

CNF Guide to Layout BEAMER v 4.0 and SCELETON

CONTENT:

1. LAYOUT BEAMER OVERVIEW

2. Converting Patterns QUICK START

3. PROX correction QUICK START

4. SCELETON QUICK START

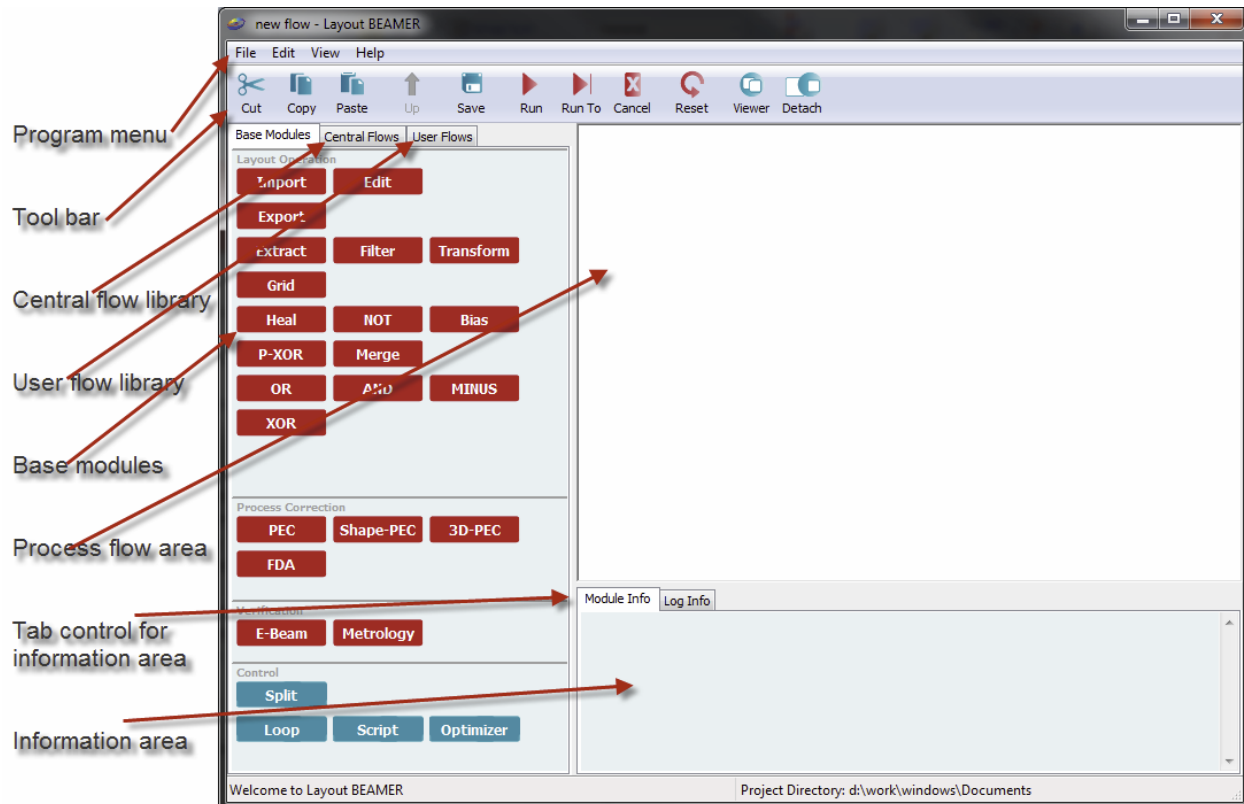
5A. LAYOUT BEAMER TONE REVERSAL QUICK START - Method 1

5B. LAYOUT BEAMER TONE REVERSAL QUICK START - Method 2

For questions or comments email: **rob@cnf.cornell.edu**

1. LAYOUT BEAMER OVERVIEW

Layout BEAMER provides a new innovative GUI framework for the database driven, modular design of complex layout process flows. Start **Layout BEAMER** by logging into korat or minx using the icons on your desktop. On Windows, also start X-Windows, either Exceed or Xming. By typing **LayoutBEAMER** at the prompt you will see the following main window appear:



The **Layout BEAMER** Graphical User Interface (GUI) consists of the left side **Tool Window** pane, the main **Process Flow Design** workspace window pane, and the lower **Information Window** pane. Within the **Tool Window** pane's **Module library** under the **Edit Tab**, you see all available process modules in the following groups:

- **Layout Process modules** (Import, Export, Extract, Transform, PEC)
- **Data Prep modules** (Heal, NOT, Bias, P-XOR, MINUS, OR, AND, XOR)
- **Modeling modules** (E-Beam, Resist)
- **Control modules** (If, Loop, Merge, Split)

The **Tool Window** pane also has **User Flows & Central Flow Tabs**, where common user-defined process flows can be stored to build up a database for later retrieval and re-use.

