
Veritas Manual

Veritas Staff

Mar 11, 2024 - 17:02 UTC

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Welcome to the manual for the Veritas beamline.

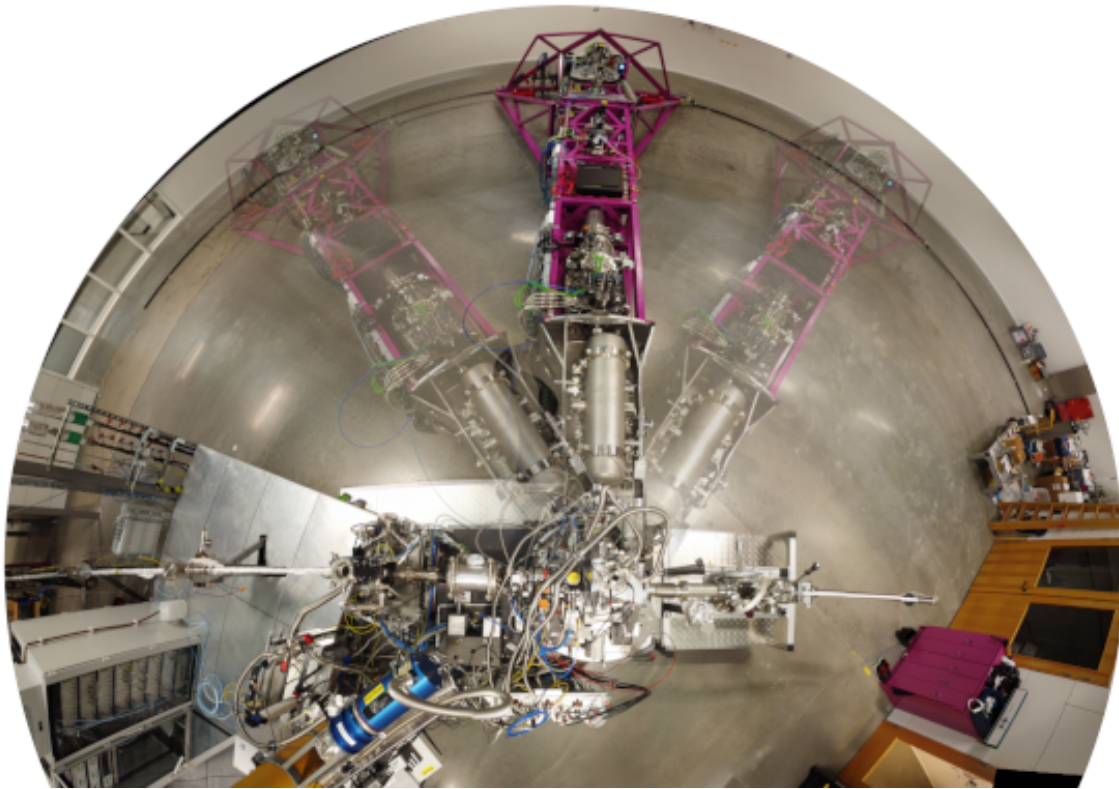


Fig. 1: Fisheye of the Veritas spectrometer from above the sample position. Photo: L. Kjellsson

Offline PDF documentation can be downloaded here: [veritasmanual.pdf](#).

Build time: Mar 11, 2024 - 17:02 UTC

THE VERITAS BEAMLINE

If you are a user that needs information about running the beamline. For detailed beamline specifications and optics, please visit the [webpage](#).

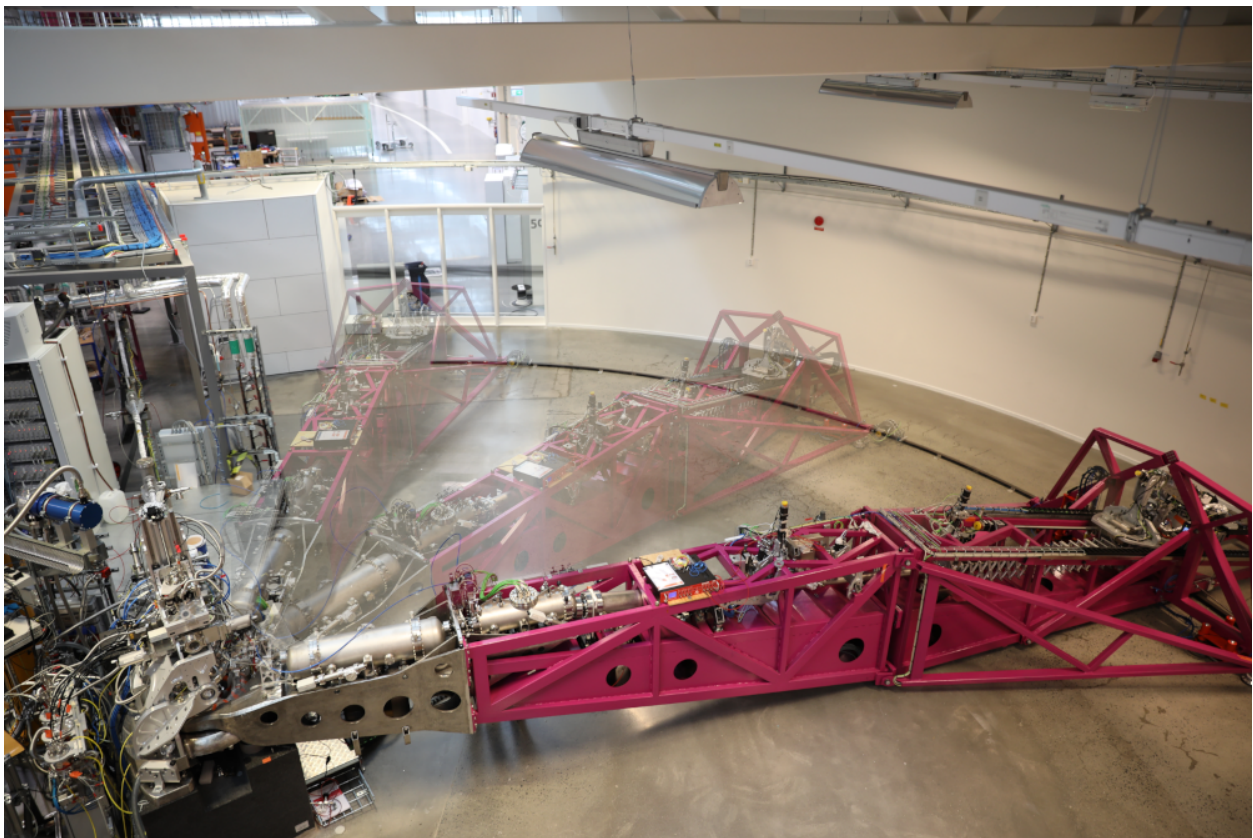


Fig. 1: The Veritas spectrometer at 3 different Q-angles. Photo: L. Kjellsson

THE ENDSTATION AND SAMPLE ENVIRONMENTS

We can operate in all three sample environments, Solid, Liquid and Gas. And, based on the sample environments we modify our endstation from very subtle to radical.

2.1 Endstation for Solid and gas samples

For solid and gas samples, we use the Q-chamber (measurement chamber), upper chamber and load lock chamber as shown in the figure. We can also set different scattering angles, thanks to the rotatable Q-chamber. The only difference is the requirement to swap the sample rods.

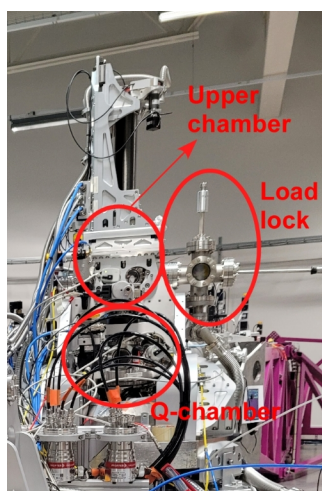


Fig. 1: Endstation for solid and gas experiments

2.1.1 Solid state sample rod

2.1.2 Sample rod for gas experiments

2.2 Endstation for Liquid samples

For liquid samples, the changes are more radical as we need to swap the Q-chamber with a differential pumped chamber to accommodate the liquid jet sample rod, cold trap and ice breaker. Since this chamber is not rotatable, we are limited to 90 deg scattering angle.

