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Standard Operating Procedure (SOP)

Elionix ELS-7500EX

(EBL-01)

Version 1.1.0, Updated 5/6/2022

In case of emergency please call 911

For any other major safety concern contact EHRS at: 215-898-4453 or via email: ehrs@ehrs.upenn.edu

If there is an error on the system/tool please report it on IRIS, and staff will address it

Please *DO NOT* run diagnosis without a staff member's approval

General safety tips and common mistakes

- If the system is not running, make sure you are logged into the tool on IRIS.
- Outgassing materials and materials with a high vapor pressure are not allowed in the chamber
- Samples should be secured with the clips on the sample holder. Tape should not be used.
- Pattern and sample prep should be completed in advance of the EBL reservation
- Make sure not to overtighten the load arm or the load arm lock when loading or unloading the sample
- When run is finished, the tool should be left with the Iso. Valve closed and the beam blanked
- This SOP is written to ONLY provide some key operational procedures in a step-by-step manner. Neither this SOP nor any other documentation is a substitute for training and qualification to use the tool.

Elionix ELS-7500EX

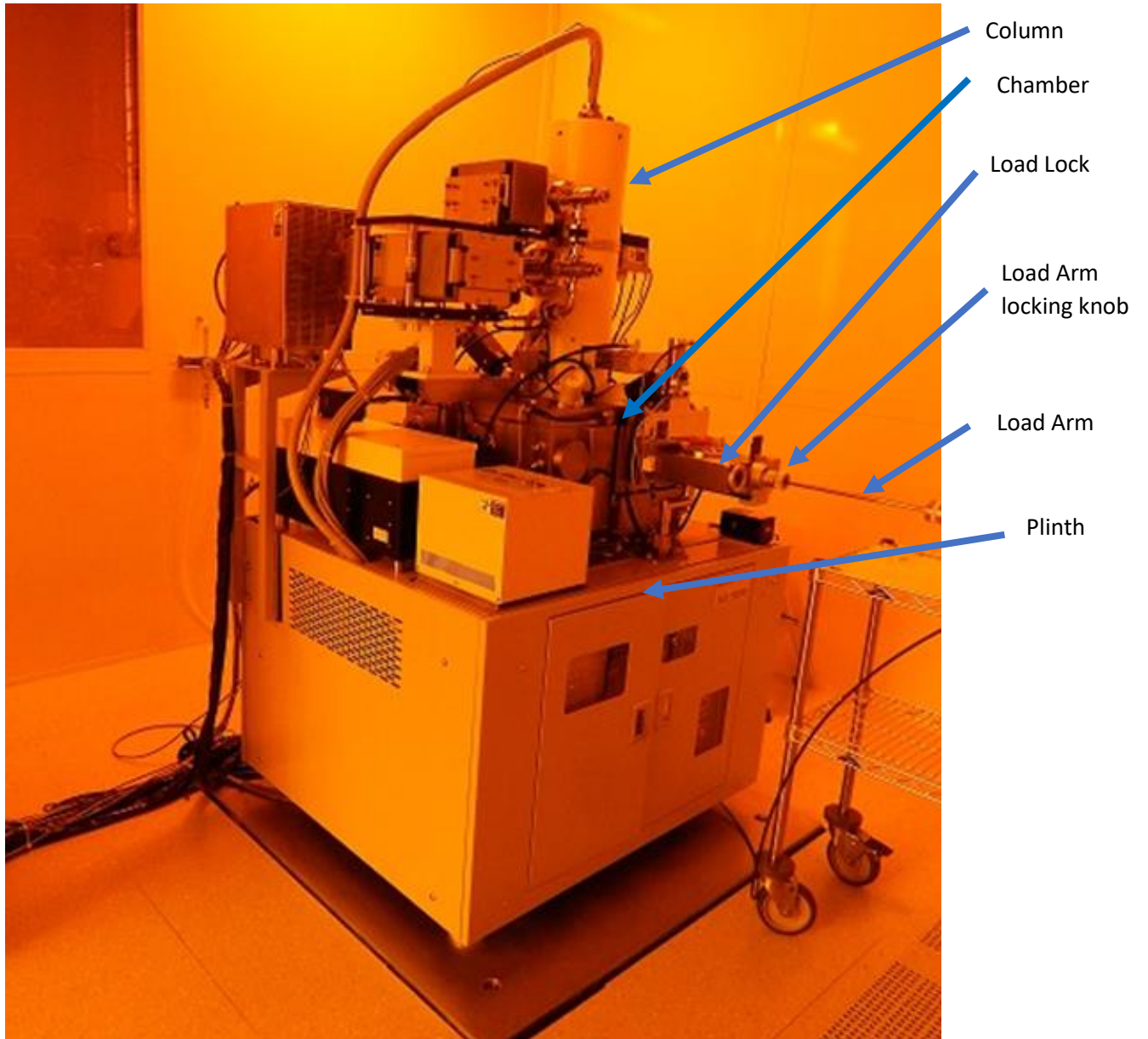


Procedure Overview

- Load sample
- Adjust height and set current
- Prepare schedule file
- Run field correction
- Run exposure
- Unload sample

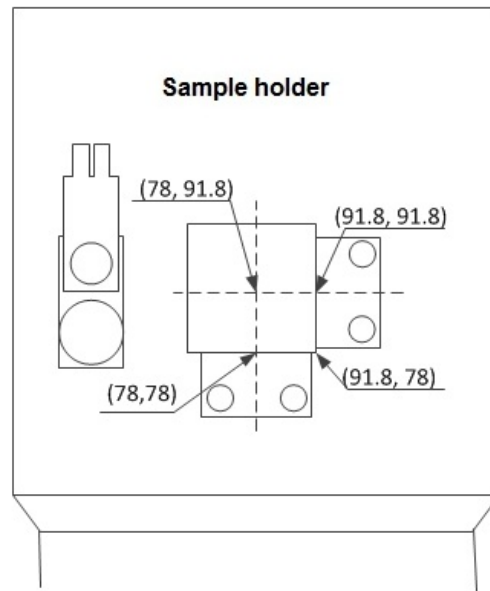
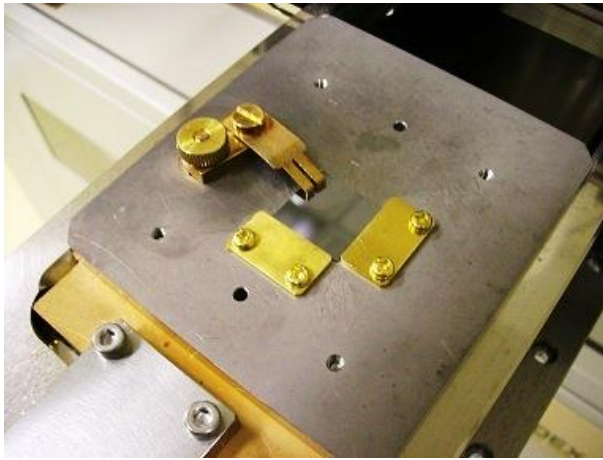
Tool Overview

Hardware Overview



Sample Holders

Piece Part Holder



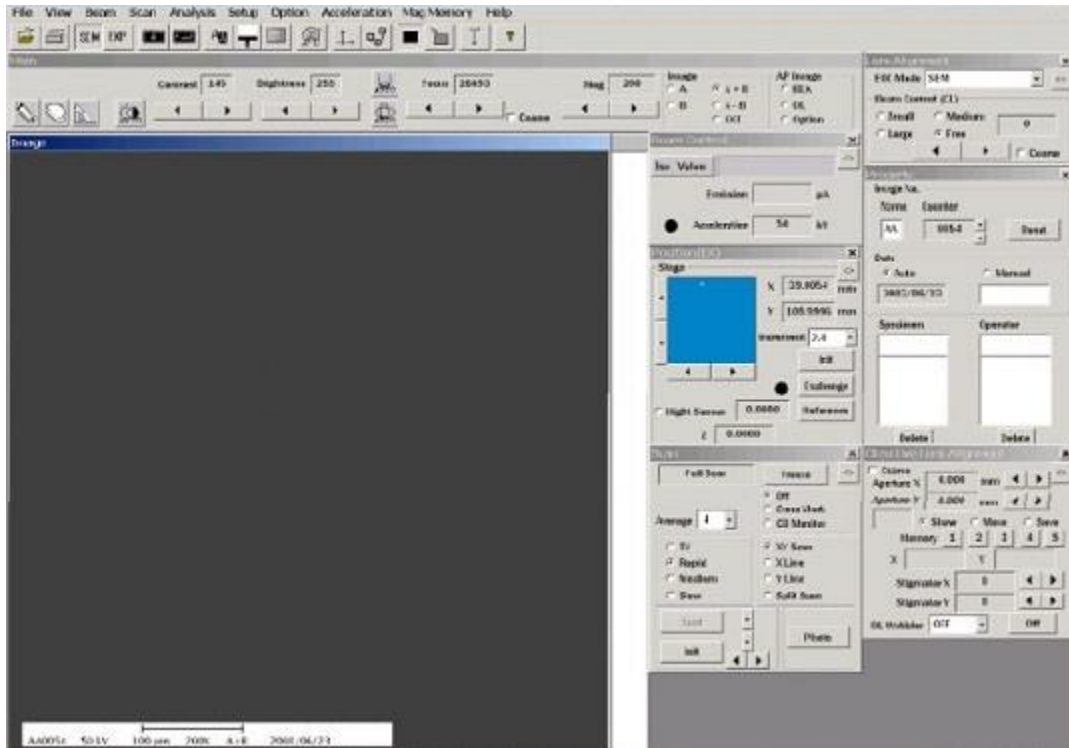
Left: Photograph of piece part holder with chip loaded. **Right:** Schematic of piece part holder. Coordinates are the approximate values (in mm) of the global stage coordinates of these locations when the holder is loaded into the tool.

