_1" "RefEvalWin_1" "Both" "NoReplace" "Eval")

(sdedr:define-gaussian-profile "AnalyticalProfileDefinition_1" "BoronActiveConcentration"
"PeakPos" 0 "PeakVal" 1e19 "ValueAtDepth" 2.5e12 "Depth" 2 "Gauss" "Factor" 0.8)



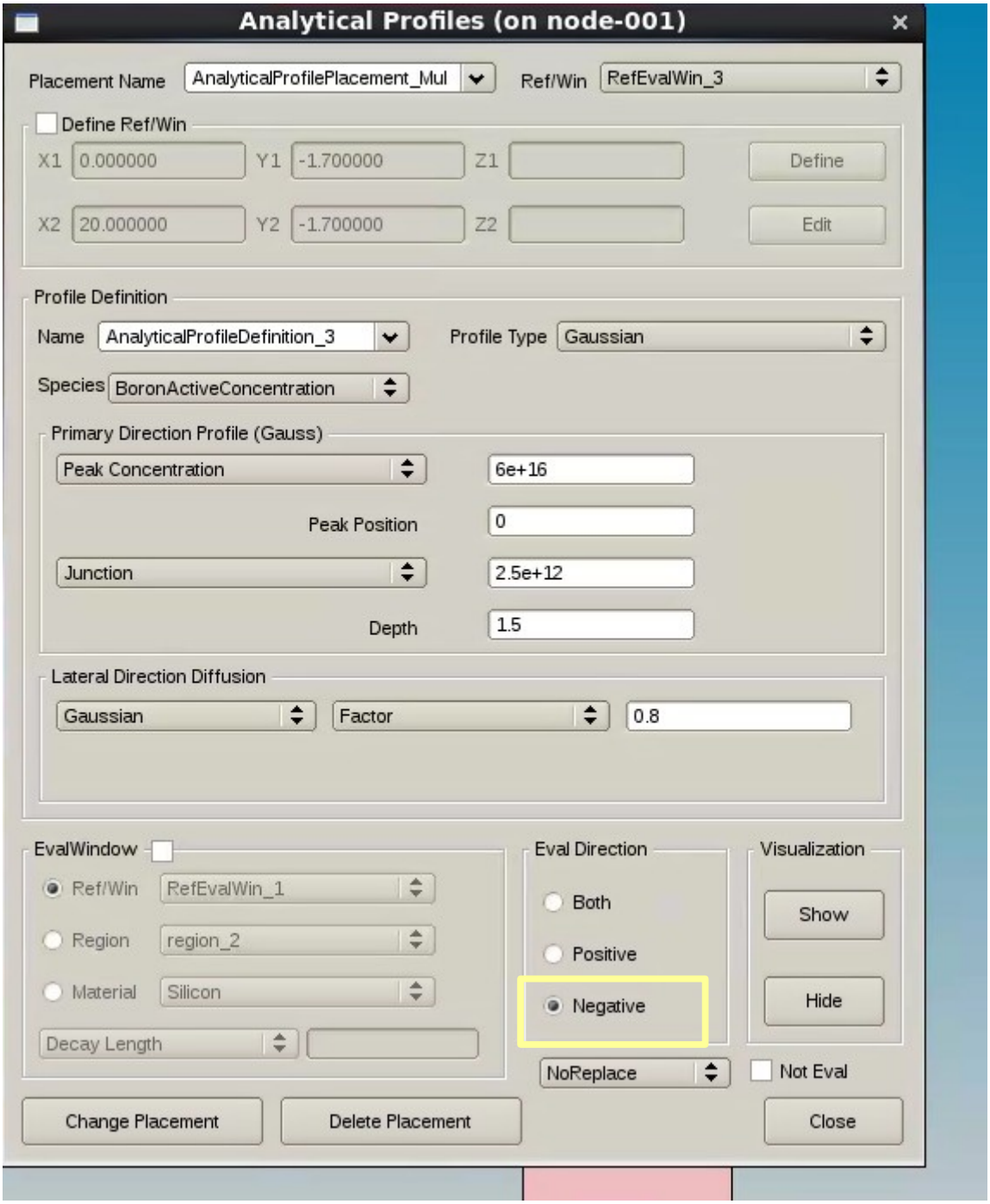
(sdedr:define-analytical-profile-placement "AnalyticalProfilePlacement_P" "AnalyticalProfileDefinition_2" "RefEvalWin_2" "Both" "NoReplace" "Eval")

