

114 user videos

GDA setting and scanning



Setting up the GDA session

GDA is continuously evolving, so in order to get the latest release & updates, type: 'gdaclient --reset' in a terminal at the beginning of your experiment (as shown below), to launch the more updated version

If the GDA freezes during the beamtime, you can close it (and the Log Panel), and just type: 'gdaclient' for re-launching it or the full 'gdaclient --reset' for a new reset

A screenshot of a terminal window titled 'FedID@i14-ws002:~'. The window has a menu bar with 'File', 'Edit', 'View', 'Search', 'Terminal', and 'Help'. The terminal prompt is 'FedID@i14-ws002 ~]\$' and the command 'gdaclient --reset' has been entered.

```
FedID@i14-ws002:~  
File Edit View Search Terminal Help  
FedID@i14-ws002 ~]$ gdaclient --reset
```

A more comprehensive restart may be needed if the GDA refuses to work, which can be triggered by typing 'gda servers', but please inform your local contact before doing so

Setting up the GDA session

Data Acquisition Client - Beamline I14 - 9.29.0

File Tools Map Detector Window Help

Send Feedback Live Background XY Scan Plot Scan Type Run

Mapped Data Search:

Map

Mapping Experiment Setup Standards Scans Custom script

Configure Beamline Configure Focus

Script Files

Other Scan Axes

dcm_energ 13.000

Detectors

Xspress3 software 0.1

XRD/XRF 0.01

XRF/Eiger imaging 0.01

Eiger Imaging 0.001

XRF scanning 0.01

XRF/Imaging 0.01

Map points: 25 Total exposure time: 00:00:00
Smallest steps: X = 0.001250; Y = 0.001250; Absolute = 0.001250

Queue Scan

Jython Console Queue Live Stream

```
Setting up alignment tools
Setting up GDA XANES scan
Setting up sparse xanes scan
Setting up Ptychography scan
Exporting dcm_energ
Initialising detectors...
Error initialising detector Excalibur
Initialising array plugin for Merlin: ad_base_pv = BL14I-EA-DET-03:DET: ndarray
Using ImageMode to take one image
Initialising array plugin for Xspress3: ad_base_pv = BL14I-EA-XSP3-01: ndarray
Using ImageMode to take one image
Error initialising detector Xray Eye
Detector initialisation complete
Defining shutter controls
Initialisation Complete
>>>
```

Status - user x

Machine

Ring current 298.98 mA

Time to refill 168 s

Detector Cover

Position 19 mm

Unknown

Beamline

ID Gap 5.82 mm Bragg 6.307 degrees

Energy 18.001 KeV No beam

OH1 Shutter State Open

OH2 Shutter State Open

OH3 Shutter State Open

EH2 Nano Shutter Processing State Closed Processing Running

Open

Detector Data

Live Controls

Stage controls

Sample X	Sample Y	Sample Z
0.19993 mm	-0.59771 mm	-0.50230 mm
- 0.025 +	- 0.025 +	- 0.025 +
Stop	Stop	Stop

Endstation configuration

Run Ready

Watchdogs

beam_available_watchdog topup_watchdog

DCM energy

DCM energy 18.001 keV

- 0.1 +

Stop

41.083, 15.574

gqz18237 Baton held No Scan running

No Script running Stop All

gqz18237@i14-ws002:~ GDA Log Panel Data Acquisition Client - Beamline...

Setting up the GDA session

The 'Endstation configuration' menu at the centre of the screen would prepare the instruments accordingly:

- **Sample transfer:** Detectors out of the way, safe position for the users to go inside the hutch
- **Reset stages:** Automatically reset the stages for an accurate positioning (use after every sample change)
- **Microscope:** Move the microscope at the back of your sample, looking for the focus position
- **XRF/Imaging:** Place the Merlin detector at the back of the sample for phase contrast imaging, detector cover out of the way, preparation to allow beam on
- **XRD/XRF or XRF/Eiger:** Similar to above but placing the Excalibur detector for XRD or the Eiger in position

The screenshot displays the GDA software interface. On the left, there are two plot windows: 'Map' and 'Detector Data', both showing a grid with axes from 0 to 100. The main window is titled 'Mapping Experiment Setup' and contains several panels. The 'Configure Beamline' panel shows 'Script Files' and 'Other Scan Axes' with a 'dcm_enrg' field set to 13.000. The 'Detectors' panel lists various detectors with checkboxes and values: Xspress3 software (0.1), XRD/XRF (0.01), XRF/Eiger imaging (0.01), Eiger imaging (0.001), XRF scanning (0.01), and XRF/Imaninn (0.01). Below this is a 'Queue Scan' button. The 'Jython Console' at the bottom right shows a list of status messages, including 'Setting up alignment tools', 'Setting up GDA XANES scan', 'Setting up sparse xanes scan', 'Setting up Ptychography scan', 'Exporting dcm_enrg', 'Initialising detectors...', 'Error initialising detector Excalibur', 'Initialising array plugin for Merlin: ad_base_pv = BL14I-EA-DET-03:DET: Using ImageMode to take one image', 'Initialising array plugin for Xspress3: ad_base_pv = BL14I-EA-XSP3-01: r Using ImageMode to take one image', 'Error initialising detector Xray Eye', 'Detector initialisation complete', 'Defining shutter controls', and 'Initialisation complete'. The 'Run' button is highlighted with a red dashed box, and a red arrow points to it from the text 'Remember to wait until the symbol "Ready" appears after each selection (or look at the progress messages at the jython console)'. A blue arrow points from the text 'Click "Run" after selecting your preferred scripted position' to the 'Run' button.

