

Raith 100 Electron Beam Lithography



Electron-beam (e-beam) lithography is a lithographic process used to transfer patterns onto silicon or other substrates. It employs a focused beam of electrons to expose a pattern into the electron-sensitive resist applied to the surface of the substrate. The main advantage of e-beam lithography is that it can offer much higher patterning resolution than the conventional optical lithography which is limited by the diffraction of light, thus it is extremely suitable for fabrication of nanoscale features [2].

This document describes how to setup an exposure in a step-by-step manner. Most of these steps must be done in the correct order. Only change the order if you are familiar with the system operation and know that it is possible to do so. The best advice is to gain an understanding of each module before deviating from the given outline. A common user is REQUIRED to talk with NCF staff on any operation beyond this guide. Detailed documentation is available in the reference section, along with a helpful website.

Patterns for writing can be drawn using GDSII editor native to the E-line software. It is also possible to import a pattern from other editors such as AutoCAD, but it is recommended to use the internal editor, mainly because it allows

for some unique manipulations to each feature in the pattern. Creation of a pattern isn't covered in this manual, but can be found in the accompanying E-line Software Manual pdf.

Abbreviations used in this manual

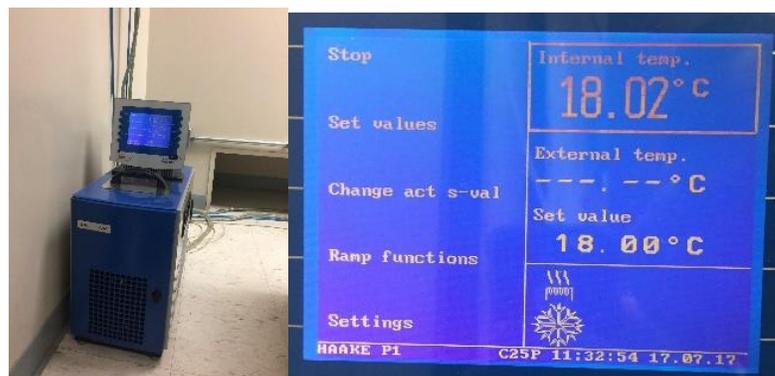
Abbreviation	Meaning	
CPC	Column PC (right monitor)	SEM window
LPC	Lithography PC (left monitor)	Writing parameters are set here
WF	Write Field	Area exposed to beam
WFA/AWF	Write Field Alignment/ Align Write Field	Stitching together patterns while writing
WD	Working Distance	Distance from beam column to sample
Area Dose	-	Dosage required to fully develop out an area of the resist
Area Dwell Time	-	Time the beam stays at each location
Area Step Size	-	Length the beam moves between each dwell time

I. System Operation

By policy, the system is always on, so any operation by an NCF user is limited to starting the software, loading and unloading samples, e-beam writing, and general-purpose SEM.

Load/Unload Samples

1. Check the system chiller. The temperature should be 18°C. If the chiller temperature is above 18°C, please call the NCF office.



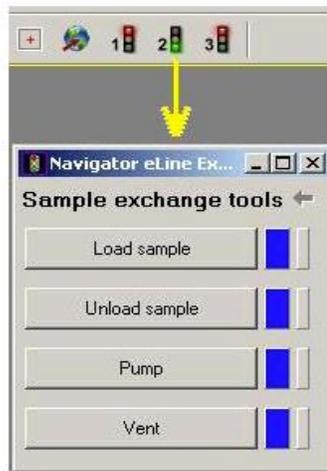
2. Turn on both monitors. If the software is running already, make sure there is no red warning or error at the bottom of the left monitor. Close the software and log back in with your credentials.



3. Double click on the *e-Line software* on the desktop and login with your username and password. If you have forgotten your password, please let a member of the NCF Staff know so it can be reset for you.
4. Open the Nitrogen tank and turn on the HEPA filter.



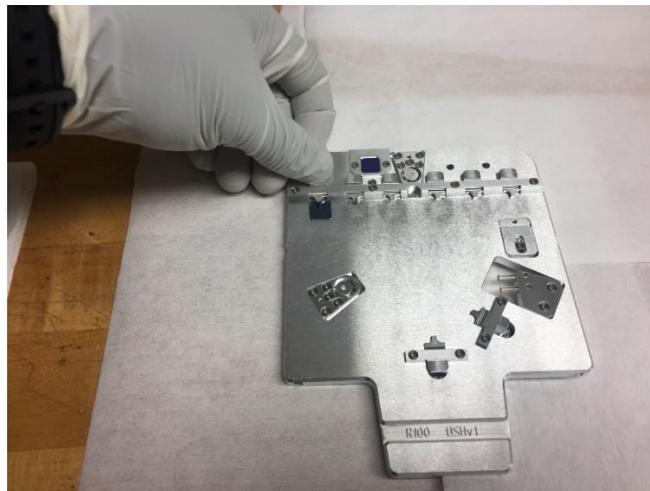
5. On the left monitor, click **Unload Sample** on the **Navigator Exchange** window. If this window is not present, click the second traffic light icon on toolbar to open it.



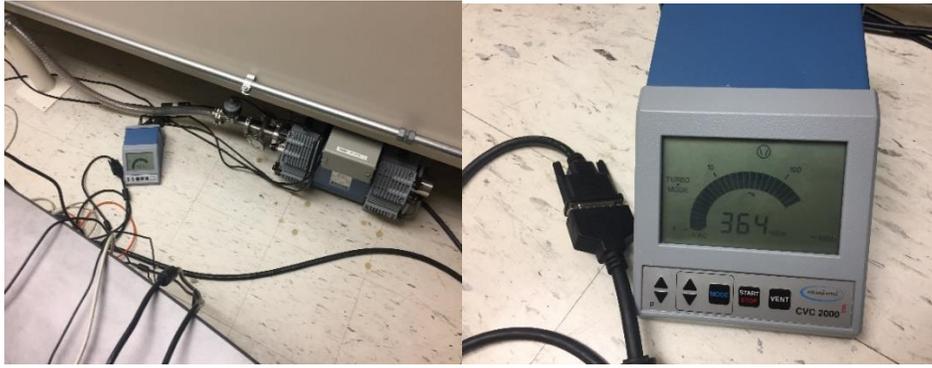
6. Click **Ok** on the next two dialog boxes that pop up.
7. It takes about 3-5 minutes to vent the chamber. When the gap between the door and the chamber is about 2mm wide, then door can be pulled open. The door is heavy, so try to be gentle and slowly pull it out.
8. Take out the sample holder and put it down on a clean room wipe.



9. If the sample has PMMA to be written on, use a **plastic tweezer** to mount sample on the holder. Push down the spring clamp and slide the sample underneath, then release the spring clamp.
 - a. The holder has 6 clips that can be used for loading flat samples. There is an additional clip at the bottom that can be used to hold whole wafers in place as well.
 - b. There is also a slot for loading samples at 90° for doing cross-sectional SEM. However, it's recommended to use a sample holder with the desired angle you want for your imaging



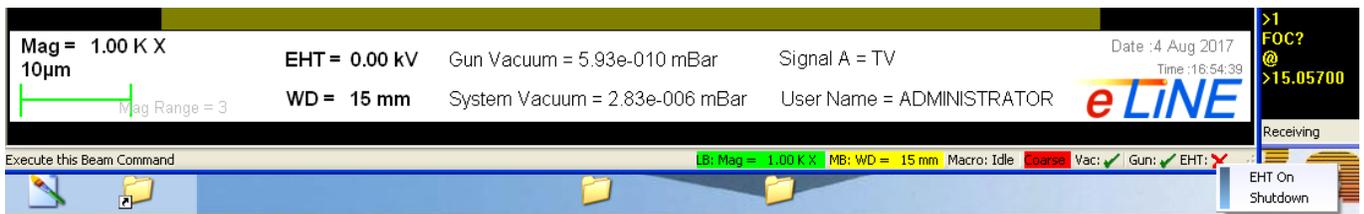
10. If loading an un-patterned sample that has PMMA on it, after placing the sample in its clip, use a **metal tweezer** to scratch any corner of the sample.
11. Place the sample holder back into the chamber. Click **Load Sample** on the **Navigator Exchange** window and click **OK** on the dialog boxes that come up.
12. Slowly close the chamber and firmly hold it closed until the backing pump turns on and starts to pump the chamber. Hold the chamber door closed for about 2 minutes. Check the pump on the floor, behind the monitors to make sure the pressure is going down.



13. Close the Nitrogen tank and flip the HEPA filter switch to the off position.
14. The system takes approximately 15 to 20 minutes to pump to high vacuum, although some samples might require more time if they are slowly outgassing. It is not necessary to stay in the room while the chamber pumps down.

II. Operation

15. At the end of load procedure, turn on EHT on the right monitor. (Right-click on “EHT” in the lower right corner of the SMART-SEM window and select **EHT On**.)



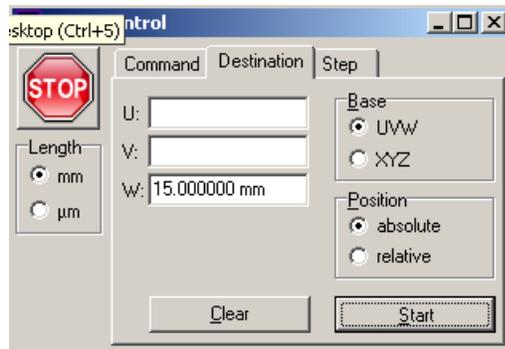
16. On the left monitor, click **YES** to reset the UV adjustment, then enter the following values into the next 3 dialog boxes that come up respectively: **Accelerating Voltage = 10KV, Aperture = 30um, Working Distance = 10mm.**
17. Click **YES** to drive the stage to Home position. When at the Home Position, a dialog box indicating a successful loading sequence will pop up. If necessary, you can input a sample name as well.



III. Taking SEM

Using the mouse to hover over the icons in the SMART-SEM toolbar shows a text box indicating what the icon is.

18. If not already on, turn on EHT on the right monitor. (Right-click on "EHT" in the lower right corner of the SMART-SEM window and select EHT On.)
19. On the left monitor, in the **Stage Control** window, under the **DESTINATION** tab, input the desired WD in and click **START**.



20. Make sure the **Beam** is **OFF**; the icon should look as such . Move to the clip where the sample is located by clicking the **Command** tab and then clicking the appropriate clip in the **Stage Control** window.