Other Holders

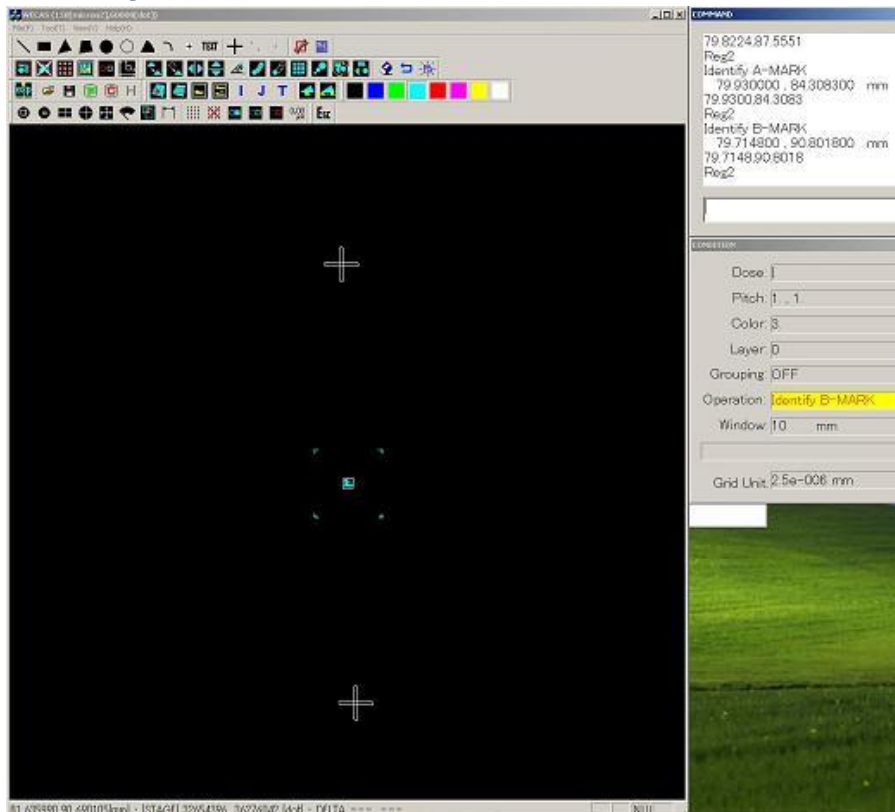
Wafer and mask holders are also available. These are rarely used. Consult staff for instructions on using these if needed.

Software Overview

SEM Software



Patterning Software


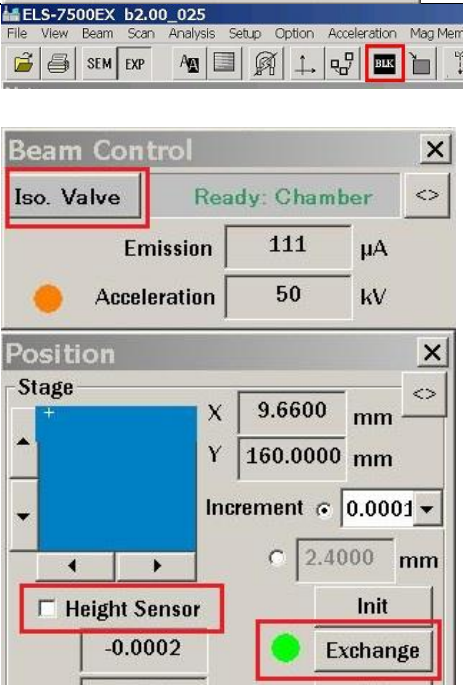
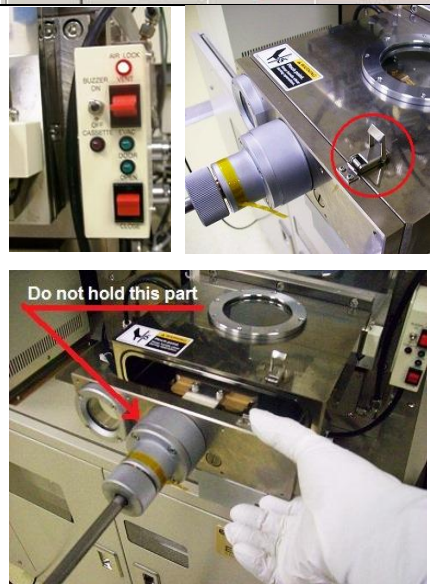


Scheduling Etiquette for the Elionix

- Reserve only time that you intend to use
- Cancel reservations as soon as you know you will not be able to use them
- If you need to cancel a reservation less than two days prior to its start, email all users to let them know that the time is available
- If you finish with more than an hour left on your reservation, email all users to let them know that the time is available
- Log in as soon as you start, and log out as soon as you finish
- Do not log in from outside of the cleanroom
- Data conversion/pattern prep should be done in advance to the greatest possible extent
- Your sample prep should be done by the time your reservation starts
- Remember:
 - All cancellations and unused reservations are monitored
 - Abuse of the reservation system or consistent failure to display proper etiquette and respect for other users can result in loss of access to the tool

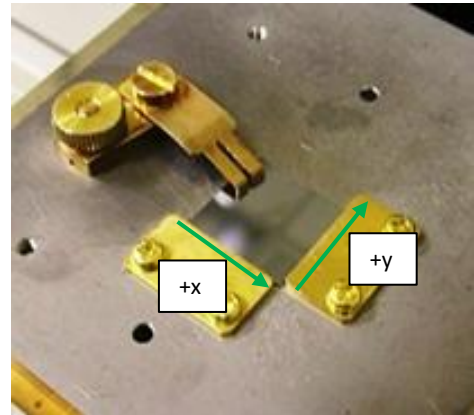
Full Procedure

1. Sample Loading

<p>Log into the tool via IRIS. After logging in, press 'retry' in the pop-up prompt in the SEM GUI to clear the pop-up.</p>	
<p>1.1. Make sure that the tool is in the appropriate state for sample loading</p> <ul style="list-style-type: none">1.1.1. The SEM software should be showing. If it is not, press the 'ctrl' key twice1.1.2. The beam should be blanked1.1.3. The isolation valve should be open (Iso. Valve button is gray)1.1.4. The height sensor should be off (unchecked)1.1.5. The stage should be at 'Exchange' position. The circle next to the exchange button will be green. <p>Note: Often, the previous user of the tool will ask the current user to unload their sample. In this case, follow the instructions in section 6 to unload the sample.</p>	
<p>1.2. Vent the loadlock</p> <ul style="list-style-type: none">1.2.1. Press the red switch up to the "VENT" position1.2.2. Wait until the red LED stops blinking and shows solid red1.2.3. Undo the latch on the top of the load lock1.2.4. Gently slide the sample holder out of the loadlock. Do not touch any part of the load arm.	

1.3. Mount Sample

- 1.3.1. Place sample with lower right corner firmly in contact with brass stops
- 1.3.2. Make sure that the orientation of the sample is correct. Coordinate orientation is shown in the image
- 1.3.3. Fasten in place with the clip



1.4. Evacuate loadlock and load tool

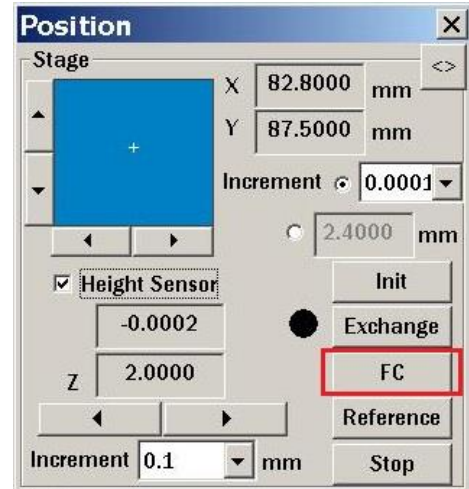
- 1.4.1. Close and latch the loadlock
- 1.4.2. Evacuate the load lock by pressing the top red "AIR LOCK" switch down to the "EVAC" position. Wait until "EVAC" LED stops blinking.
- 1.4.3. Open the gate valve by flipping the bottom red ("DOOR") switch up to the "OPEN" position.
- 1.4.4. Hold the end of the load arm and gently loosen the load arm locking knob
- 1.4.5. Slowly slide the load arm into the tool until it is fully inserted. The stainless steel cylinder should fully cover the locking knob.
- 1.4.6. Turn the load arm counterclockwise several turns until it is fully disengaged from the sample holder. There is no harm in turning it more than necessary.
- 1.4.7. Retract the load arm fully, and gently tighten the locking knob until the arm remains in place when you release it
- 1.4.8. Flip the DOOR switch down to close the gate valve



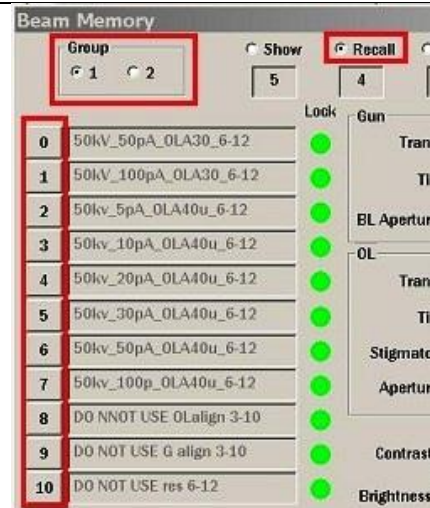
2. Setting Beam Current

Note: Beam current should be chosen based on the requirements of the pattern. This decision should be made during the design phase. See Appendix B for information about choosing a beam current