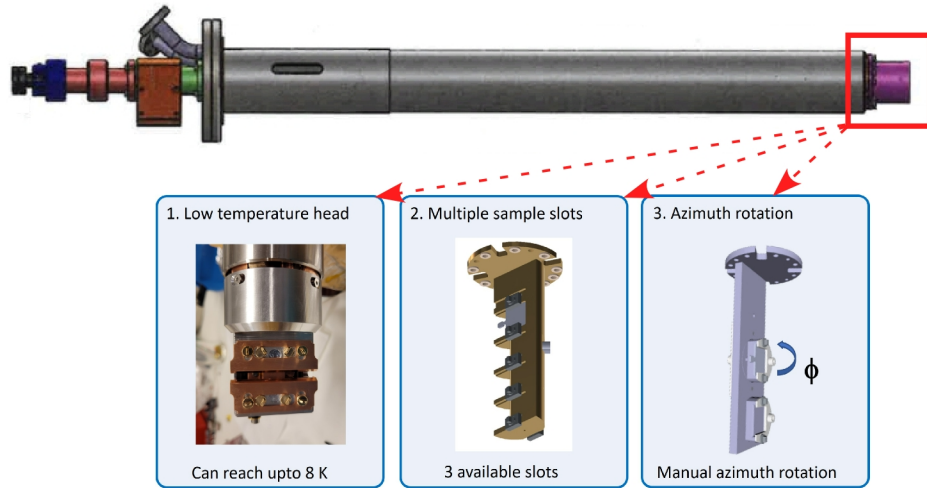


Fig. 2: Solid state sample rod with detachable heads according to user need

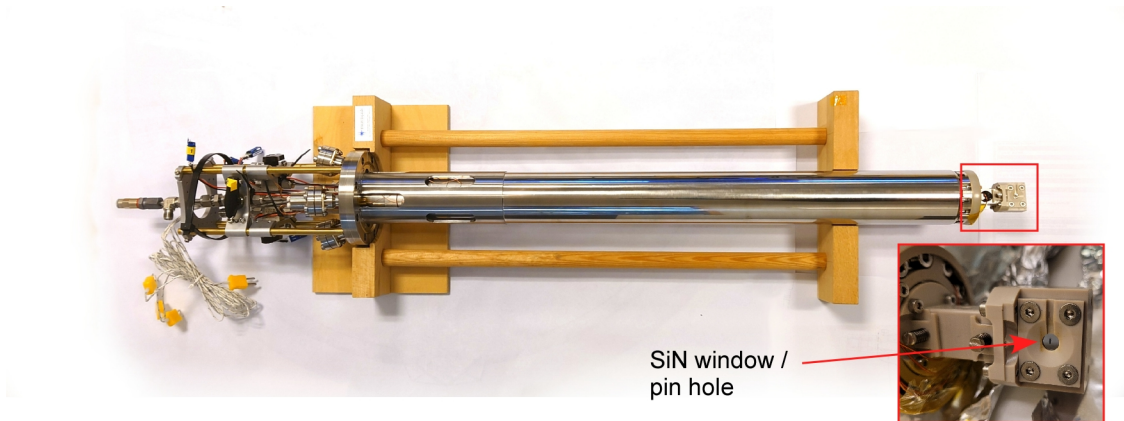


Fig. 3: The sample rod with a gas-cell (inset). Photo: L. Kjellsson

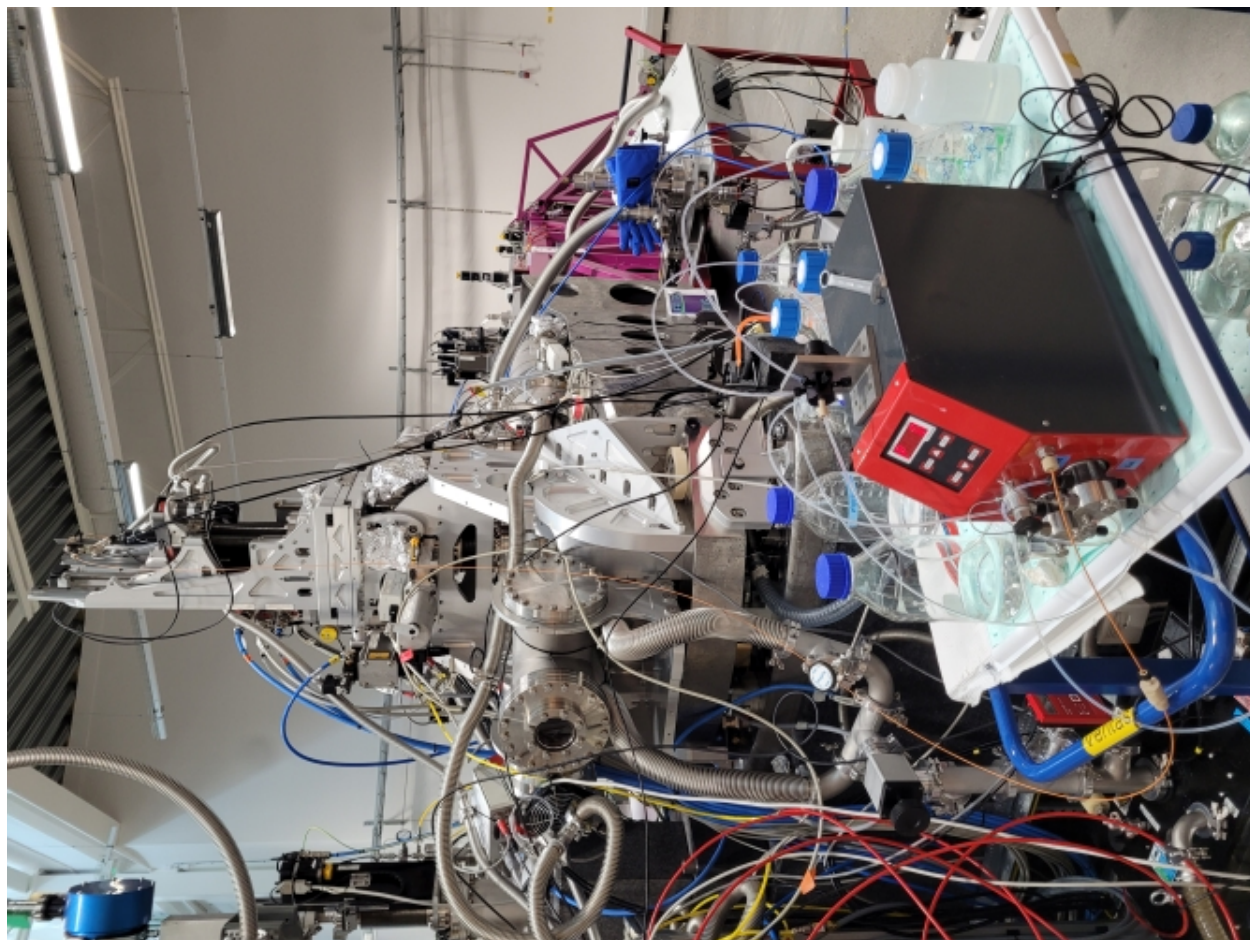


Fig. 4: Endstation for liquid experiments

2.2.1 Sample rod for liquid experiments

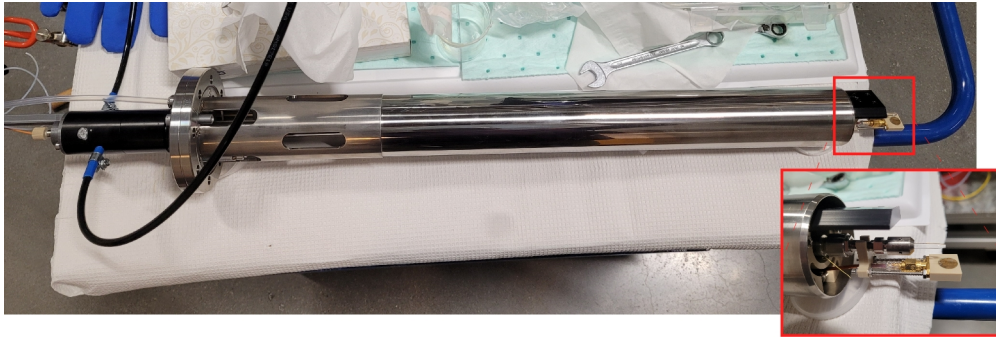


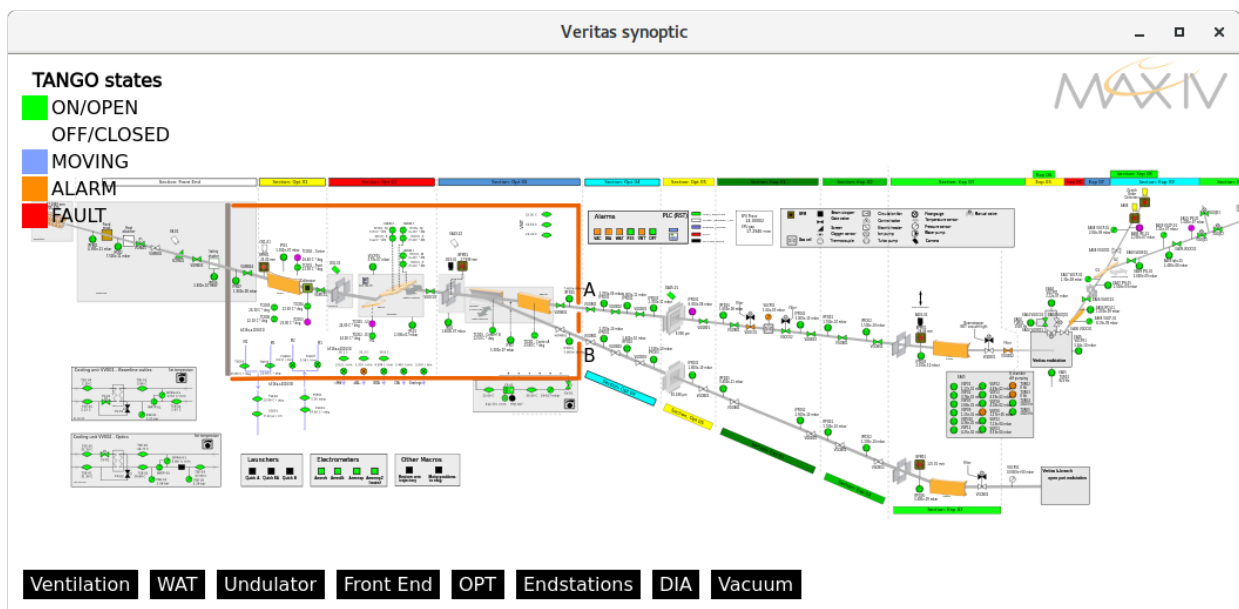
Fig. 5: The liquid jet sample rod

BEAMLINE SOFTWARE

Here is a short intro to what user interfaces is needed for what task.

- General beamline control: *Synoptic* and *QuickGUI*
- Scanning, for XAS-measurements (or RIXSmaps): *Scangui*
- RIXSmeasurements: *Rixsclient*

3.1 Synoptic



How to start it:

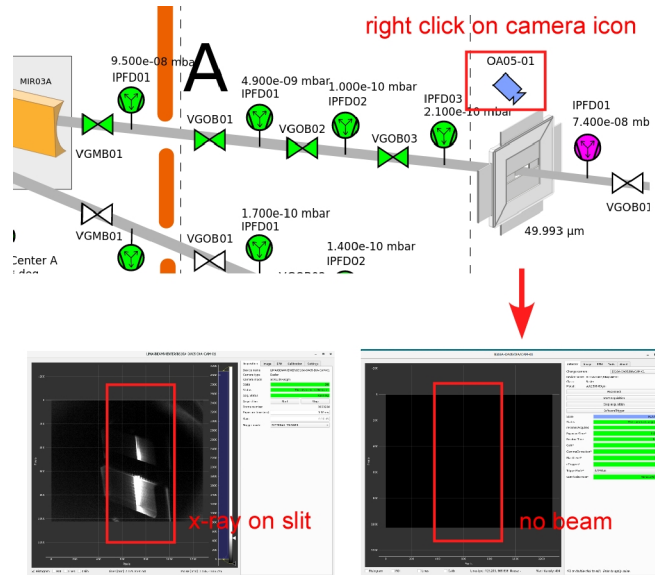
- Icon on desktop
- In menubar: "MAXIV": "MAXIV Veritas synoptic"
- Run in terminal "ctveritassynoptic"

What does it do?

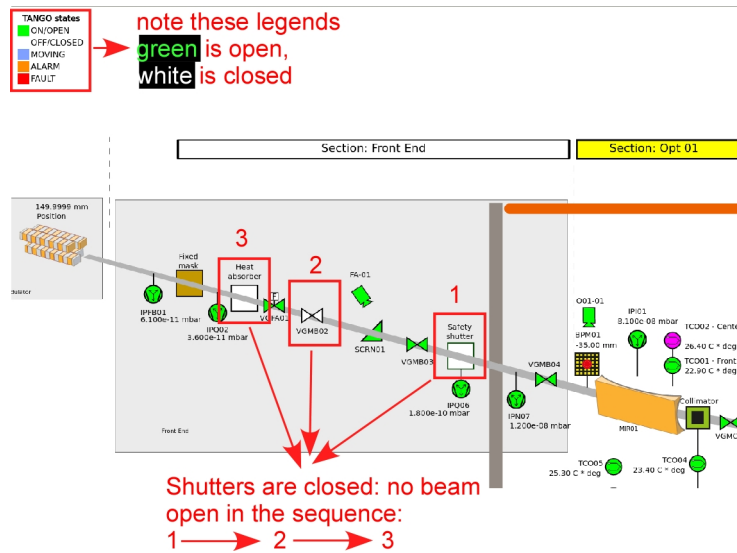
The Synoptic gives a graphical representation of the beamline and spectrometer. Here you can check pressures, open valves, and open to the frontend.

Check if there is beam

- Right click on the camera icon over the exit slit and a window will open (see figure with and without beam).



- Start the camera acquisition and if the beam is still not there check if the front end (FE) is closed or if there is a beam dump.
- If the FE shutters are closed (white) open them following a strict sequence, starting from downstream all the way to the Heat absorber. Prior to opening, check if there is current in the 3 GeV ring (approx. 400 mA). Open “Safety Shutter” first, followed by “VGMB02”, and in the end, when their colors change to green, open “Heat absorber” (see figure below).



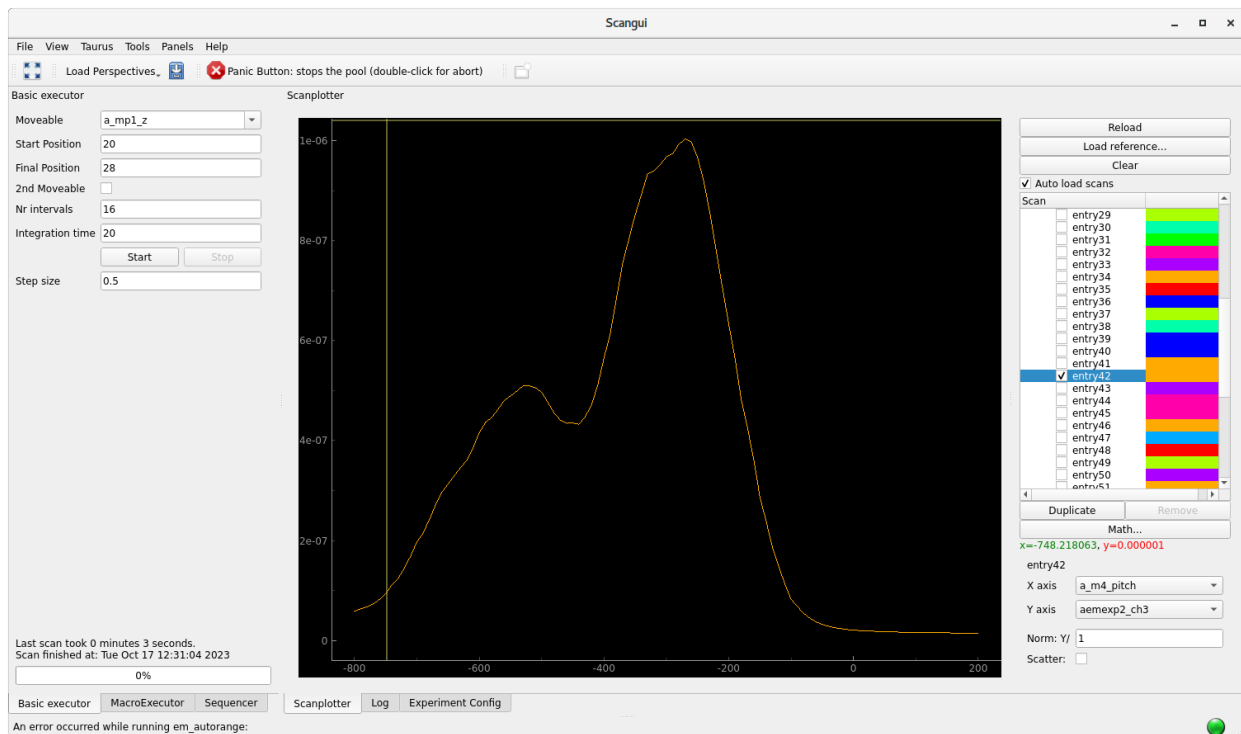
NOTE: if at any point you feel uncomfortable to open any valves / shutter, please feel free to contact the **floor coordinator** (+46 (0)46 222 16 61 / +46 73 597 3055) or the beamline local contact.

When do I need to use it

- During sample transfer
- Opening the FE after a beam dump

- Troubleshooting a “Why is there no beam?”-scenario

3.2 Scangui



How to start it:

- In menubar: “MAXIV Scangui”
- In terminal: “scangui”

What does it do?

The scangui is a general purpose scanning tool. It is used for scanning motors or combined motions (such as beamline energy).

When do I need to use it

- Making a RIXSmap
- Finding the sample by scanning the manipulator
- Setting up sequences to automatically measure XAS or RIXSmaps at different sample positions.

3.2.1 Making an XAS-measurement

1. Open up the Scangui
2. Go to the tab “Experiment Config”, make sure the correct measurementgroup is selected. If it is correct the skip to step 5.
3. Click the radiobutton “Edit Mode”
4. Click on the drop-down menu next to “Active measurement Group”, select e.g. “XAS”
5. Click “Apply” in the bottom right corner.
6. Now you can go back to the tab “Scanplotter”
7. Go to the tab “Basic executor”
8. Set the moveable to: “beamline_energy”
9. Set Start position “400” (eV), and stop position 402 (eV)
10. Choose the number of steps for the scan, either by writing the number of intervals (which is 1 less than steps), or by writing the stepsize “0.1” (eV)
11. Click “Start” to run it
12. In the scanplotter, you have to select the correct x and y axis, both for the “Livedata” and for the scan loaded from file “entry1337”

3.2.2 Sequencer tab (advanced measurement mode)

It is possible to automate measurements using custom macros. In the sequencer tab one can load, modify, save and run such macros using a graphical interface. (The sequencer macro is saved as an *.xml file, and can also be modified in a text editor).

Macro	Description	Optional	Save output
ascan	Scan in Basic executor		
mesh	Raster scan two motors, data will be saved in a single entry	bidirectional = True to snakescan	Single entry
a2scan	Scan along a line across two dims defined by the start and end-points for the two motors	a	
seqmotion	Outer loop scan, will NOT generate an entry		
rixsaqstart	will trigger rixsaq to initiate a scan		
rixsaqstop	will trigger rixsaq to stop a scan		
mv	move a single motor to a specified value		

Nested scans

Making a raster scan of the sample

A mesh scan or raster scan can be used to find the sample. You need to select two motors or pseudo motors, for example `a_mp1_x` and `a_mp1_y` (x and y manipulator axii), and similarly as to the regular scan you, you also need to specify the start and stop for the two motors.

1. Open up the Scangui
2. Go to the tab “Experiment Config”, make sure the correct measurementgroup is selected. If it is correct the skip to step 5.
3. Click the radiobutton “Edit Mode”
4. Click on the drop-down menu next to “Active measurement Group”, select e.g. “XAS”
5. Click “Apply” in the bottom right corner.
6. Now you can go back to the tab “Scanplotter”
7. Go to the tab “Sequencer”
8. In the drop-down menu , select **mesh** and press +
9. Set the 1st moveable to: “`a_mp1_x`”
10. Set the 2nd moveable to: “`a_mp1_y`”
11. Set Start position and stop position for the two motors to appropriate values
12. Choose the number of steps for the scan by writing the number of intervals (which is 1 less than steps)
13. Click “Start” to run it
14. In the scanplotter, you have to select the correct x and y axis, both for the “Livedata” and for the scan loaded from file “entry1337”

Gitlab link: <https://gitlab.maxiv.lu.se/kits-maxiv/app-maxiv-scangui3>

3.3 Quickgui

3.3.1 Quickgui: Veritas A

How to start it:

- Icon on desktop
- Run in terminal: “`quickgui /mxn/home/veritas-user/quickgui/veritas_a.yml`”

What does it do?

This is a general interface for moving motors in the beamline.

When do I need to use it

This is typically used for beamline optimization.