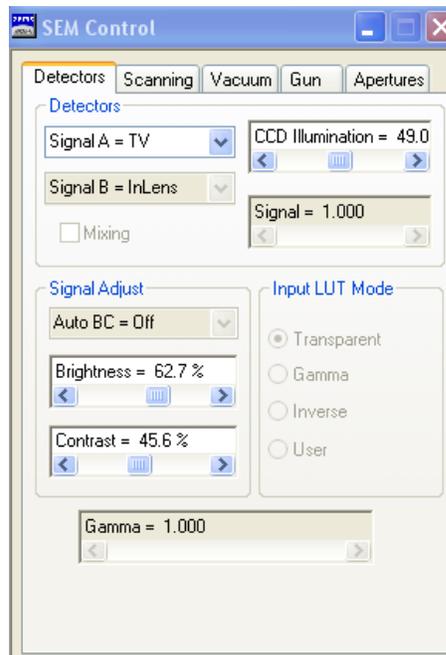
21. Once at the destination, turn the **Beam ON**; the icon should look as such . Click on the **Normal Scanning**  icon on right monitor. This exposes the sample to the electron beam.

The LPC mouse uses the left button as the magnification and the middle button as the focus. Clicking and dragging either button left or right will change the magnification or focus.

22. Find your sample using **Stage Joystick** control. If the SEM image seems to be moving slowly, push the **High-Speed** button on the **Stage Joystick** control and make sure the **2nd** scan speed is selected on the left monitor.



23. On the right monitor, under the **SEM Control** window, select the **Detector** tab. Under **Signal Adjust**, select **Auto BC**.

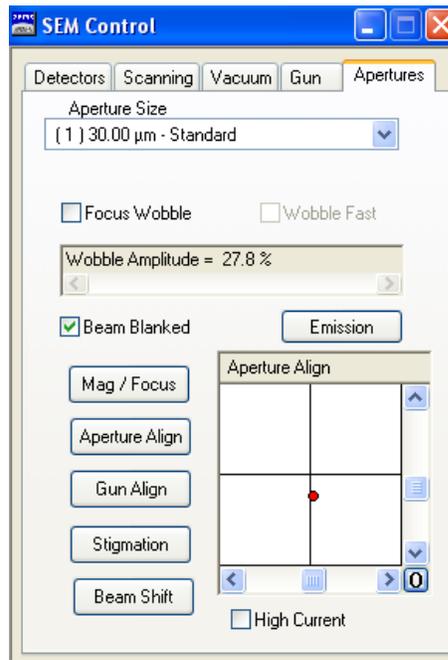


24. Place the right mouse cursor on the SEM image. Focus by holding down the middle button of the mouse and dragging it left and right.

25. Zoom in by holding down the left button on the same mouse as in step 24 and dragging it left and right.

26. Adjust both focus and magnification until the clearest image of a particle can be seen at $\sim 20kX$ magnification. This particle should be at around 200nm scale bar.

27. On the right monitor, under the **SEM Control** window, click on the **Apertures** tab and enable **Focus Wobble** by clicking on the box next to it. The particle you are focused on will begin to move in and out of focus.



28. If there is not a small box on the screen, click on the **Raster Icon**  in the toolbar on the right monitor. This brings a box on screen and restricts the beam to a small area around the particle you are looking at.
29. On the right monitor, under the **SEM Control** window, click on **Aperture Align**. The objective is to stop the image from moving side to side and up and down. Do this by clicking the arrows in the square window until the image stays in one position while coming in and out of focus.
30. On the right monitor, under the **SEM Control** window, click on **Stigmation**. Use the arrows to try and correct any stretching and blurring of the image on screen.

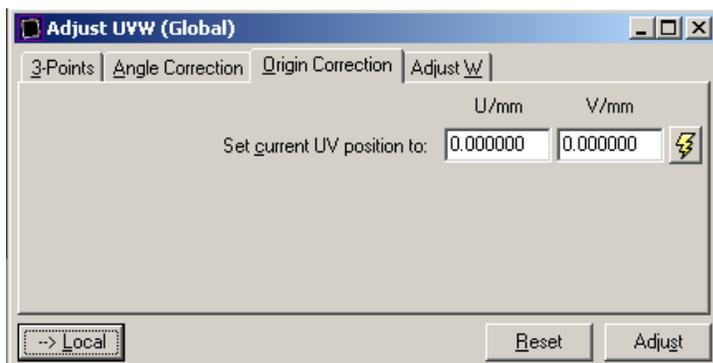
31. Deselect **Focus Wobble** by clicking on the box next to it. Click on **Mag/Focus** or click the  icon and try focusing.
32. Repeat steps 24-31 until a very clear and sharp image can be seen on screen. If it's still there, remove the raster box by clicking on its icon again in the toolbar.
33. Find what you would like to take an image of and click on the **4th** scan speed on the right monitor and save the image.

34. You can stop the image from continuously scanning by clicking **Pause**  in the toolbar of the SEM window on the right monitor.
35. To save the image, on the SEM window on the right monitor, click **File** → **Save Image**. In the dialog box that comes up, click on **Change Directory** and find yours and click **OK**.
36. Enter a name for your sample. If you would like to save multiple images of the same spot on your sample, click on the **Settings tab** in the same dialog box and enter a number in the **Next** field.
37. Click on  icon to save the image.
38. Once done image, unload you sample by following steps 4-14.

IV. Performing Lithography

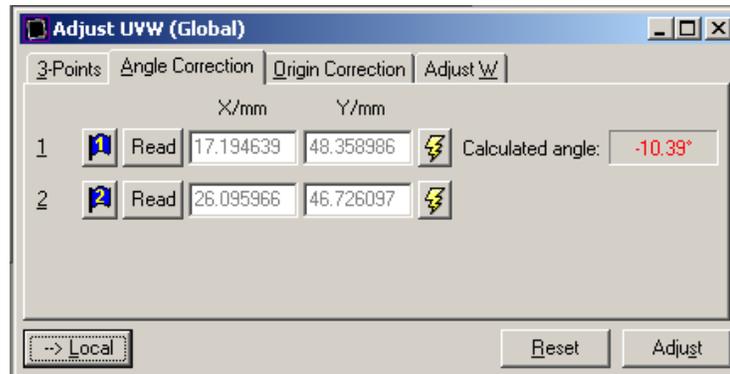
The Raith 100 uses two type of coordinate systems. The first is the Global Coordinate System denoted by XYZ. This is the coordinate system used by the stage when one moves from one part of the stage to another. The second, is the Local Coordinate System denoted by UVW. This refers to the sample as your move from one part of your sample to the other.

39. Refer to steps 15-21 for the initial steps required in performing e-beam writing.
40. Find a corner (preferably the scratched one) of the sample using **Stage Joystick** control. If the SEM image seems to be moving slowly, push the **High-Speed** button on the **Stage Joystick** control and make sure the **2nd** scan speed is selected in the SMART-SEM window.
41. Click on the crosshairs in the toolbar of the right monitor and center them on the edge of the sample.
42. On the **Adjust UVW** window in left monitor by clicking on the **ORIGIN CORRECTION tab**.
43. Ensure that it is in mode **Global**; if it is in mode LOCAL, click on the button at the bottom of the window once to change it.

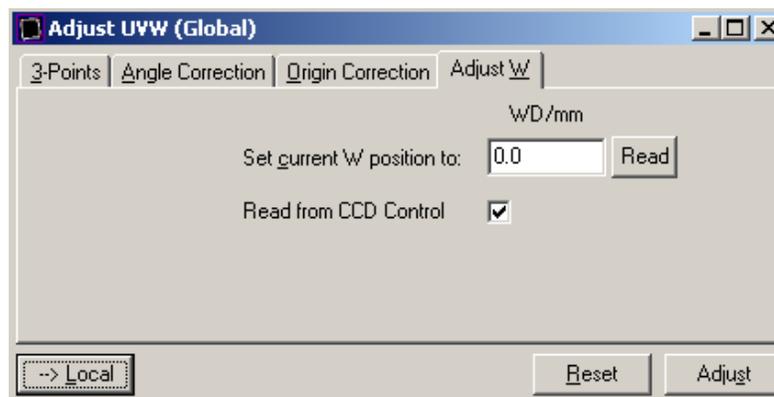


Note that clicking on the **lightning icon**  at any time will move the stage back to the origin you have just set.

44. Click **ADJUST**. This sets the current location in the local UVW coordinate system as the origin.
45. In the same window, click the **ANGLE CORRECTION tab** and then click **READ** in location **1** to record the XY location of point 1.



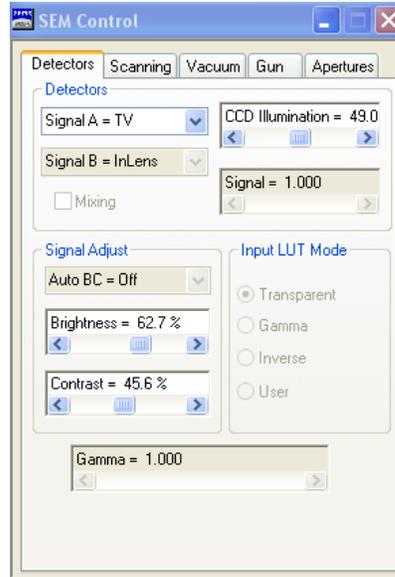
46. Using **Stage Joystick** control, drive the stage to the opposite corner of the sample. Click **READ** in location **2** to record the XY location of point 2.
47. Click **ADJUST** to calculate transformation angle between XY and UV coordinates. NOTE: the computer assumes +U direction to be along the vector from point 1 to point 2.
48. In the same window, and while in focus (described in detail in the next section), select the **Adjust W** tab. Click the **READ** button to set the current W position to 0. Then click on **ADJUST**.



V. Focusing

49. Under the **ORIGIN CORRECTION tab**, click on the flag icon to move the stage back to the origin you set.
50. Turn the **Beam ON**  and find the corner you scratched earlier. Find particles around the scratch.

51. On the right monitor, under the **SEM Control** window select the **Detector** tab. Under **Signal Adjust**, select **Auto BC**.