- Click "Run" after selecting your preferred scripted position

- Remember to wait until the symbol "Ready" appears after each selection (or look at the progress messages at the jython console)

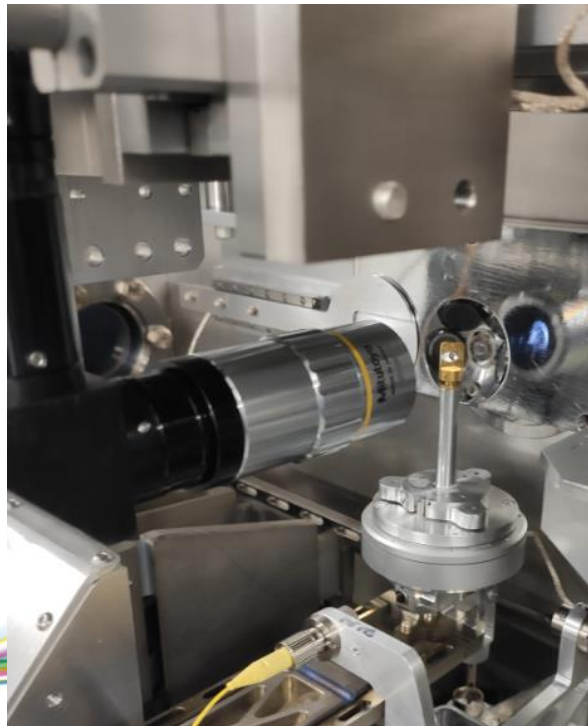


Setting up the GDA session

The 'Endstation configuration' menu at the centre of the screen would prepare the instruments accordingly:

- **Microscope:** Move the microscope at the back of your sample, waiting until the completion message appears at the jython console (or until you can see the camera stops through the webcams inside the EH2)

- At the 'Live Stream' tab, the "sample microscope camera" can be opened by double-clicking or selecting connect.
- That would open a microscope tab at the top-centre (red-ellipse), in which the exposure time (0.01 below) may be adjusted to increase/decrease the brightness of the view and start/stop the camera using the symbols.
- Once you are looking at the live view, the X,Y, Z stages should be moved using the differential value below (+ or -) until the region of interest is located at the cross displaying on the camera view.



The screenshot displays the GDA software interface. The top window, titled 'sample_microscope_cam: MJPEG', shows a live video feed of the microscope camera. The exposure time is set to 0.01. Below the video feed, the X and Y coordinates of the sample are shown as 11.44 and 11.74, respectively. The 'Live Controls' panel on the right shows the stage positions: Stage X is 11.800 mm, Stage Y is 1.0000 mm, and Stage Z is -9.0200 mm. The 'Endstation configuration' panel shows the system is 'Ready'. The 'Jython Console' at the bottom shows the 'Sample microscope camera' selected.

Setting up the GDA session: Mapping

The 'Mapping Experiment Setup' tab allows controlling how to submit all the analysis requested at I14:

- **Detectors:** The small gear would allow to "clean" the area, by selecting only the detectors in use (XRF/Imaging would trigger the XRF detector at backscatter position and the Merlin photon counting detector (at transmission geometry))

The screenshot displays the 'Mapping Experiment Setup' window. A 'Choose from available detectors' dialog box is open, showing a list of available detectors on the left and a 'Selected' list on the right. 'XRF/Imaging' is selected in the 'Selected' list. In the main window, the 'Detectors' section lists various detector types with their respective exposure times. A small gear icon next to the 'XRF/Imaging' entry is highlighted with a red dashed box. A red arrow points from the text in the list to this gear icon. Another red arrow points from the gear icon to the 'Queue Scan' button. A blue arrow points from the 'Mapping Experiment Setup' title bar to the 'Configure Beamline' button. The 'Queue Scan' button is highlighted in orange. The 'Jython Console' at the bottom shows the following output:

```
Setting up alignment tools
Setting up GDA XANES scan
Setting up sparse xanes scan
Setting up Ptychography scan
Exporting dcm_engr
Initialising detectors
```

Setting up the GDA session: Mapping

The 'Mapping Experiment Setup' tab allows controlling how to submit all the analysis requested at I14:

- Ensure that the desired detector is selected

Then select the value for the dwell time (scanning time per point). Usually 15 ms, but may need higher values for low-conc samples

- Switch the scan path to "Raster"

Subsequently selecting the desired resolution below as sampleX and sampleY Step (higher ~300-500 nm values are adequate for coarse scanning, while 50-100 nm will be for high-resolution maps)

- Select the mapping (X,Y) size

About 50 micron is good for low-resolution then adjust to lower values for high-res

- Set the "Sample name" for clarity

- The 'Total exposure time' will provide an estimation on how long the scan proposed is going to take

The screenshot shows the 'Mapping Experiment Setup' interface with several key elements highlighted by colored arrows:

- Other Scan Axes:** A checkbox for 'dcm_enrg' is set to 13.000.
- Detectors:** The 'XRF/Imaging' detector is selected with a dwell time of 0.015.
- Region shape:** Set to 'Centred Rectangle'.
- Scan path:** Set to 'Raster'.
- SampleX Centre:** 0.5 mm
- SampleX Step:** 100 nm
- SampleX Range:** 5 µm
- SampleY Centre:** 0.5 mm
- SampleY Step:** 100 nm
- SampleY Range:** 5 µm
- Alternating:** Unchecked
- Continuous:** Checked
- Orientation:** Horizontal
- Sample Name:** An empty text field.
- Map points:** 2,601
- Total exposure time:** 00:00:39
- Smallest steps:** X = 0.0001000; Y = 0.0001000; Absolute = 0.0001000
- Queue Scan:** A red button to start the scan.