Building a Process Flow is simply done by **drag & drop** (using the left mouse button) of the desired process modules from within the **Edit Tab** (Module Library) into the **Process Flow Design** workspace window or double click on the desired process

Module and it will automatically be connected to the last Module added into the Process Flow Design workspace.

Module Status

The status of a module is shown by the module color and the icon marker located at the right side of the module. A module which has not had its parameters set is identified as an orange colored module, whereas a red color and a triangular-shaped Run To button signifies that parameters have been set but the module has not been run yet. A module which has been run and the results are ready, is shown with an overlapping-box View icon. A progress bar is shown while the process is being computed . If a module has been selected with the mouse or with the Ctrl-A command, it will have four red dots surrounding the module. Moving your mouse over a module will display the module name and any comments that have been assigned to that module.



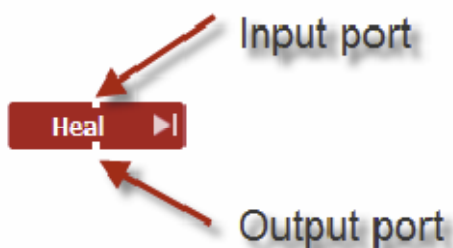
Single Port Modules

A port is used to connect modules. There are input and output ports. A single port module has only one port at the bottom center of the module signifying that it has only output connectivity capability. It can be connected to another module, but has no input capability within the flow. A module's ports are identified as a small, white-colored box.



Dual Port Modules

A dual port module has a connectivity port at both the top and bottom center of the module, signifying that it has both input and output connection capability in a flow.

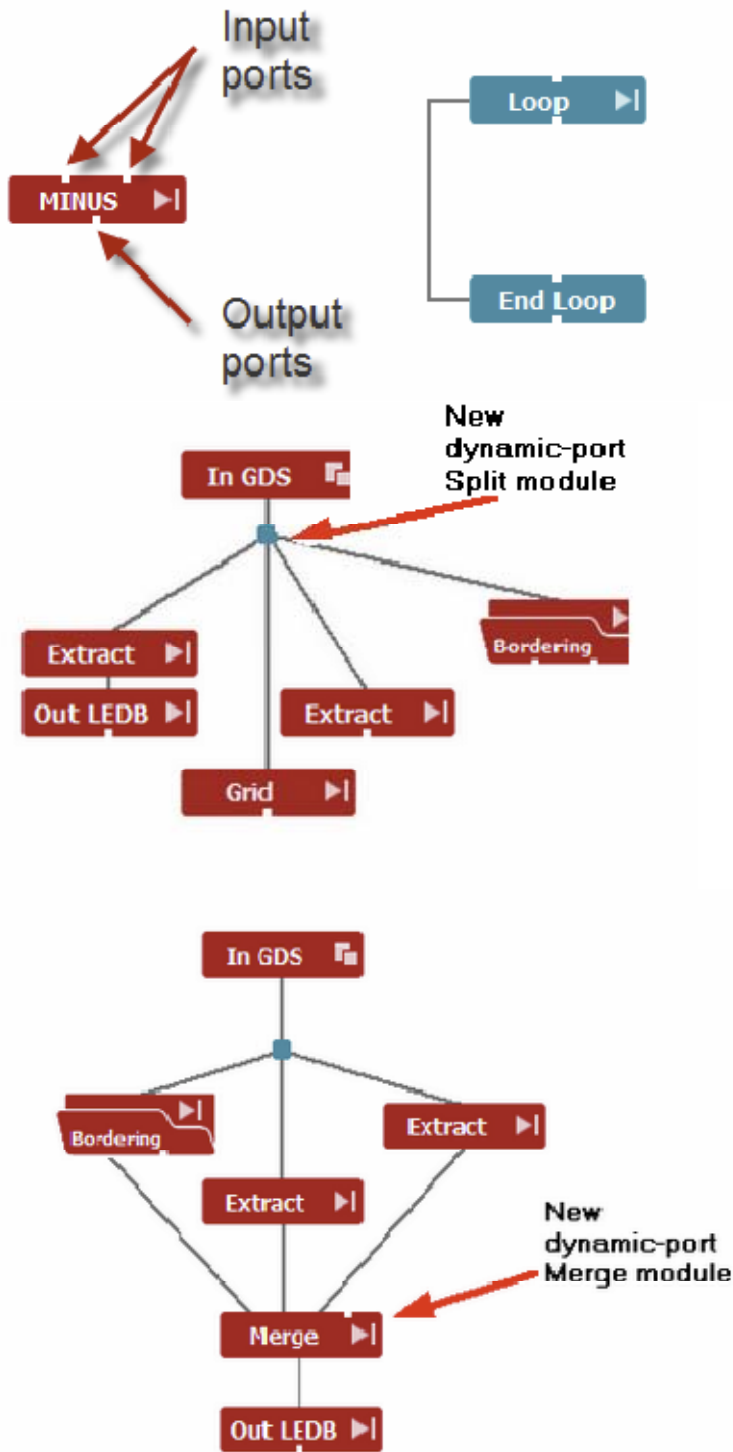


Dual port modules include: Extract, Filter, Transform, Grid, Heal, NOT, Bias, P-XOR, PEC, Shape-PEC, 3D PEC, FDA, Export, E-Beam and Metrology.