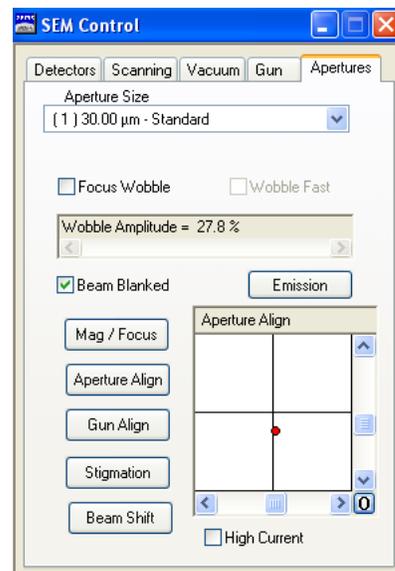


52. Place the right mouse cursor on the SEM image. Focus by holding down the middle button of the mouse and dragging it left and right.

53. Zoom in by holding down the left button on the same mouse as in step 51 and dragging it left and right.

54. Adjust both focus and magnification until a sharp image of a particle can be seen at ~20kX magnification. This particle should be at around 200nm scale bar.

55. On the right monitor, under the **SEM Control** window, click on the **Apertures** tab and enable **Focus Wobble** by clicking on the box next to it. The particle you are focused on will begin to move in and out of focus.





56. If there is not a small box on the screen, click on the **Raster Icon** in the toolbar on the right monitor. This brings a box on screen and restricts the beam to a small area around the particle you are looking at.
57. On the right monitor, under the **SEM Control** window, click on **Aperture Align**. The objective is to stop the image from moving side to side and up and down. Do this by clicking the arrows in the square window until the image stays in one position while coming in and out of focus.
58. On the right monitor, under the **SEM Control** window, click on **Stigmatism**. Use the arrows to try and correct any stretching and blurring of image on the screen.
59. Deselect **Focus Wobble** by clicking on the box next to it. Click on **Mag/Focus** and try focusing.
60. Repeat steps 51-58 until a very clear and sharp image can be seen on screen. If it's still there, remove the raster box by clicking on its icon again in the toolbar.
61. The result should be a well resolved image of the particle at a magnification of ~20KX-30KX or higher.

The key of the aperture alignment is to minimize the image shift during the wobble sequence. You might be able to improve the aperture alignment even further by repeating the same procedure at higher magnification and reduced wobble amplitude. If the dust particle is becoming too large at high magnification, move to a smaller dust particle and continue the optimization.

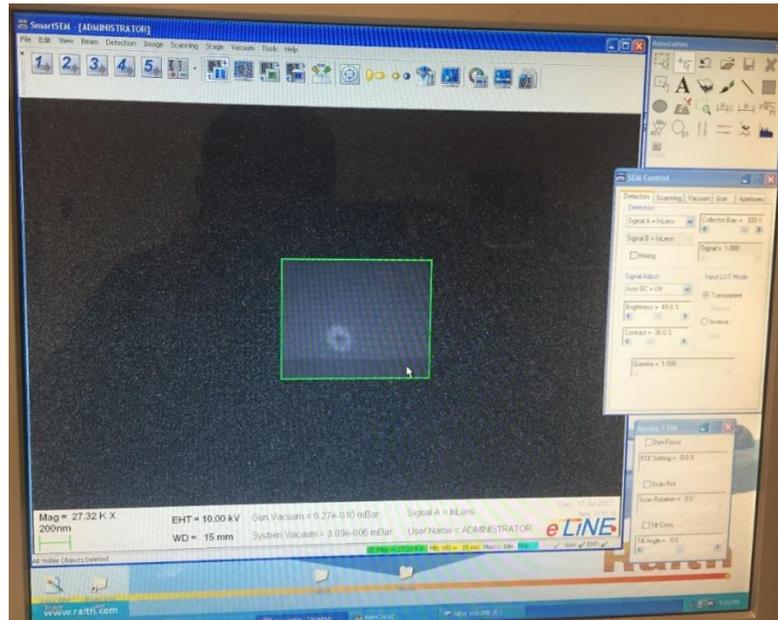
Further E-beam Optimization

62. Perform the **Aperture alignment** again at higher magnification and reduced wobble amplitude. Perform the **Stigmatism** correction again at a higher magnification.
63. Deselect **Focus Wobble** and continue the alignment optimization using alternating **Aperture Alignment** (left mouse button) and the manual focus (middle mouse button). This method allows a more precise adjustment than the automatic wobble and is recommended for the final optimization steps.
64. Repeat the same procedure between the optimization of **Aperture Alignment** and **Stigmatism** correction until no further improvement can be achieved.

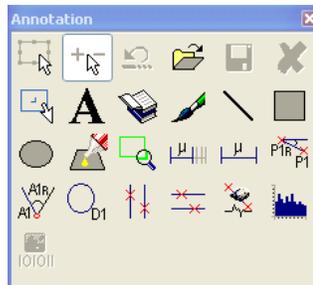
Creating a Spot Shot - for the final optimization of the aperture alignment and astigmatism correction

65. Once done, move to an unexposed region of the sample (preferably the far away from the scratch).
66. Zoom in until at a magnification of ~27kX – 30KX around 200nm scale bar.

67. **Quickly**, click on the **Spot Shot Icon** in the toolbar of the **SEM window** on the right monitor. Focus on the spot shot then click on the **4th** scan speed and then click **Pause** in the toolbar. The system will burn a dot into the resist for ~3 seconds.



68. Measure the width of the beam with the tools in the **Annotations window**. The dot should be circular with a diameter less than 100nm.

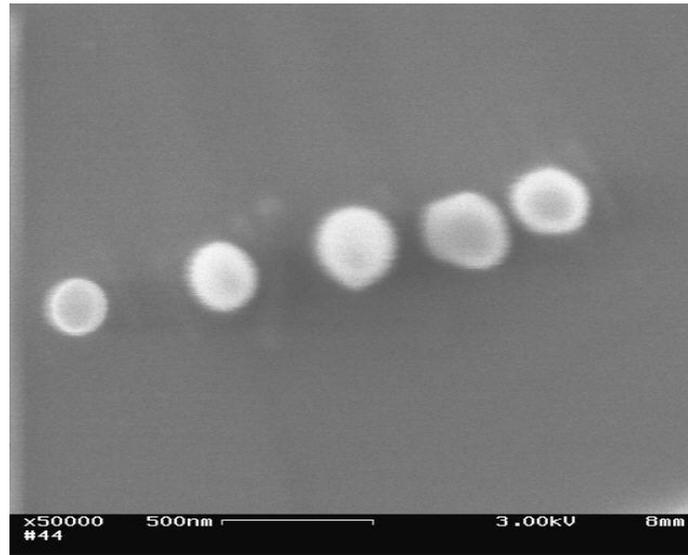


69. If you were not able to burn a visible contamination dot, click on the middle mouse button which will start the dot exposure. Wait for 1 minute while the dot is burned into the sample and click the middle mouse button again to end the dot exposure.

70. Move the stage and burn another spot shot. The new dot should be smaller since the focus has been improved.

If the dot is not round, apply the aperture alignment and then the astigmatism correction again, using this dot. Using such alternating routines, it is possible to achieve an ideal round dot, which grows within a few

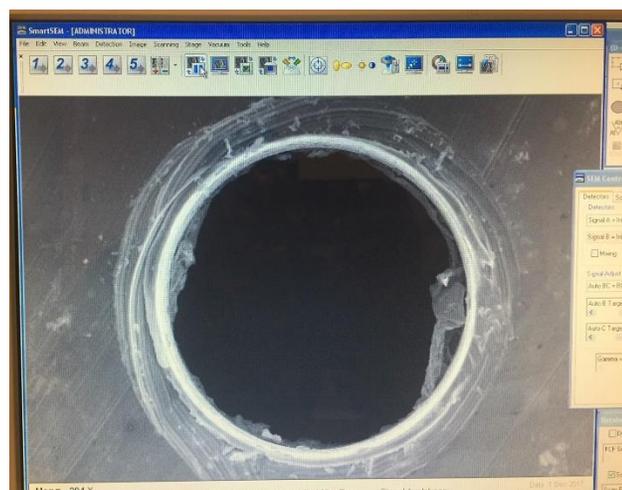
seconds of exposure time and shows perfect alignment. The optimization on this dot now provides the optimized conditions for a real exposure nearby.



An example of spot shots is shown.

Measuring E-beam Current

71. Under the **Command** tab in the **Stage Control** window, click **Free** and then click **Go** to move to the **Faraday Cup** on the stage.
72. Zoom out to the lowest magnification and focus. You will see a hole on screen. Zoom in on the hole to a magnification of >30KX. This is to ensure that all the electrons enter the **Faraday Cup**.



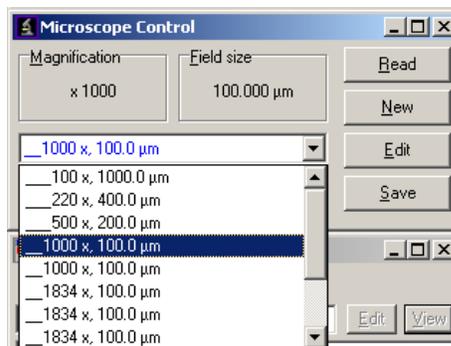
73. On the left monitor, Click **Measure** on the **Current** window to measure the beam current and record it along with the other required parameters in the logbook.



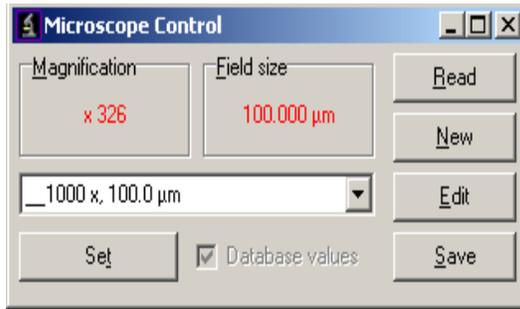
VI. Write field alignment

The laser-interferometric stage is the reference coordinate system. It is supposed to be a "perfect", x- and y-axes, exactly perpendicular, and of the same scale. The coordinate system for the e-beam deflection inside the column is not perfect and has long term drift in its components. The u- and v-axes are not perpendicular, nor parallel to either of the stage's x- or y-axes and they have different scaling. All these imperfections are compensated for in software with the Write Field Alignment procedure which minimizes the stitching error that comes from writing the pattern in parts. This procedure must be done prior to writing, since the long-term drift changes the compensation from day to day.