Setting up the GDA session: XRF windowing

The 'Mapping Experiment Setup' tab allows controlling how to submit all the analysis requested at I14:

- **Processing:** The 'Add Processing' button allows selecting some automatic postprocessing of the data.

- At the 'Specify application and setup config', the 'i14-xrf' option can be selected

The screenshot shows the 'Mapping Experiment Setup' dialog box with the 'Processing Template and Detector Selection' section. The 'Specify application and setup config' radio button is selected. The dropdown menu for 'Specify application and setup config' is open, showing a list of options: beam_known, beam_unknown, dawnlegacy, dawn, dpc, i14-xrf (highlighted with a blue dashed box), jupyter, jupyter-live, ptyypi14, savu, xrd, and xrf_windowing. A blue arrow points from the text above to the 'i14-xrf' option. The 'Add Processing...' button is highlighted with a red dashed box, and a red arrow points from the text above to it. The background shows the 'Mapping Experiment Setup' window with various parameters like 'dcm_enrg' and 'Detectors'.

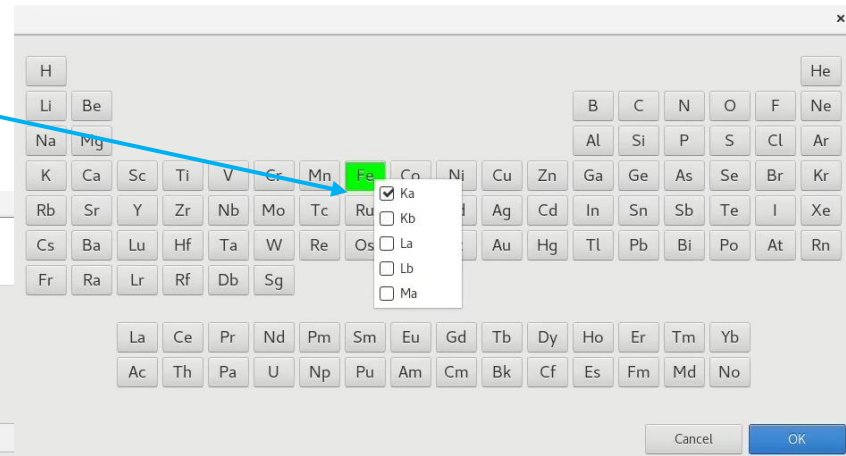
Setting up the GDA session: XRF windowing

The 'Mapping Experiment Setup' tab allows controlling how to submit all the analysis requested at I14:

- **Processing:** The 'Add Processing' button allows selecting some automatic postprocessing of the data.

The 'i14-xrf' template would allow some live visualisation of the data

- Change the 'Width' value to 20, and then click at the "XRF" button
- Then select the electronic transition to be displayed for the targeting elements
- Click "Finish"



Processing Template and Detector Selection

Select the processing template file to use and the detector to apply it to.

Detector: Xspress3 software

Create a new processing file from a template:

Processing Template File: xrf_windows.nxs

Use an existing processing file:

Processing File:

Specify application and config. file:

App Name:

Config File:

Specify application and setup config:

i14-xrf XRF element window integration

Name	Value	Unit
Element List		XRF
Width	20	

< Back Next > Cancel Finish

Setting up the GDA session: Mapping

The 'Mapping Experiment Setup' tab allows controlling how to submit all the analysis requested at I14:

- **Processing:** The 'Add Processing' button allows selecting some automatic postprocessing of the data.

The 'i14-xrf' template would allow some live visualisation of the data

- The corresponding processing chain will be selected by default, which could be discarded by unclicking the small square at the left

- If the detector is in place (look info advancing two more slides), you could use 'Queue Scan' to submit a singular scan in the sample X,Y range selected

(Note: If the beam is OFF the 'Queue Scan' button will be red-coloured, meaning that it need to be turned ON before submission, which will happen automatically when selecting the detector)

- ✓ An autogenerated processing chain will be displayed
When selected, it will generate a scan in the /mgxxxx-y/processed/ directory to investigate the data.
Also the same scan will be loaded back in the "Mapped Data" space at the left of the GDA console, for a live assessment

Mapping Experiment Setup Standards Scans Custom script

dcm_energ 13.000

Detectors

XRF/Imaging 0.015

Region shape: Centred Rectangle Scan path: Raster

SampleX Centre 0.5 mm SampleX Step 100 nm

SampleX Range 5 µm SampleY Step 100 nm

SampleY Centre 0.5 mm Alternating

SampleY Range 5 µm Continuous

Orientation Horizontal

Sample Name Test_sample Edit metadata...