(sdedr:define-gaussian-profile "AnalyticalProfileDefinition_2" "PhosphorusActiveConcentration" "PeakPos" 0 "PeakVal" 1e+19 "ValueAtDepth" 2.5e+12 "Depth" 2 "Gauss" "Factor" 0.8)

d. multiplication region (optional)

mesh> define refeval window> line
(sdedr:define-refeval-window "RefEvalWin_3" "Line" (position 0 -1.7 0) (position 20 -1.7 0))

device> analytical profile placement



(sdedr:define-gaussian-profile "AnalyticalProfileDefinition_3" "BoronActiveConcentration" "PeakPos" 0 "PeakVal" 6e+16 "ValueAtDepth" 2.5e+12 "Depth" 1.5 "Gauss" "Factor" 0.8)

(sdedr:define-analytical-profile-placement "AnalyticalProfilePlacement_Mul" "AnalyticalProfileDefinition_3" "RefEvalWin_3" "Negative" "NoReplace" "Eval")

4. define the mesh

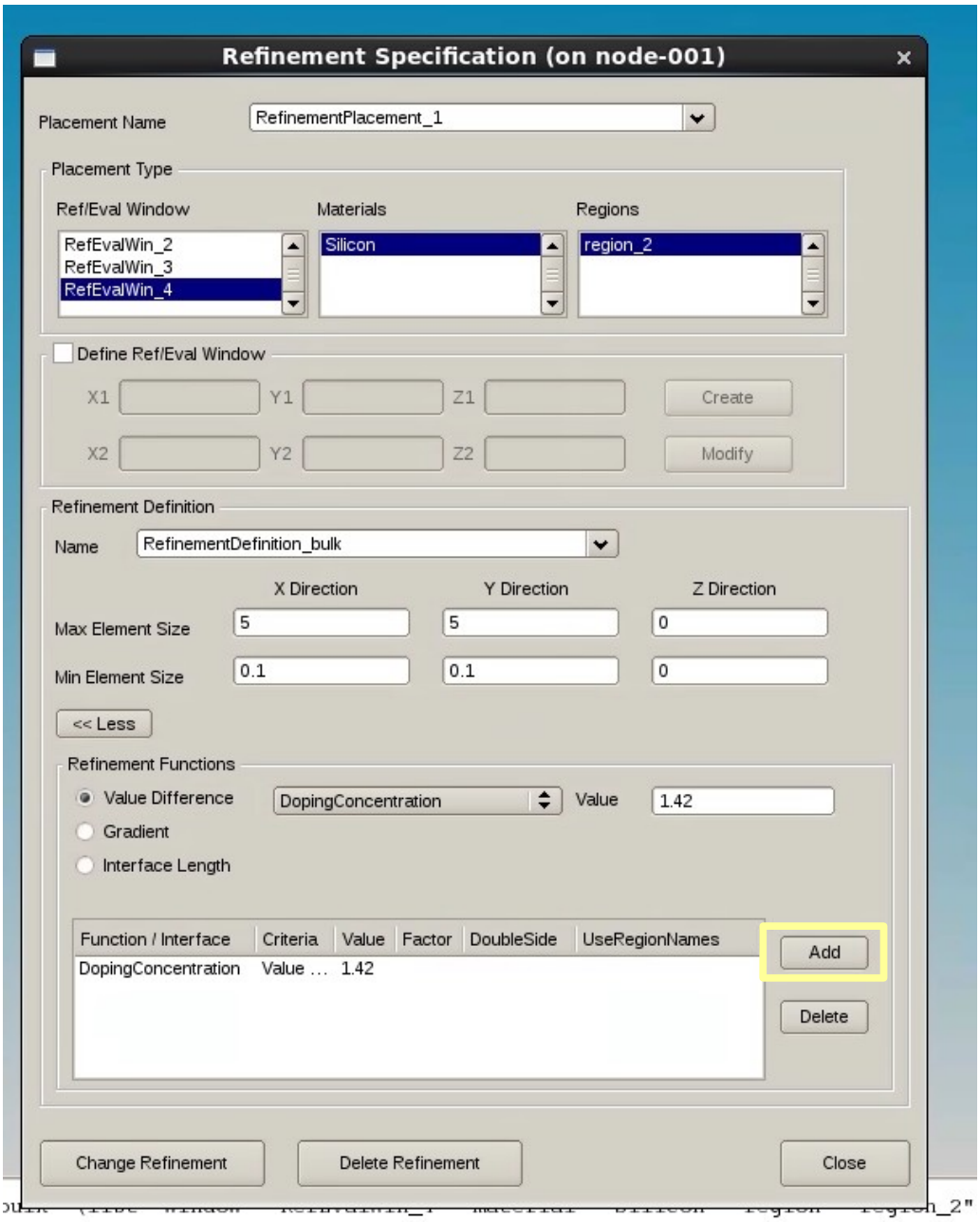
a. global mesh
mesh> define refeval window > rectangle
define a rectangle covering the whole bulk