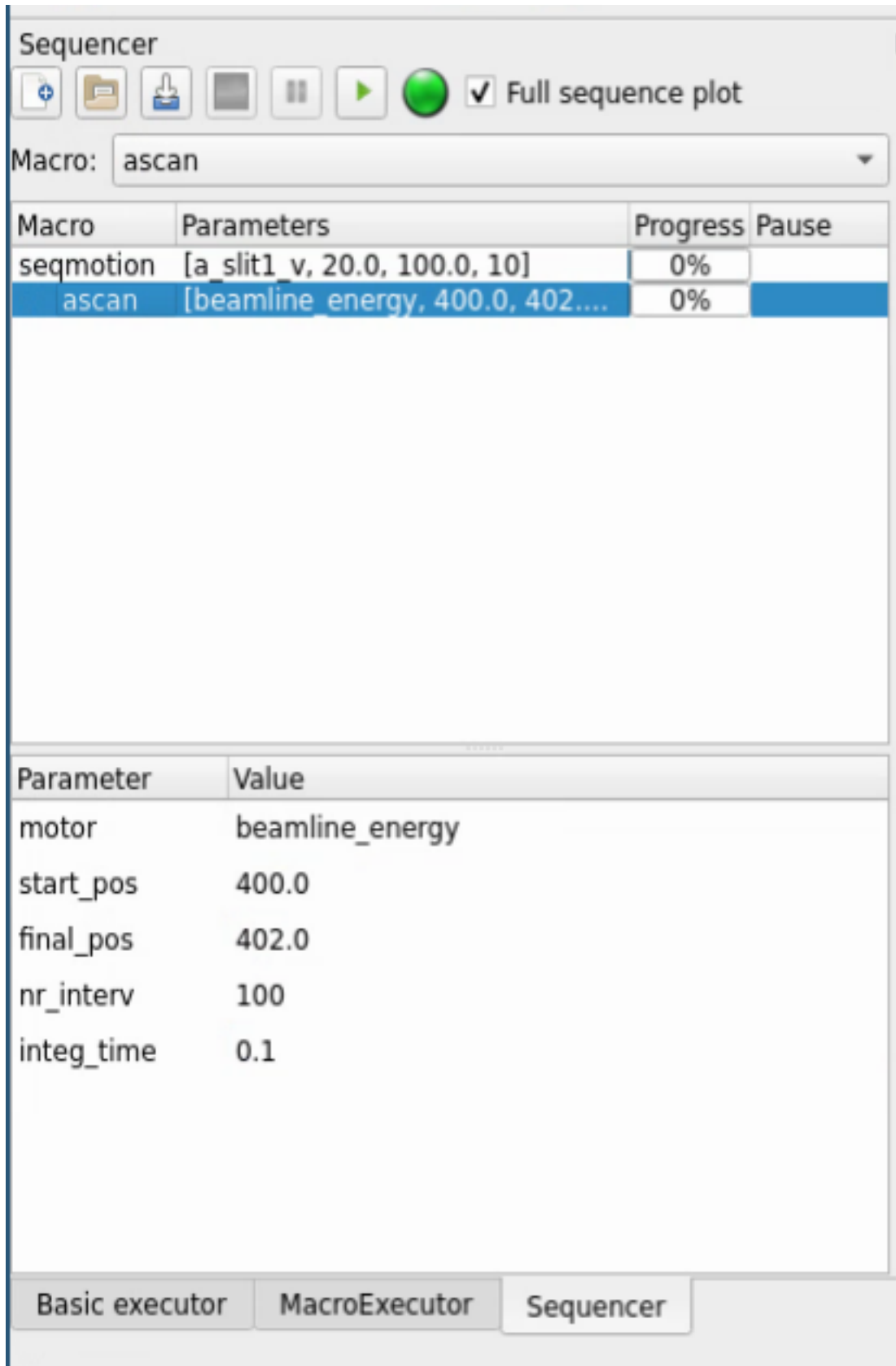
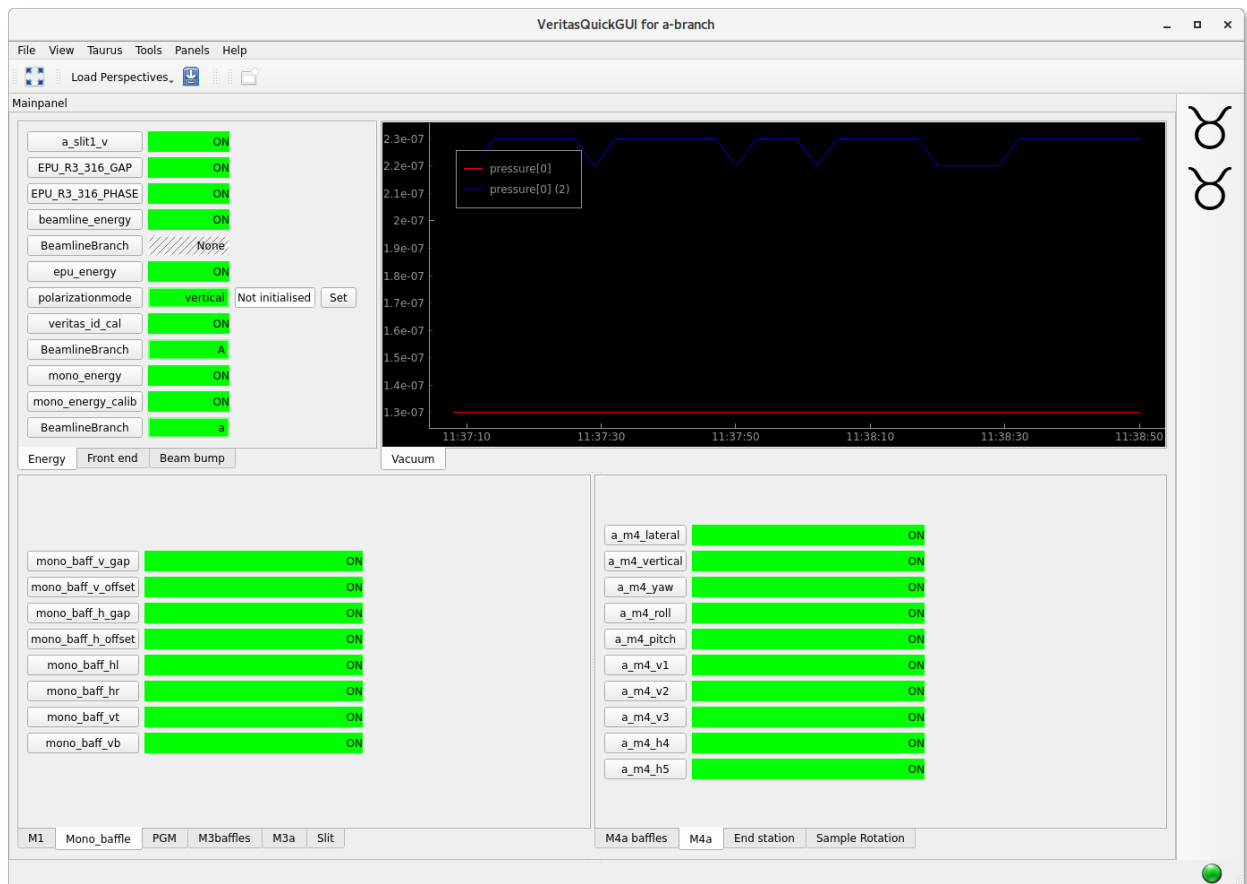
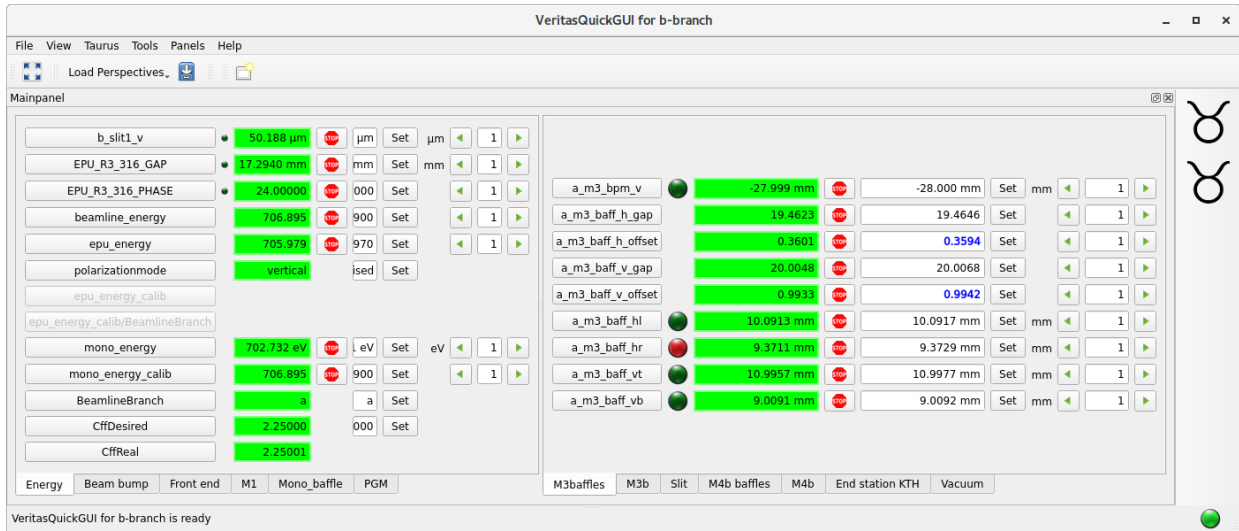


Fig. 1: An example sequence which scans the slit from 20um to 100um and makes a XAS-measurement at every slitopening.



3.3.2 Quickgui: Veritas B



How to start it:

- Icon on desktop
- Run in terminal: “quickgui /mxn/home/veritas-user/quickgui/veritas_b.yml”

What does it do?

It is used for moving motors on the open-port branch of the beamline.

When do I need to use it?

You will use this if you are a user at the B-branch. Beamline optimization, set monochromator exit slits and beamline energy.

3.3.3 Quickgui: Veritas A endstation

How to start it:

- Icon on desktop
- Run in terminal: “quickgui /mxn/home/veritas-user/quickgui/endstation_a.yml”

What does it do?

This is a general interface for moving motors needed to operate the big spectrometer.

When do I need to use it?

- *Sample transfer*
- Moving and rotating the sample
- Changing beamline energy, monochromator exit slit
- Changing Q-angle of the spectrometer
- Changing energy of the spectrometer.

VeritasQuickGUI for a branch Endstation

File View Taurus Tools Panels Help

Load Perspectives

Mainpanel

Endstation Vacuum Beamline Vacuum Sample Temperature AEMEXP2

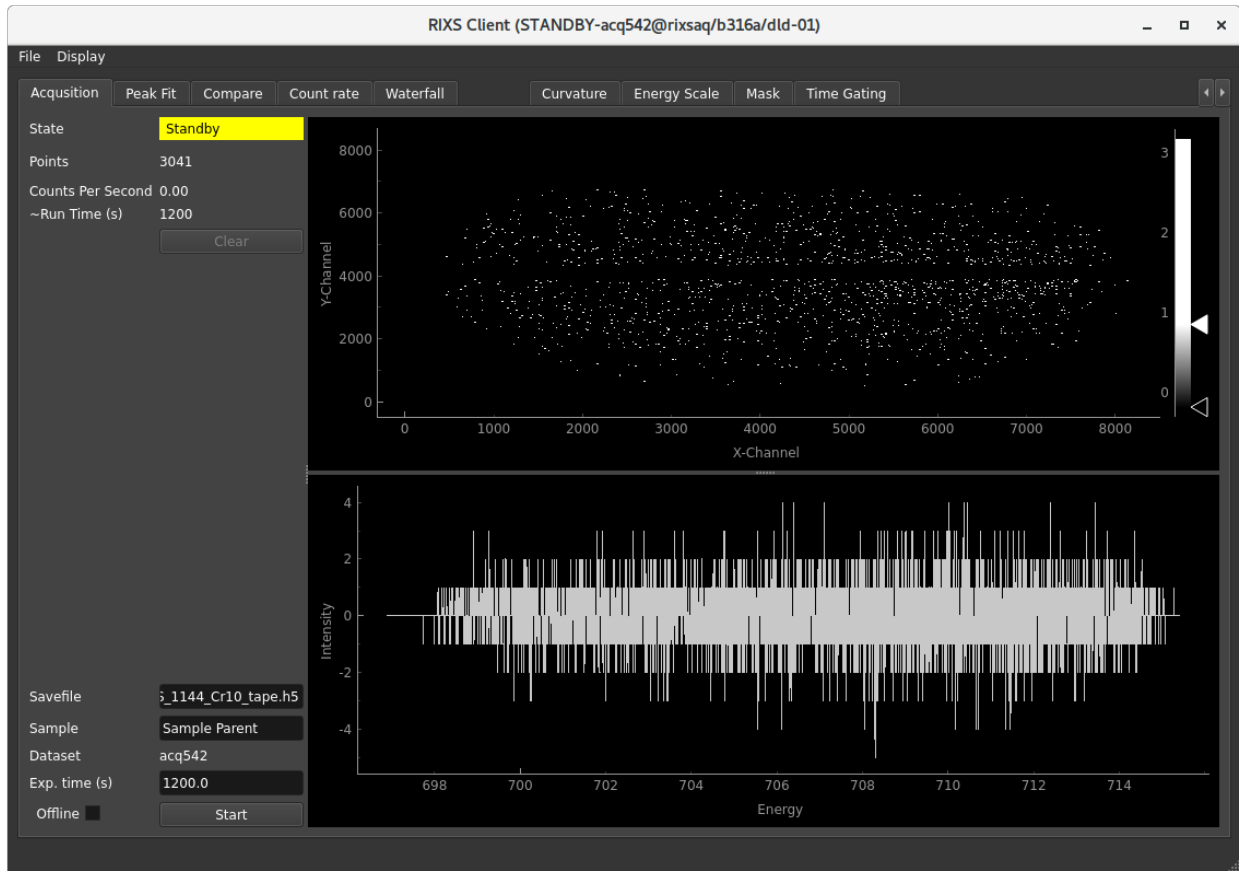
a_slit1_v	9.990 μm	STOP	10.000 μm	Set	μm	1
beamline_energy	706.894	STOP	706.900	Set		1
EPU_R3_316_GAP	17.2940 mm	STOP	17.2939 mm	Set	mm	1
EPU_R3_316_PHASE	24.00000	STOP	24.00000	Set		1
polarizationmode	vertical		Not initialised	Set		
veritas_id_cal	706.91	STOP	706.90	Set		1
mono_energy_calib	706.900	STOP	706.900	Set		1
CffDesired	2.25000		2.25000	Set		
CffReal	2.25002					

Energy Endstation Manipulator Sample scanner Sample temperature Liquid jet setup

a7_gr_baff_v_gap	12.99	STOP	13.00	Set		1
a7_gr_baff_v_offset	4.50	STOP	4.50	Set		1
a7_gr_baff_h_gap	8.01	STOP	8.00	Set		1
a7_gr_baff_h_offset	-0.00	STOP	0.00	Set		1
a7_gr_baff_hl	4.00 mm	STOP	4.00 mm	Set	mm	1
a7_gr_baff_hr	4.004 mm	STOP	4.000 mm	Set	mm	1
a7_gr_baff_vb	1.99 mm	STOP	2.00 mm	Set	mm	1
a7_gr_baff_vt	11.00 mm	STOP	11.00 mm	Set	mm	1

Gr Baff Gratings DLD Q-motion Expert

3.4 RIXS Client



How to start it:

- In menubar: “MAXIV Rixsaqclient DLD1”
- In terminal: “/usr/local/bin/ctrixaq rixsaq/b316a/dld-01 rixsaqfit/b316a/dld-01”

What does it do? It records RIXS data, it can be great for experiments.

When do I need to use it?

Gitlab link: <https://gitlab.maxiv.lu.se/species/app-maxiv-rixsaq>

3.4.1 Calibration

Each photon hitting the detector is recorded, but to produce a final spectrum a few calibration steps are taken. The points are processed in the following order:

Understanding

The calibration routines in the data pipeline is processed on a point-by-points basis. N.b. that in some cases it might be beneficial to instead work on imagedata. The calibration is applied in the following order:

1. **Time gating** is used to filter out the photon hits that occurred between the light flashes of the synchrotron.
2. A **curvature correction** algorithm is applied to the points
3. **Masked** portions of the detector area is removed
4. The 2D image is summed along the vertical axis, creating the spectrum
5. The dark spectrum is subtracted.

Correctly setting a calibration

This should be repeated after every move of energy in the emission spectrometer.

Here are the steps needed to make a nice calibration, note that it is important to do this before setting an energy scale, since the curvature correction can move the peaks slightly on the emission axis.

0. Make a measurement with a line in the center of the detector.
1. Go to the tab “Time gating” move and adjust the green marker so that it selects the area with synchrotron light. If the x-axis on the histogram is very different from the example, the modulo might need to be changed. Change to “expert mode” to view it.
2. If you will do long exposures, it might be beneficial to also check “Subtract dark”, and to move the red-area to a suitable position.
3. Go to the tab “Mask”, and make sure the masks are not covering the edges of the line. We need as much as possible of the line for a good curvature correction. The line-finding in the curvature correction is working on masked data (although the raw image is displayed).
4. Go to the tab “Curvature”, select the curvature in the list and click “-” to remove it.
4. Adjust the intensity so that you can see the line clearly by dragging the white marker towards lower values.
5. Drag the edges of the box so that it covers the line, but not much more.
6. Make sure the red line finds the measured line nicely, you can drag the white pieces of each slice for manual adjustments
6. Click the “+”-button to add the curvature. You see a preview of the correction to the right
7. Click the button “Apply correction”
8. Go to the mask-tab and add or adjust the masks as needed. They are moved by dragging them with the mouse, their size is adjusted by dragging the small marker in their top-right corner. Don’t forget to click “Apply”
9. Now you have made the calibration, and you are ready to set an energy scale.