Processing Add Processing...

App	Name
<input checked="" type="checkbox"/>	i14-xrf {"element_list":["Fe-Ka"],"window_width":20}

Map points: 2,601 Total exposure time: 00:00:39
Smallest steps: X = 0.0001000; Y = 0.0001000; Absolute = 0.0001000

Queue Scan

Jython Console x Queue Live Stream

i14-248220_xrf.nxs

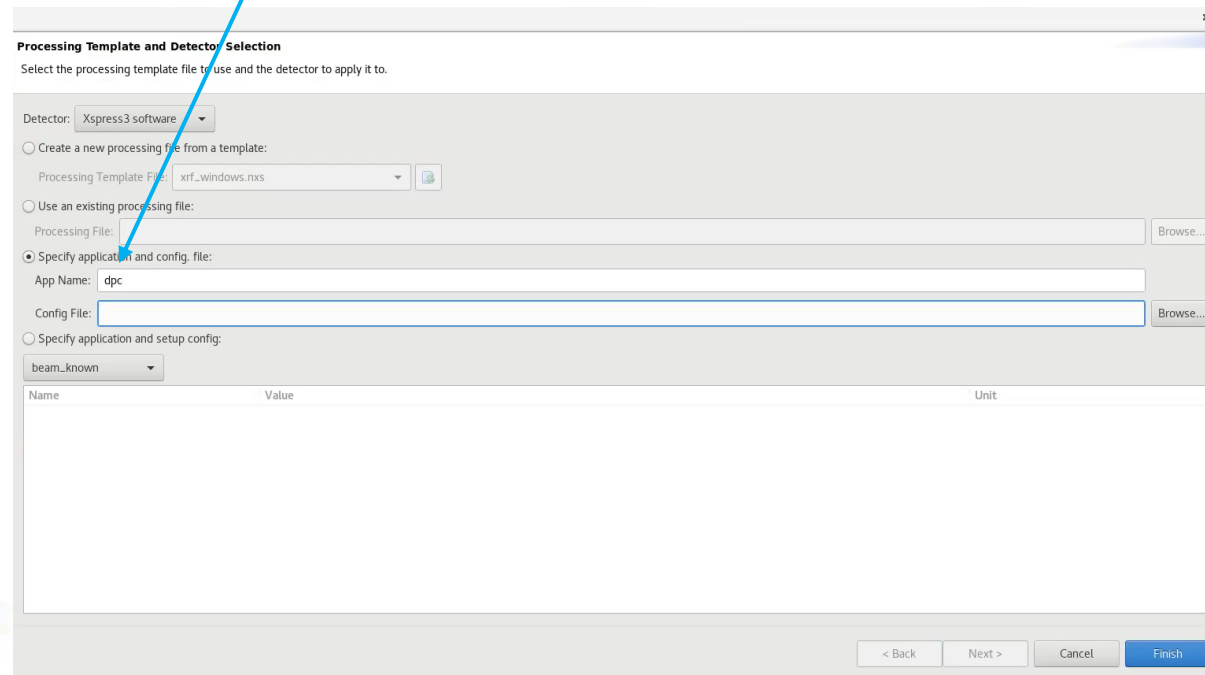
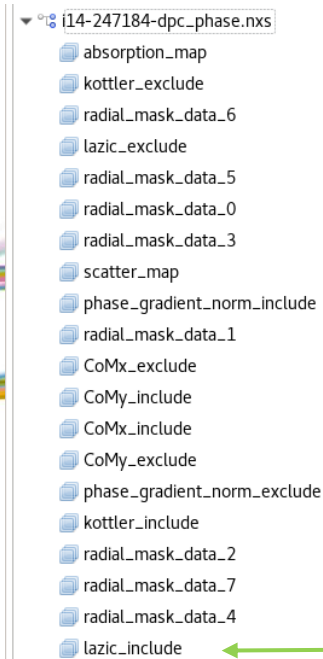
- mca
- IO_4
- It
- result
- Y-Ka
- IO_2
- IO_1
- W-La**
- Zr-Ka
- IO_3

Setting up the GDA session: DPC

The 'Mapping Experiment Setup' tab allows controlling how to submit all the analysis requested at I14:

- **Processing:** The 'Add Processing' button allows selecting some automatic postprocessing of the data.

- The 'i14-xrf' template would allow some live visualisation of the data
- In the third section "specify application and config file", type 'dpc' at the App Name space. This will trigger an automatic differential phase contrast (DPC) reconstruction of the transmitted signal acquired from either the Merlin or the Eiger detector, which will be loaded back at the "Mapped Data" area, as 'i14_XXXXXX_dpc_phase.nxs' file at the left of the GDA console
- Click "Finish"



- The 'lazic_include' filter will generally provide a nice phase contrast image

Scanning at GDA: Placing the detector in position

Before scanning, remember to select the appropriate detectors to be used at the 'Endstation configuration' menu:

- **XRF/Imaging:** Place the Merlin detector at the back of the sample for phase contrast imaging, detector cover out of the way, preparation to allow beam on
- **XRD/XRF or XRF/Eiger:** Similar to above but placing the Excilbur detector for XRD or the Eiger in position