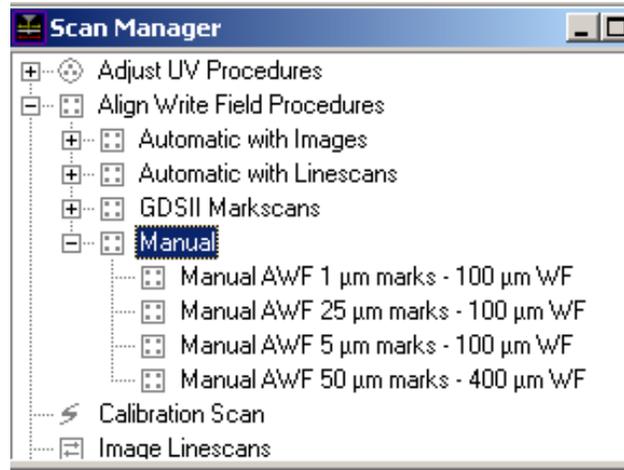
74. For un-patterned sample, align the WF to a particle with a sharp edge on the sample
- On the right monitor, find a particle with a sharp edge at $\sim 1\mu\text{m}$ scale bar.
 - In the **Microscope Control** window select **Magnification and Write field size 1000 X 100 μm** . It is possible to select another write field size, however, the larger the size, the lower the accuracy of the beam writing.



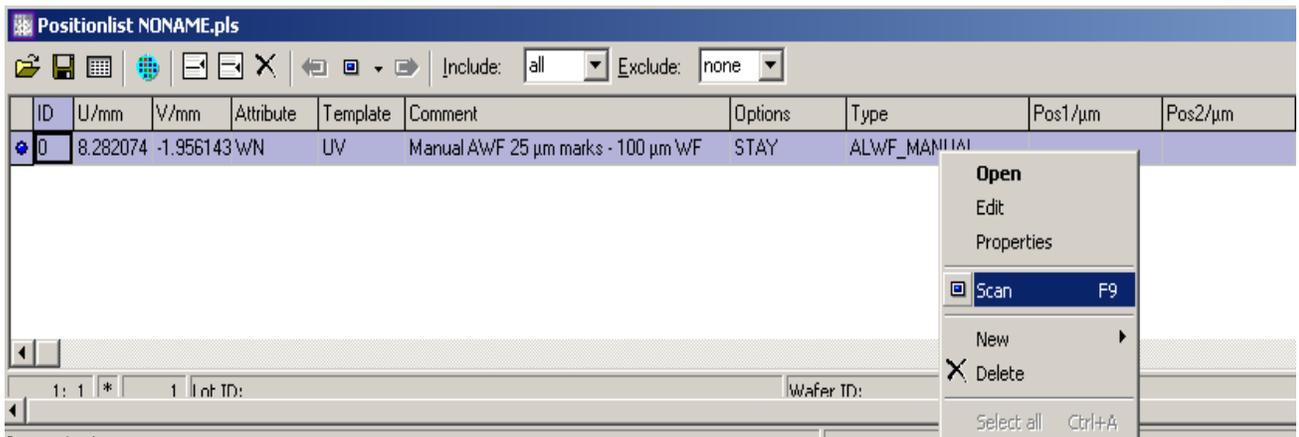
- Make sure the box labeled **Database Values** is checked. Click **Set** to confirm.



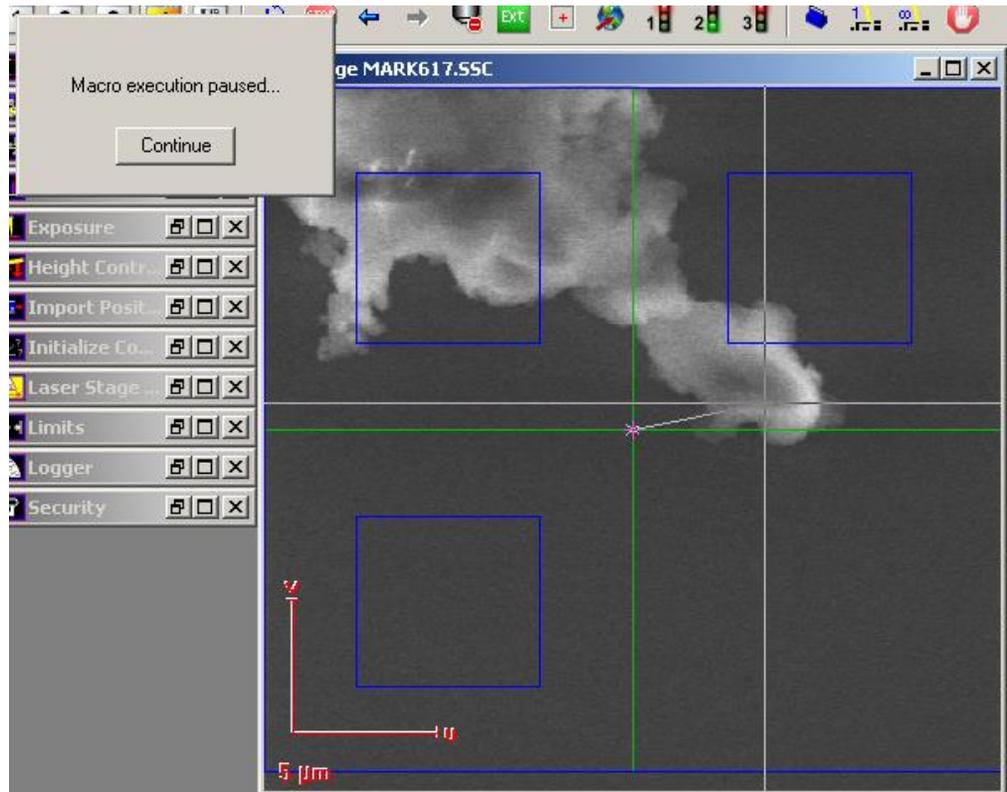
- d. Open the **Scan Manager** window. Select **Align Write Field Procedures** → **Manual** → **Manual AWF 25μm - 100μm WF**.



- e. On the right monitor, under the **SEM Control window** select the **Detector tab**. Under **Signal Adjust**, select **Auto BC OFF**.
- f. Drag and drop the file in part e into the **PositionList** window. Right click on it and select **SCAN** to perform the write field alignment. Delete any old files that were already there.



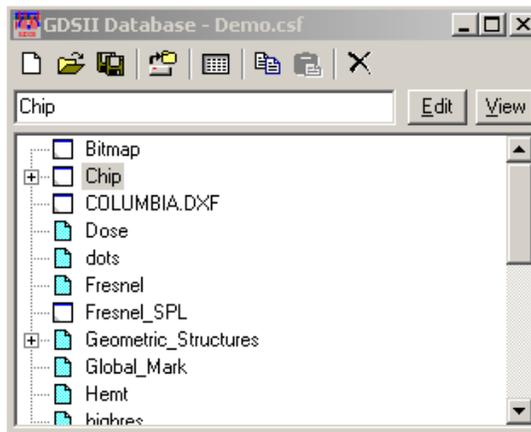
- g. A new window will pop up. On the left monitor, hold down the **Ctrl button and left click** and drag the center of the image to the sharp edge of the particle.



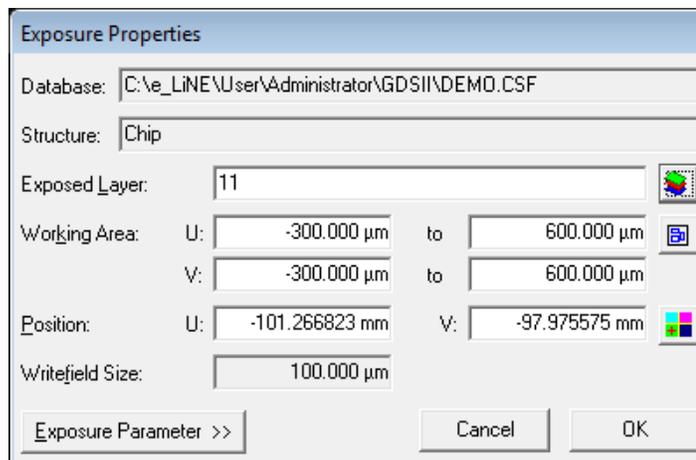
- h. Click **Continue** and repeat 'part h' twice. Click **Ok** when asked to accept the WF parameters.
- i. Repeat parts e – h for sequentially smaller marks: **Manual AWF 5μm - 100μm WF** and **Manual AWF 1μm - 100μm WF**.
- j. The correction value can be checked at c:\e_LiNe\Protocol\Protocol.html. For optimal stitching, final scan size should be $\leq 1\%$ of Write field size. (1 μ for 100μ WF.)

VII. Exposure

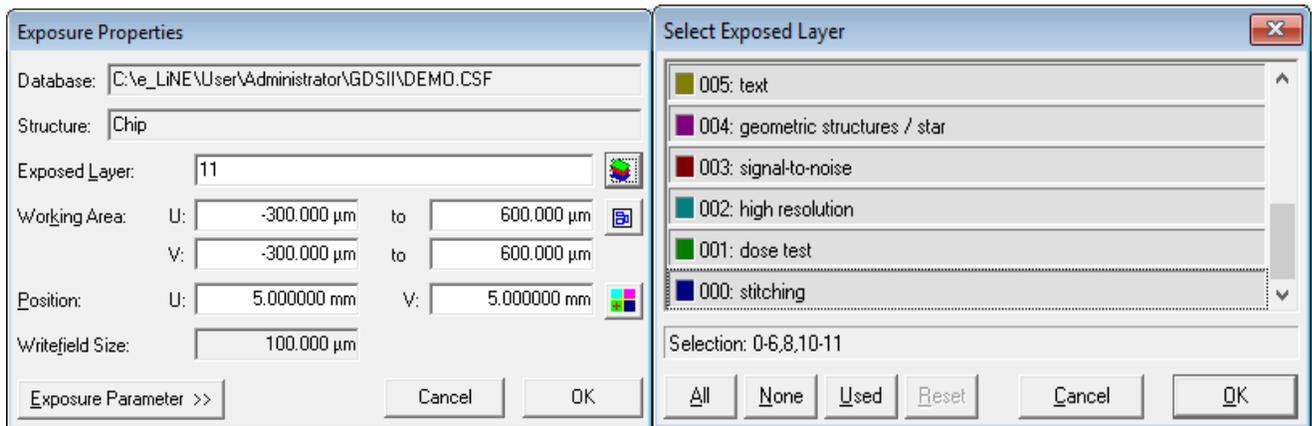
75. Open the pattern file you are going to write from **GDSII Database window**. For the training, open '**Demo.csf**' and click on the file name '**Chip**'