Multi Port Modules

A multi port module usually has three ports with a few exceptions. The multi port modules have two input ports at the top on the module and one output port on the bottom. Some specialty modules will have one input and two output modules while others, such as Loop and Optimizer, will combine two modules as a single process,

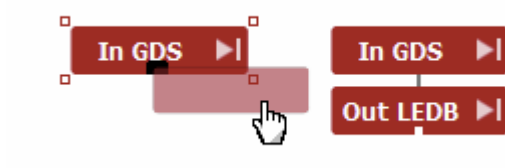
each with input and output connectivity capability. The other exception is the new Merge and Split modules which transform into a hub with a dynamic number of ports.



Multi port modules include: OR, MINUS, AND, XOR, Split, Merge, Loop and Optimizer.

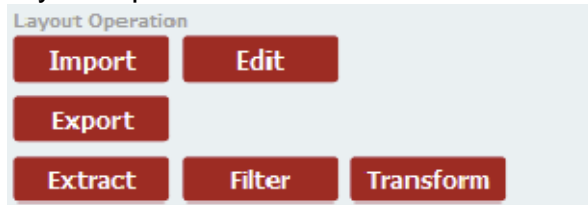
How To Connect Modules

There are three ways to connect modules. Drag and drop a module from the library onto the target module in the flow until the small white connection port turns black, then release the mouse and the modules will be connected. Modules can also be manually connected by using the right mouse button, held down, to draw a line between open ports. Finally, double clicking a module in any library will automatically send it to the Process Flow Design window, and connect it to a *selected* module in the flow.

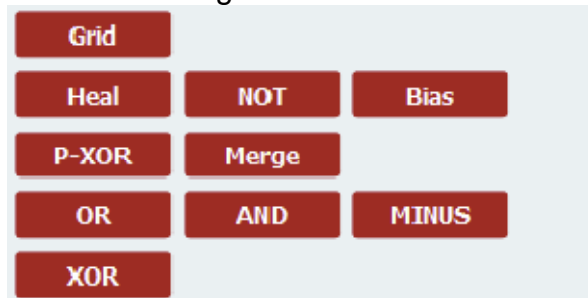


Base Module Library Overview

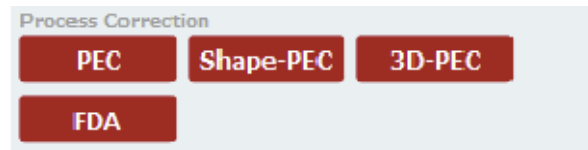
Layout Operation:



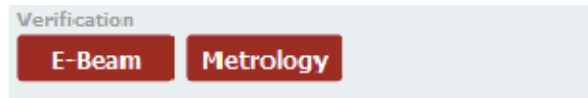
Post Processing



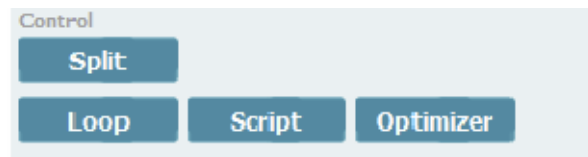
Process Correction



Verification





Control



2. Converting Patterns QUICK START

1. For short run conversions you could use a Windows machine to run LayoutBEAMER. This is accomplished by starting a session of Exceed or Xming, putty over to your korat or minx account and type **LayoutBEAMER**

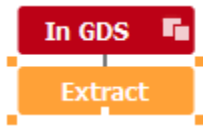
NOTE: Longer conversions, or any PEC related work, you must use the SUN Rays. You can let the conversion run in the background. Log into **korat** or **minx** through a SunRay and type **LayoutBEAMER**

2. Drag & Drop the **Import** Module from the Module Library into the Process Flow Design area workspace. Navigate to a folder with your GDSII file. Either accept the default Import Layout settings (Layer Set * & Datatype Set *) which means all available layers will be imported, or choose the layers you wish to import. Execute the **Import** module by selecting **Run To** from the module option menu with a right mouse button click on the **Import** module as below. Following completion the icon  dot will turn into .

3. Drag & drop the **Extract** module into the Process Flow Design area workspace, dropping it directly on top of the **In GDS** module, releasing the **Extract** module when the **In GDS** module output port turns black as shown below.