Map

Mapping Experiment Setup Standards Scans Custom script

Configure Beamline

Script Files

Other Scan Axes

dcm_engr 13.000

Detectors

Xpress3 software 0.1

XRD/XRF 0.01

XRF/Eiger imaging 0.01

Eiger imaging 0.001

XRF scanning 0.01

XRF/Imaginn 0.01

Map points: 75 Total exposure time: 00:00:00
Smallest steps: X = 0.001250; Y = 0.001250; Absolute = 0.001250

Queue Scan

Jython Console Queue Live Stream

```
Setting up alignment tools
Setting up GDA XANES scan
Setting up sparse xanes scan
Setting up Ptychography scan
Exporting dcm_engr
Initialising detectors...
Error initialising detector Excilbur
Initialising array plugin for Merlin: ad_base_pv = BL14I-EA-DET-03:DET:
Using ImageMode to take one image
Initialising array plugin for Xpress3: ad_base_pv = BL14I-EA-XSP3-01:
Using ImageMode to take one image
Error initialising detector Xray Eye
Detector initialisation complete
Defining shutter controls
Initialisation Complete
>>>
```

Detector Data

Microscope

Sample Y: -0.59771 mm

Sample Z: -0.50231 mm

Run Ready

Watchdogs

beam_available_watchdog topup_watchdog

DCM energy

13.000 keV

- 0.1 +

Stop

- Click "Run" after selecting your preferred scripted position
- Wait until the symbol "Ready" appears after each selection (or look at the progress messages at the jython console)
- The right detector should be selected afterwards (clicking the small square), as well as defining the dwell time value (*XRF/Imaging fastest speed would be 0.015 s*)

Scanning at GDA: Checking the beam status

On the searching icon, type 'status' and select the "Status – staff" option

Find Actions

Views

- Stats and Maths (Data Analysis)
- Status - staff (14 Views)**
- Status - user (114 Views)
- Server status (Other)

Commands

- Maximize Active View or Editor - Toggles maximize/res...
- Reset Perspective - Reset the current perspective to its...
- Show In (Server status)
- Show In (Stats and Maths)
- Show In (Status - staff)
- Show In (Status - user)
- Show View (Server status) - Shows a particular view
- Show View (Stats and Maths) - Shows a particular view
- Show View (Status - staff) - Shows a particular view

Preferences

- Editors - General

Resources

- StaticCharAtlas.js
- StaticCharAtlas.js.map
- StaticCharAtlas.ts
- Stats.js
- stat.js
- stata.py
- stata_dark.py
- stata_light.py
- state.js

Machine

Ring current 298.98 mA

Time to refill 168 s

Detector Cover

Position 19 mm

Unknown

Beamline

ID Gap 5.82 mm Bragg 6.307 degrees

Energy 18.001 KeV No beam

OH1 Shutter State Open

OH2 Shutter State Open

OH3 Shutter State Open

EH2 Nano Shutter Processing

State Closed Processing Running

41.083, 15.574

gqz18237 Baton held No Scan running

No Script running Stop All

Scanning at GDA: Checking the beam status

On the searching icon, type 'status' and select the "Status – staff" option

That will open a secondary tab at the bottom left

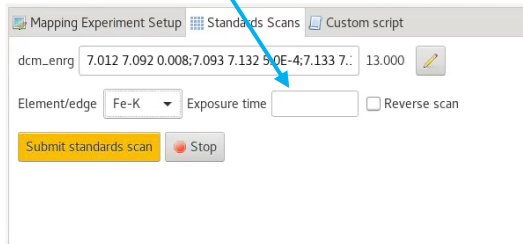
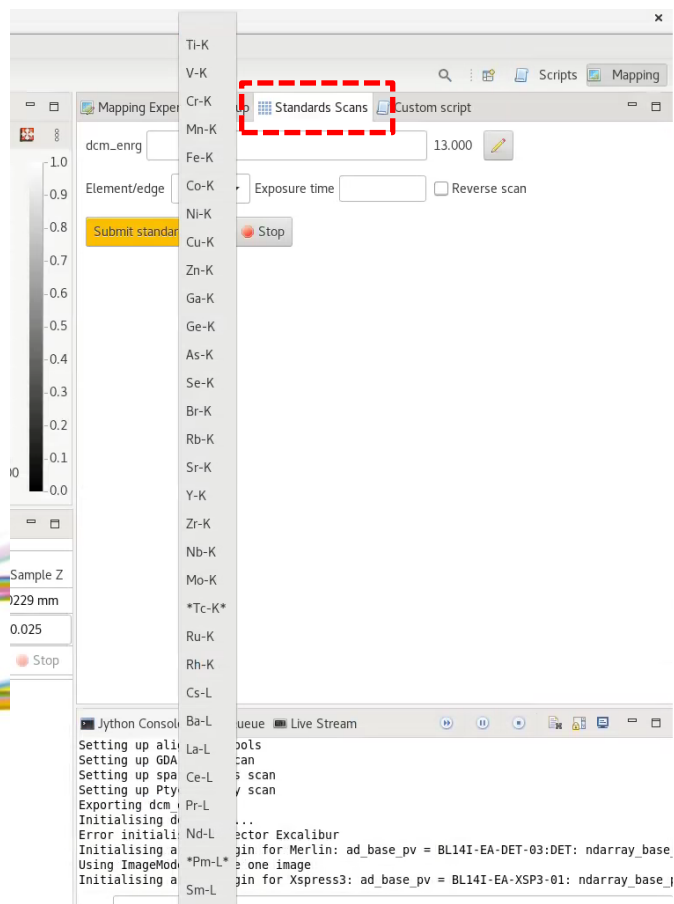
- If the "EH2 Nano Shutter" is closed, click the 'Open/Close' button