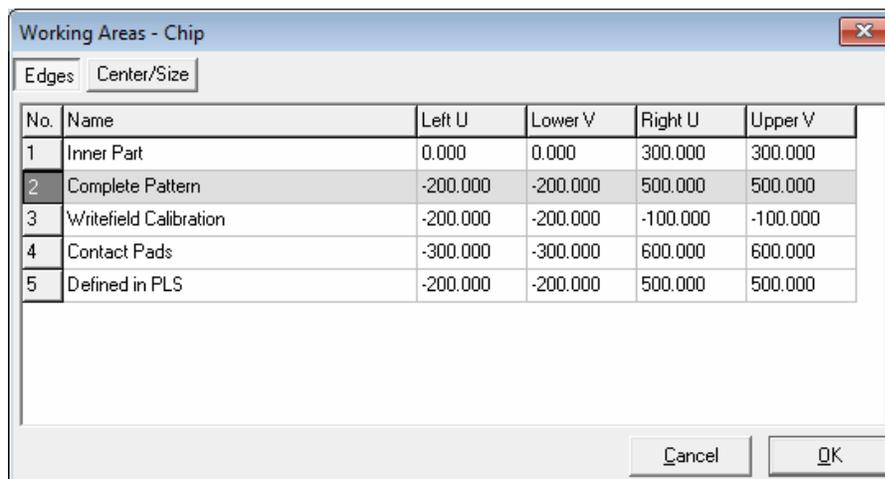
76. To find the layer on which the GDSII file is to be written, right click on the file name and select **Properties**. In the **GDSII Structure Properties** window, 'Used Layer' indicates the layer for writing this GDSII file. Select Layers 11.



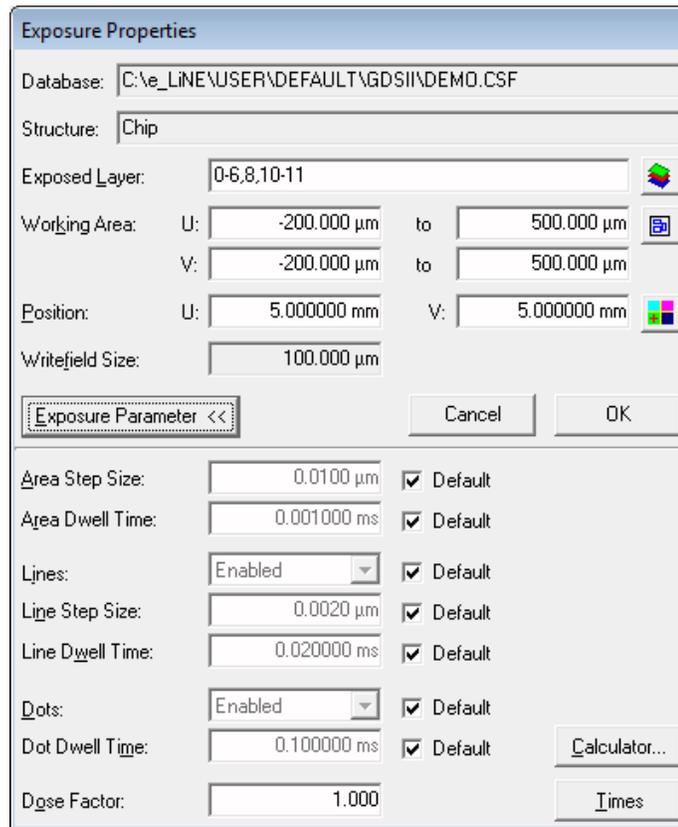
77. Drag and drop the **GDSII file** into the **POSITIONLIST** window. Right click on the file and select **Properties**.
78. In the **Exposure Properties** window, use the **Layer tool**  to select correct layers to expose. Click **OK**.
79. In the **Position section**, type in UV coordinates corresponding to center of the sample or wherever you would like to write.



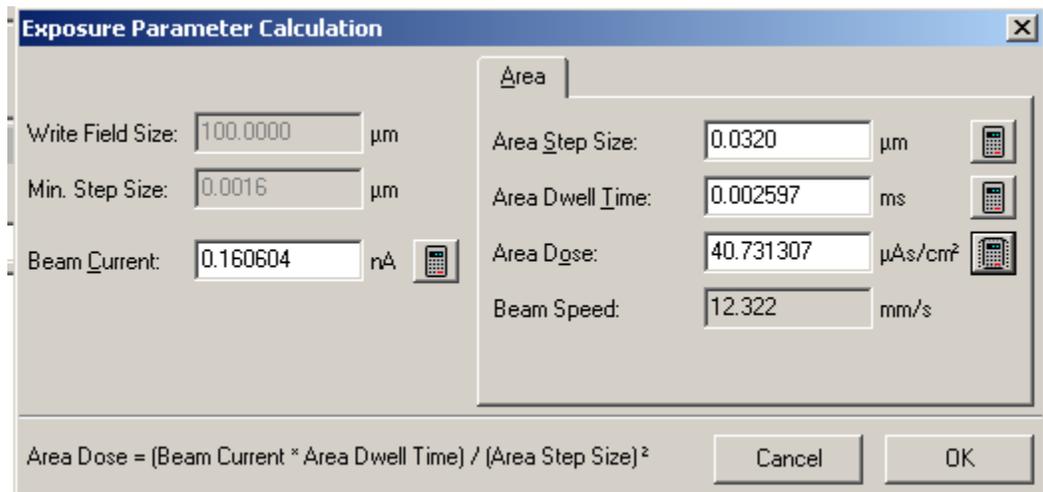
80. In the same dialog box click on the **Working Area icon**  and select the **Working Area 'Complete Pattern'** and click **OK**.



81. Click on **Exposure Parameters**.



82. Click on **CALCULATOR** to set up dosage according to the measured beam current.



83. Click **OK** to confirm. For reasonable results, the beam speed should not exceed 15 mm/s.

84. Click on the **Calculator icon** next to the area dose. You can change any other parameter to suit your needs but make sure to click the calculator icon of the other parameters to update them.

85. Calculation of the area dose follows the equation

$$\text{Area Dose} = \frac{(\text{Area Dwell Time}) \cdot (\text{Beam Current})}{(\text{Area Step Size})^2}$$

86. Click **OK** to confirm.

For example, if you use PMMA 950 k molecular weight, thickness 100 nm, and beam voltage of 10 keV, the area dose should be 100 $\mu\text{As}/\text{cm}^2$. Click on the Line. The corresponding Line dose should be of 300 pAs/cm, so you can calculate dwell time. Then click on the Dot. The corresponding Dot dose should be of 0.08 pAs /cm, so you can calculate dwell time.

87. Click the **TIMES** button at the bottom of the **Exposure Properties** window to estimate writing time.

88. Click **OK** on the **Exposure Properties** window to confirm the exposure parameters.

89. Right click on the GDSII file and click **SCAN** to perform the writing.

Developing the sample

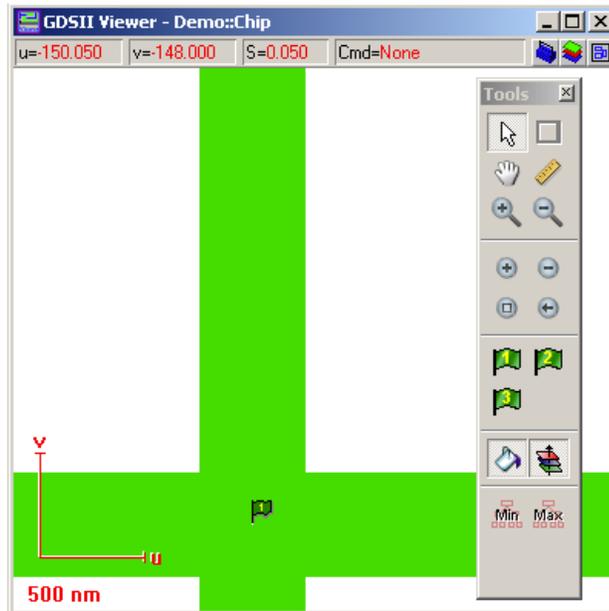
Unload the sample. Develop the resist according to its type, i.e. dipped into MIBK:ISO=1:3 developer for 30 seconds and immediately afterward for 15 seconds in isopropanol.

VIII. Mix & Match Exposure (3 – Point Alignment) for Pre-Patterned Samples

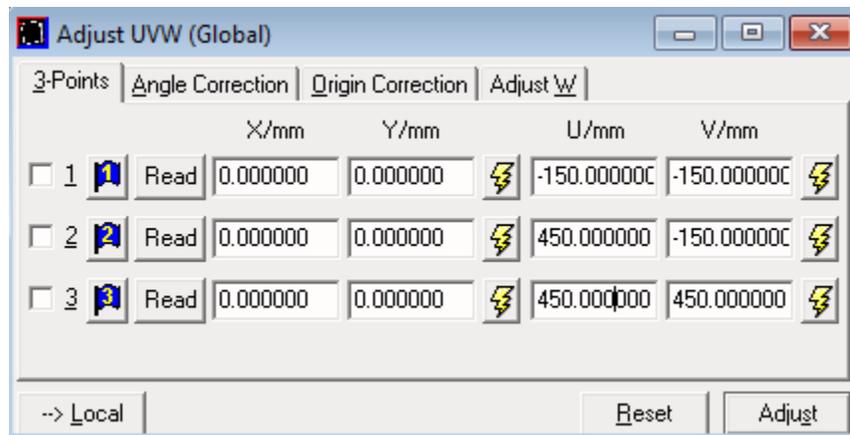
To perform mix and match exposure, you will have to perform the steps in sections 4,5, and 6 of this manual.

Task 1: Defining UV positions of marks

1. Open the GDSII Viewer with your corresponding pattern. In our example, open '**Demo.csf**' and '**Chip**'. Locate **mark 1** within your pattern. In our example the mark is located at U=V= -150 μm . Drag and drop the **green flag 1** onto **your mark 1**. The UV coordinates for mark 1 will now be displayed in the **Adjust UVW window** under the **3-Points** tab.



