Instructions for the Elionix S50-EX

Pattern creation

1. Create your pattern in either a DXF or GDSII format. You can use Autocad to create DXF files, or KLayout to create either DXF or GDSII files. Both programs are free.
2. If using DXF files, make sure to save it as Autocad2000/LT format.
3. On the CAD pc, transfer your files to your folder. It is a good idea to make a new subfolder for each different pattern.
4. On the CAD pc, open WecaS.
5. Convert your file to the CELL format using either the DXF to GDSII converter buttons.
6. For complex, repetitive patterns, like photonic crystals, you can use a computer language, like matlab or python, to script the creation of DXF, GDSII, or CELL files. There are multiple python libraries for DXF and GDSII files. To script the creation of a CELL file, it is easiest to reverse engineer CELL files that you already have.
7. Optionally, you can assign doses to different shapes in your CELL file. This can be useful if different parts of your pattern need to get different doses. You will have the opportunity to assign doses later during the schedule creation.
8. Save your CELL file.
9. If you are using a previous CELL file, load it now, by pressing “Place Cell,” or use the command “PC.” Enter an offset such that all marks in your pattern will have positive coordinates.
10. Press the orange button “Select Field Size/Dot” to input the field and dot parameters.
11. The keyboard command “PZ” will zoom in to show your pattern.
12. Place “chips” or write fields. This can be one manually or automatically. Enter the command “PW” or press the chip placement button to do this. Input the chip placement parameters, give it a name, and press ok.
13. Optionally, you can add registration marks to this file. You can also add them to a separate SCON file.
14. Save the .SCON “configuration” file, which includes the pattern and chips, in your directory.

Sample loading

1. Make sure the sample is at the exchange position in the SEM program. The exchange position light will be green.
2. On the loadlock, flip the switch up to “evac.”
3. When the evac light is green, flip the gate valve switch to open.
4. Unlock the transfer rod, slide it in, and screw it into the stage.
5. Retract the stage, and then lock the rod.
6. Close the gate valve.
7. Vent the chamber.
8. Place your sample on the sample holder.
9. Evacuate the loadlock.
10. When the light turns green, open the gate valve, making sure the rod doesn't slide in.

11. Slide the stage in, and unscrew the rod. Once the rod is unscrewed, you can give the stage a little push to make sure it is in the correct spot.
12. Retract the rod, lock it, and close the gate valve.
13. If you have switched sample holders, it is a good idea to wait 20-30 minutes for the holder to thermalize.

Beam conditioning

1. Drive to the reference position.
    a. Stage->Reference
2. Recall the beam condition, and unblank it
    a. Beam Adjustment -> Beam
    b. Make sure the “Recall” button is selected, and then click on the configuration number you want. Wait a few minutes for the lenses to degauss.
3. Open the isolation valve with Beam Adjustment -> Isolation Valve
4. Condition the beam on the reference.
    a. Unblank the beam (top menu)
    b. Manually focus and stigmate with the mouse or use Auto focus/stigmate
    c. If needed, check the dynamic focus
5. Drive to the faraday cup, measure, and adjust the beam current.
    a. Stage->Reference
    b. Beam adjustment -> Beam Current -> Measurement
    c. Adjust the beam current with the arrows.
    d. Click Beam adjustment -> Beam Current -> Measurement to turn off the measurement.
6. Drive to the starting point on your sample.
    a. If you already know the coordinates of your sample, you can manually drive to it.
    b. Otherwise, in WecaS, on the “Exp. Graphics” menu, press “Move Stage.” This can be accessed from the “Edit Schedule Execution” icon.
    c. Select your stage.
    d. On the “Exp. Graphics” menu, press “Move Stage”
        i. If you want to click on the desired point, you may need to click on the command window, and then press escape.
    e. Move to the desired point. Moving without the height sensor is ok.
    f. It is a good idea to verify that the height sensor works on your sample.
    g. You can make a contamination dot to confirm proper beam conditioning. When you do this, take care not to expose parts of your pattern.
        i. On the SEM program, increase the magnification to > 50,000 and put the beam
    h. If using marks, drive to the first mark.

Schedule creation

1. Click the “Edit Schedule Execution” icon in WecaS.
2. Use the dose calculator to calculate the dwell time per dot, making sure that it is not too small. The minimum time is 10 ns.

3. To perform a dose test, use the Matrix Con option, to vary the dose.
    a. The dose time field will modulate the dose time specified in the SCON file.
    b. The dose coef field will modulate doses specified in the CELL file.
4. Save the schedule file.
5. Press “Set_option” to set a bunch of scheduling options.
    a. Here you can set whether or not to use the height sensor, marks, height map, etc.
6. Press “Next.”
7. To properly position the pattern, press “Display Sample Holder” on the “Exp. Graphics” menu
8. Now select “Move Pattern.”
    a. Optionally, you can left click on the sample holder. If you then press ok, the center of the pattern will be moved to where you clicked.
    b. There is also an option to read the current stage coordinates. In this case, the center of the pattern will be moved to the current stage coordinates. If you moved the stage to the center of your pattern, or to the first mark, then it is a good idea to do this. For this to work, you may need to click the command window and then press escape to bring up the dialog to read the stage coordinates.
9. This is also a good time to measure the sample inclination and configure your SCON file to use the height map.

Exposure

1. On the Exp. Graphics menu, press “Next.”
2. You can estimate the writing time here.
3. It is a good policy to always do a field correction before you write.
4. Expose.

Unloading

1. Unload your sample using the process described above, making sure to insert the stage back into the main chamber.
2. Develop your sample according to your recipe. A good starting point for PMMA is to develop in 1:3 IPA:MIBK for 60s at room temperature with an IPA rinse. Different chemicals and temperatures can be used, with different results.

Using alignment marks

1. These need to be placed in the con file.
2. Difference between local and global marks.
3. Manual vs automatic marks.

Questions: alignment still on the SEM screen