In GDS and **Extract** modules appear connected as



Choose a cell, layer and datatype range, select extents (automatic extent is default). Click **OK**. The modules appear as:



Right click **Extract** select **Run To**. The modules appear as:

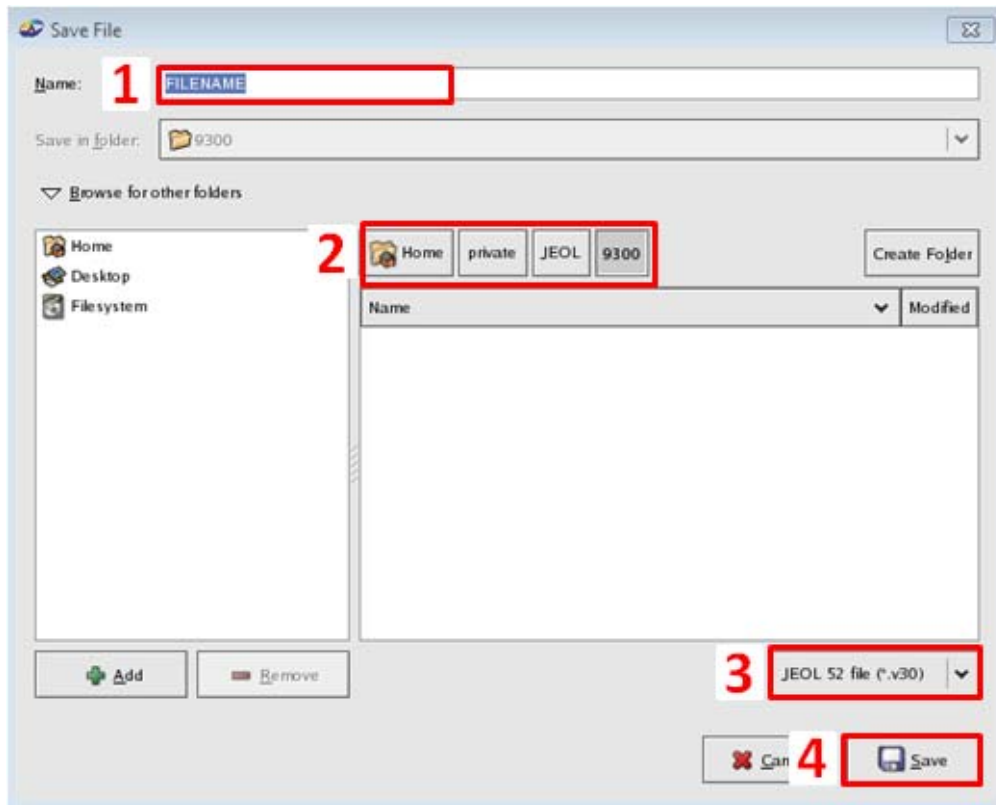


To view data right click **Extract** select **View Layout**.

4. Drag & drop the **Export** module on top of **Extract**. Click **Browse for other folders** in the **Save File** window.



In the expanded **Save File** window, type in a file name, navigate to the correct folder, choose **JEOL 52 file (*.v30)**, and click **Save** (steps 1-4 in the below figure).



For the JEOL, in the **General** tab make sure that the machine type is either JBX-9300FS (100kV) or JBX6300FS. Choose appropriate pattern units and shot pitch units. Fracture Mode 1 is the typical fracturing mode. Fracture Mode 2 uses the algorithm developed by Don Tennant at

Lucent that snaps ebeam pixels to pattern edges. Consequently within this mode increased number of fractured shapes are produced. When mapping layers to shot modulated clocks, within the *Advanced* tab, under *Dose Mapping*, choose **Layer to Class**.

Fixed main field option stacks fields in a boustrophedonic/serpentine/meander manner, whereas **Floating** allows placement of the main fields such that the structures are written with minimal stage movement for the areas of interest.

For the JBX63000FS: After choosing JBX-6300FS under the Machine Type settings under the **General** tab. Click on the **Tool** tab, choose:

EOS Mode 3 4th Lens mode, 500um field size, 1nm pixels

EOS Mode 6 5th Lens mode, 62.5um field size, 0.125nm pixels

Then go back to the **General** tab and modify settings.

Right click **Export** select **Run To**.

FILE TRANSFER TO JEOL6300

```
ftp jeol6300
user name:   jeoleb
password:    Jeoleb
cd pattern/user
bin
put FileName.v30
```

FILE TRANSFER TO JEOL9300

```
ftp jeol
user name:   ebtest
password:    EBtest
cd pattern/user
bin
put FileName.v30
```


3. PROX correction QUICK START

Complete steps 1-3 in section 2. Drag & drop the **PEC** module on top of **Extract**.