- Repeat the same procedure for **marks 2 and 3**. In our example, mark 2 is located at $U = 450 \mu\text{m}$ and $V = -150 \mu\text{m}$ and mark 3 is located at $U=V=450\mu\text{m}$. **Uncheck the boxes of all 3 positions in the 3-Points tab.**

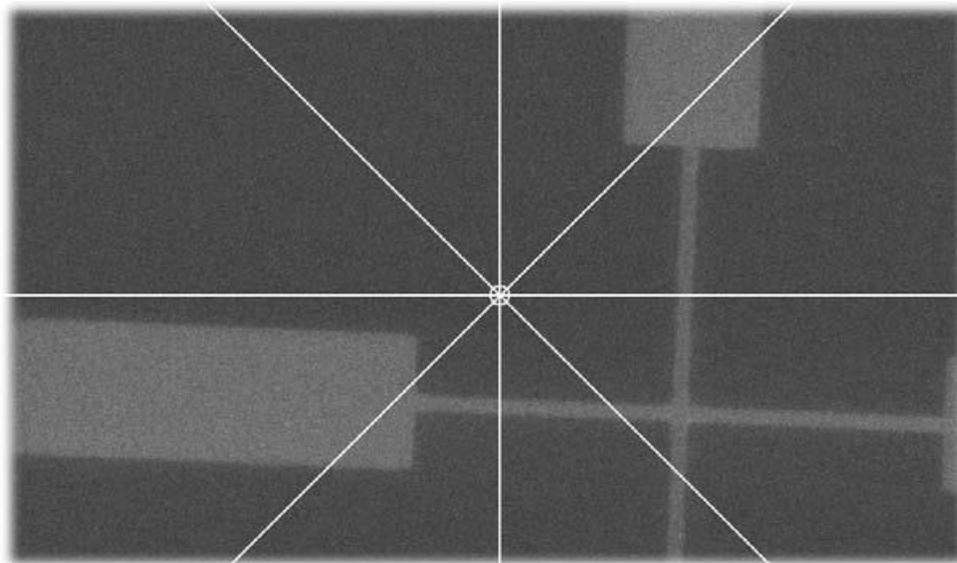


Task 2: Locating the first mark on the sample

- To find the first mark, in the **Stage Control window**, enter the value 5 mm for U and V. Click on Start.



4. On the right monitor select a magnification of 3000x. Click the **crosshair icon**  and turn on the beam. The first mark should now be visible.

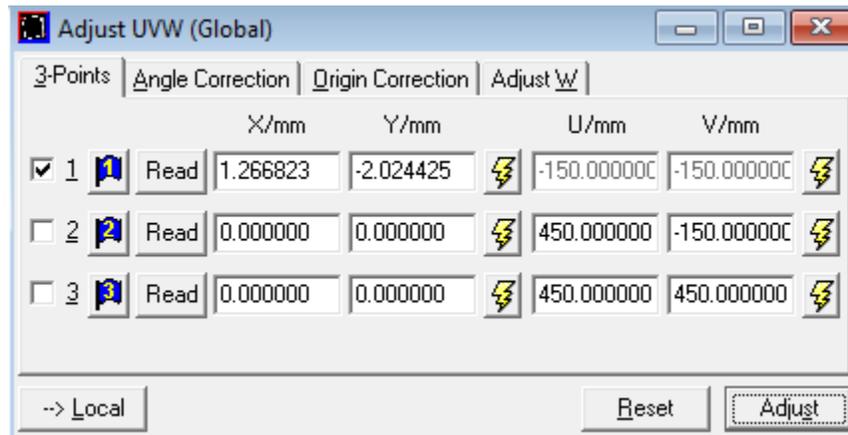


5. Using the joystick, move the crosshair over the mark then **switch off the beam**. The next task is to perform a 3-Point Adjustment.

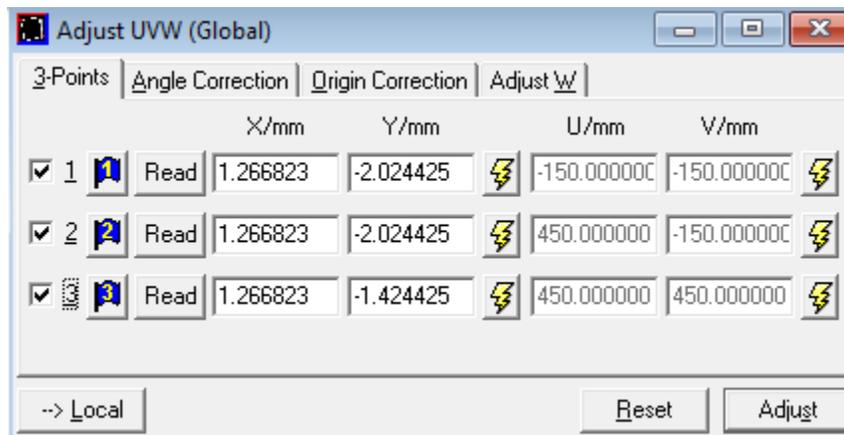
Task 3: 3-point adjustment

6. Open the **ADJUST UVW window** and select the tab, 3-Points.
7. Ensure that it is in mode **LOCAL**; if it is in mode GLOBAL, click on the button at the bottom of the window once to change it.
8. Click **Read** to update the current XY coordinates of the first mark position. Select the checkbox the same position. Click **Adjust** to confirm the position positions.

In this step, we have performed, in principle, an origin correction, this means that the origin of the coordinates system has been redefined.



9. Click on the lightning icon  of mark 2 related to the UV coordinates. This will move the stage to the second mark.
10. Select a high magnification again, (approximately 3000x) and repeat steps 4-8 for marks 2 and 3.

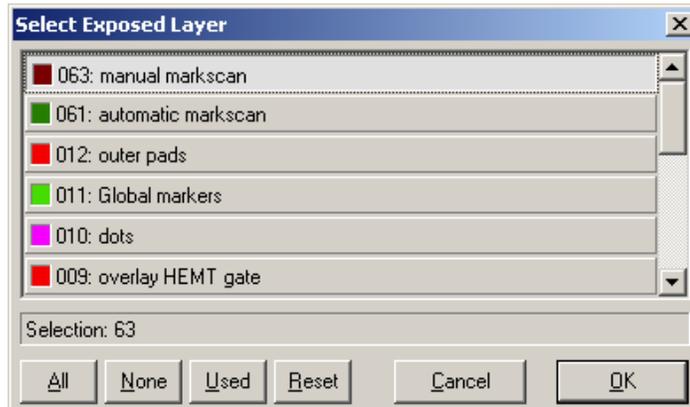


You may proceed to exposing the resist and writing your pattern after this step by skipping to Task 4 in this section. If you choose to do so, do not select layers 61 or 63 in step 38 in Task 4. However, this means the alignment is done with the user's approximated locations of his/her alignment keys, meaning accuracy of the writing will not be very good.

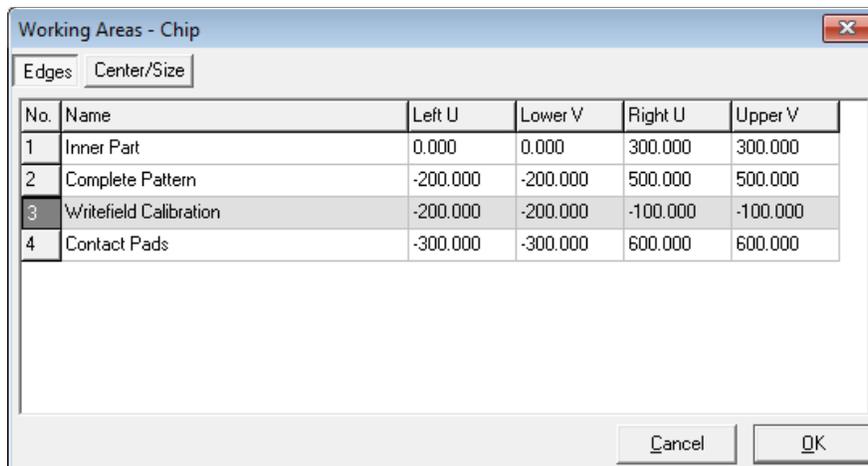
Semi-automated write field alignment

In several cases, you may not be required to set-up a fully automated write field alignment. For example, if only a small number of alignments are necessary, or difficult mark detection conditions exist, a semi-automated procedure is more appropriate. This procedure can save time and with the interaction of the operator, more reliable results can be achieved. In the following, we will describe the semi-automated procedure first to familiarize you with the concept. The next task will describe the automated procedure, which is more complex.

11. Move the stage back to the first mark.
12. In the **Microscope Control window** select **Magnification and Write field size 1000 X 100µm**.
13. Make sure the box labeled **Database Values** is checked. Click **Set** to confirm.
14. Select the structure '**Chip**' from the database **Demo.csf** and drag & drop it into the **Positionlist**.
15. Right click on the file name and select **Properties**. Click on the layer icon  and select layer 63.



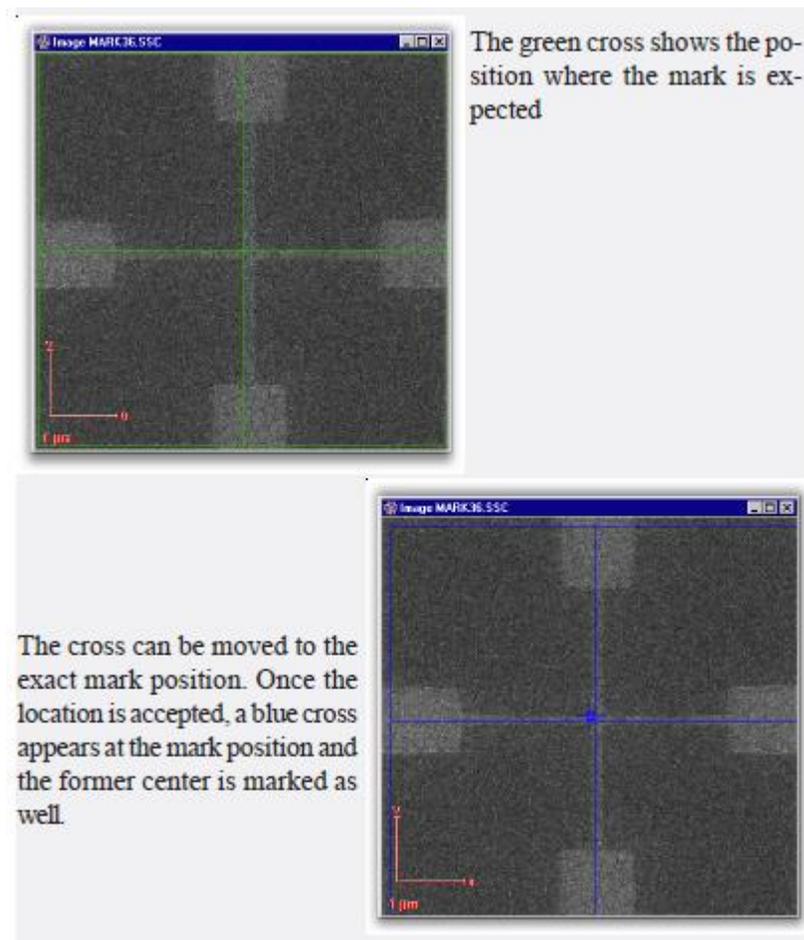
16. Click on the **Working Area icon**  and select the **Working Area 'Write field Calibration'** and click **OK**.