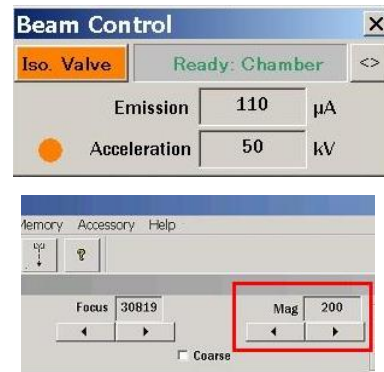
- 2.1. Move the stage to the Faraday cup
 - 2.1.1. Click the “FC” button in the position window
 - 2.1.2. Wait until the stage stops moving



- 2.2. Load a beam from memory
 - 2.2.1. From the top menu, click “Beam” and then “Beam Memory”
 - 2.2.2. Make sure the “Recall” radio button is selected at the top of the “Beam Memory” window
 - 2.2.3. Click the number next to your desired beam
 - 2.2.3.1. There are two groups, so if you don’t find the beam you are looking for, try switching to the other group
 - 2.2.3.2. Each beam name includes its current, its aperture, and the date it was last updated
 - 2.2.4. Close the “Beam Memory” window



- 2.3. Center the SEM on the Faraday cup (FC)
 - 2.3.1. Open the isolation valve. The button will turn orange.
 - 2.3.2. Unblank the beam
 - 2.3.3. Make sure the scan is in TV mode. You should see a live SEM image, with the FC visible
 - 2.3.4. Right click on the SEM image, and select “Move Stage (Center)” from the menu
 - 2.3.5. Left click on the FC to bring it to the center
 - 2.3.6. Increase magnification to ~1000x

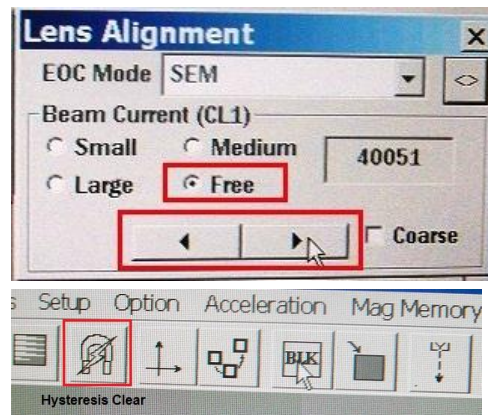


2.4. Measure and adjust the current

- 2.4.1. In the “Scan” window, press “Freeze” and then “Spot” to fix the beam in the center of the FC
- 2.4.2. On the picoammeter in the electronics rack, press the “ZERO CHECK” button. The green LED in the button should turn off
- 2.4.3. Adjust the range using the up button until it is suitable for the selected beam current. See the table to the right for how to set the range and read the current
- 2.4.4. Adjust the CL1 setting in the “Lens Alignment” window until the current reading on the picoammeter is the same as the desired beam current
 - 2.4.4.1. Make sure the “Free” radio button is checked
 - 2.4.4.2. For large adjustments, the “Coarse” box should be checked
 - 2.4.4.3. Usually, the left button causes the current to increase and the right button causes it to decrease
 - 2.4.4.4. When the current is satisfactory, press the “Zero Check” button again to disable the meter reading
- 2.4.5. Degauss the lens by pressing the “Hysteresis Clear” button in the toolbar
- 2.4.6. Press “Zero Check” to enable measurement on the meter and make sure the reading has not changed. If it has, go back to 2.4.4 and repeat until the current is stable
- 2.4.7. After degaussing, it is usually necessary to reset the Spicer active EMF cancellation system by pressing the reset button
- 2.4.8. Press “Zero Check” and lower the sensitivity all the way down on the picoammeter
- 2.4.9. In the “Scan” window, press “Freeze” and select the “TV” radio button to return to SEM operation
- 2.4.10. Blank the beam



Current (pA)	Range	Scale
10	3×10^{-11}	Bottom
20	3×10^{-11}	Bottom
30	1×10^{-10}	Top
50	1×10^{-10}	Top
100	3×10^{-10}	Bottom
200	3×10^{-10}	Bottom
500	1×10^{-9}	Top
1000	3×10^{-9}	Bottom
2000	3×10^{-9}	Bottom
5000	1×10^{-8}	Top
6000	1×10^{-8}	Top
10000	3×10^{-7}	Bottom
20000	3×10^{-7}	Bottom



<p>2.4.11. In some cases, it may be advisable to focus and stigmatize the electron beam on your sample at this point. Instructions for that are in Appendix A.</p>	
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3. Setting Sample Height

Note: This procedure is for using the laser displacement meter to set the height. On transparent or very small samples, it may not be possible to use the laser. If this is the case, see Appendix A for other options.

3.1. Navigate to the location on your sample that you intend to pattern

3.1.1. Click the “Stage Memory” icon in the toolbar

3.1.2. In the “Stage Memory” window, enter the absolute coordinates of your pattern center in the X and Y fields at the top of the window

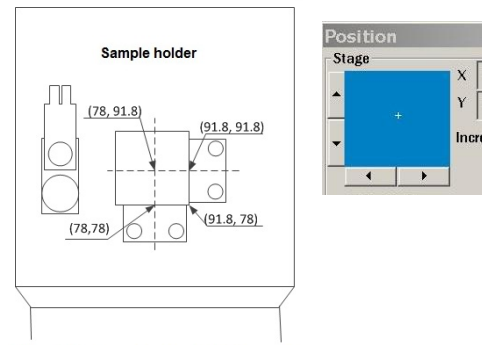
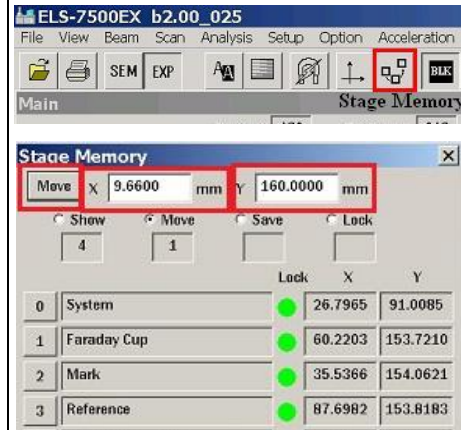
3.1.2.1. For unaligned writes, Choose the position that you would like to be the [0,0] position from your CAD

3.1.2.2. For aligned writes, see the complete procedure in Appendix C

3.1.3. The sample holder schematic gives some important coordinates that will help located a suitable position

3.2. Press the “Move” button to move to those coordinates

3.2.1. In the “Position” window, the small green cross will move to show the current stage position. It should be near the center when the stage is at your sample position.

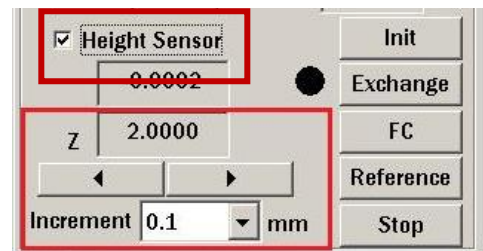


Absolute Coordinate of The Sample

3.3. Set the stage height using the laser height sensor

3.3.1. Check the ‘Height Sensor’ box in the “Position window to turn on the height sensor

3.3.2. Bring the stage up by increasing its Z position



Note: The zero position of the height sensor corresponds to the optimized working distance for lithography in this tool. For a standard 525 μm sample, the stage Z position should be ~ 3.4 mm.

3.3.2.1. Select the appropriate increment (usually start with 1 mm). Click the



right arrow to move the stage up by this increment. When the sample is in range of the sensor, the sensor button on the IWATSU unit will become illuminated, and the digital display will begin showing a correct value.

3.3.2.2. Continue to modify the increment and increase the height as needed until the display reads 0.0000 mm. It should be stable there to within 0.0001 mm.

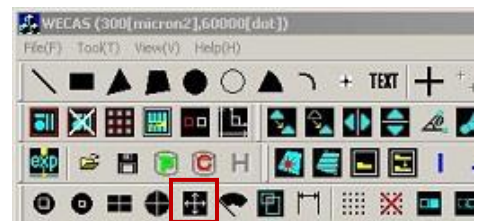
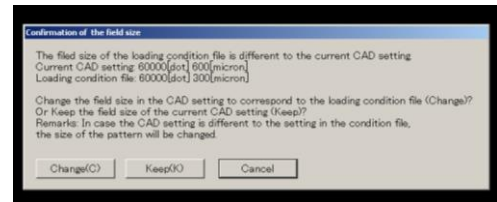
3.3.3. Record the stage position in X, Y, and Z. These values will be necessary during job creation.

4. Preparing and Scheduling Exposure

Note: It is strongly encouraged that pattern data be prepared in a CAD program such as LayoutEditor and fractured and exported for EBL using Beamer. These instructions assume that a .CO6 file (and other associated files) containing the pattern data are ready. Appendix D contains information on pattern conversion from .gds or .dxf format in the WECAS software, though this is not recommended.

4.1. Load .CO6 File

- 4.1.1. Press Ctrl twice on the keyboard to switch to the patterning PC
- 4.1.2. Transfer data files to PC via USB
 - 4.1.2.1. Files should be placed in "D:\\users\\your_username\\"
 - 4.1.2.2. All associated files should be transferred in a single folder
- 4.1.3. Open WECAS software if it is not already open
- 4.1.4. Select File -> Load CO6
- 4.1.5. If prompted, choose to change settings to those of the loaded file
- 4.1.6. Press the "Zoom Area" button to zoom to the location of the patterns. Check that they look as expected.
- 4.1.7. If these are aligned patterns, the alignment marks need to be added now. See Appendix C for instructions.