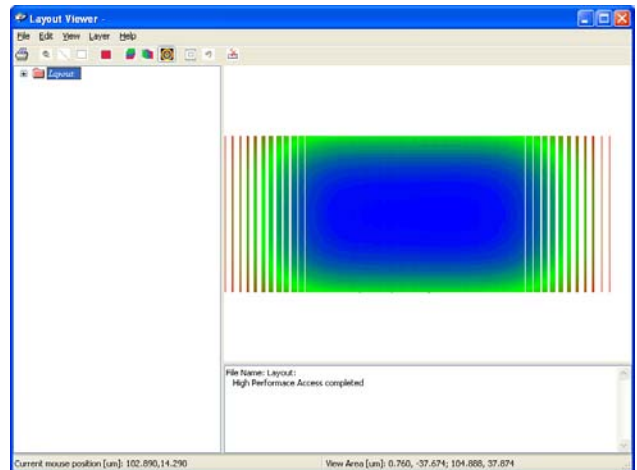
General tab: With “*Gaussian Approximation*” enabled, enter the *Beta* and *Eta* parameters. Checking “*Include Short Range Correction*” enables the *Alpha* parameter. At 2nA or lower on the JEOL *Beam FWHM[um]* parameter is around 0.004.

Computing the parameters using SCELETON generated data: Choose “*Numerical PSF*”, click Browse and select the SCELETON xrz file (see next section on generating a SCELETON file). Set the *Beam FWHM[um]* to the appropriate beam diameter (at 2nA, the beam diameter is around 5nm). Within the *Accuracy* tab, within *Dose Class Definition*, default *Accuracy* setting: PEC will only generate the number of dose classes needed to get the defined accuracy. The default setting is 1% with the max number of 256 dose classes. This means that you will get less dose classes if the accuracy of 1% can be reached by lower number of dose classes. Choosing *Fixed Number* allows user defined number of dose classes, default is 64 dose classes. The isodose grid defines the grid between adjacent doses. For Manhattan geometries a minimum figure size can be specified. Click **OK**.

Click **OK**. Right click **PEC** select **Run To**. To view the proximity corrected pattern, right click **PEC** select **View Layout**. Within the *Layout Viewer* choose View > Color by Layer > Dose.

Export data (see Section 2 item 4). For the JEOL, exporting a v30 file will automatically generate a **jdi** file containing modulated doses (see below). Paste this data into the job file.

```
MOD001: MODULAT (( 0, 19.17 ) , ( 1, 20.00 ) , ( 2, 20.85 )
- , ( 3, 21.69 ) , ( 4, 22.55 ) , ( 5, 23.41 )
- , ( 6, 24.28 ) , ( 7, 25.15 ) , ( 8, 26.03 )
- , ( 9, 26.91 ) , ( 10, 27.81 ) , ( 11, 28.70 )
- , ( 12, 29.61 ) , ( 13, 30.52 ) , ( 14, 31.43 )
- , ( 15, 32.36 ) , ( 16, 33.29 ) , ( 17, 34.22 )
- , ( 18, 35.17 ) , ( 19, 36.11 ) , ( 20, 37.07 )
- , ( 21, 38.03 ) , ( 22, 39.00 ) , ( 23, 39.98 )
- , ( 24, 40.96 ) , ( 25, 41.95 ) , ( 26, 42.95 )
- , ( 27, 43.95 ) , ( 28, 44.96 ) , ( 29, 45.98 )
- , ( 30, 47.01 ) , ( 31, 48.04 ) , ( 32, 49.08 )
- , ( 33, 50.13 ) , ( 34, 51.18 ) , ( 35, 52.24 )
- , ( 36, 53.31 ) , ( 37, 54.39 ) , ( 38, 55.47 )
- , ( 39, 56.56 ) , ( 40, 57.66 ) , ( 41, 58.77 )
- , ( 42, 59.89 ) , ( 43, 61.01 ) , ( 44, 62.14 )
- , ( 45, 63.28 ) , ( 46, 64.43 ) , ( 47, 65.58 )
- , ( 48, 66.74 ) , ( 49, 67.92 ) , ( 50, 69.09 )
- , ( 51, 70.28 ) , ( 52, 71.48 ) , ( 53, 72.68 )
- , ( 54, 73.90 ) , ( 55, 75.12 ) , ( 56, 76.35 )
- , ( 57, 77.58 ) , ( 58, 78.83 ) , ( 59, 80.09 )
- , ( 60, 81.35 ) , ( 61, 82.63 ) , ( 62, 83.91 )
- , ( 63, 85.20 ))
```



4. SKELETON QUICK START

Log into **korat** through a SunRay NOTE: On **minx** skeleton command is **skeleton32**

Also SunRays must be used for skeleton.

Copy **skeleton.mda** and **skeleton.rsc** from **~rob.ilic/public/skeleton** into a directory where skeleton will run. Typing **cp ~rob.ilic/public/skeleton/skeleton.* .** will copy both files into your current working directory.

30nmHSQsoi.sip example file

```
#-----  
# Skeleton run for Rob (rob@cnf.cornell.edu)  
# SOI - 110nm SiN on top of 1um SiO2  
#  
ResultFileName      30nmHSQsoi  
StackDescFileName   30nmHSQsoi  
InjectionEnergy/eV  100000.0  
ElectronsToTrace    3000000  
Verbosity           2  
IntervalInfo/s      60.0  
IntervalWrite/s     600.0  
#-----
```

NOTE: Compiling this .sip file will read in 30nmHSQsoi.stk and generate 30nmHSQsoi.srz for 3 million 100keV electrons, it will display results every 60seconds, and write results to file every 600 sec.