17. Click on the **ADJUST UV position** icon  in the **Exposure Properties** window. This command will use the pre-defined working area and the write field size to calculate the correct sample UV position.
18. In the **Positionlist window**, right click on the file and select **Scan**. The stage will now drive to the corresponding position and the exposure on Layer 63 will be initiated.

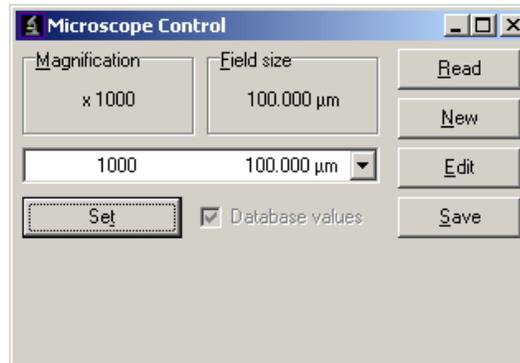
The software will generate the positionlist 'Align.pls'. The positionlist will be filled with the corresponding Marks scan. The scanning of the positionlist will start automatically and after the first image, the software will pause to await interaction with the user. The green cross displayed in the center of the image defines where the mark is expected. At this stage, the mark will probably not be at the center, but it can now be defined manually.

19. To define the position of the mark, hold down the **Ctrl button and left click** and drag the mark to center of the image. Click **Continue**.



Automated write field alignment

20. Move the stage back to the first mark.

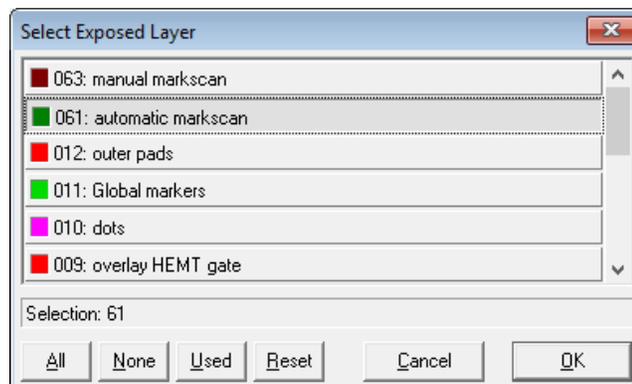


21. In the **Microscope Control window** select **Magnification** and **Write field size 1000 X 100µm**.

22. Make sure the box labeled **Database Values** is checked. Click **Set** to confirm.

23. Select the structure '**Chip**' from the database **Demo.csf** and drag & drop it into the **Positionlist**.

24. Right click on the file name and select **Properties**. Click on the layer icon  and select layer 61.



25. Click on the **Working Area icon**  and select the **Working Area 'Write field Calibration'** and click **OK**.

No.	Name	Left U	Lower V	Right U	Upper V
1	Inner Part	0.000	0.000	300.000	300.000
2	Complete Pattern	-200.000	-200.000	500.000	500.000
3	Writefield Calibration	-200.000	-200.000	-100.000	-100.000
4	Contact Pads	-300.000	-300.000	600.000	600.000
5	Defined in PLS	-200.000	-200.000	500.000	500.000

26. Click on the **ADJUST UV position** icon  in the **Exposure Properties** window. This command will use the pre-defined working area and the write field size to calculate the correct sample UV position.
27. In the **Positionlist window**, right click on the file and select **Scan**. The stage will now drive to the corresponding position and the exposure on Layer 61 will be initiated.

Exposure Properties			
Database:	C:\RAITH150\User\Andi\GDSII\DEMO.CSF		
Structure:	Chip		
Exposed Layer:	61		
Working Area:	U:	-200.000 μm	to -100.000 μm
	V:	-200.000 μm	to -100.000 μm
Position:	U:	-0.150000 mm	V: -0.150000 mm
	Writefield Size:	100.000 μm	
Exposure Parameter >>		Cancel	OK

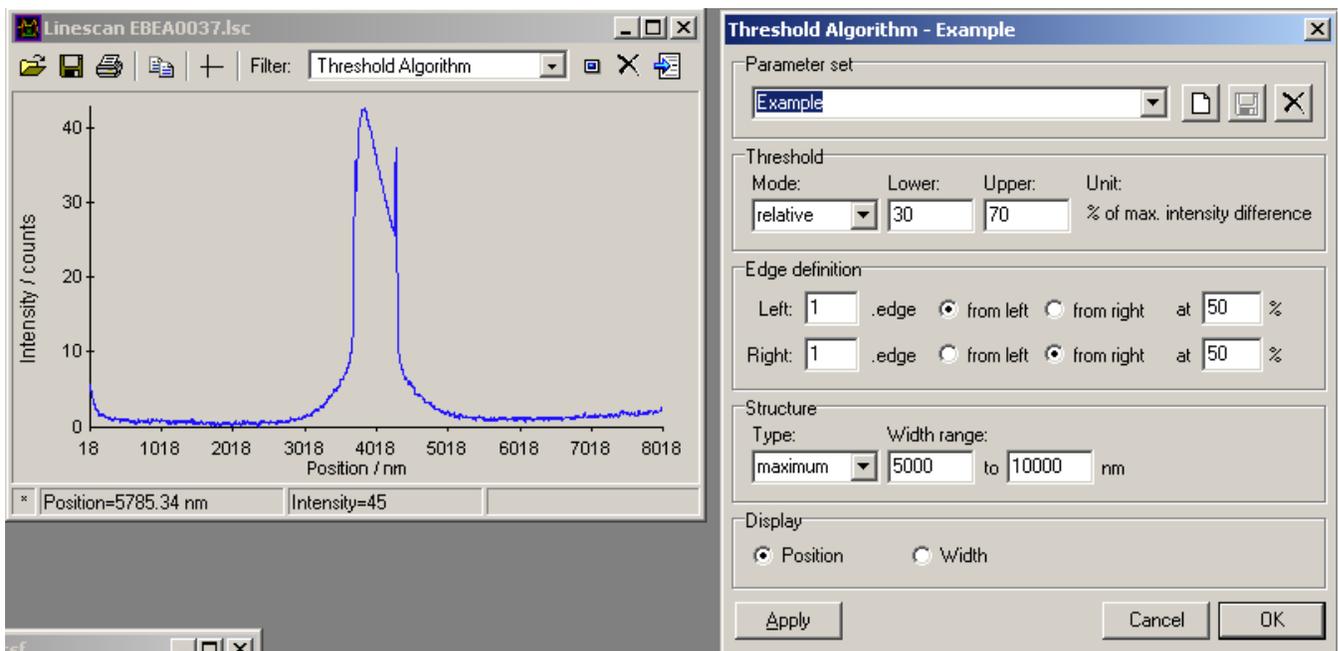
The software will open a new positionlist, called 'Align.pls'. A set of mark detections is stored within this positionlist and executed automatically, and we will be able to observe its progress. Several Line scans will be displayed, but it is unlikely that there will be a valid parameter set for mark detection within the line scanning and many errors will be shown. Once the execution of the positionlist is completed, the software will close 'Align.pls' which will close all the Line scans. The next step is to find a parameter set such that during the automated align write field procedure, the software will be able to detect all the marks.

28. Go to **File** → **Open Positionlist** and open the positionlist **'Align.pls'**, which has been stored in your user directory **'Data'**.

ID	U	V	Attribute	Template	Comment	Options	Type	Pos1	Pos2
0	-0.036500	-0.040000	LE*	dUV	Autoalign V1	STAY;	RAUTOSCAN	-40.597	-39.398
1	-0.040000	-0.036000	LS*	dUV	Autoalign U1	STAY;	RAUTOSCAN	-41.194	-38.797
2	-0.036500	0.040000	LE*	dUV	Autoalign V2	STAY;	RAUTOSCAN	39.403	40.602
3	-0.040000	0.044000	LE*	dUV	Autoalign U2	STAY;	RAUTOSCAN	-41.194	-38.797
4	0.043500	-0.040000	LS*	dUV	Autoalign V3	STAY;	RAUTOSCAN	-40.597	-39.398
5	0.040000	-0.036000	LE*	dUV	Autoalign U3	STAY;	RAUTOSCAN	38.806	41.203
6	0.043500	0.040000	LE*	dUV	Autoalign V4	STAY;	RAUTOSCAN	39.403	40.602
7	0.040000	0.044000	LS*	dUV	Autoalign U4	STAY;	RAUTOSCAN	38.806	41.203
8	0.000000	0.000000	h	dUV	Alignment m	STAY;	MACRO		