All the indicators at the 'Status' tab should be green, showing them as "Open". If that is the case the 'Queue Scan' button will be white coloured, signalling that everything is ready to take the beam

```
Setting up alignment tools
Setting up GDA XANES scan
Setting up sparse xanes scan
Setting up Ptychography scan
Exporting dcm_eng
Initialising detectors...
Error initialising detector Excalibur
Initialising array plugin for Merlin: ad_base_pv = BL14I-EA-DET-03:DET: ndarray
Using ImageMode to take one image
Initialising array plugin for Xspress3: ad_base_pv = BL14I-EA-XSP3-01: ndarray
Using ImageMode to take one image
Error initialising detector Xray Eye
Detector initialisation complete
Defining shutter controls
Initialisation Complete
>>>
```

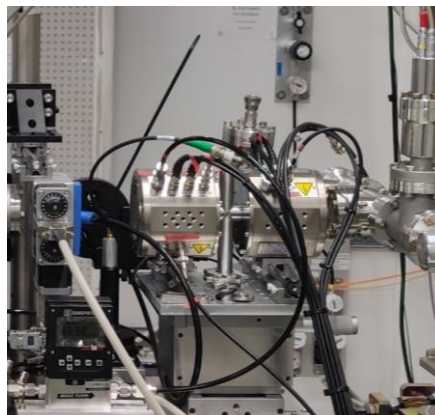
Scanning at GDA: point XANES

Point XANES or standard XANES acquisition: The 'Standards Scan' tab (red rectangle below) allows performing point xanes acquisition on a fixed location of the sample as well as measuring the XANES pellets. In there, the 'Element/edge' to analyse should be selected from the drop-down list (i.e., Fe-K) as shown at the left below, which will populate the energy list accordingly (right image). The exposure time (dwell time) should be typed (for example to 0.1 s).



Things to notice before submitting this analysis:

- The beam may need to be manually opened beforehand
- For point XANES, double click on the position of interest firstly in the mapping area to move the stages (*a warning message will appear to confirm the movement*)
- Standard XANES: The pellet should be placed between the ion chambers at the EH2, and **remember to remove it** straight away once finishes!

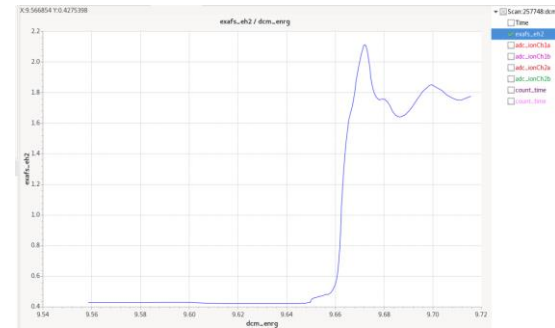


Scanning at GDA: point XANES

Point XANES or standard XANES acquisition: The 'Standards Scan' tab (red rectangle below) allows performing point xanes acquisition on a fixed location of the sample as well as measuring the XANES pellets. In there, the 'Element/edge' to analyse should be selected from the drop-down list (i.e., Fe-K) as shown at the left below, which will populate the energy list accordingly (right image). The exposure time (dwell time) should be typed (for example to 0.1 s).

Standard XANES pellet

The running scan will generate a new tab: 'Scan Plot' at the right of the Queue and the jython console, in which the signal between the ion chambers may be selected: eh2_exafs



Point XANES

After selecting a region of interest on the mapping area (double click will move the stages first!), a point XANES on that nano-region can be submitted. In this case the data will NOT be live on the 'Scan Plot' tab, which only shows the ion chambers signal. For reconstructing the point xanes, check this [video](#) on the [I14 website](#), on how to load jupyter notebooks. Then: 1) select: /dls_sw/i14/ops/notebooks/centralised_notebooks/point-XANES_XRF-standard.ipynb, 2) update the 'inpath' details, and 3) "Cell" – "Run all"

```
In [1]: inpath = {"nexus": "/dls/i14/data/2023/mg33564-1/scan/i14-247146.nxs",
                "window_low": 805-10,
                "window_high": 805+10
            }
```

```
In [2]: outpath = {"txt": "/dls/i14/data/2023/mg33564-1/processing/point_xanes/i14-247146_Cu-xanes.txt"}
```

If the standard is collected at the sample position using
scan xsp3_addetector 1.0
or
standards_scan_xsp3(*energies)
This can be used to extract the spectrum.

- The channel value for the windowing will be 1/10 of the Ka1 fluorescence line (i.e., Cu = 8046 eV), or the corresponding La1 line for some elements



Scanning at GDA: XRF Mapping

At the 'Scan Type' icon (red rectangle below), the main analysis techniques available at I14 can be selected. Remember to select the 'Mapping' option for XRF imaging.