30nmHSQsoi.stk example file 30nm HSQ on top of SOI (110nm Si/ 3um SiO2/Si substrate)

```
#-----  
StackDescriptor:    HSQ/SOI  
NumberOfLayers:    4  
#-----  
MaterialDescriptor: HSQ  
Thickness/nm:      30  
LayFlag:           1  
#-----  
MaterialDescriptor: Si  
Thickness/nm:      110  
LayFlag:           0  
#-----  
MaterialDescriptor: SiO2  
Thickness/nm:      3000  
LayFlag:           0  
#-----  
MaterialDescriptor: Si  
Thickness/nm:      700000  
LayFlag:           0  
#-----
```

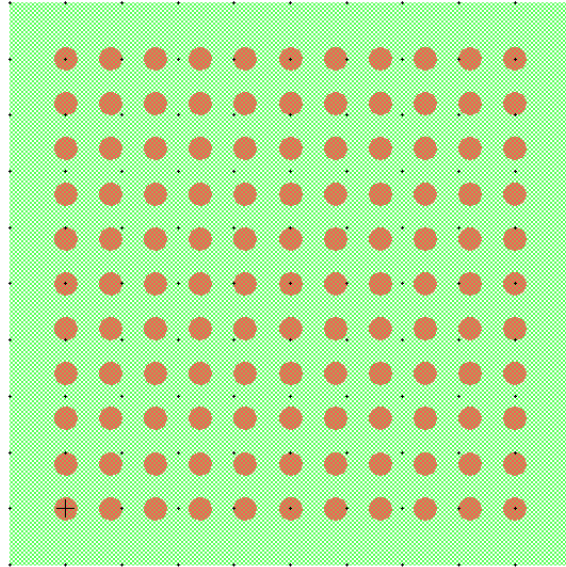
NOTE: Layer thickness is expressed in nm. LayFlag = 1 for the resist layer.

skeleton 30nmHSQsoi.sip generates 30nmHSQsoi.srz (defined by ResultFileName)
(NOTE: on **minx** the command would be **skeleton32 30nmHSQsoi.sip**)

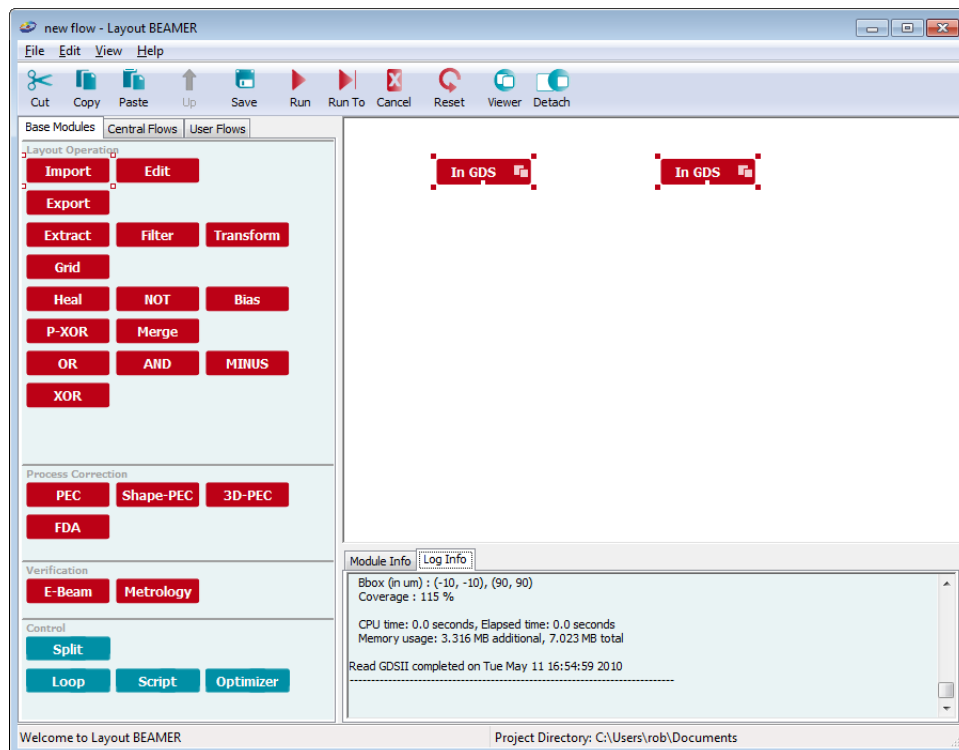
Extract the data half-way through the plane of the resist, in this case 15nm:
skeleton 30nmHSQsoi.srz 15 generates 30nmHSQsoi_z15.xrz

5A. LAYOUT BEAMER TONE REVERSAL QUICK START - Method 1

You should have a bounding box around your features. The bounding layer must be different than the feature layer. As an example, consider 10 x 10 array of circles (red layer) with a bounding box (green layer).