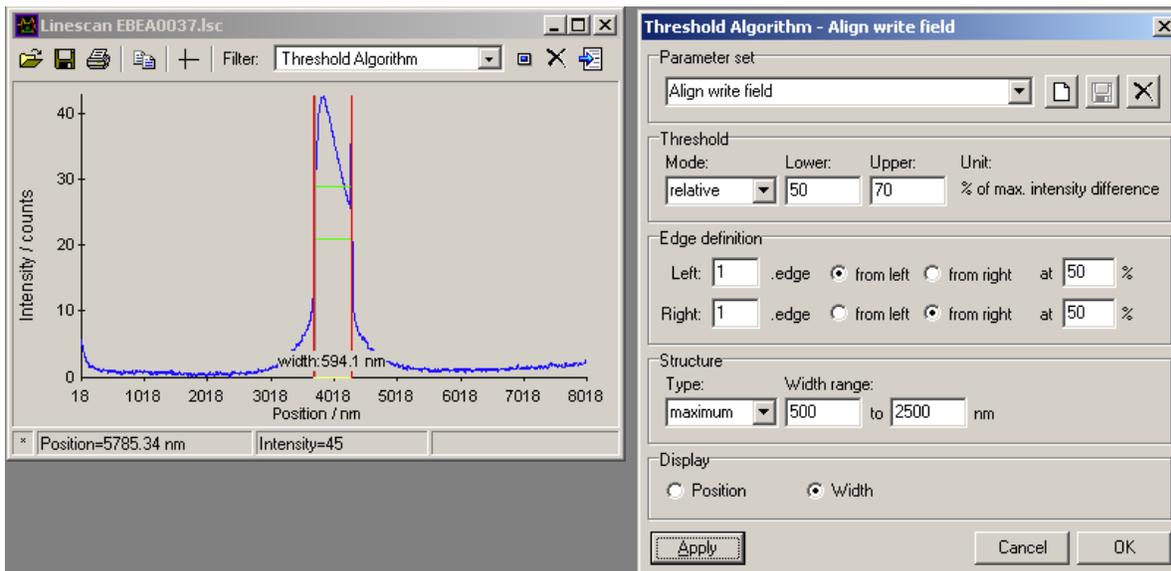
As we have not completed the optimization yet, the light is displayed in red, since the Line scan could not be completed successfully. The corresponding Attributes show LE meaning Line scan error.

29. Double click on one of the lines with an error and the corresponding Line scan will be opened. Select the **'Threshold Algorithm'** from the dropdown list and click the **Apply** button.

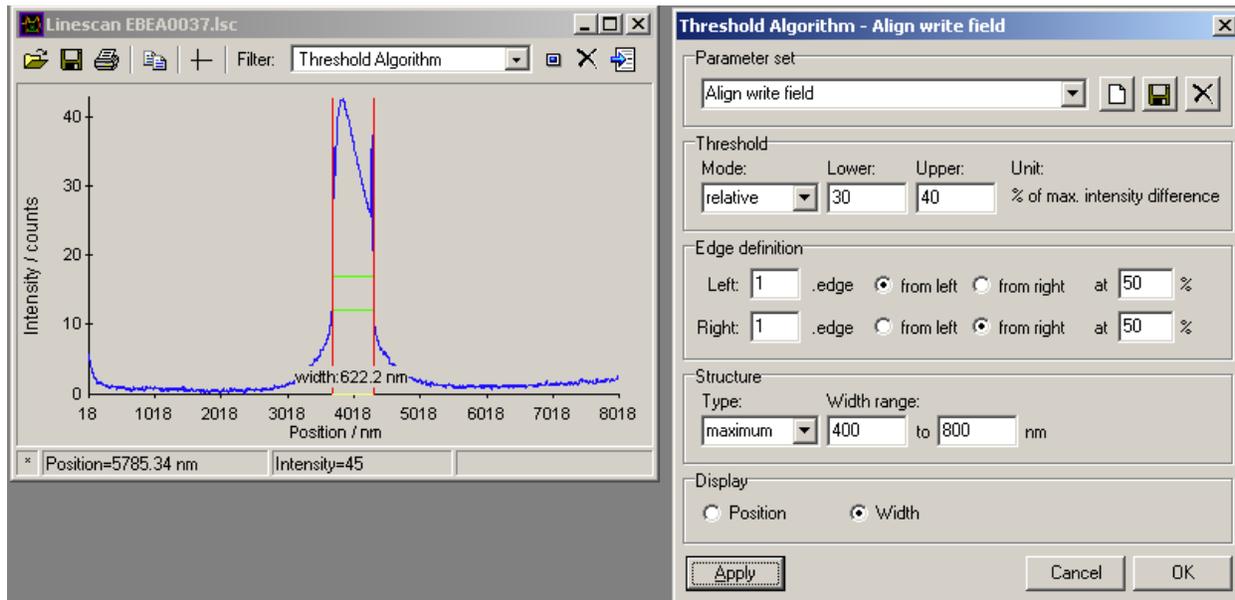


30. Select the parameter called 'Align Write field' from the dropdown list and click **Relative**. For **Lower** select **50**, for **Upper**, select **70**. For **Edge Definition**, select **1st edge from left** and **1st edge from right**.
31. For both edges select **50%**. For **Structure** select type **Maximum** and a **Width range** from **500 nm** to **2500nm**. Click **Apply**.

The software now applies the threshold algorithm with the parameter set chosen to the corresponding Line scan. If you were able to detect a mark, then the corresponding result will be displayed in the line scan by plotting red bars and a line width bar. The next step is to optimize the parameter set.



32. In our example, the width was 594 nm, which means that we restrict the width range. In the **Parameter Set window**, select a **structure width range of 400-800**. Click **Apply**.
33. Try reducing the thresholds for **Lower** to **30** and **Upper**, to **40**. Click **Apply**.



As we have now defined the parameter set. The software will now be able to detect the line successfully in the Threshold Algorithm window. The next step is the verification of the parameter set.

34. Click **OK** in the **Parameter Set** window. You may close **Line scan window** but leave the **Positionlist 'Align.pls'** open.
35. In the **Positionlist 'Align.pls'**, in the menu bar, go to **Scan > All**. The software will start scanning the positionlist again.
36. After the **Positionlist 'Align.csf'** has been performed successfully, close the window.

If the positionlist could not be performed successfully, you will need to change the parameters for the Threshold Algorithm.

Task 4: Exposure

37. Select the first **Positionlist** file. Right click and select **Properties**.
38. Now select the layers to be exposed. Click on the **Layer icon**  and select layers 7 and 9. Also, depending on the type of alignment you want to do, semi-automated or automated, select 61 or 63.
39. Click **OK**. Click on the **Working Area**  icon and select **Working Area, 'Complete the Pattern'**. Click **OK**.
40. Click on the **ADJUST UV position** icon  in the **Exposure Properties** window. This command will use the pre-defined working area and the write field size to calculate the correct sample UV position.

41. Click on **Exposure Parameters**, which will give you access to the complete set of exposure parameters, which are disabled, prior to selecting calculator.
42. Click on **CALCULATOR** to set up dosage according to the measured beam current.
43. Click on the **Calculator icon** next to the area dose. You can change any other parameter to suit your needs but make sure to click the calculator icon of the other parameters to update them.
44. Click **OK** to confirm.
45. Execute the **Positionlist**. Depending on if you have chosen automated procedure (Layer 61) or semi-automated procedure (63), user interactions might be required.

IX. Appendix

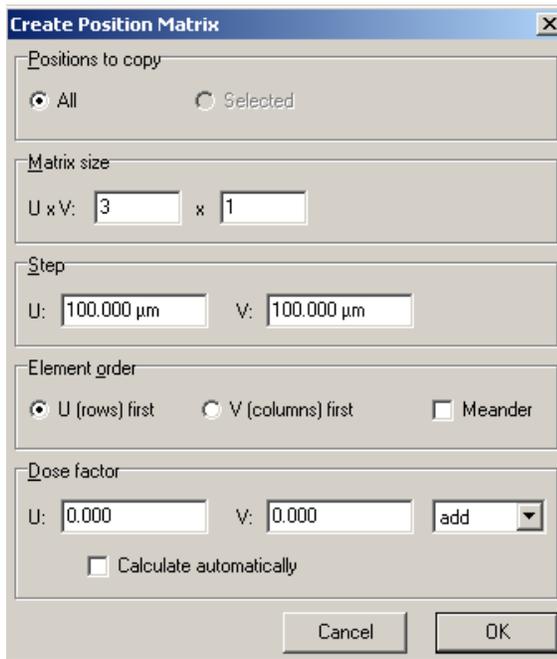
Dosage Testing

If the correct dose for your resist is known, it is not necessary to follow this task. If the correct dose is not known, perform exposure of the same pattern with different doses to reduce the dose parameter range values.

1. You can create copies of your pattern for dosage tests by clicking **FILTER** then **MATRIX COPY** from main menu.



2. You can set the spacing between copies and the dosage for each new copy.



Note that you can select the mathematical function (add, multiply, etc.) you want your dose factor to follow for augmenting the dosage.

- The **PositionList** window will then look as such. You can change the dose factor for each file.

ID	U/mm	V/mm	Attribute	Template	Comment	Options	Type	Pos1/µm	Pos2/µm	Pos3/µm	Link	File	Layer	DoseFactor	Time	MarkSeq
0	-62.97315	25.88516	>N	UV	Boxes		EXPOSURE	50.000	50.000				%Root%	1.000		
1	-62.97315	25.88516	>N	UV	Boxes		EXPOSURE	50.000	50.000				%Root%	1.000		
2	-62.77315	25.88516	>N	UV	Boxes		EXPOSURE	50.000	50.000				%Root%	1.000		

Checking the leveling limits – after Spot Shot

It is likely that your sample surface is tilted to the beam. This can be checked by the following tasks, but this task is not necessarily required prior to an exposure.

- Switch to a lower magnification and move the stage for a relatively long distance, i.e. 1 mm. Ensure that you notice the direction of movement to relocate the previous contamination dots.

2. Burn another dot and view the result. This dot now is likely to be larger than the previous one, but this time the focus adjustment should be sufficient for the optimization. It should not be necessary to perform the Aperture Alignment and Astigmatism correction again.
3. Perform some experiments to establish the stage travel distance, at which you need to refocus the sample surface. To improve the leveling of small samples, it is recommended to use two opposite clamps.

X. References

- [1]. E-Line Software Operatonal Manual. © 2005 by Raith GmbH. All rights reserved.
- [2]. Li Pengcheng. A Review of Proximity Effect Correction in Electron-beam Lithography. Department of Electrical and Computer Engineering, Auburn University, Auburn, AL, USA.
- [3]. Liljeborg, A. (n.d.). Raith 150 E-beam Lithography Software. Retrieved July 12, 2017, from Albanova Nanofabrication Facility, Albanova University, Stockholm, Sweden
- [4]. http://www.nanophys.kth.se/nanophys/facilities/nfl/manual/index.html#_Intro
- [5]. <http://www.nanophys.kth.se/nanophys/facilities/nfl/manual/raith-v-5.0/overv.html>