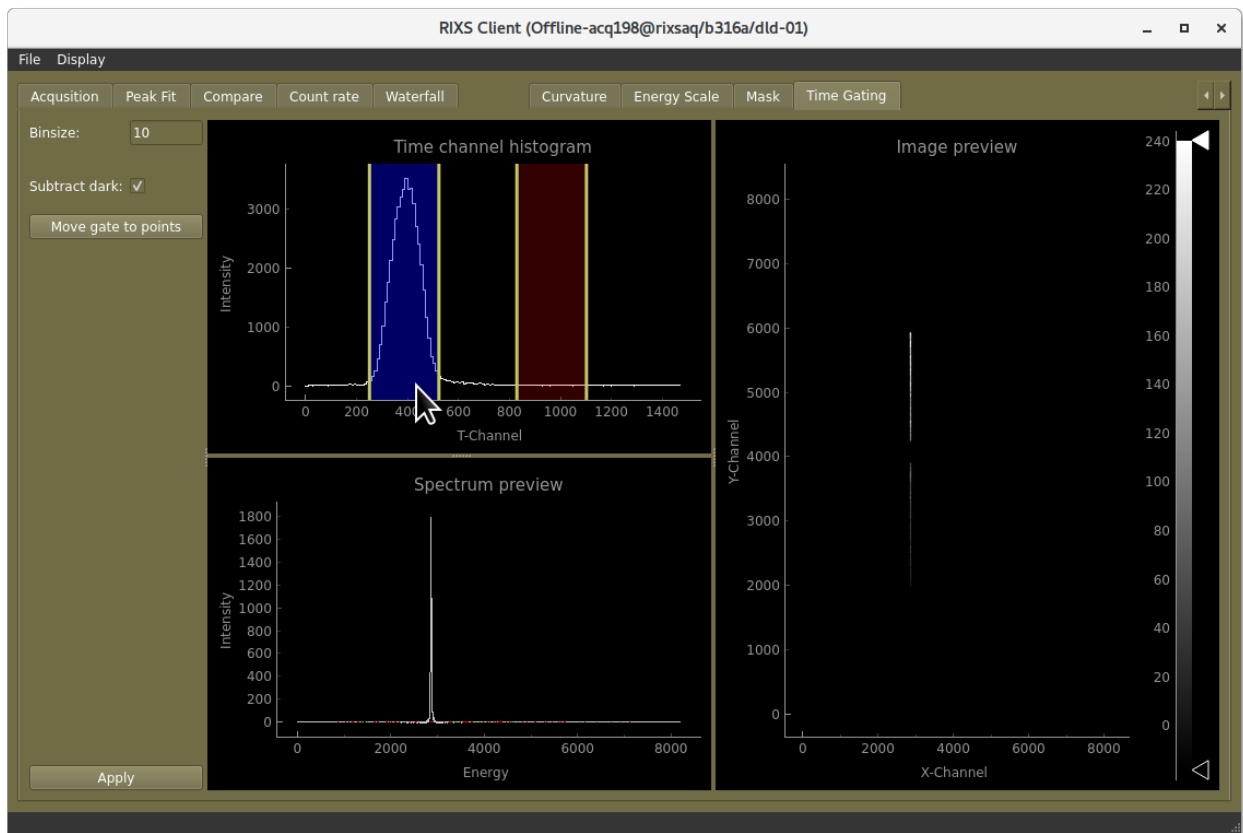


Fig. 2: Drag the green-area to select where in time you want to select the hits on the detector

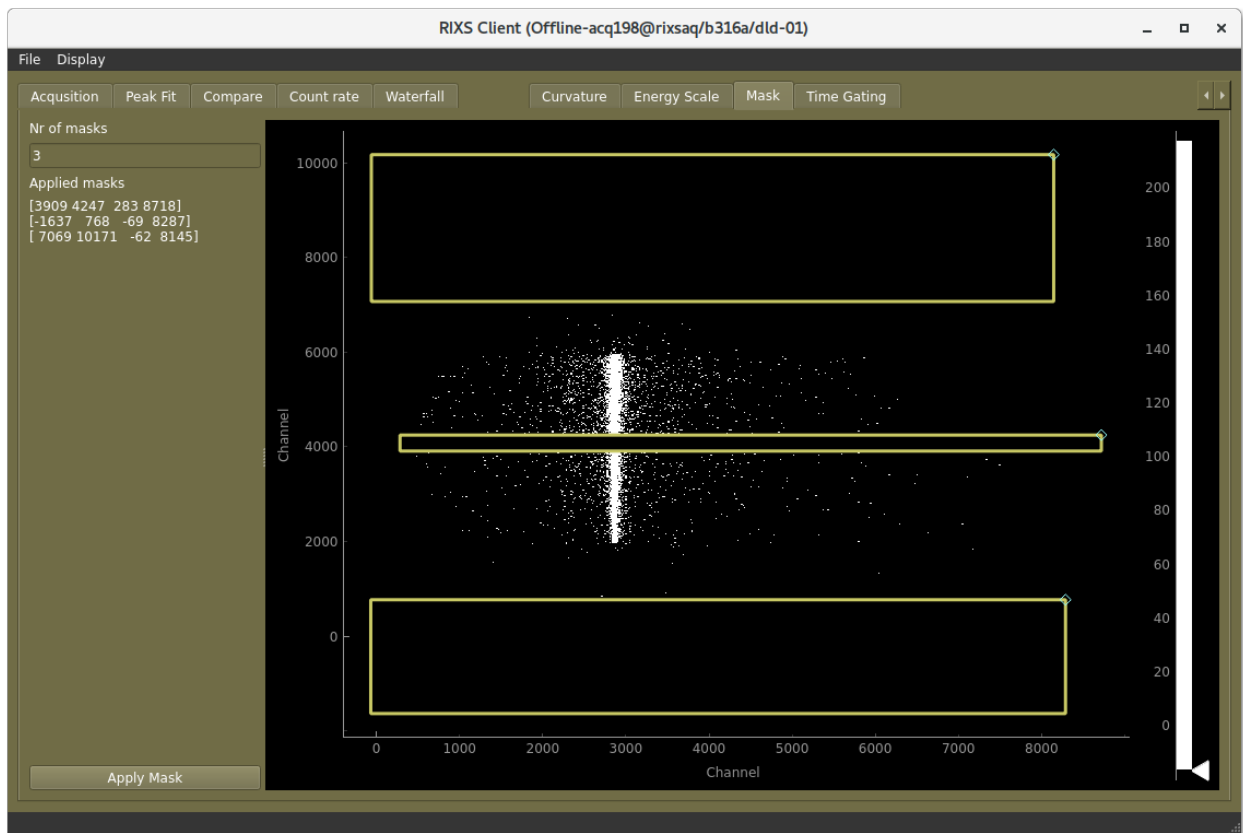


Fig. 3: Make sure the line is not masked out

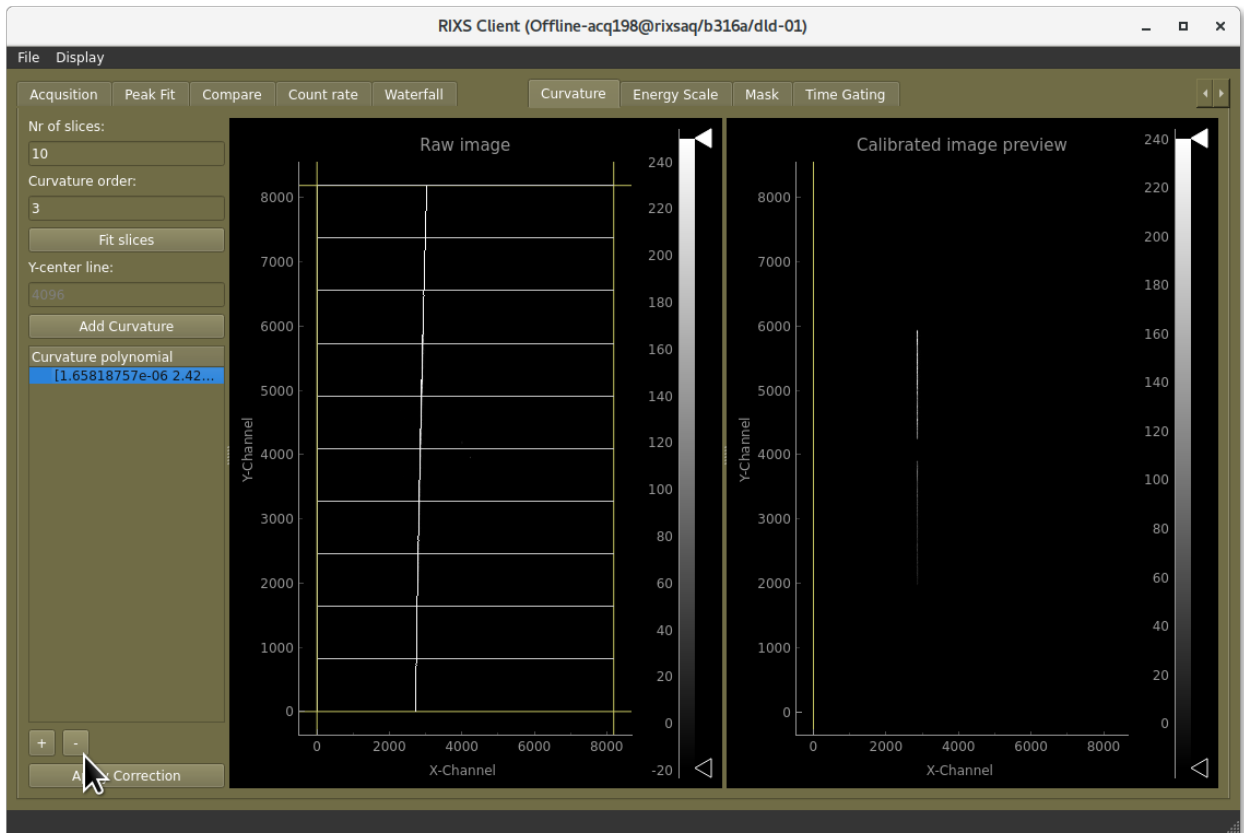


Fig. 4: Remove the old curvatures

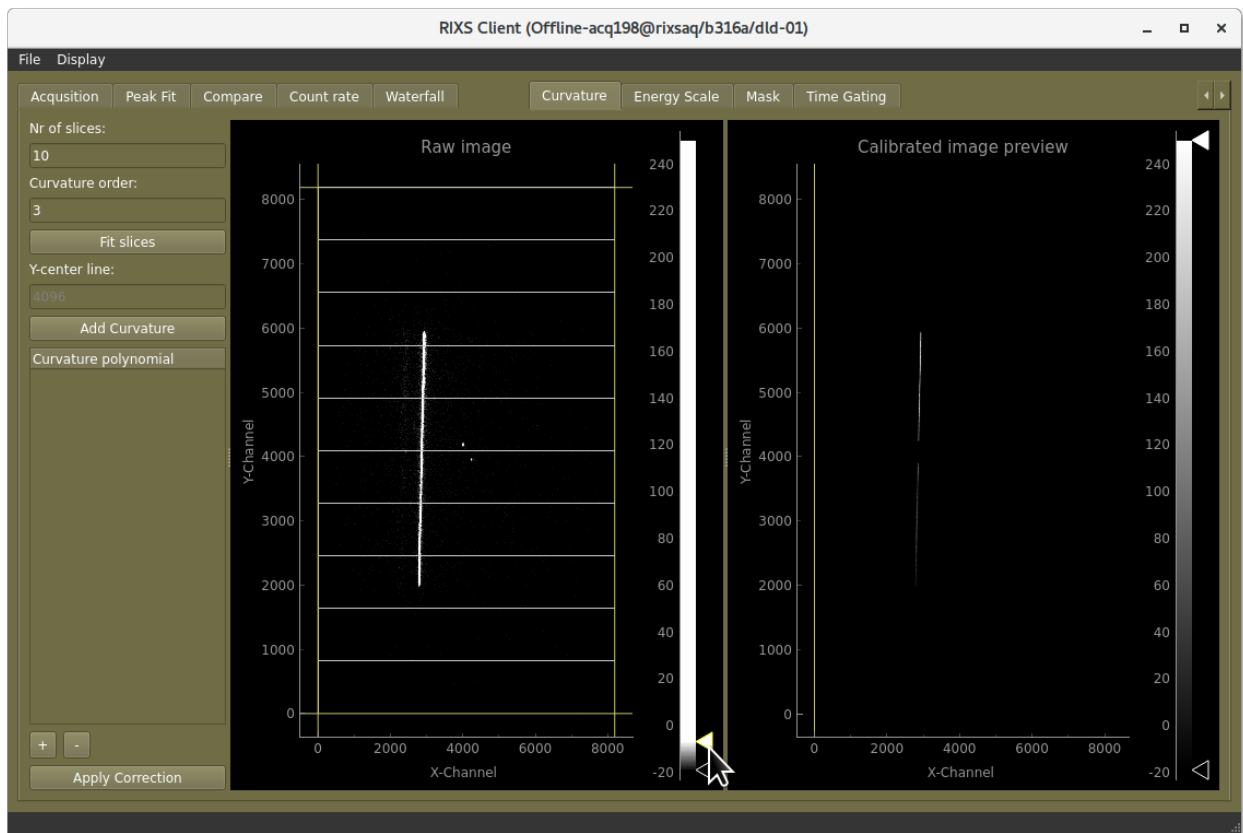


Fig. 5: Adjust the intensity so that you can see the line clearly.