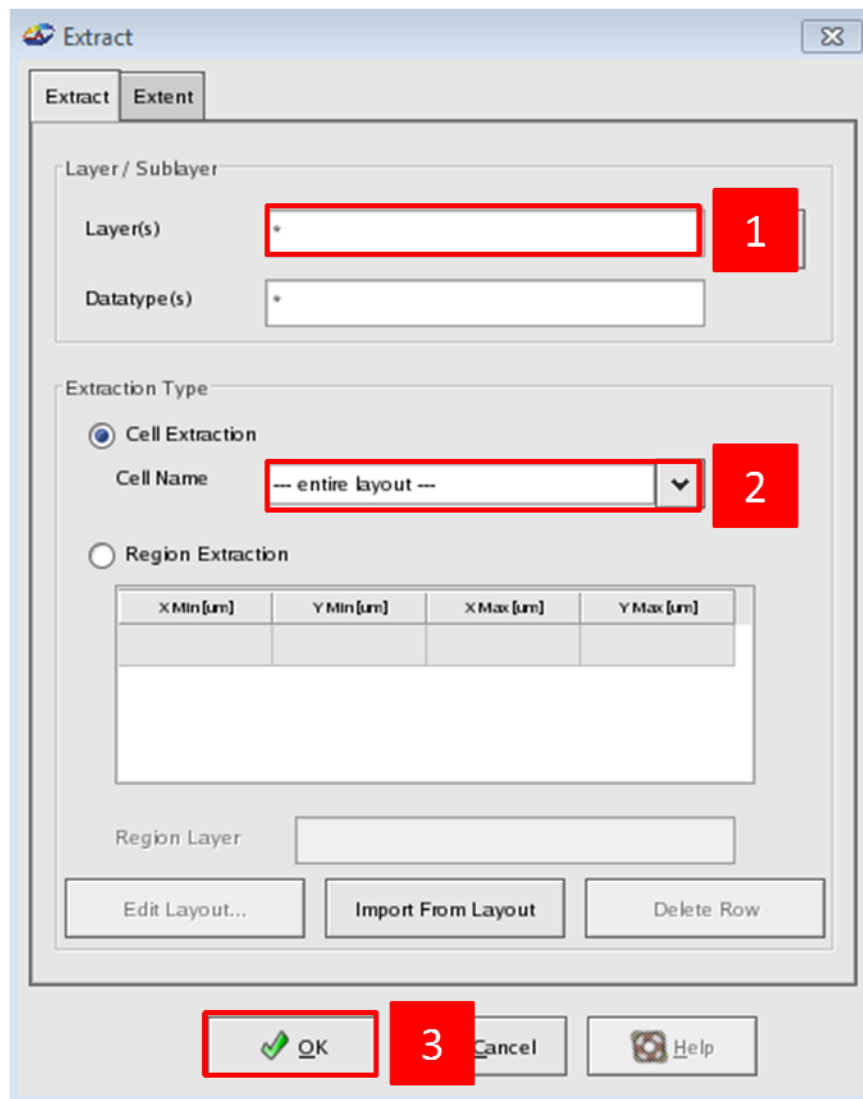
1. Drag & Drop 2 instances of the **Import** module and choose the same gds file (see below figure). Right click each **Import** and select **Run To**. Layout BEAMER will appear as:



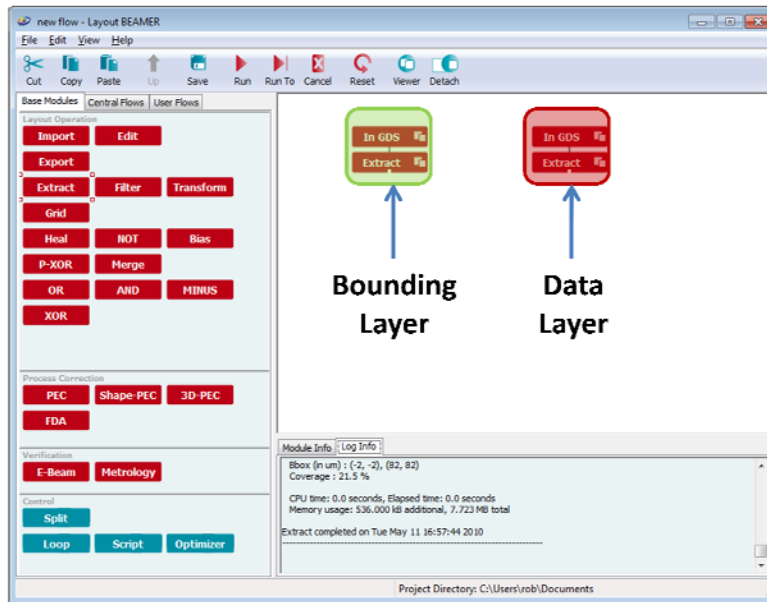
2. Drag & Drop 2 instances of the **Extract** module over the existing **Import** modules. To accomplish this, drag and drop a module from the library onto the target module in the flow until the small white connection port turns black, then release the mouse and the modules will be connected.



