



EECS 143 Microfabrication Technology

SIMPL Manual

1. GETTING STARTED RUNNING SIMPL

In order to run SIMPL on Ara, you need to have an account on the Ara/Cory cluster. If you are running the software directly from the host workstation (e.g. in 111 Cory), you can skip to Section III. If you are running remotely (i.e. from a non-Ara cluster workstation), you need to do the following. Let's say you are working from a hypothetical machine called e143.eecs and you want to run SIMPL from bootes.eecs.eecs.berkeley.edu (an Ara machine). From e143.eecs, type "xhost bootes.eecs.berkeley.edu" to allow bootes.eecs.berkeley.edu access to your host machine. Then log onto bootes.eecs.berkeley.edu; once in bootes.eecs.berkeley.edu, type "setenv DISPLAY e143.eecs.berkeley.edu:0.0" to display X-windows on your host machine. (Replace e143.eecs.berkeley.edu with the appropriate name) Now go on to Section III.

For a list of Ara clients, type "clients" on your Ara account.

If you are running SIMPL from a PC in the ee143 instructional laboratory, you need to set up the appropriate files in order to run the X-emulator software. Proceed to Section II.

2. INITIALIZING XREMOTE (if running from a PC using PC-Xware)

The PCs in the ee143 lab use a X-emulator software called PC-Xware to run X-windows. Read the Xremote.help file in /usr/pub and follow the directions to initialize the PC-X display and xhost settings on your ara.eecs.berkeley.edu account. After initialization, you will have a file called xremote.start, which you can execute upon logging onto your ara.eecs.berkeley.edu account from the PC-Xware terminal.

In order to start PC-Xware from the PC, you need to run Microsoft Windows. Type "win" at the prompt to enter Windows. Once in Windows, click on the icon PC-Xware. An annex window will come up, prompting you to log in. Type "rlogin machine -l account" and enter your password to log in. The "machine" is where you want to log on, and "account" is your account name. Once you are logged on, type "xremote.start" to initiate the Xremote process. You will get two Xterm windows to work with. The fore/background color can be altered by editing your .xinitremoterc file present in your account.

3. RUNNING SIMPL & COPYING DEMO DIRECTORIES AND FILES

SIMPL on Ara is installed in the directory /cad/simpl_sys5. All you need is to have /cad/bin in your path, or start simpl-dix with the command /cad/bin/simpl-dix.

/cad/simpl_sys5 has the following directory structure:

- /cad/simpl_sys5/bin
- /cad/simpl_sys5/lib
- /cad/simpl_sys5/demo
- /cad/simpl_sys5/demo/cmos
- /cad/simpl_sys5/demo/nmos

```
/cad/simpl_sys5/demo/npn2
/cad/simpl_sys5/demo/dram
```

To run a process, copy the selected sub-directories from the "demo" directory (such as cmos) into your home directory. "cd" into your newly-copied sub-directory and run SIMPL from there. If you just want to look at the SIMPL layouts and cross-sections without running the simulation files, you don't have to copy them; instead, just cd to the directory in /cad/simpl_sys5.

For example, to look at the cmos demo, type from the prompt:

```
% cd /cad/simpl_sys5/demo/cmos
% ls
./
../
cmos.cif
cmos.final.cross
cmos.init.cross
cmos.pattern
cmos.process
```

The files above are described below:

cmos.cif = layout file

cmos.final.cross = cross section of the wafer after cmos.process has been applied to cmos.init.cross, with the layout cmos.cif

cmos.init.cross = initial cross section of the substrate

cmos.pattern = pattern file for simpl-dix only. has no physical information

cmos.process = process description to run in batch mode

This is how you look at the final profile [Be sure to have /cad/bin in your path]:

```
% simpl-dix -pf cmos.pattern cmos.cif
```

(For a listing of command line options, see the Appendix section.)

Now, simpl-dix should display a window. The left and right windows show patterns. The upper main windows shows the layout, and the lower window shows the cross section. The menu is at the very bottom. You should see the following menu:

Select "CALL EDIT COMMANDS"

In the next menu, select "EDIT PROFILE"

A window appears "SIMPL-2 PROFILE FILE NAME?" and enter 'cmos.final.cross'. The profile will appear.

Now you can zoom in with the following sequence: (1) Click on ZOOM (2) move the mouse button into the profile window, click and drag the mouse to another position. For example, let's zoom over the gate region of a MOSFET.

Repeat (1) and (2) until you like what you see and hit the Enter (Return) Key. If you want to back out of zooming, hit the ESC key.

It may be a good idea to play with the other options, such as "FORCESCALE 1:1", or "SHOW DOPANT" to selectively show boron, arsenic, and other doping, or the net doping (default).