4.2. Set exposure parameters in schedule file

- 4.2.1. Click the "exp" button
- 4.2.2. A warning dialog box about unsaved data on the CAD screen will pop up. Click "OK"
- 4.2.3. In the "Edit Schedule File" window, select the "Ref" button, and choose your CO6 file. If you correctly loaded your CO6 file in step 4.1, it will be available in the pop-up window.



4.2.4. Enter the stage coordinates of your pattern origin in the X and Y fields and press enter

4.2.4.1. This should be the stage coordinates where you want the 0,0 position of your CAD file to be on your chip. You should have chosen and recorded this position in step 3.

4.2.5. Set the dose parameters

4.2.5.1. See Appendix B for more information about choosing correct dose parameters

4.2.5.2. Dose time (or dose shift) should usually be set to 0 if you converted your patterns in Beamer

4.2.5.3. Dose slope is a multiplier on the base dose. This can be useful for dose arrays. If you set your base dose time in Beamer to 1, the dose slope should be the base dose time at which you want to expose your samples. If you set your base dose time in Beamer, this should be 1.

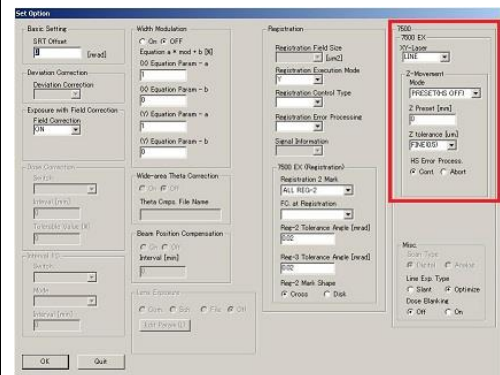
4.2.6. Click “Set Option”

4.2.6.1. In the pop-up window, set the relevant options. Usually these are only the laser settings in the rightmost column:
XY – Laser: Line
Mode: Preset (HS ON)
Z Preset (mm): Z position of sample found in step 3.3
Z tolerance (µm): Fine (0.5)

4.2.6.2. If the laser height sensor does not work well on your sample, discuss these settings with staff, and see Appendix A for other options

4.2.6.3. For options related to alignment, see Appendix C

4.2.7. Click OK to confirm these options



4.2.8. Save your schedule file by clicking “Save Sch” and entering a filename

Note: If you want to expose the same pattern multiple times on the same chip, or if you want to do a dose array of a single pattern. The “Matrix Con” option can be used. See Appendix E for details. Exposure arrays can also be set up in Beamer instead.

5. Running Exposure

5.1. Check exposure

5.1.1. In the “Edit Schedule File” window, press “Exposure” to open the viewer

5.1.1.1. Use the zoom functions to find your patterns on the screen. You may need to zoom out significantly to find the correct location. Patterns should be at the stage coordinates where you will write them if you converted your CAD in Beamer. At first, only the fields will be visible.

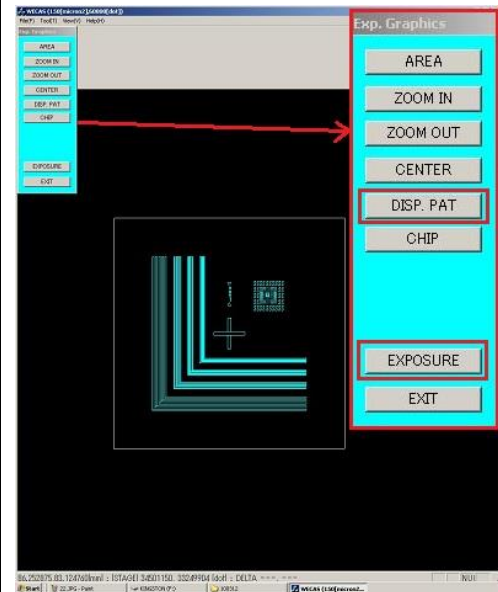
5.1.1.2. Press “DISP. PAT” to show the patterns within the fields

5.1.1.3. If everything looks right, press “EXPOSURE”

5.1.2. If a dialog box asking to initialize the XY-Laser comes up, click Yes

5.1.3. In the Exposure window, press the “Estimate” button and then click “Calc” to check the exposure time

5.1.3.1. Make sure that all values in the estimate are reasonable

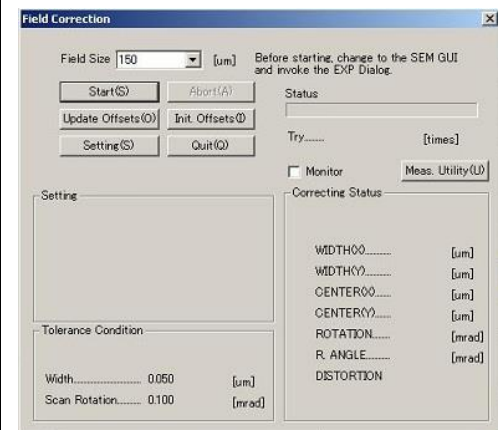


5.2. Run Field Correction

Note: Field correction corrects for the size, position, and rotation of the EBL field. It can be skipped with caution and the understanding that a ~1-4% error in feature size/pitch should be expected. It should never be skipped if field stitching or overlay alignment is required. If you intend to skip field correction, you must focus and stigmatize the SEM image prior to starting your exposure

5.2.1. Click the “Field Corr.” button

5.2.1.1. Tolerances can be adjusted by clicking “Settings,” though this should be done with caution



5.2.1.2. If you change the settings, they should be returned to the defaults when you are done:

Width: 0.050 μm

Scan Rotation: 0.100 mrad

5.2.2. Click "Start." This will move the stage to the reference sample, which is high contrast gold nanoparticles. Unblank the beam when the stage is finished moving.

5.2.3. Adjust focus and stigmation iteratively until the SEM image is optimized

5.2.3.1. If focus and stigmation were already corrected (either directly on the sample or on the reference sample), this step can be skipped

5.2.3.2. Choose between focus, stigmation, and stage movement by right clicking on the SEM image

5.2.3.3. Focus is adjusted by left clicking on the image (with focus selected) and then dragging the mouse left and right to move the focus.

5.2.3.4. Stigmation is adjusted by left clicking on the image (with stigmation selected) and then dragging left and right for x- and up and down for y-stigmation

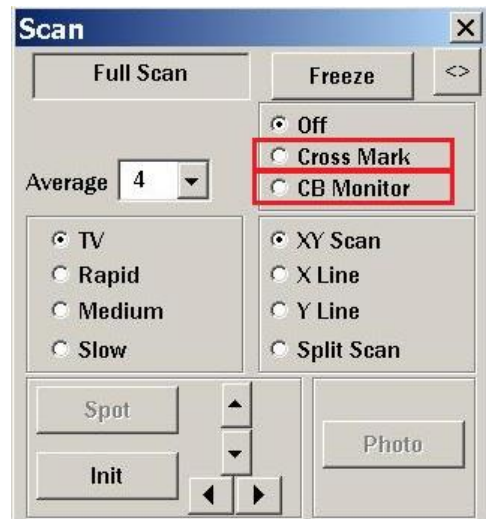
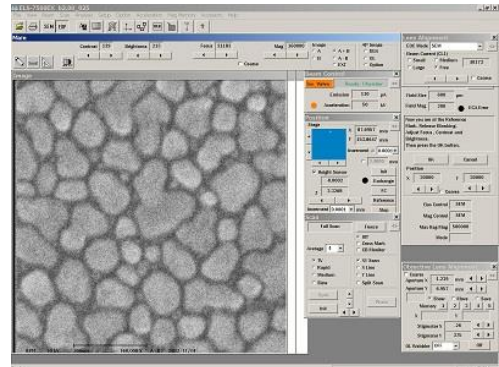
5.2.3.5. The SEM image should be optimized at a magnification of at least 160,000x. 10-20 nm gold particles should be clearly visible.

5.2.4. When image quality is sufficient, blank the beam and click "OK" in the Exposure window

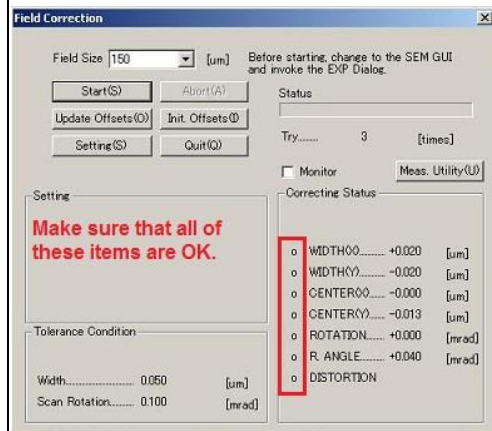
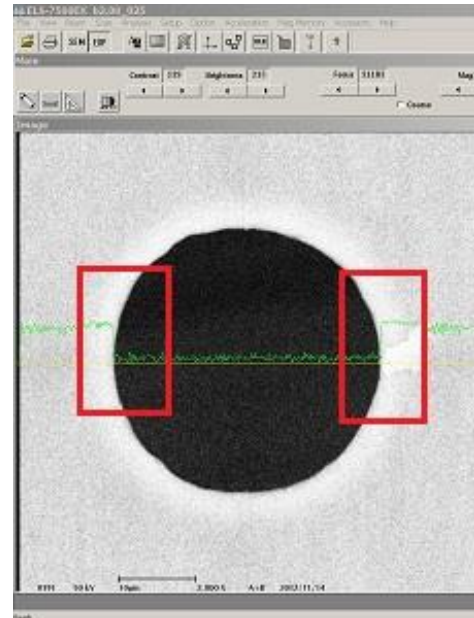
5.2.4.1. If the Exposure window is not open, click the EXP button in the toolbar