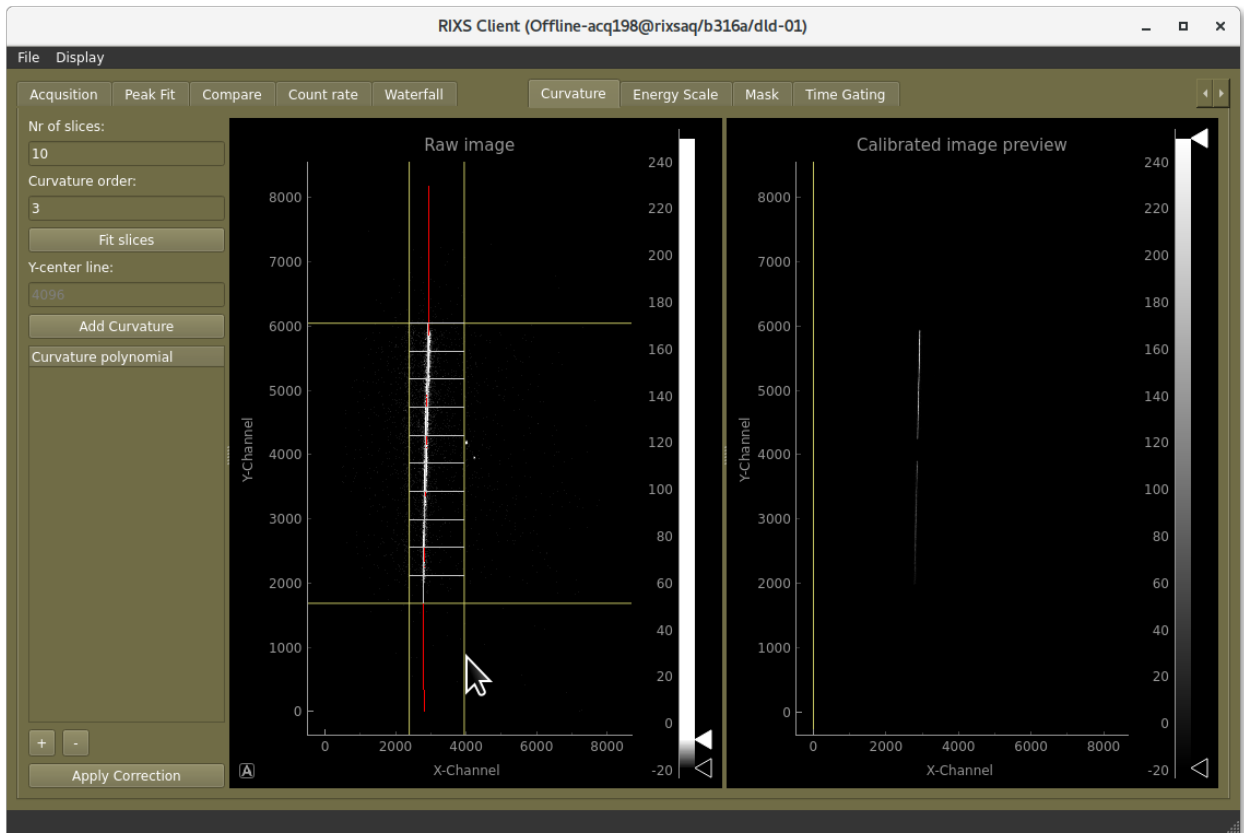


Fig. 6: Adjust the corners of the box so that it covers the line.

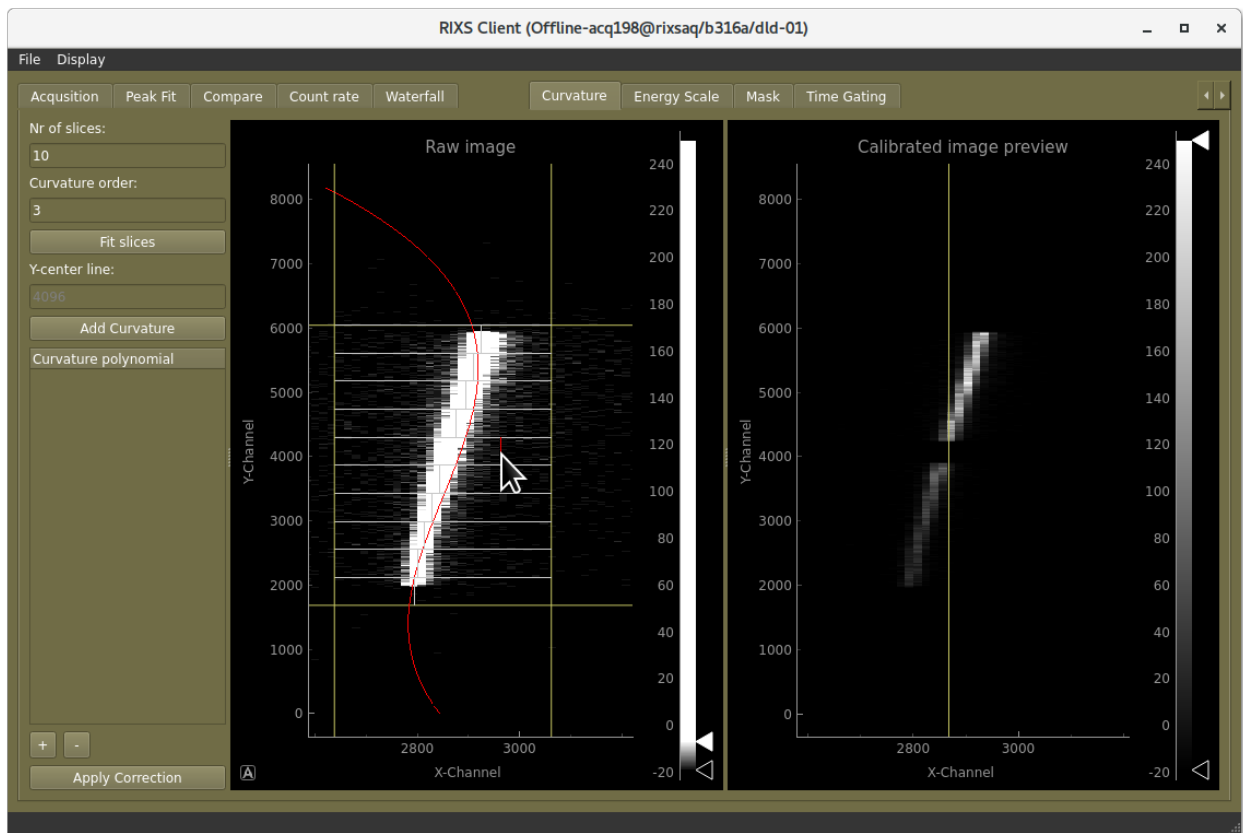


Fig. 7: Adjust the fits if needed.

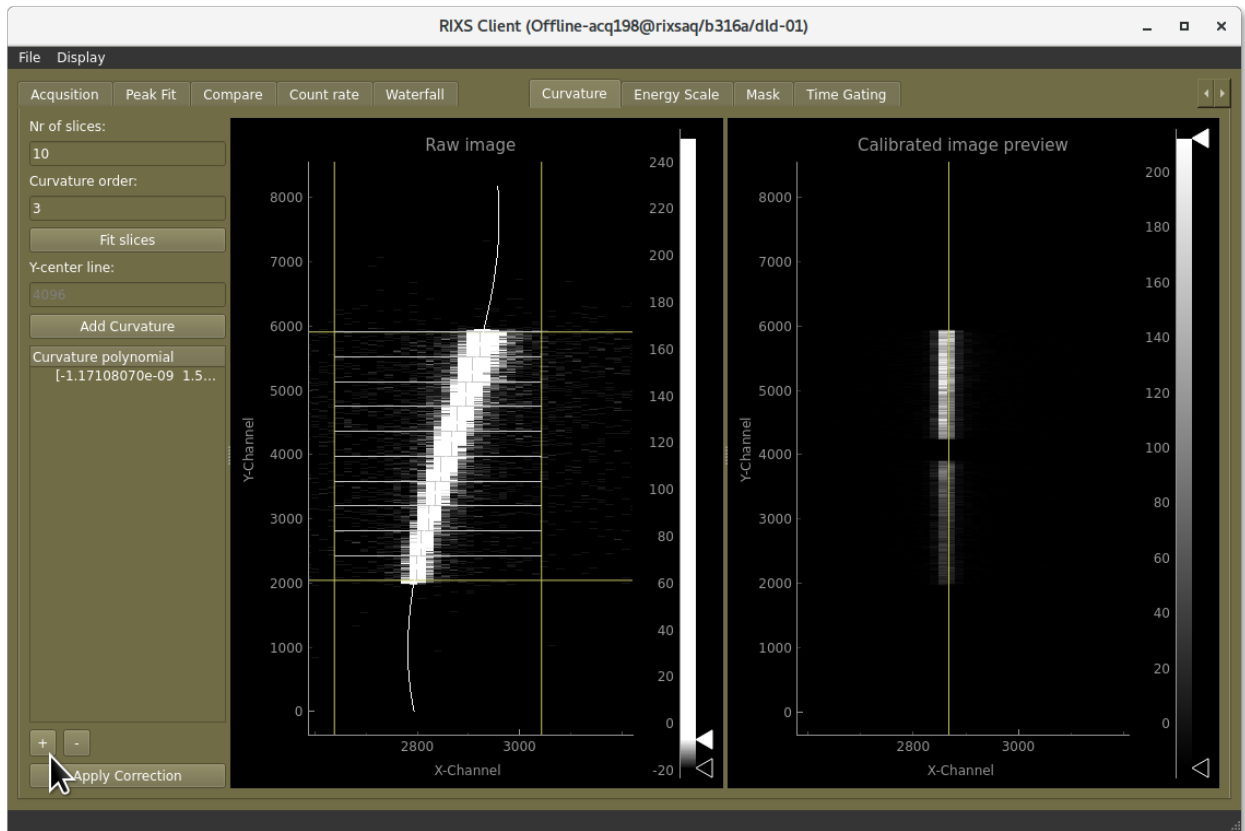


Fig. 8: Click the “+”-button to add the curvature

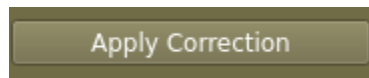


Fig. 9: Don't forget to apply the curvature correction

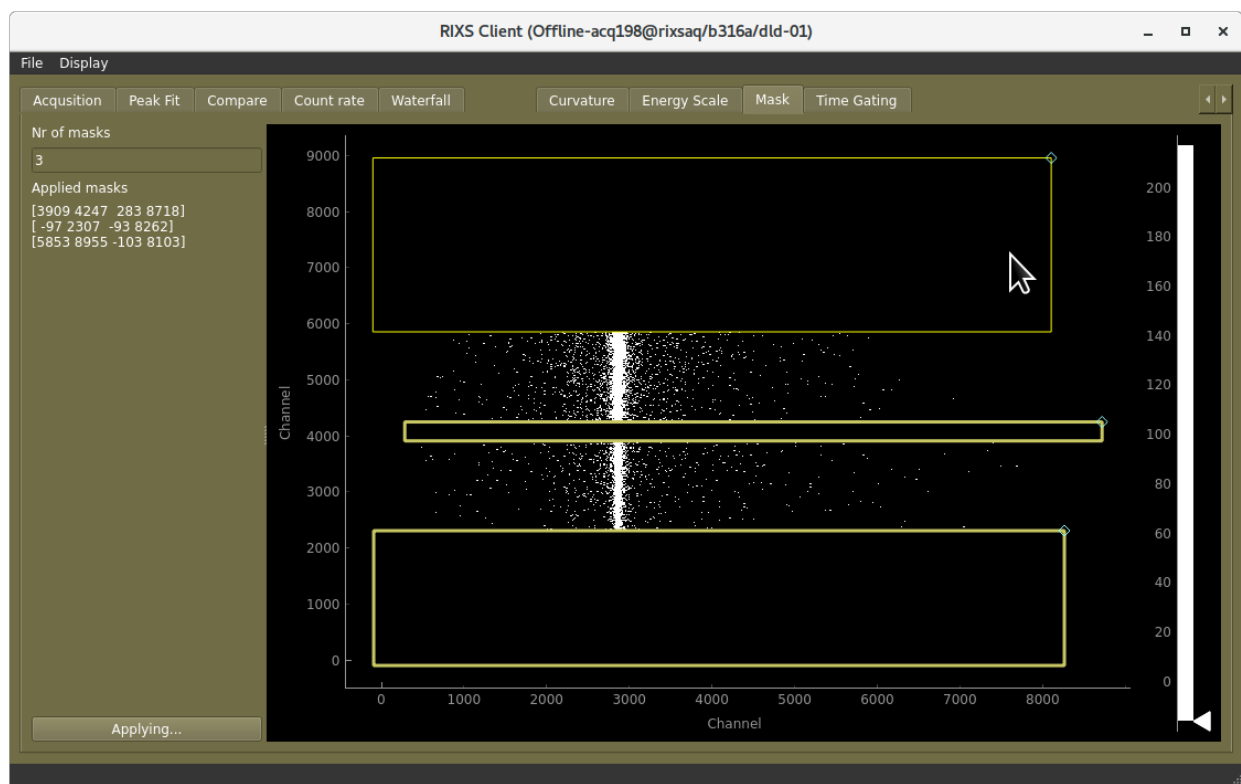


Fig. 10: Adjust the masks to cover areas you don't want included.

Setting an emission energy scale

1. First make sure you have set up the other steps of the calibration
2. Go to the tab "Energy scale", remove the old energy scale by clicking the "--" button then clicking "Apply scale"
3. Measure a few known lines across the detector, for example elastic lines with known monochromator energy.
4. Fit or otherwise estimate the channel number for each energy.
5. Add the to the table in the "Energy scale"-tab by clicking "+" to add a row then adjusting its energy, and channel number. You can also drag the line to the right to set the channel.
6. Apply the scale

3.5 Alba elektrometer gui

How to start it:

- Go to the webbrowser: and go to the appropriate URL
1. aemexp2: <http://b316a-a101630-aem-temp-01:8888> (**This is the primary for the endstation**)
 2. aemexp: <http://b316a-ea03-ctl-aem-01.maxiv.lu.se:8888>
 3. aemoh: <http://b316a-o02-ctl-aem-01.maxiv.lu.se:8888>
 4. aemslit: <http://b316a-ea01-ctl-aem-temp-01:8888>

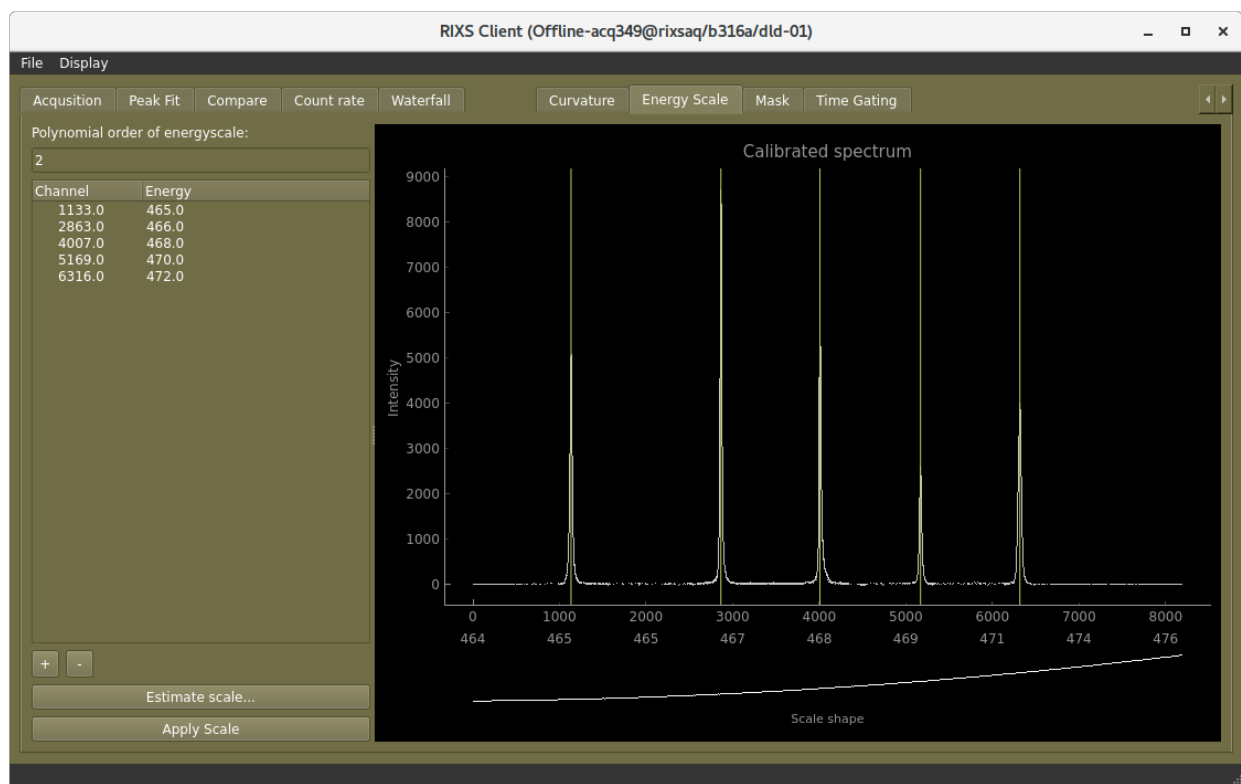


Fig. 11: The energy scale is set by inputting a table of detector channels with corresponding photon energies.