You can click on any pattern (left or right). If the pattern is a pattern of a layout mask, the following happens:

- Left Button : Flash Layout, and draw polygon filled
- Middle Button : Flash Layout, and draw polygon outlined
- Right Button : Flash Layout, and hide polygon

[Running from the PC with a mouse of only 2 buttons will limit your options.]

This mainly helps identify what is what. Sometimes, materials or layouts have similar colors, so this is a way to separate them. If the pattern is for a material only (such as OXID) or doping spectrum (such as P17), then the material flashes in a different color.

Running a Process:

First of all, change into one of the demo directories which you copied to your own personal account (e.g. cd ~/simpl_sys5/demo/cmos if you created a /simpl_sys5 directory)

Then type the following to run:

```
% simpl-dix -pf cmos.pattern cmos.cif
```

Click on "RUN SIMPL-2", and click "no" when asked "START NEW SIMULATION?".

When asked "SIMPL-2 PROFILE FILE NAME ?" enter "cmos.init.cross"

Click "BATCH MODE" and enter "cmos.process"

The status window (upper most windows) prints some status information, such as "RUNNING PROCESS ETCH".

The process will run until it finishes.

4. OTHER FEATURES - NEW OUTLINE

You can draw a new outline for any particular layout and observe the evolution of the cross-section corresponding to that new outline.

From the main menu, select "CALL EDIT COMMANDS"

In the next menu, select "EDIT LAYOUT"

Now, select "NEW OUTLINE" and then "RETURN" twice to return to the main menu.

Select "RUN SIMPL-2". You will be asked whether to start a new simulation or not? Click "YES".

You will then be asked several questions to initialize your substrate. Enter the desired dopant (B, As, P, or Sb) and doping level (e.g. $1e15$). The initialized substrate cross-section will appear with the color corresponding to the appropriate doping level. If you are running the process "cmos.process", type in B and $1e15$, respectively.

If you want, you can save your initialized substrate profile in a file so you can run the process with the new outline in the future, select "INPUT MODE". In the next menu, select "SAVE PROFILE". Enter a file name with a ".init.cross" extension for easy identification (e.g. cmos2.init.cross). Do not overwrite the default cmos.init.cross file!

Select "BATCH MODE" and enter in the process you want to run corresponding to the particular .cif (layout) file loaded already.

5. CAVEATS

Simpl-dix does not have an option to print to a postscript printer (or, for that matter, any printer). You can give the flag '-rv' to simpl-dix to run in reverse video, and then do a screen dump, and convert that to postscript, and send it to the printer. Usually, these files are large, and take time to print.

When you play around and try to run SIMPL, don't run SUPREM4 implantation, as no SUPREM4 binary is accessible on Ara.

When running ETCH and you specify SAMPLE NONPLANAR ETCH, you need to specify a file containing etchrates. For now, just give it a generic file "/cad/simpl_sys5/lib/etchrates". You can copy the file and modify it to your needs.

IMPORTANT: Given the 6 Mb disk quota limit for each Ara/Cory account, we suggest after each SIMPL run that you DELETE all SIMPL files in your directory which were generated from running SIMPL so you don't exceed the quota and receive a warning message from the system administrator.

Lastly, this is of course an abridged SIMPL manual to help you get started. Feel free to play around with the features (e.g. dopant profile, ZOOM) and share with other students features or options which other students may find useful in this course.

Good luck.

6. SUGGESTED EXERCISES

1. After running any of the demo processes (e.g. nmos, cmos, npn), attempt to draw a new outline, and initialize your substrate (See section III). Before running the process for the new outline, take some time to visualize and draw out what actual cross section-section is. When you have completed this exercise, run the process and evaluate whether you are correct or not.

2. Jot down the masking step used as the process is evolving in front of you on the screen. Consider why that particular step is used. What is the tradeoff if you don't use that particular masking step at all? Is there a better process step to replace it?

7. Appendix (List of SIMPL command line options)

Usage: simpl-dix [display] [geometry] [options] [CIF files]

Available Options:

- ar (Enable auto-raise mode)
- b (Enable bell mode)
- bd color (Set border color)
- bg color (Set background color)
- bw width (Set border width)
- d (Enable debug mode)
- df file (Set debug file)
- fg color (Set foreground color)
- fm font (Set menu font)
- fn font (Set normal font)
- ft font (Set title font)
- hl color (Set highlight color)
- if file (Set SIMPL-2 interchange file)
- m (Enable monochrome mode)
- ms color (Set mouse color)
- n name (Set window name)
- pf file (Set pattern file)
- rv (Enable reverse video)
- tb (Enable title bar)

James Chan, Andrej Gabara, Spring 1994