(sdedr:define-refeval-window ":" "Rectangle" (position -1 1 0) (position 21 -101 0))

mesh > refinement specification

select “RefEvalWin_4”, “Silicon”, “region_2”

refinement functions> value difference> doping concentration
value = 1.42
add



create refinement

```
(sdedr:define-refinement-size "RefinementDefinition_bulk" 5 5 0 0.1 0.1 0 )

(sdedr:define-refinement-placement "RefinementPlacement_1" "RefinementDefinition_bulk"
(list "window" "RefEvalWin_4" "material" "Silicon" "region" "region_2" ) )

(sdedr:define-refinement-function "RefinementDefinition_bulk" "DopingConcentration"
"MaxTransDiff" 1.42)
```

b. electrodes mesh
same as before:
mesh> define refeval window > rectangle ...
mesh > refinement specification ...

N electrode

```
(sdedr:define-refeval-window "RefEvalWin_N" "Rectangle"  (position -1 0 0) (position 21 -10 0))

(sdedr:define-refinement-size "RefinementDefinition_N" 2 0.2 0 0.5 0.1 0 )
(sdedr:define-refinement-placement "RefinementPlacement_N" "RefinementDefinition_N"
"RefEvalWin_N" )

(sdedr:define-refinement-function "RefinementDefinition_N" "DopingConcentration"
"MaxTransDiff" 1.42)
```

P electrode

```
(sdedr:define-refeval-window "RefEvalWin_P" "Rectangle"  (position -1 -100 0) (position 21 -100
0))

(sdedr:define-refinement-size "RefinementDefinition_P" 2 0.5 0 0.5 0.1 0 )
(sdedr:define-refinement-placement "RefinementPlacement_P" "RefinementDefinition_P"
"RefEvalWin_P" )

(sdedr:define-refinement-function "RefinementDefinition_P" "DopingConcentration"
"MaxTransDiff" 1.42)
```