What does it do?

Allows you to see the current currents and change settings

When do I need to use it?

- When doing XAS-measurements, you need to have the appropriate measurement range on the elektrometer. Go here to change the range

How to change range

- Copy the hostname in the top right e.g. b316a-a101630-aem-temp-01.maxiv.lu.se
- Unlock the settings by clicking the small lock, the hostname is the password
- Set the range for your channel

3.6 Sample tracker

How to start it

- On desktop: "Sampletrackergui"
- In terminal: `"/mxn/groups/veritas/ludde/startsampletrackergui.sh"`

What does it do? The sample tracker consists of two components.

1. A plotter for meshscans, useful for mapping and finding your sample
2. A red line that displays where on the sample you have previously measured.

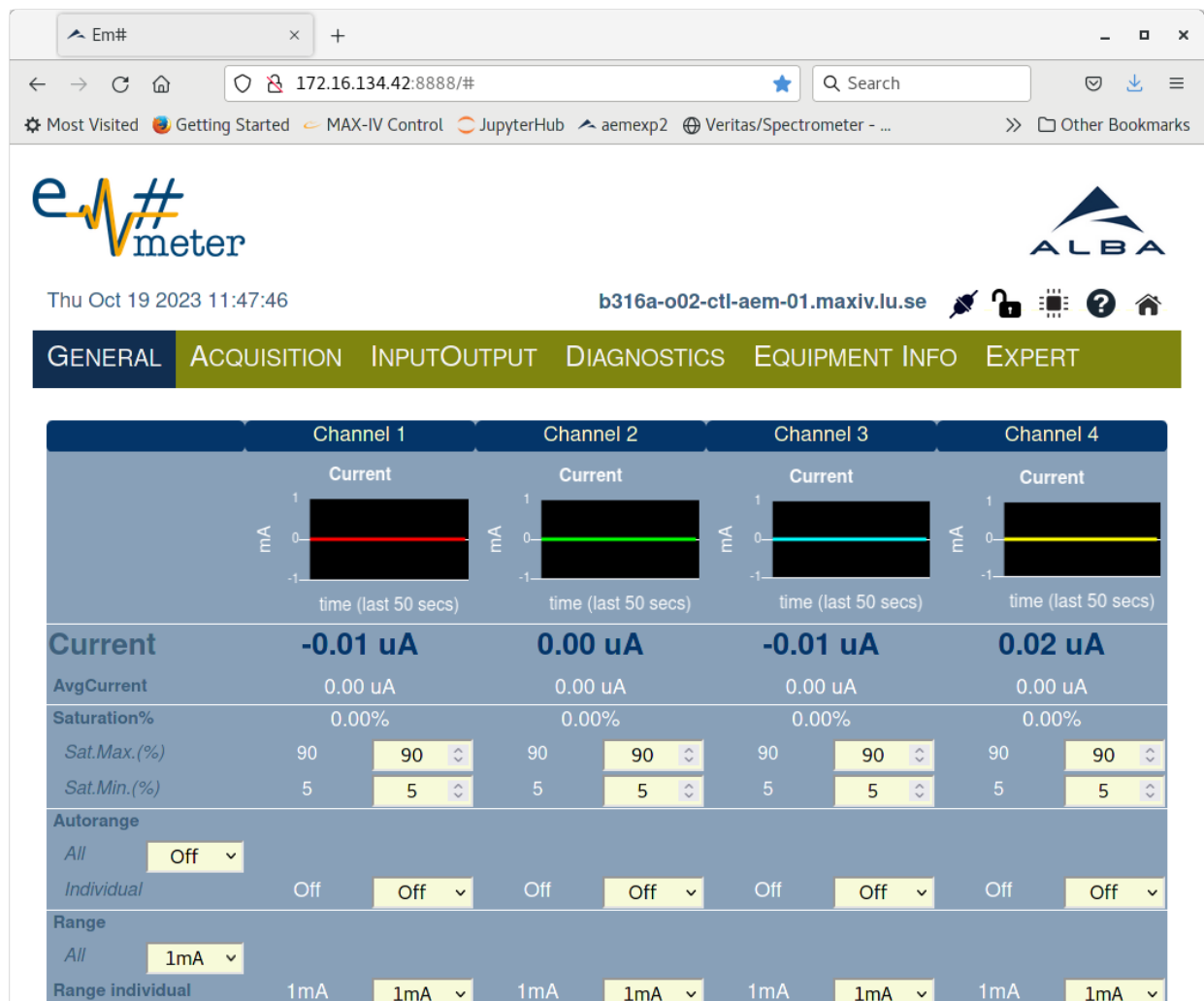
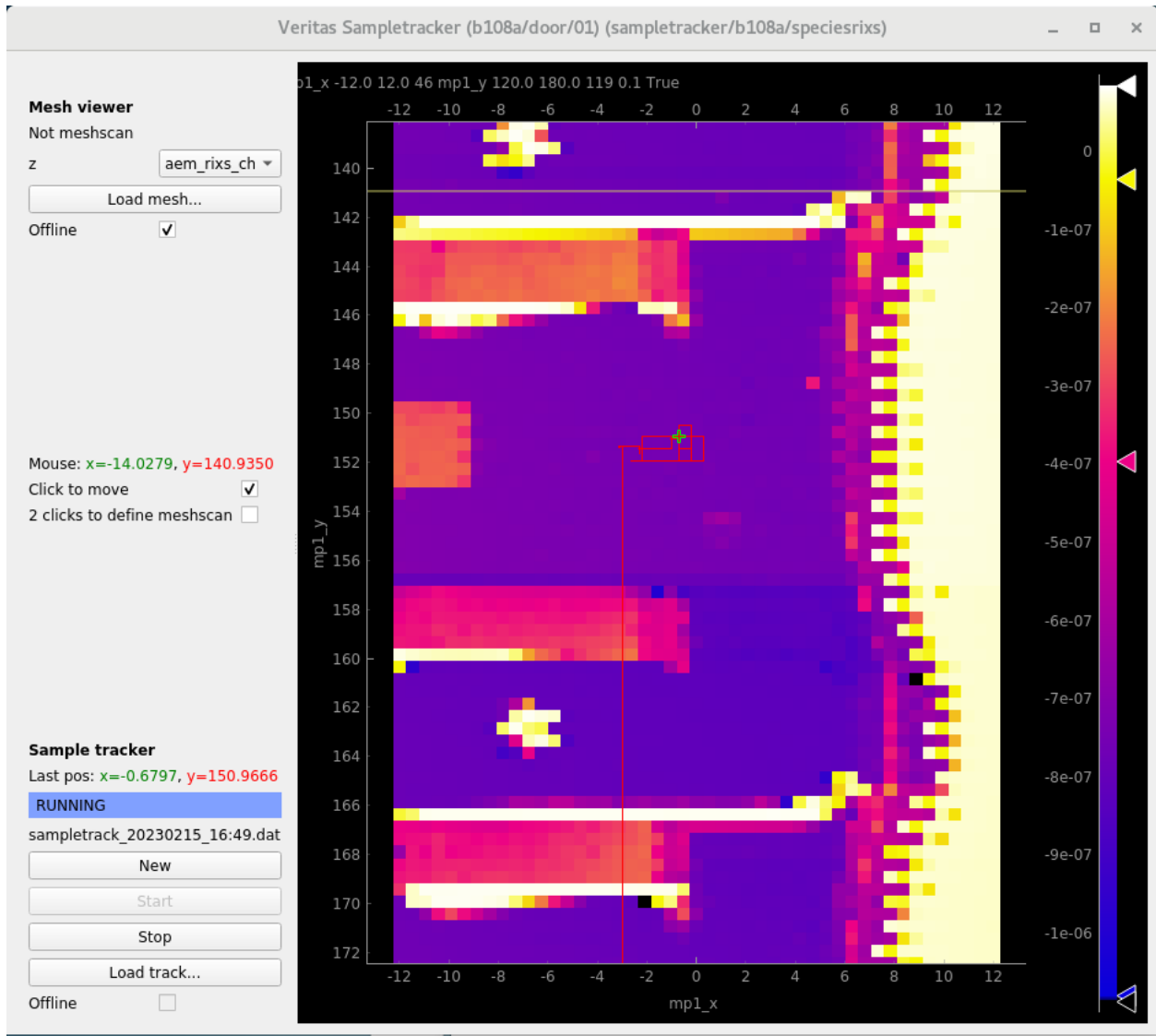


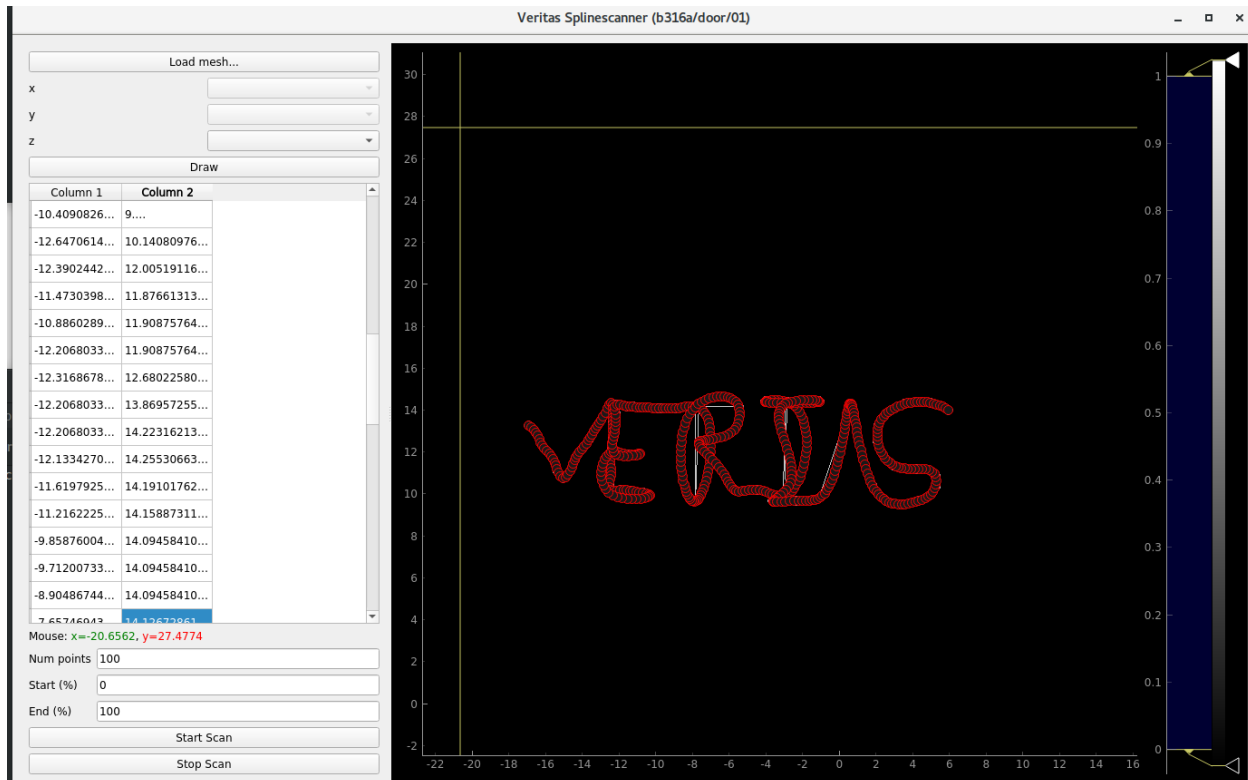
Fig. 12: The alba electrometers are mainly controlled by a web interface



When do I need to use it? To plot meshscans, to keep track of where you have measured.

Gitlab link: <https://gitlab.maxiv.lu.se/veritas/app-maxiv-rixs-sampletracker>

3.7 Splinescanner



How to start it:

- On desktop: “Splinescannergui”
- In terminal: “/mxn/groups/veritas/ludde/app-maxiv-splinescannergui/startit.sh”

Gitlab link: <https://gitlab.maxiv.lu.se/veritas/app-maxiv-splinescannergui>

3.8 Scanlog

How to start it:

- Go to the webbrowser: <https://scanlog.maxiv.lu.se/>

3.9 Astor

3.10 Spock

3.11 Jive

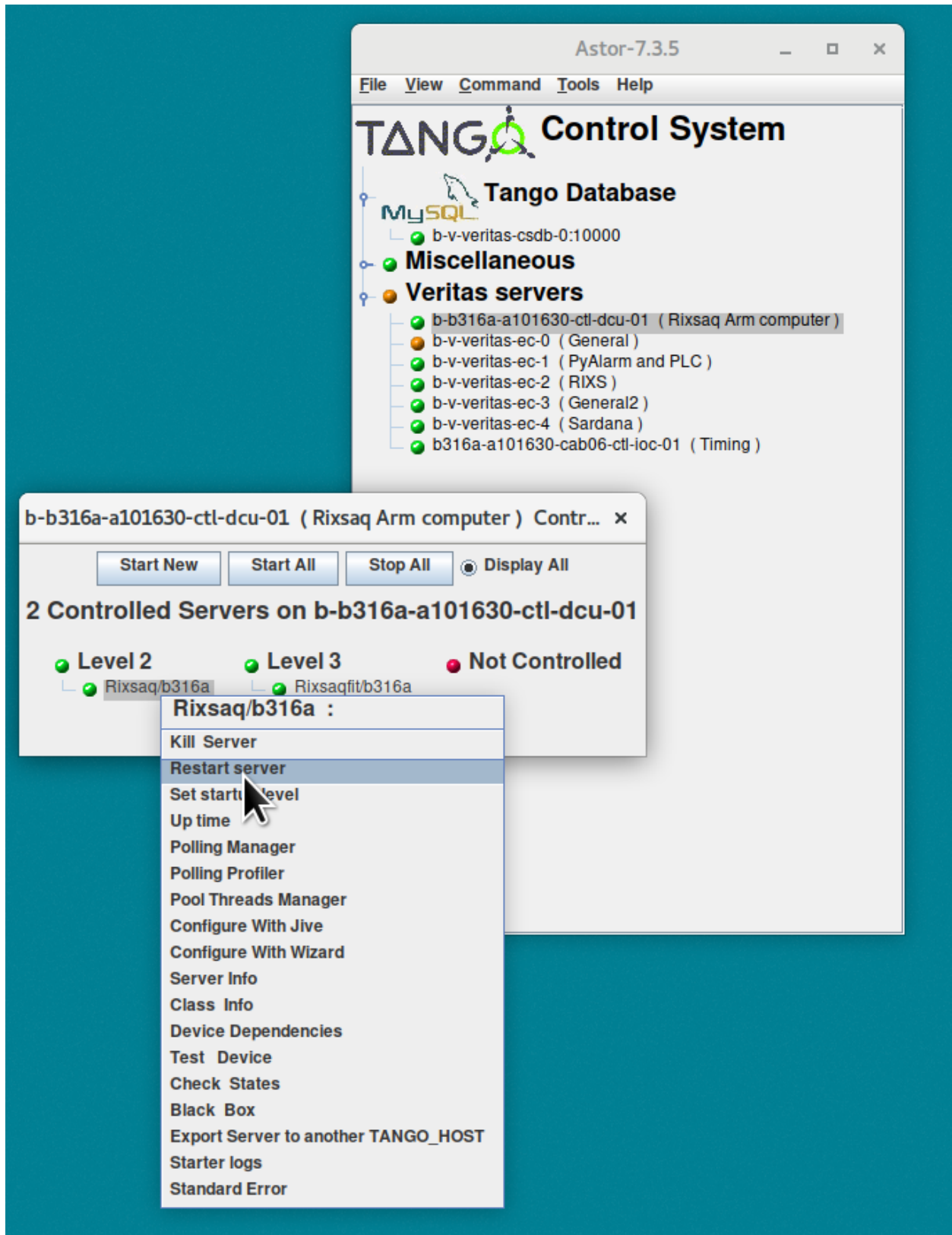


Fig. 13: Astor is used to restart tango devices

```

IPython: home/veritas-user
File Edit View Search Terminal Help
object? -> Details about 'object'. ?object also works, ?? prints more.

IPython profile: spockdoor
Connected to Door_B316A

Door_B316A [1]: MainThread WARNING 2023-10-19 11:46:20,627 TaurusRootLogger: Qtdefault None.None[0]: Qt: Ses
sion management error: None of the authentication protocols specified are supported
Door_B316A [1]: ascan dmot01 > 10 10 0.1
This operation will not be stored persistently. Use "expconf" or "newfile" to configure data storage (or eventual
ly "senv ScanDir <abs directory>" "senv ScanFile <file name(s)>")
Scan #9 started at Thu Oct 19 11:46:39 2023. It will take at least 0:00:03.928427
#Pt No dmot01 aemexp_timer aemexp_ch1 aemexp_ch2 aemexp_ch3 aemexp_ch4 dt
0 0 0.1 2.77108e-07 1.34083e-06 1.94403e-08 5.84431e-08 0.11796
1 1 0.1 2.76195e-07 1.34172e-06 2.03695e-08 5.87243e-08 0.802553
2 2 0.1 2.76802e-07 1.3421e-06 1.98804e-08 5.87977e-08 1.3727
3 3 0.1 2.76128e-07 1.34147e-06 1.95626e-08 5.87855e-08 1.92
4 4 0.1 2.76053e-07 1.34117e-06 2.11153e-08 5.79907e-08 2.46241
^C
Ctrl-C received: Stopping...
Stopping Motion(['dmot01']) reserved by ascan
Motion(['dmot01']) stopped
Stopping aemexp reserved by ascan
aemexp stopped
Scan #9 ended at Thu Oct 19 11:46:42 2023, taking 0:00:03.358032. Dead time 84.3% (setup time 0.8%, motion dead t
ime 40.8%)
Executing ascan.on_stop method...
Stopping done!

Door_B316A [2]:

```

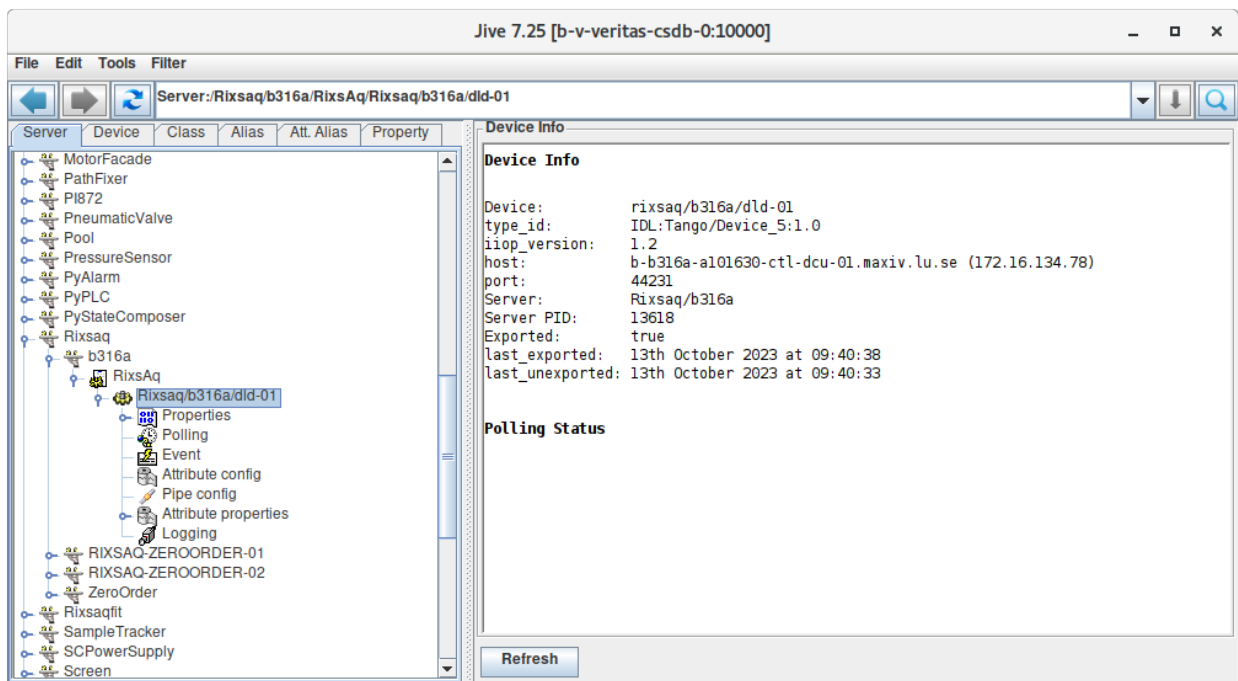


Fig. 14: Jive can be used for advanced control system operations

START YOUR BEAMTIME

Here is a short introduction to start the experiment. Please open the following three interfaces to view, move, control and scan the required (pseudo) motors in order to execute your experiment during the beamtime.

- General beamline control: [Synoptic](#) and [QuickGUI](#)
- Scanning, for XAS-measurements (or RIXSmaps): [Scangui](#)
- RIXSmeasurements: [Rixsclient](#)

4.1 Samples handling

At the RIXS endstation in Veritas beamline, you can carry out experiments with solid, liquid and gas samples. Here is a brief introduction of the sample environment, sample handling and preparation (particularly solid state samples).

4.1.1 Solid state samples

Get to know the endstation chambers

As already mentioned in the [previous section](#), the Veritas RIXS endstation has three chambers, for solid and gas samples, as labeled in the figure:

- Load Lock (LL) chamber
- Upper chamber or transfer chamber. This chamber receives the sample plate(s) from LL chamber. This chamber also houses the sample rod (which is also the closed cycle He cryostat).
- Q-chamber or the measurement chamber. It allows continuous motion of the scattering arm without breaking the vacuum.

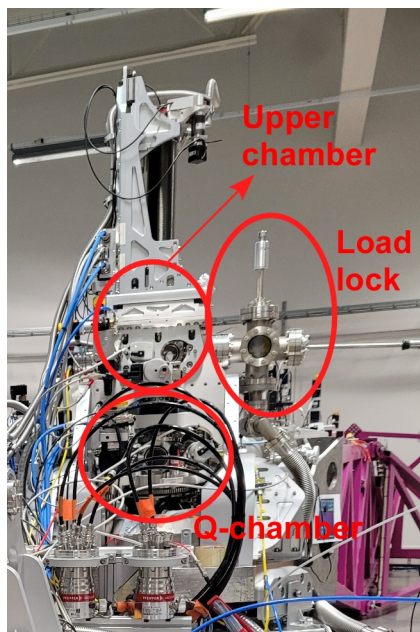
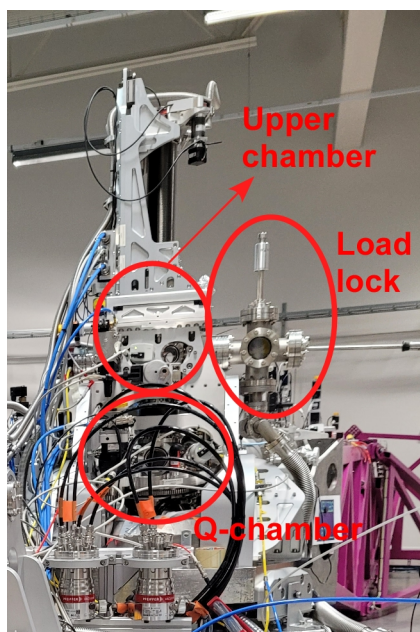


Fig. 1: RIXS endstation chambers.



The solid samples can be in the form of powder (pelletized), single crystals or thin films. Here is a brief introduction of the steps you may follow to introduce your sample finally into the main chamber.

Here is a flowchart of the process that we usually follow.

NOTE: If your sample is air sensitive, you can use the argon suitcase and mount it directly on the load lock. To avail this, you must use the glove box facility available in one of the chemistry labs.

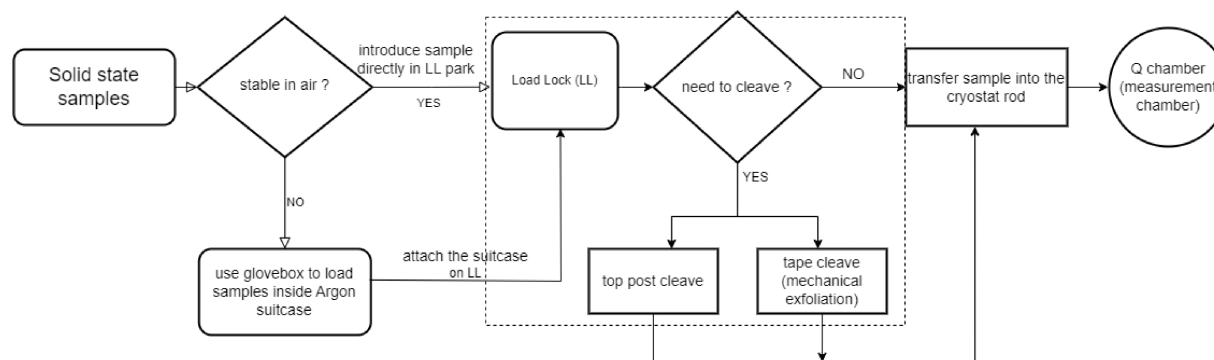


Fig. 2: Solid state sample handling.

Sample plate

We use Omicron flag-style sample plate and the sample is glued on it either using both-side copper tape (if you are not cleaving the sample) or some conductive epoxy (example: Epotek H21D conductive epoxy, or Epotek E4110 conductive epoxy). Currently we have stainless steel and copper sample plates, and if you need, we can ship a few plates to the your address. For this, the you must approach the beamline responsible atleast one month ahead of the scheduled beamtime.

The sample gluing on the sample plate must be done within one of the shaded regions depending on the choice of cryostat head during experiment. You may glue multiple samples in one sample plate (if the azimuth cryo-head is not used), however, it is recommended to follow the orientation as shown in the figure.

All dimensions are in mm

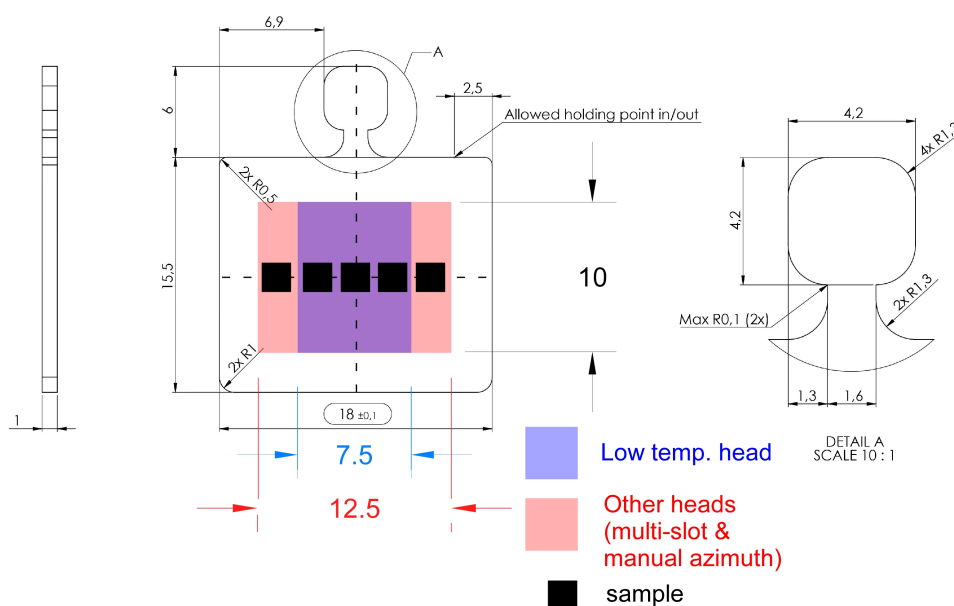


Fig. 3: Sample plate and sample gluing regions.

Load Lock

The load lock (LL) is attached to the upper chamber, and equipped with a linear transfer arm constituting of a sample bank to store four sample plates.

If your sample is air sensitive and cleaving may not be possible, please contact the beamline responsible and we will exchange the linear transfer system with an argon suitcase constituting of four sample plates bank. In this case, you, the user, may use Ar glove box available in one of the Chemistry labs at MAX IV to transfer samples into the samples plate bank of Ar suitcase. Purge the LL with Ar several times (5-6 times) before opening the suitcase valve, after which start the roughing pump followed by the turbo pump and wait till the pressure in LL is lower than 5×10^{-7} mbar.

If you want to cleave the sample, you dont need to use the Ar suitcase. Introduce the sample plates from the LL door into the sample bank. After reaching appropriate pressure in the LL (lower than 5×10^{-7} mbar), you may cleave with the transfer wobble stick.

How to Cleave ?

1. Top-post cleave Glue a post on the sample surface using conductive epoxy (example: Epotek H21D conductive epoxy, or Epotek E4110 conductive epoxy). It is recommended to use a post of similar surface area as that of the sample. Inside the LL, after reaching appropriate pressure, knock off the post using the transfer wobble stick to expose a clean sample surface.

2. Tape cleave (mechanical exfoliation) You can also exfoliate the sample surface using tape (typically we use kapton tape). See the figure.

Transfer sample to the sample rod in upper chamber

Now its time to transfer the sample plate(s) to the sample rod in the upper chamber (UC). Prior to transfer, the manipulator must be set to sample transfer positions in order to receive the sample plate. Let us know how to do this :

You need the following softwares to align the sample rod's sample holder surface parallel to the sample plate:

Open these softwares

Prior to sample transfer and subsequent experiments lets open and get familiar with the following two control panels / softwares:

1. QuickGUI
2. Scangui

Sample transfer positions

The sample transfer will differ depending on the samplerod and environment currently in use. Please not the differences when indicated Please continue working on the list below.

Using the [QuickGUI](#), Move manipulator to the following positions depending on the choice of the sample rod head:

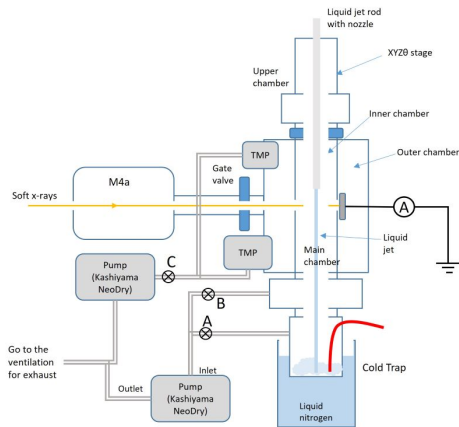
Sample transfer positions for the low temperature head at 10 K:

Positions	Low temperature head	multi slot head	azimuth head
a_mp1_x	66.65 mm		
a_mp1_y	374 mm		
a_mp1_z	17.5 mm		
a_mp1_yaw	2 deg (tight/loose), 357 deg (to insert / remove sample plate)		

Transfer process: Follow the following steps to transfer the sample plate into the sample rod in the UC.