The screenshot displays the 'Data Acquisition Client - Beamline I14 - 9.29.0' interface. The 'Scan Type' icon in the top toolbar is highlighted with a red dashed box. A dialog box titled 'Choose the scan type' is open, with 'Mapping scan' selected. The 'Mapping Experiment Setup' panel on the right shows the following configuration:

- Detectors: XRF/Imaging 0.015
- Region shape: Centred Rectangle
- Scan path: Raster
- SampleX Centre: 0.5 mm
- SampleX Step: 100 nm
- SampleX Range: 5 μm
- SampleY Centre: 0.5 mm
- SampleY Step: 100 nm
- SampleY Range: 5 μm
- Alternating:
- Continuous:
- Orientation: Horizontal
- Sample Name: Test_sample
- Processing: Add Processing...
- App Name table:

App	Name
<input checked="" type="checkbox"/> i14-xrf	{'element_list': 'Fe-Ka', 'window_width': 20}
<input checked="" type="checkbox"/> dpc	
- Map points: 2,601 Total exposure time: 00:00:39
- Smallest steps: X = 0.0001000; Y = 0.0001000; Absolute = 0.0001000
- Queue Scan button

Scanning at GDA: XANES spectromicroscopy

Scan type → XANES

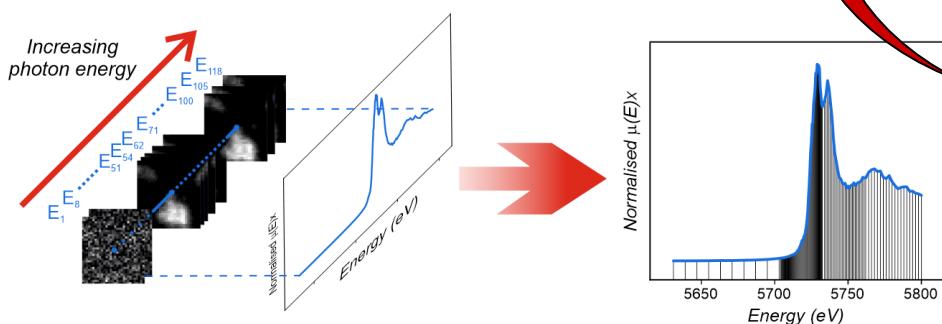
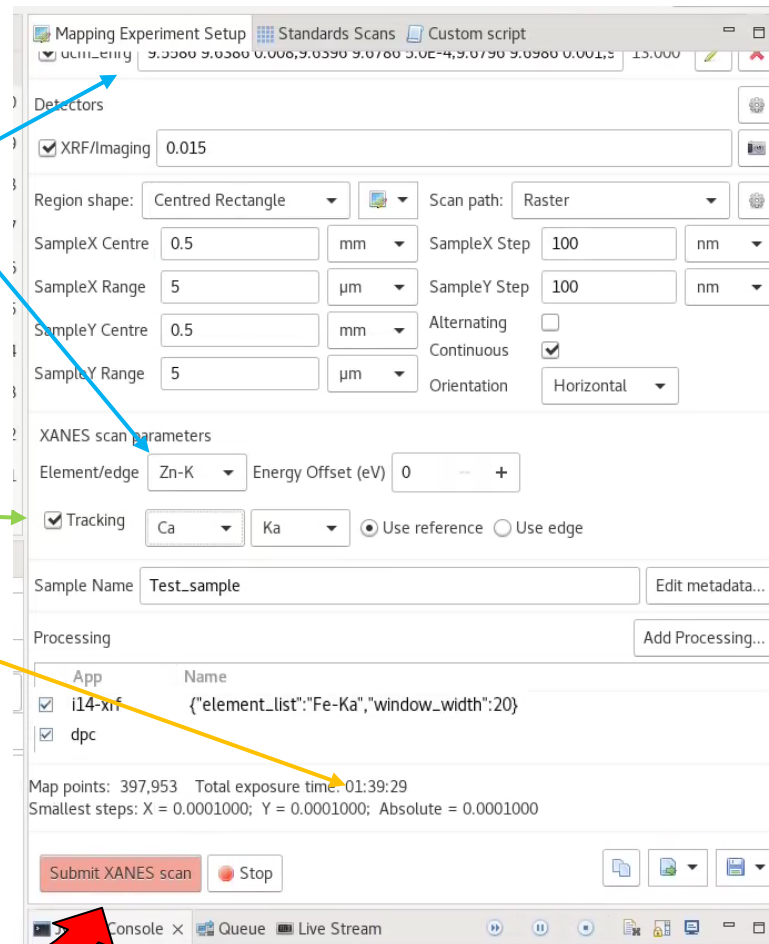
The 'Mapping Experiment Setup' tab will change its layout, adjusting to this acquisition methodology.

In there, the 'Element/edge' to analyse should be selected from the drop down list (i.e., Zn-K) as shown at the image, which will populate the energy list accordingly at the top.

The "Tracking" allows to select a background element (i.e., Ca) and an electronic transition (i.e., Ka) whose signal should be constant. Hence, please select an element/transition with an energy lower than the edge/element for XANES. This [published methodology](#) (Quinn *et al.* J. Synchrotron Rad. (2021). 28, 1528-1534) automatically adjusts the sampling area at the beginning of each scan to ensure that the microstructure remains in the field of view.

The 'Total exposure time' will be an estimation based on the submission of the ~150 individual scans, but some time on overheads, tracking and energy changes should be accounted (usually around ~1 hour more)

Again, the 'Submit XANES scan' button will be red-coloured if the beam is OFF. Please, ensure that this is activated before submission.