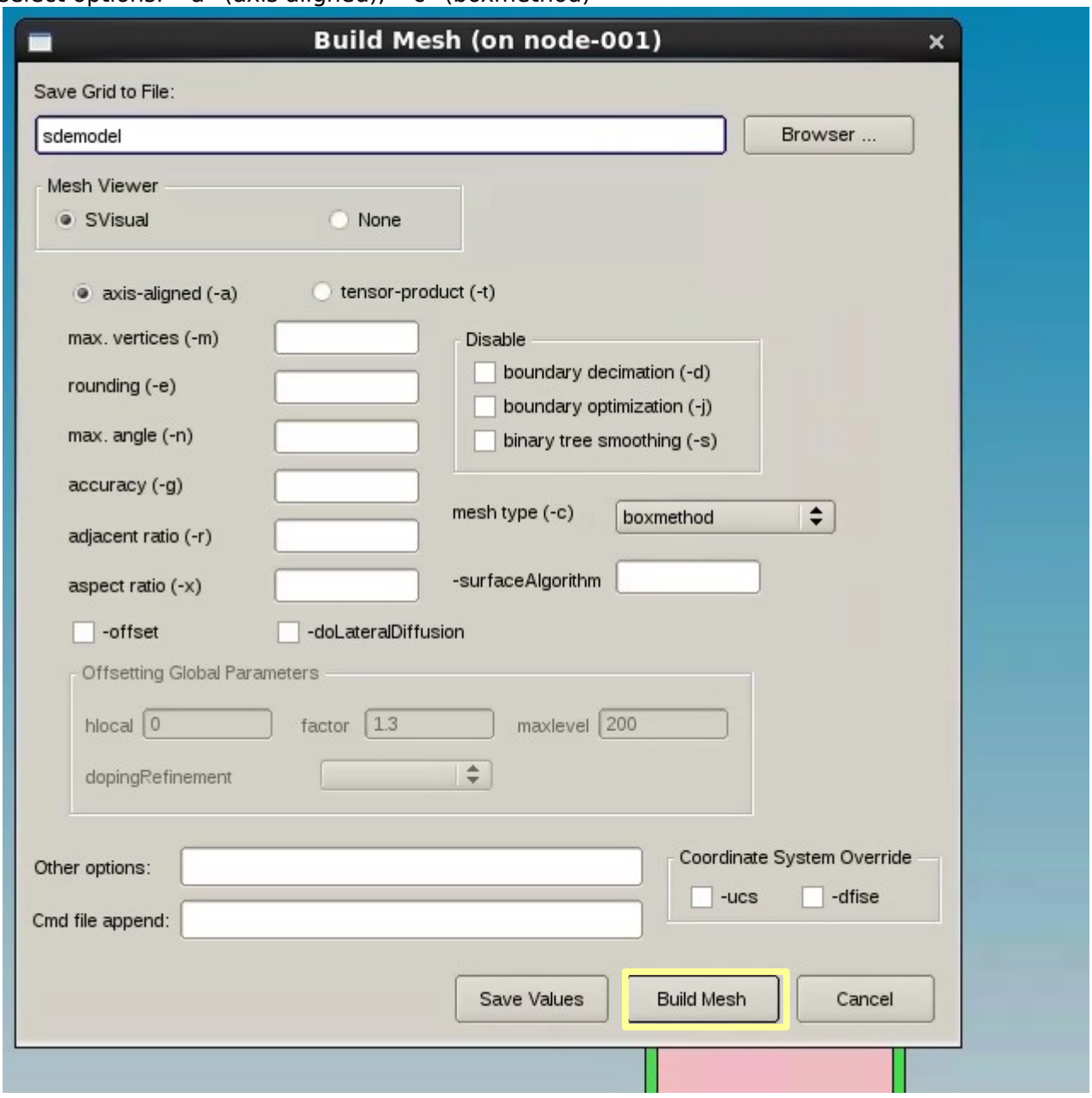
gain implant

```
(sdedr:define-refeval-window "RefEvalWin_mul" "Rectangle"  (position -1 -1 0) (position 21 -3.5
0))

(sdedr:define-refinement-size "RefinementDefinition_mul" 2 0.1 0 0.05 0.1 0 )
(sdedr:define-refinement-placement "RefinementPlacement_mul" "RefinementDefinition_mul"
"RefEvalWin_4" )

(sdedr:define-refinement-function "RefinementDefinition_mul" "DopingConcentration"
"MaxTransDiff" 1.42)
```

5. build the mesh

mesh> build mesh

select options: “-a” (axis aligned), “-c” (boxmethod)



build mesh

OR

put in the command file the following lines (best option, sde does it automatically):

```
(sde:save-model "p@node@")
(sde:build-mesh "snmesh" "-a -c boxmethod" "n@node@")
```