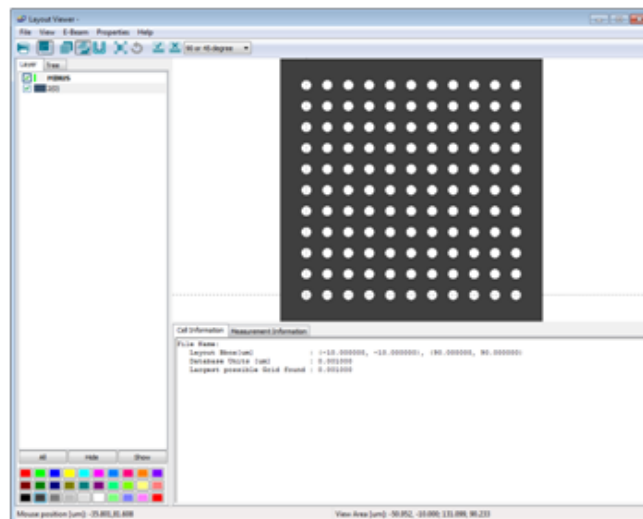
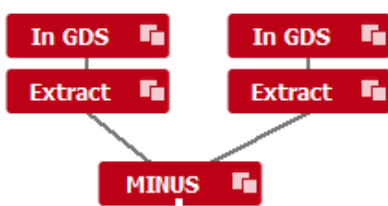
Over the left **Extract** choose the bounding layer and boundary cell, over the right **Extract** choose your data layer and respective cell, then click **OK**.



Right click each **Extract** and select **Run To**. The screen should appear as:



3. Drag & Drop the left side of the **Minus** module over the left **Extract** and the right side of the **Minus** module over the right **Extract**. Right click **Minus** and select **Run To** (see left figure below). Right click **Minus** and choose **View Layout**, then **View -> Fill Shapes** (right figure below shows the output of the **MINUS** operation)



4. Drag & drop the **Export** module on top of **Minus**. Choose the file format (most likely GDS). Right click **Export** select **Run To**.

5B. LAYOUT BEAMER TONE REVERSAL QUICK START - Method 2

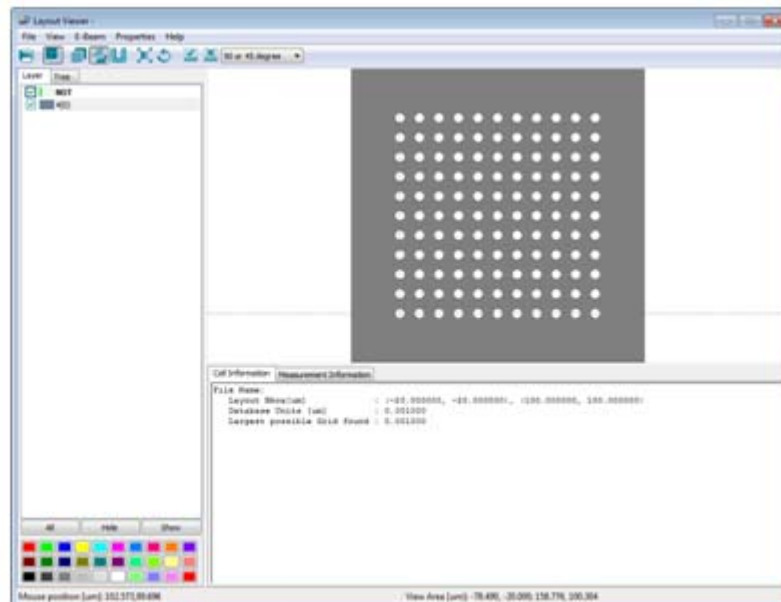
This method does not need a drawn bounding box. Pattern extents are user defined.

1. Drag & Drop an instance of the **Import** module and choose a gds file. Drag & drop an instance of the **Extract** module over the **Import** module. To accomplish this, drag and drop a module from the library onto the target module in the flow until the small white connection port turns black, then release the mouse and the modules will be connected.



Right click on **Import** and select **Run To**. Drag & drop an instance of the **Extract** module over the **Import** module. Choose the cell and layer within the **Extract** tab. Click on the **Extent** tab. Default extents are **Automatic** extents defined by your pattern. Click **User** to manually specify user extents for the Boolean operation.

2. Drag & Drop an instance of the **NOT** module on top of the **Extract** module. Right click on **NOT** and select **Run To** (see left figure below). Right click on **NOT** and select **View Layout**, then *View -> Fill Shapes* (right figure below displays the output of the **NOT** operation).



Drag & drop the **Export** module on top of **NOT**. Choose the file format (most likely GDS). Right click **Export** select **Run To**.