5.2.5. The stage will drive to the mark location for automatic field correction

5.2.6. Optimize brightness and contrast to run field correction



- 5.2.6.1. Zoom in to ~1000x and center the stage on the nearest black dot.
 - 5.2.6.2. Click “CB Monitor” in the “Scan Window”
 - 5.2.6.3. The trace in the center of the screen shows the grayscale value of the SEM image at that point in the image. To allow the automatic procedure to work, the contrast at the edge of the hole should be maximized.
 - 5.2.6.4. Increasing brightness shifts both the top and bottom of the trace up
 - 5.2.6.5. Increasing contrasts moves the top and bottom further apart while also shifting both up.
 - 5.2.6.6. If the trace does not move at all in one direction, that means it is saturated on that end
 - 5.2.6.7. Brightness and contrast should be adjusted until both the bright and the dark parts are nearly, but not quite saturated
- Note:** For very low beam currents, the noise makes this more difficult. It can help to increase the frame averaging in the SEM. It can also be better to adjust contrast slightly high and brightness a slightly low, even if this means some parts of the trace are saturating



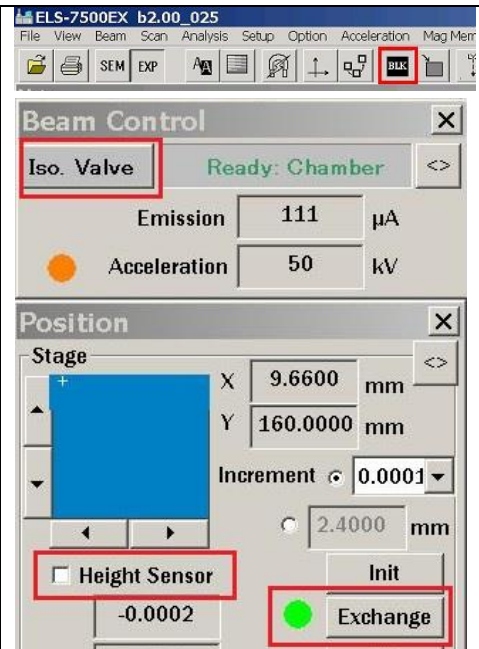
- 5.2.7. Press “OK” in the Exposure window, and return to the Patterning PC. The field correction routine can often take ~15 minute to complete.

- 5.2.7.1. In the Field Correction window, the current try is displayed. It should normally take ~3 tries to reach the tolerance.

<p>5.2.7.2. The window shows the status of the parameters being corrected. An x next to the parameter means it is out of spec, and a circle means it is in spec</p> <p>5.2.8. When all values are in spec, return to the SEM PC and press “OK” in the Exposure window</p>	
<p>5.3. Run Exposure</p> <p>5.3.1. Switch to the Patterning PC and press “Exposure” and then “Yes” in the dialog box</p> <p>5.3.2. For alignment, it is necessary to confirm mark positions. See Appendix C for instructions</p> <p>5.3.3. For unaligned exposures, no input is required until the exposure is finished</p> <p>5.3.4. When the exposure is finished, another dialog box will pop up. Click “OK”</p> <p>5.3.5. The stage will drive to the FC. Return to the SEM PC</p>	

6. Sample Unloading

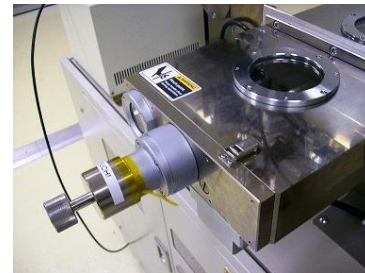
- 6.1.** Return that the tool is in the appropriate state for sample transfer
- 6.1.1.** The SEM software should be showing. If it is not, press the 'ctrl' key twice
 - 6.1.2.** The beam should be blanked
 - 6.1.3.** The isolation valve should be open (Iso. Valve button is gray)
 - 6.1.4.** The height sensor should be off (unchecked)
 - 6.1.5.** The stage should be at 'Exchange' position. The circle next to the exchange button will be green



- 6.2.** Evacuate the loadlock
- 6.2.1.** Press the red switch down to the "EVAC" position
 - 6.2.2.** Wait until the green LED stops blinking and shows solid green
 - 6.2.3.** Open the gate valve by flipping the bottom red ("DOOR") switch up to the "OPEN" position.



- 6.3.** Retrieve Sample Holder
- 6.3.1.** Unlock the load arm and slowly slide it into the tool until it is fully inserted. The stainless steel cylinder should fully cover the locking knob.
 - 6.3.2.** Turn the arm clockwise until it just barely encounters some resistance. Then loosen it by ¼ turn
 - 6.3.3.** Withdraw the arm and lock it in place
 - 6.3.4.** Close the gate valve by flipping the bottom red "Door" switch down to the "CLOSE" position



6.4. Remove Sample

- 6.4.1.** Press the red switch up to the “VENT” position to vent the load lock. Wait until the red “AIR LOCK” led stops blinking
- 6.4.2.** Undo the latch on the top of the load lock
- 6.4.3.** Gently slide the sample holder out of the load lock. Do not touch any part of the load arm.
- 6.4.4.** Release clip and carefully remove sample
- 6.4.5.** Tighten clip slightly so it stays in place
- 6.4.6.** Close the load lock, secure the clip, and flip the top switch down to “EVAC” to evacuate the load lock



6.5. Clean up your workspace and log out of the tool in IRIS

Appendix A: Height Control

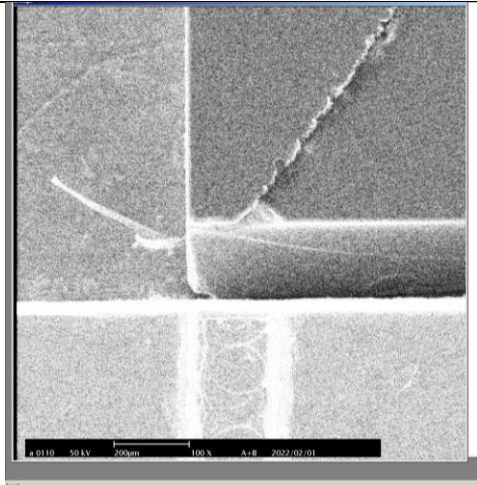
Normally, the tool reflects a laser off of the top surface of your sample to measure its height, and then moves the stage z position to keep the top surface of the sample at the focal plane of the electron beam. There are three main cases where this does not work well:

1. When the sample is transparent. There is not a sufficient reflection off of the top surface of the sample to get an accurate height reading.
2. When the combination of thickness and refractive index of resists results in destructive interference of the laser reflection. This is fairly rare.
3. When the tool attempts to measure the height within ~1mm of the edge of the sample. Scattering of the laser from the edge results in bad readings. For very small samples, there could be minimal (or no) space on the sample where a good height reading can be taken.

For the first two cases, the easiest option is to coat the sample with a thin conductive layer. Thermally evaporated or sputtered Al or Au ~10-20 nm thick are commonly used. This metal layer is then stripped before developing. E-beam evaporation is usually not recommended because there is a chance that the resist can be partially exposed during the evaporation.

For small samples, writing near the edge of a wafer, or if a reflective coating is not possible, it may not be possible to use the laser height sensor. If the writing area is small and there are features near the writing area that can be used to focus the SEM, writing can usually be done without the laser. Below is an example of a procedure that can be used.

- A.1.** Before loading, use a diamond scribe to make a small scratch at the edge of the sample
- A.1.1.** Use a nitrogen gun to blow away any dust from the scratch
- A.1.2.** The tip of the scratch should ideally be within a few mm of the desired writing location
- A.1.3.** Load the sample and set the beam current as normal. Skip section 3 of the SOP (Setting Sample Height).



A.2. Use the scratch to set sample height

A.2.1. Navigate to the end of your scratch

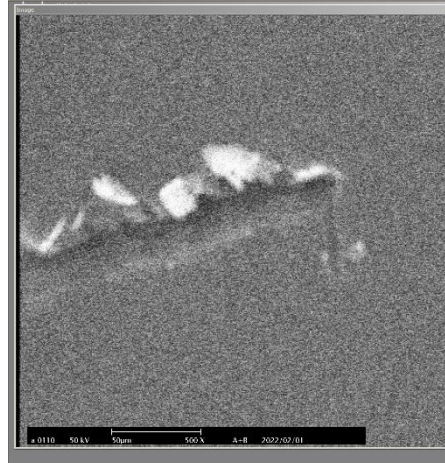
A.2.1.1. Start by finding it along the edge of the chip. Then carefully move along the scratch into the center of the chip.

A.2.1.2. Remember that any area on the chip that you see in the SEM is being exposed. As you near the tip of the scratch, begin to zoom in to minimize the exposed area near the tip.

A.2.2. With the laser off, begin to move the Z stage up, just as you would when setting the height with the laser.

A.2.2.1. As you move the stage up, look at the focus of the SEM image. Optimize the focus as much as you can by moving the stage. Once you are close, you should zoom in on a small particle.