Scanning at GDA: underscanning XANES

Scan type → sparse XANES

This is based on a published [undersampling methodology](#) (Townsend *et al.* Optics Express (2022). 30, 43237-43254) for reducing the dose and scanning times. This is achieved by skipping rows within scans and reconstructing the X-ray spectromicroscopy data using low-rank matrix completion.

The 'Mapping Experiment Setup' tab will change its layout, adjusting to this acquisition methodology.

Only the XRF detector can be triggered in this analysis, since missing-rows would make the photon counting detectors to fail. This is automatically selected by default, but remember to re-select XRF/Imaging or XRD/XRF when transitioning back to the "Mapping" scan type.

The 'Element/edge' to analyse should be selected from the drop down list (i.e., Zn-K) as shown at the image, which will populate the energy list accordingly at the top.

An 'Energy Offset' may be inputted if the energy calibration has been done in advance. Please, input only non-decimal numbers (in eV units) either positive or negative according to the calibration.

The 'Percentage' of undersampling may be adjusted if needed, but a 20% missing data is adequate, and it has been scientifically proven.

The 'Total exposure time' is an estimation based on the submission of the ~150 individual scans with FULL ROWS. Hence, the scan will be considerably faster (total time about 1/3 of the estimated time)

Again, the 'Submit Sparse XANES scan' button will be red-coloured if the beam is OFF. Please, ensure that this is activated before submission.

The screenshot shows the 'Mapping Experiment Setup' window with the following configuration:

- Other Scan Axes:** dcm_enrg [9.5586 9.6386 0.008; 9.6396 9.6786 5.0E-4; 9.6796 9.6986 0.001; ...] 13.000
- Detectors:** XRF/Imaging 0.015, XRF scanning 0.01
- Region shape:** Centred Rectangle, **Scan path:** Raster
- SampleX Centre:** 0.5 mm, **SampleX Step:** 100 nm
- SampleX Range:** 5 µm, **SampleY Step:** 100 nm
- SampleY Centre:** 0.5 mm, **Alternating Continuous:**
- SampleY Range:** 5 µm, **Orientation:** Horizontal
- XANES scan parameters:** **Element/edge:** Zn-K, **Energy Offset (eV):** 0, **Percentage (%):** 20
- Sample Name:** Test_sample
- Processing:** Add Processing
- Map points:** 397,953, **Total exposure time:** 01:06:20, **Smallest steps:** X = 0.0001000; Y = 0.0001000; Absolute = 0.0001000
- Buttons:** Submit Sparse XANES scan (red), Stop
- Ython Console:** Setting up alignment tools, Setting up GDA XANES scan, Setting up sparse xanes scan, Setting up Ptychography scan

Scanning at GDA: Ptychography

Scan type → **ptychography** (*currently under development*)

This methodology is still “under development”, so please speak with your local contact before trying it.

Once triggered, the GDA will automatically move the stages 800 μm out of focus (positive Z, making the beam bigger at the point of exposure), adjust the stage offset, submit the ptychography scan plus the associated reconstruction strategies, and place the stages back to the focus position upon scan completion.

The ‘Mapping Experiment Setup’ tab will reflect the ideal mapping resolution (sampleX and Y Step), which is 100 nm (although this may be decreased to ~ 50 nm to ensure enough data overlapping).

There will be some [PtyPy](#) reconstruction algorithms triggered by default (listed at the right of the ‘ptypy14’ app), which should be evaluated upon completion at the ‘/mgxxxxx-y/processed/ptychography_ptypy/’ directory (Please, allow at least 2-3 hours for completion depending on the dataset size).

Again, the ‘Submit ptychography scan’ button will be red-coloured if the beam is OFF. Please, ensure that this is activated before submission.

The screenshot shows the 'Mapping Experiment Setup' window with the following parameters:

- Other Scan Axes:** dcm_enrg: 13.000
- Detectors:** XRF/Imaging: 0.015, XRF scanning: 0.01
- Region shape:** Centred Rectangle, **Scan path:** Raster
- SampleX Centre:** 0.5 mm, **SampleX Step:** 100 nm
- SampleX Range:** 5 μm , **SampleY Step:** 100 nm
- SampleY Centre:** 0.5 mm, **Alternating:** , **Continuous:**
- SampleY Range:** 5 μm , **Orientation:** Horizontal
- Sample Name:** Test_sample
- Processing:** Add Processing...
- App List:**

App	Name
<input checked="" type="checkbox"/> i14-xrf	{'element_list': 'Fe-Ka', 'window_width': 20}
<input checked="" type="checkbox"/> dpc	
<input checked="" type="checkbox"/> ptypy14	i14_known_probe_dm_template.yaml
<input checked="" type="checkbox"/> ptypy14	i14_unknown_probe_dm_template.yaml
<input checked="" type="checkbox"/> ptypy14	i14_known_probe_dm_posref.yaml
- Map points:** 2,601, **Total exposure time:** 00:00:39, **Smallest steps:** X = 0.0001000; Y = 0.0001000; Absolute = 0.0001000
- Buttons:** Submit ptychography scan (red), Stop

Scanning at GDA: XRD

Scan type → Mapping

This

- To be completed

Scanning at GDA: Tomography

Scan type → tomography

This

- To be completed