A.2.2.2. During this process, be aware of a sensible Z value based on the thickness of your sample, and do not stray far from that value



A.3. Use the SEM focus and stigmatism to fine tune the SEM image

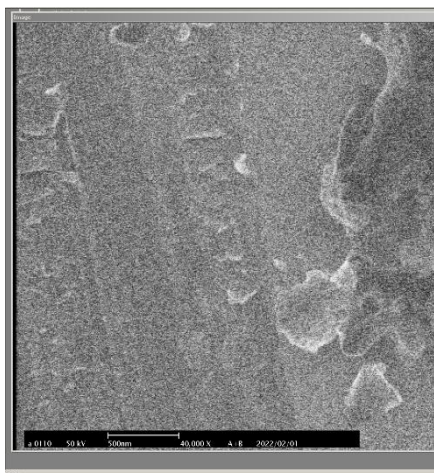
A.3.1. Choose an appropriate small particle near the end of the scratch

A.3.1.1. Focus and stigmatize on this particle just as you would on the reference sample

A.3.1.2. When you have a good image at >150,000x magnification and can resolve features on the order of 10s of nm, that is sufficient

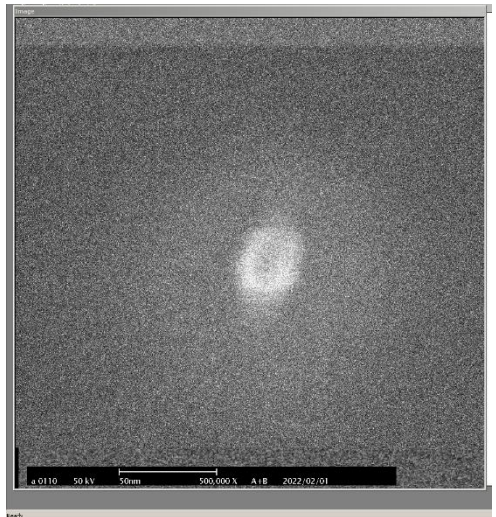
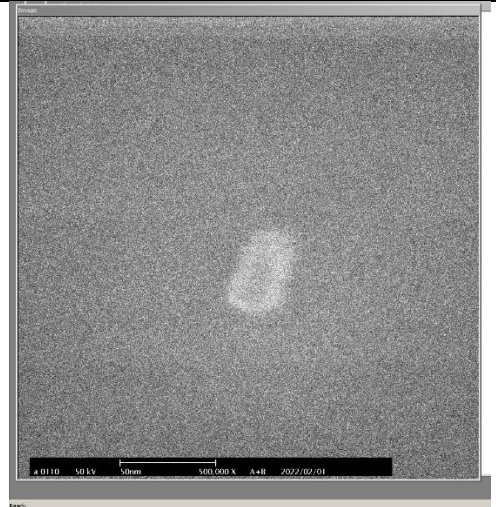
A.3.2. Record the X, Y, and Z positions once you are satisfied with the image

A.3.2.1. The X and Y coordinates you record are the coordinates from which you will reference your sample position in the schedule file



A.4. Check and fine tune focus and stigmation by burning spots

- A.4.1.** At low current (usually <200 pA), burning spots in resist can be a very effective way to check and optimize the beam condition.
- A.4.2.** Move the stage a small amount away from the area you have been looking at
- A.4.2.1.** It is a good idea to move in the opposite direction that you intend to write to avoid damaging important parts of your sample
- A.4.3.** Immediately after moving to an unexposed area, click “Freeze” and then “spot” in the Scan window.
- A.4.3.1.** The mag should be at least 100,000x
- A.4.4.** Wait for ~30 seconds and then return to video mode on the SEM
- A.4.5.** You should see a small donut shaped mark in the center of the SEM window
- A.4.5.1.** If this mark is blurry or asymmetrical, this means your focus or stigmation is off
- A.4.6.** Iteratively adjust focus and stig and move to a new location to burn a new spot until you are satisfied with the quality.
- A.4.6.1.** You should be able to decrease the length of time in spot mode as the beam quality gets better.
- A.4.6.2.** In the final step, the spot time should be as short as possible, and the resulting spot should be <20nm in diameter
- A.4.6.3.** Keep in mind that the spots will change as you observe them, so it is necessary to work quickly and move on once a spot is degraded



A.5. Run the exposure without height control

- A.5.1.** In the exposure options, choose “PRESET(HS OFF)” under Z-Movement and enter the Z height from A.3.2 in Z Preset
- A.5.2.** During field correction, do not adjust focus or stigmatism at all on the reference. Skip to step 5.2.6.



Appendix B: Choosing Writing Parameters

Choosing appropriate writing parameters is a critical part of successful lithography. Writing parameters are not independent and must all be considered together. Changing one without considering the effect on the others can be disastrous. The following parameters should be considered during the design of the pattern and completely chosen at the time of data prep:

- Field Size
- Field Dot Number
- Pitch Number (or Shot Pitch)
- Current
- Aperture
- Dose time

Field Size, Field Dot Number and Pitch Number

The field size options in the Elionix are 75 μm , 150 μm , 300 μm , 600 μm , 1200 μm , and 2400 μm . A smaller field gives the potential for higher resolution, but also slower writing and an increase in the number of stitching boundaries. Larger fields also result in more aberration at the edge of the fields, as a greater beam deflection is required, so the field uniformity is not as good. Usually, 300 μm or 600 μm fields are chosen. Unless critical pattern dimensions are very small (maybe below ~ 50 nm) the damage to the pattern caused by stitching is much greater than that caused by the limitations of a 600 μm field, so it is better to choose a larger field to eliminate stitching. Fields larger than 600 μm should not be used for fine features.

The field dot number is the number of discrete dots in x and y that the tool will divide the field into. Each dot is a specific location in the field that the tool can place the beam and dwell for a fixed amount of time to expose the resist. The Elionix allows us to choose 20,000 dots, 60,000 dots, or 240,000 dots. 60,000 dots is almost always chosen. 20,000 dots exists for legacy purposes and should probably never be used. 240,000 dots may be necessary if you are trying to push to the resolution limits and pattern features smaller than 10 nm. For most patterns, it gives no advantages and results in much slower writing.

Dividing the field size by the number of dots gives the size of each of those dots. This is sometimes (confusingly) called the resolution, but it is more accurately the machine grid.

By adjusting the pitch number, we can choose to expose not every single dot on the machine grid, but a square effectively made up of several dots on each side by skipping a certain number of dots in each direction. For example, if we choose a field size of 300 μm and a dot number of 60,000, dividing those gives a machine grid of 5 nm. A pitch number (or shot pitch) of 2 would mean that we skip exposing every other dot, meaning our shots are placed 10 nm apart. 10 nm is our exposure grid.

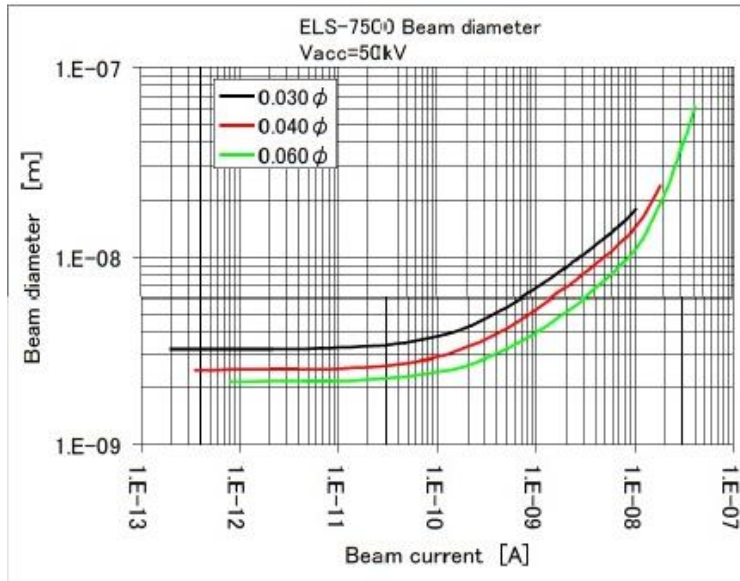
It is critical that our feature sizes and positions in our pattern are placed at multiples of the exposure grid in order to ensure accurate pattern placement. For example, if we have a 20 nm exposure grid and have two lines placed 90 nm apart, one of those lines will be shifted by 10 nm during fracturing because two shots cannot be placed 90 nm apart. Our features will be either 80 or 100 nm apart.

In general, the grid chosen depends on the features in the pattern. It is usually a good idea to have the minimum feature size at least 4-5x larger than the exposure grid.

Current and Aperture

The current and objective lens aperture settings chosen affect the actual diameter of the beam. They also strongly affect the dose time.

Ideally, the physical beam diameter should be slightly larger than the exposure grid. This is not a strict rule as the beam size only weakly affects the pattern feature sizes, and dose considerations are generally more important for selecting current and aperture. The graph below shows the relation between current, aperture, and theoretical beam diameter. In practice, the beam diameters are likely somewhat larger and various beam blur effects will further broaden the effective size of the beam.



The chart below shows the available current and aperture settings in the tool and the nominal beam diameter for each.

Current (pA)	Aperture (μm)	Nominal Beam Diameter (nm)
10	40	2.5
20	40	2.5
30	40	2.5
50	30	3.5
50	40	3
100	30	4
100	40	3
200	40	3.5
500	60	3.5
1000	60	4
5000	60	8
6000	60	9
10000	60	10
20000	60	20

Dose and Dose Time

The dose required to expose a pattern is mainly a function of the resist used and the accelerating voltage, and more weakly a function of resist thickness, pattern density, feature size, and development conditions. Usually this value is determined empirically for a particular pattern, though good resist and process characterization can allow one to fairly accurately choose a dose directly.

Dose cannot be entered into the tool directly. Instead, it is entered as dose time, which is the amount of time the beam dwells on one particular shot before moving on to the next. The two are related by the dose equation:

$$Dose = \frac{It}{A}$$

Where I is the beam current, t is the dose time, and A is the shot area. Solving for dose time and substituting $A = S^2$ (shot area is exposure grid squared) gives the following:

$$t = \frac{Dose * S^2}{I}$$

Adding units and the necessary conversion factor, the equation can be used as follows:

$$t [\mu s] = \frac{Dose \left[\frac{\mu C}{cm^2} \right] * S [nm]^2}{I [pA] * 100}$$

Note that the equation above is linear with dose and current and quadratic with exposure grid. This means that the most powerful way to control dose time is to adjust the exposure grid, either by modifying the field size or (usually) the shot pitch.

In the Elionix, there are several parameters that go into the dose time calculation:

Base Dose Time – this is the base dose with no corrections applied to it. For optimized patterning, this is the dose that gives equal sized lines and spaces when patterning an array of lines with 50% duty cycle. The base dose time can be set in the Beamer export module.

Dose Factor – a multiplier on the base dose time set in Beamer. PEC and FDA modules in Beamer apply a dose factor.

Dose Slope – a multiplier on the base dose time set in WECAS. Applying a dose slope is the recommended method to run a dose array in WECAS. If you set a base dose time of 1 in Beamer, the dose slope can be used in WECAS to set the base dose.

Dose Shift – an additive factor on the dose time, which is applied after the dose factor and dose slope are applied to the base dose.

Combining all of these parameters, the following equation defines the dose time in WECAS:

$$Dose\ Time = Base\ Dose\ Time * Dose\ Slope * Dose\ Factor + Dose\ Shift$$

In the Elionix, the dose time is constrained by the limitations of the pattern generator to a minimum dose time of 0.1 μs with increments of 0.05 μs .

The main practical consequence of this is that if the exposure grid is small, the beam current must be extremely low in order for the tool to be capable achieving the dose time for most reasonable doses. This results in very slow writing, and also increases the severity of stitching and alignment errors caused by drift. It is good practice to write patterns at the highest current and largest exposure grid that can achieve the desired features. There is a dose time calculator in the WECAS software, but it should be used with caution because it does not account for changes made to the pitch number and can give bad data because of this. A dose time calculator in a spreadsheet is available with the tool process data.

Proximity Error Correction

Proximity error correction (PEC) is an important consideration for many EBL patterns, the details of which are beyond the scope of this document, but it deserves a brief mention because it affects dose times and thus current selection. To perform PEC, we use Beamer to computationally vary the dose within our pattern to account for various electron beam scattering effects and keep the effective dose of all parts of our pattern uniform. Because of the limitations of dose times in the Elionix, if we use a high current, the desired doses based on the computation do not match up with the available doses from the allowed dose times. This leads to low dose accuracy and poor patterning. The required dose accuracy and the beam current which will enable that dose accuracy are important considerations for PEC.

Appendix C: Alignment

Alignment Marks

Aligned patterning is used to precisely position a pattern with respect to another pattern that already exists on the sample. The known, previously patterned features that are used to match the second pattern with the first are called alignment marks. Any shape that can be identified in the SEM, and whose position relative to the features to be patterned is precisely known, can be used as a mark. The easier it is to see the mark and find its center, the better the alignment will be. At 50 kV, resist can be used, but makes a poor mark. Noble metals (~20 nm thick or more) make very good marks. Etched marks can be used, but they need to be much thicker than deposited noble metals. Metals with atomic numbers near Si such as Ti, Cr, and especially Al, do not make very good marks. The tool is capable of automatically detecting circles and cross shapes, though automatic alignment is rarely used. Most commonly, cross shaped markers are used and located manually. Crosses with a smaller width can allow more precise alignment, but are also harder to locate. A hierarchical design with larger markers that are easier to locate and smaller ones that are more precise can be a good idea.

Keep in mind that the only way to find marks (automatically or manually) is to use the SEM to look at them, which means that the resist is being exposed. This means that marks should be kept far away from any parts of the device that can be damaged by exposure to subsequent process steps.


Alignment in the Elionix is limited to global alignment with two marks. You may have as many marks on your sample as you'd like for your convenience in navigating, but the tool will look for only two, which are defined as the registration A- and B- marks. Marks that are further apart will result in better alignment. At minimum, it is a good idea for the marks to be at least 3 mm apart. Alignment accuracy is highly dependent on the pattern, marks, and operator. Any alignment better than ~30 nm should be considered a best effort basis, and not consistently achievable.

Alignment Procedure Overview

To perform alignment in the Elionix, the following steps beyond the requirements for an unaligned write should be performed:

1. CAD positions of the registration marks should be defined in the CO6 file. The tool will not accept positions $< 0.25\text{mm}$, so consider this in the CAD design phase.
2. The exact stage position of at least one alignment mark needs to be found and used to precisely set the pattern position in the schedule file.
3. Correct settings for alignment need to be chosen in the exposure settings.
4. During exposure, both marks need to be identified in the SEM with the greatest possible precision.

Detailed Alignment Procedure

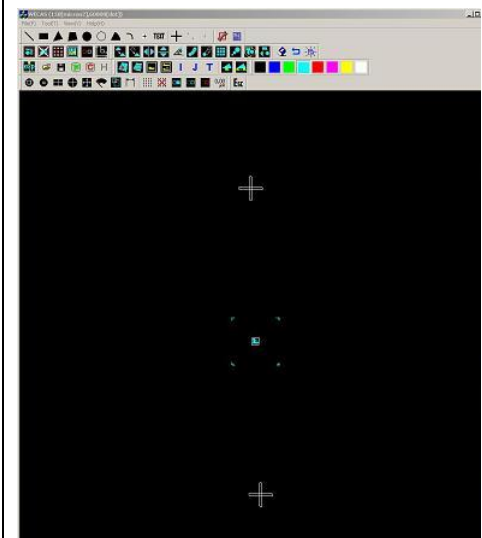
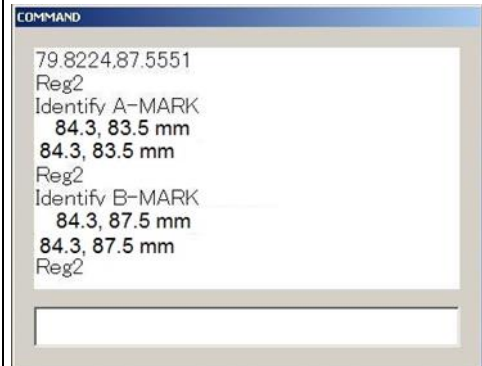
<p>C.1. Locate alignment mark</p> <p>C.1.1. This should be done during step 3 of the full procedure (setting sample height)</p> <p>C.1.2. Instead of driving to an arbitrary location in the center of your sample, you should carefully navigate to the position of a known alignment mark</p> <p>C.1.2.1. There are many methods of finding a mark, and they are highly dependent on your sample</p> <p>C.1.2.2. The mark you find does not have to be one of your Registration A or B marks, it just needs to have a known position with respect to those. However, to avoid the chance of a mistake in location or a problem with your marks ruining the write, it is often a good idea to find the exact position of at least one of your registration marks.</p> <p>C.1.3. Set the height of the sample at this location as in step 3 of the full procedure</p> <p>C.1.4. Use the SEM to precisely find the location of this mark. It may be helpful to focus the SEM, but it is not strictly necessary.</p> <p>C.1.5. Record the stage position of the mark</p>	
<p>C.2. Define Registration A and B marks</p> <p>C.2.1. This should be done during step 4 of the full procedure (preparing and scheduling exposure) immediately after loading CO6 file into WECAS</p> <p>C.2.2. Select “Reg2 MARK” from the toolbar in the WECAS Software</p> <p>C.2.2.1. In the COMMAND window, enter the coordinates (in mm) of the first marker (A-MARK). The coordinates must have a decimal place, so if your mark is at 5 mm, you must enter 5.0.</p> <p>Note: If you prepared your data in Beamer and properly set your extents, the positions entered for A-</p>	 <p>The screenshot shows the WECAS software interface. The title bar reads 'WECAS (150[micron2],60000[dot])'. The menu bar includes 'File(F)', 'Tool(T)', 'View(V)', and 'Help(H)'. The toolbar contains various icons for file operations, navigation, and editing. A red box highlights the 'Reg2 MARK(R2)' button, which is represented by a grid icon. Other visible icons include a line, a square, a circle, a triangle, a plus sign, and a text box.</p>

MARK and B-MARK will be exactly the same as their positions in your CAD in Beamer. If you converted your data in WECAS, these coordinates are much less obvious.

C.2.2.2. Enter the coordinates of B-MARK in the same manner. If these were entered correctly, you will see them as two large crosses in the pattern display window. Make sure that their position with respect to your pattern is correct.

C.2.3. Click file and choose "Save the active CON file" and click yes in the dialog box

C.2.3.1. This newly saved CO6 file is the one you should choose in your schedule, not the original from Beamer



C.3. Precisely set pattern position in the Schedule file

C.3.1. The x and y position in the schedule should be the stage position of the origin from your Beamer Export

C.3.1.1. This can be calculated from the stage position of the known point determined in step C.1 as follows:
$$[x,y]_{sch} = [x,y]_{mark,stage} - [x,y]_{mark,CAD}$$
For example, if the mark position in your CAD is [1,1] and on the stage you found it at [75,75], the [x,y] coordinates you enter for the schedule are [74,74]. This is the position of your origin in the stage coordinates.

C.4. Set the alignment options in the schedule options window before saving schedule file

- C.4.1.** Registration Execution Mode: Y
Registration Control Type: Usually 'Manual'
Registration Error Processing: Relevant only for auto alignment

Registration 2 Mark: Usually "All REG-2". This matters if a pattern with alignment marks is instanced in an array. All REG-2 will perform alignment at each pattern, while 1st Reg-2 Only will perform the alignment only once.

FC at Registration: Usually "No"
Reg-2 Tolerance Angle [mrad]: Usually 0.02.
Adjust this with caution

Registration

Registration Field Size
0 [um2]

Registration Execution Mode
Y

Registration Control Type
MANUAL

Registration Error Processing
E

Signal Information
N

7500 EX (Registration)

Registration 2 Mark
ALL REG-2

FC. at Registration
ALL REG-2

Reg-2 Tolerance Angle [mrad]
0.02

Reg-3 Tolerance Angle [mrad]
0.02

Reg-2 Mark Shape
 Cross Disk

C.5. During exposure, precisely locate alignment marks

C.5.1. When exposure starts, the stage will drive to the nominal position of A-Mark.

C.5.1.1. Make sure the mag is sufficiently high to avoid excessive exposure, and unblank the beam

C.5.1.2. The alignment mark should be visible. If it isn't, carefully zoom out. If the position is significantly off so that you can't find the mark without moving the stage, it is best to abort and check the previous steps.

C.5.1.3. Once the alignment mark is visible, turn the Cross Mark on and switch to slow scanning

C.5.1.4. Center the alignment mark with the Cross Mark on the screen. It is best to move the position of the mark using the X and Y position buttons in

[Reg 2 A-MARK]

Release BEAM BLANKING and move the MARK to the CENTER of SEM CRT with SDU.
Then press the OK button.

OK Cancel

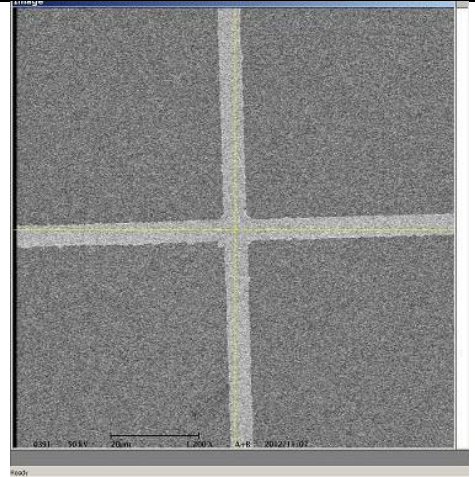
Position

X 30000 Y 30000

Coarse

the Exposure window, but if the larger movements are required, it is acceptable to move the stage with the mouse

- C.5.1.5.** Zoom in to the highest reasonable mag and make sure the marks are as closely centered as possible. Blank the beam and press "OK" in the Exposure window.
- C.5.1.6.** The stage will automatically drive to the B-MARK. Repeat the process to center the B-MARK. You must select the B-MARK at the same magnification as the A-MARK.
- C.5.1.7.** The exposure will proceed. When it is finished, follow the standard procedure from step 5.3.4.




Appendix D: File Conversion in WECAS

The WECAS Software can be used as a CAD program for drawing patterns. This is not recommended and no further information on this will be included here. It can also be used to convert a gds or dxf data to cel and con files required by the tool for writing. This is done instead of exporting the CO6 file in Beamer.

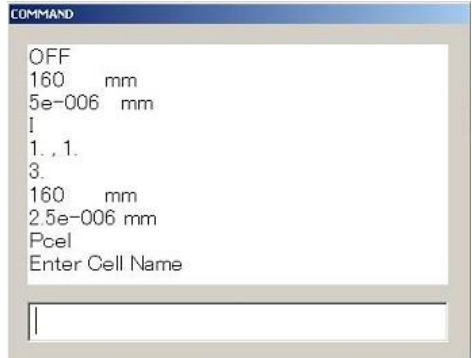
There are many advantages to using Beamer, including much faster conversion, greater control of feature ordering, greater control of the exposure grid, proximity error correction, dose control within a pattern, the ability to handle circles, arcs, and certain other shapes in a much more precise way, and greater clarity of pattern placement. Beamer provides tools that, if used correctly, can dramatically improve the speed and quality of patterning.

If, despite this, you prefer to convert your CAD with WECAS, instructions are provided below for legacy purposes.

<p>D.1. Set field and dot size</p> <ul style="list-style-type: none">D.1.1. Switch to the patterning PCD.1.2. Open WECAS software if it is not openD.1.3. Click on “Setting” in the toolbarD.1.4. Select FIELD SIZE [DOT] option<ul style="list-style-type: none">D.1.4.1. Usually 60,000D.1.5. Select FIELD SIZE [μm] option<ul style="list-style-type: none">D.1.5.1. Depends on pattern, but usually 300 or 600D.1.6. Click OK	 <p>The screenshot shows the WECAS software window titled 'WECAS (300microm2160000[dot1])'. The menu bar includes 'File(F)', 'Tool(T)', 'View(V)', and 'Help(H)'. The toolbar contains various icons for drawing and editing, with the 'Setting' icon (a grid with a pencil) highlighted by a red rectangular box.</p>
<p>D.2. Convert CAD file</p> <ul style="list-style-type: none">D.2.1. Click “Tool” in the menu bar and select either GDSII Converter or DXF Converter (GDS files are always preferred)D.2.2. Click Ref. and browse to your directory in D:\UsersD.2.3. Click Conv.D.2.4. In the pop-up, enter the layer number and press enter. Type “all” for every layerD.2.5. For “mm Mode (Y/N) ?”, type y. Choosing n means using dot mode, which will change your feature sizes and is not recommended unless you fully understand itD.2.6. Conversion can take a long time. When it is finished, press OK in the pop-up window.<ul style="list-style-type: none">D.2.6.1. A new Cell (.cel) file will exist in your directory. Its name will be the first 8 characters of the GDS structure name	

D.3. Place Cell File

- D.3.1.** Press “Place CELL” in the toolbar, or go to “File” -> “Open an existing CELL file”
- D.3.2.** In the pop-up window when asked to enter the Cell name, type “?” and press enter to choose your cell file from the directory
- D.3.3.** Enter the stage coordinates of the pattern center. You should now see your pattern in the display window. You may need to adjust the zoom.



D.4. Place Chip

- D.4.1.** Click “Place Chip” in the toolbar
 - D.4.1.1.** The “chip” is the field in which the patterns in your cell will be written.
- D.4.2.** Enter the chip name. The name is not critical.
- D.4.3.** Enter the stage coordinates of the center of the field. The patterns must be entirely contained within the field.
 - D.4.3.1.** If the patterns are too large for a single field, multiple fields must be placed. Care must be taken to avoid severe stitching errors.



D.5. Save con file

- D.5.1.** Go to File -> “Save the active CON file” and save the file in your directory.
- D.5.2.** Click “Yes” in the dialog box

D.6. Click “EXP” in the toolbar to go to the exposure menu.

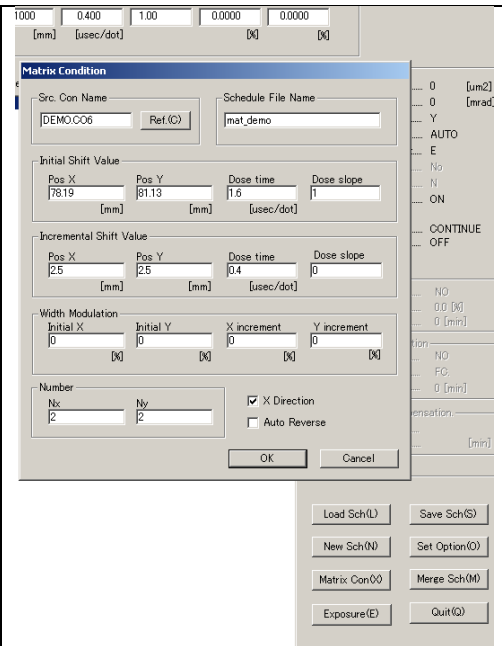
- D.6.1.** The only difference in setting up the exposure from the full procedure is that the coordinates will be [0,0] if you set your stage coordinates when placing the cell and chip.

Appendix E: Advanced Options in Scheduling

Matrix CON

If you want to write the same pattern multiple times at different places on the chip, the “Matrix Con” option in the Exposure. This can also be used to set up a dose array, as a dose step can be defined between each pattern. These functions can also be achieved in Beamer, but there can be advantages to setting this up in WECAS instead.

- E.1.** After CO6 file is loaded, click “EXP” to open the “Edit Schedule File” window
 - E.1.1.** Click “Matrix Con”
 - E.1.2.** The following parameters are required:
 - E.1.2.1.** Position of the first instance
 - E.1.2.2.** Dose time of first instance
 - E.1.2.3.** Number of instances in x and y
 - E.1.2.4.** Spacing of instances in x and y
 - E.1.2.5.** Dose shift for each pattern (This is a fixed time added to the Dose Time)
 - E.1.2.6.** Dose slope for each pattern (This is a multiplier on the Base Dose Time. Usually only one of Dose slope and Dose shift should be used.) See Appendix B for a more detailed discussion on dose shift and dose slope.
 - E.1.2.7.** Mod x and y should usually not be used
 - E.1.3.** After clicking ok, multiple copies of the con file with different parameters will be shown in the schedule file window. Check that the position and dose values are as expected. Each line can be modified individually.
 - E.1.4.** Schedule options should be set as usual
 - E.1.4.1.** If your pattern contains alignment marks, there are settings that control whether each pattern will be aligned or the alignment will only be performed for the first pattern



Combining Files

Multiple CO6 files can be combined into a single schedule in various ways. Generally, it is better to combine CAD data into a single Beamer export, but there may be some specific cases where this is not preferred. Below are some considerations:

- All files must be in the same folder
- The naming convention of CC6 and CB6 files is such that they may often have the same name. If these are overwritten, they will not write correctly. These names are referenced within the CO6 file, so renaming individual files will not work.
- The 'Merge Sch' function can be used to combine previously prepared sch files, but the schedule files and all associated pattern files must be in the same folder. After the merge, schedule options (including the laser height sensor preset) will be lost, so they must be reset
- All patterns in the same schedule must have the same field settings and current

Feel free to contact the staff members with any questions about your process and the tool.

<i>Draft</i>	<i>Date</i>	<i>Author</i>	<i>Notes on changes</i>
v.0.1.0	1/31/2022	David Barth	First Draft
v.0.1.1	2/21/2022	David Barth	Formatting Edits
v.1.0.0	3/16/2022	David Barth	Clarifications and additions from user input
v.1.1.0	5/6/2022	David Barth	Additional details and corrections about Dose Time calculation