1. Close the valve between Q chamber and UC.
2. Check LL pressure is in the order of 10^{-7} mbar.
3. Open the valve between the LL and UC.
4. Rotate the manipulator (a_mp1_yaw) to tight/loose position.
5. Tight/un-tight the screw holding the sample plate.
6. Remove if there is any sample in the sample rod and and park it in the LL sample garage.
7. Rotate the manipulator (a_mp1_yaw) to sample insert position.
8. Grab a new sample plate from LL garage.
9. Transfer it to the sample rod in the UC.
10. Rotate the manipulator (a_mp1_yaw) to tight/loose position.
11. Tight the screw.
12. Repeat the process between 5-11 if you have multiple samples.
13. Retract the transfer wobble stick and close the valve between LL and UC.
14. Open the valve between Q chamber and UC (safety feature: you cannot lower the manipulator if the valve is closed, yet its better to check and open the valve before lowering the manipulator).
15. Lower the manipulator to experimental position.
16. Now its time to find the samples. Go to “**Finding samples**” section.

4.1.2 Liquid samples

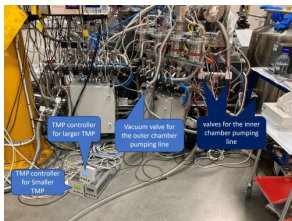


How to start pumping

1. Open angle valves (A and B) for inner chamber pumping. Wait for a min.
2. Open angle valve (C) for outer chamber pump.
3. Start two TMP for outer chamber pumping
4. Wait for the vacuum recovely

How to stop pumping

1. Confirm valves to beamline and emission specrometer is closed. it is recommended to close 3 valves from the endstation main chamber. if filter valve is used, remove filter(i.e. open filter valve) just after closing closing gate valves, to not make damage on the thin film window.
2. Close angle valve(C) for outer chamer pumping.
3. Close angle valve(B and C) for innter chamber pump.
4. Stop two TMPs for outer chamber pumping (and enable auto vent for larger TMP, if it is not enabled)
5. Wait for chmaber will be vent with air.



Procedure to Cleaning cold trap

The chamber is need to be in air pressure before starting. It is required to close top lid.

1. Prepare hot water by a electric kettle. There is a black one with around 2l capacity and white smaller one. Cold trap capacity is around 4l, so do not put more than 2l of water.
2. remove or Lower the height of the nitrogen dewer under the cold trap. if there is remalind liquid N₂. It is better not to remove cold trap since it is required to tilt the dewer to remove.
3. Add liquid nitrogen to the trap of the sample remover setup
4. Find a red line with a blank plug under cold trap. Connect a extension tube to the red tube line for put hot water into the cold trap.



5. Open the slow pumping line around B valves (in the schematic of endstation. pumping line with 6mm stainless steel tube) and slowly pump the chamber by kashiyama pump to let the cold trap to suck in the hot water. Wait for letting ice melt (around 3min). Keep through slow pumping line even after all water it goes in the cold trap. This will help not to feed the humid air to outer chamber.
6. Connect red line to the sample remover setup which is prepared beside M4 mirror of b branch.
7. Start the small pump of the sample remove setup and remove liquid from the cold trap. if glass canister becomes more than half. Stop pumping and exchange glass bin and continue pumping.
8. If cold trap still have ice go back to procedure no.5.
9. When all the sample is removed from cold trap. Put a blank plug to red line and seal it.
10. Detach glass canister of the sample remover, and store and dispose them by following the camical related rules.
11. Start pumping and wait for vacuum recovery. initially, it will be around 1mbar, but it will be comes better after start cooling cold trap. Outer chamber should be around 2 to 6E-4 after start cooling of cold trap.

If inner and outer chamber vacuum is not becoming better than 1mbar there is a lot of water somewhere in the chamber. Most case it is hot water spills in the pumping line from cold trap to the vacuum pump (large Kashiyama). Quick way to recover is exchange NW25 hose.

4.1.3 Gas samples

4.2 Finding samples

Now its time to expose your sample to x-ray photons. Prior to this, check from [synoptic](#) if we have beam on the slit, and all the valves are open. If the sample rod is still in the UC, make sure to open the valve between Q-chamber and UC.

We first start with a 2D spatial map of the sample (a_{mp1_x} vs. a_{mp1_y}), after setting a_{mp1_yaw} at normal incidence. From this point on, you are going to use the control and acquisition software named 'Scangui'. Here is how we do it:

4.2.1 Mesh scan

This is a 2D mapping of your sample using appropriate beamline energy. In the first attempt, the beamline energy does not need to be exactly the resonance energy, rather, any energy close to the resonant energy will work to get the contrast. You need to open these two softwares: **Scangui** and **Sampletracker**

After loading the sample down to the main chamber (we call it Q-chamber), you first begin with the mesh scan. This is how you can setup the mesh scan in Scangui:

go to 'MacroExecutor' or 'Sequencer' tab -> find 'mesh' macro from the 'Macro' dropdown list -> add it -> at the bottom, select the values 'a_mp1_x' and 'a_mp1_y' under parameters 'motor1' and 'motor2', respectively -> give start and final motors positions, nr_interval (number of steps), and integ_time. Set bidirectional to 'true' or 'false'.

4.2.2 Linescan

With the Scangui, you can along x or y while reading an absorption intensity

1. Start the *Scangui* and the *quickgui*
2. From the quickgui: Write down current manipulator positions: a_mp1_x, a_mp1_y, a_mp1_z, and a_mp1_yaw
3. In the quickgui, choose an appropriate beamline_energy for getting contrast when you are on the sample
4. In the Scangui, select the measurement group "NEXAFS" (see details on how to change measurement group in the entry about the Scangui)
5. In the Scangui, go to basic executor select a_mp1_x or a_mp1_y and scan around your starting guess
6. In the Scangui, plot a_mp1_x towards the appropriate alba elektrometer signal

4.3 Calibrating the emission spectrometer

See the entry under *RIXS client*

OFFLINE ANALYSIS

5.1 Data structures

During your experiment the data is recorded in two different .hdf5 files. .hdf5 files are a hierarchical data structure and behaves much like a “folder”. Each scan or rixs-acquisition has a folder in the files “entry343” or “acq1337”

5.1.1 Scangui/Sardana HDF5 files

- The data recorded for each sardana scan, is selected by the **measurement group** in the scangui. You will find for example the data from the alba elektrometer in the .hdf5 file under: “entry865/measurement/aemexp2_ch2”.
- You can find the start time of the scan under “entry865/start_time”
- You find the command that run the scan (with e.g. the beamline range) under “entry865/title”
- Before the start of each scan, a pre scan snapshot with some values is recorded. You find e.g. the sample position under “entry865/measurement/pre_scan_snapshot/a_mp1_x”

5.1.2 RIXSaq HDF5 files

Lets use “acq325” as an example. The pre-processed data can be found under: “/acq325/data/calib_x_spectrum” and “/acq325/data/energy_scale”

The raw point-by-point data can be found under: “/acq325/Instrument/DLD8080/data/points” The raw points are 12 columns, each row represent one hit on the detector. The 12 columns are:

1. x, spatial position, unit in bins 0-8192
2. y, spatial position
3. t, bunch-clock, unit: timebins, the clock is reset to 0 at every revolution of the ring.
4. t, unixtimestamp, added to the data during readout. Used e.g. for removing the last 5minutes of the measurement.
5. millisecond counter
6. start_counter, number of revolutions in the ring. +1 every time the bunch-clock is reset
7. time_tag, time in 0.5ns bins since a signal on the time_tag input. Currently connected to one of the manipulator axes.
8. master_rst_counter, not used
9. signal1bit, not used
10. Extra1 (Tango attribute set by the RIXS client, for example the beamline_energy or veritasarm_energy)

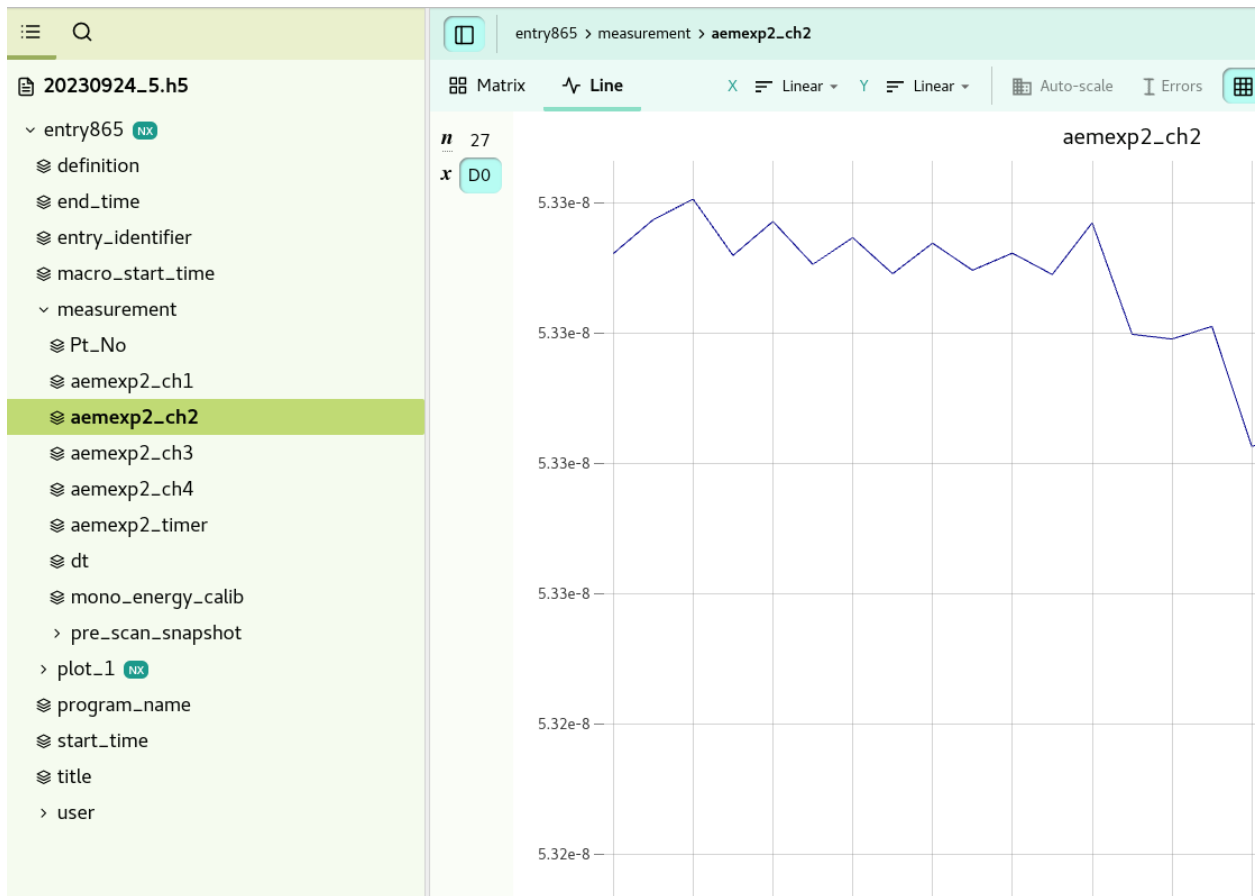


Fig. 1: The hdf5 data can be browsed using <https://jupyterhub.maxiv.lu.se/>

11. Extra2

12. Extra3

For each scan there is also metadata recorded at the start and the end, you find them in: “/acq325/startmetadata/a_mp1_yaw/position” or “/acq325/endmetadata/a_mp1_yaw/position”

throughout the rixs-measurement, some attributes are also recorded as timestamped data. You can find for example the manipulator position as a function of unixtimestamp here: “/acq325/External/a_mp1_x/position”

The calibration used for the pre-processed data can be found under: “/acq325/Instrument/DLD8080/calibration” More information about that calibration in the library: <https://gitlab.maxiv.lu.se/species/lib-maxiv-rixsaq/>

5.2 Python platform

5.2.1 Jupyter

The data measured at the beamline can be accessed from within max iv user our jupyterhubserver: <https://jupyterhub.maxiv.lu.se>

Examples of usage:

- Plotting XAS-measurements and normalizing to a current
- Fitting XAS-measurements
- Making 2D-images from meshscans
- Comparing RIXS-data

5.2.2 Contour plotter

Python script for plotting mesh-data in jupyter. Where can it be found?

5.2.3 RIXSaq python API

For the advanced user there is a python library available to process the RIXSaq data. The same library is used for the online calibration and processing, examples and information is available on the gitlab page.

<https://gitlab.maxiv.lu.se/species/lib-maxiv-rixsaq/>

To use it in e.g. jupyter, copy the rixsaqlib folder from the repository and place it in your working directory.

5.3 MatLab platform

5.3.1 Basic data reading, plotting, and saving

Users familiar in MatLab platform can also work with the data. Here are some basic commands the user can execute to view the file structures, read and plot the pre-calibrated, processed data:

Make sure that you are in the correct folder where the file is.

1. Short information about the data structure: “`h5info('abcd.h5')`”, or specifically “`h5info('abcd.h5', '/entry1234')`”

2. Detailed information: “h5disp('abcd.h5')”, or specifically “h5disp('abcd.h5', '/entry1234')”
3. Read any motor position if it is in the pre-scan snapshot of ScanGui file or metadata of DLD file; eg.: “h5read('scans-2023-04-05.h5', '/entry2791/measurement/a_slit1_v')” → reads the slit width (a_slit1_v)
4. Reads data, plot, and save the file in .txt format. Here is an example:

ScanGui

```
X=h5read('scans-2023-04-05.h5', '/entry2791/measurement/beamline_energy'); % X axis is beam-  
line_energy
```

```
Y=h5read('scans-2023-04-05.h5', '/entry2791/measurement/aem_rixs_ch3'); % Y axis is electrometer  
channel, eg. 'aem_rixs_ch3'
```

```
plot(X,Y) % plot data
```

```
A(:,1)=X; A(:,2)=Y; % storing in a matrix named A
```

```
save('filename.txt', 'A', '-ascii') % save A under the name 'filename.txt' in the same folder
```

RIXS

```
X=h5read('20230304_DLD_1.h5', '/acq002/Instrument/DLD8080/calibration/energy_scale'); % X  
axis
```

```
Y=h5read('20230304_DLD_1.h5', '/acq002/Instrument/DLD8080/calibrated_data/  
calib_x_spectrum'); % Y axis
```

```
plot(X,Y) % plot data
```

```
A(:,1)=X; A(:,2)=Y; % storing in a matrix named A
```

```
save('filename.txt', 'A', '-ascii') % save A under the name 'filename.txt' in the same folder
```

5.3.2 Software (based on MatLab platform) for general users

We can provide a complete data treatment software based on MatLab. The user can install this in their **Windows** or **MAC** computers. MatLab installation or licensing are not required to install this software. Please contact the beamline staff (Anirudha Ghosh) to get access to these softwares.

There are two software packages: “SpectraViewer” and “RIXS Analysis” for basic and advanced data treatment, respectively:

SpectraViewer

You can use this program to plot and save (in .txt format) XAS and RIXS data and generate a log file that contain all the metadata from the scans. Here are the main features of this software:

- plot single or multiple XAS or RIXS plots.
- normalize XAS plots from single or multiple electrometer channels.
- generate RIXS maps with respect to any parameter.
- generate a log table with two editable columns.
- the log table is automatically saved in .xlsx format.
- save the contents of the line spectra plot in .txt format.

You may download and install the latest version of SpectraViewer for [Windows](#) and [MAC](#) using the link.



Fig. 2: SpectraViewer interface with a few functionalities.

RIXS Analysis

Here you can do advanced analysis using the raw data from RIXS .h5 file. The figure shows the interface of the software. It has several tabs using which you can do different types of analysis, thereby utilizing the full potential of the Veritas beamline.

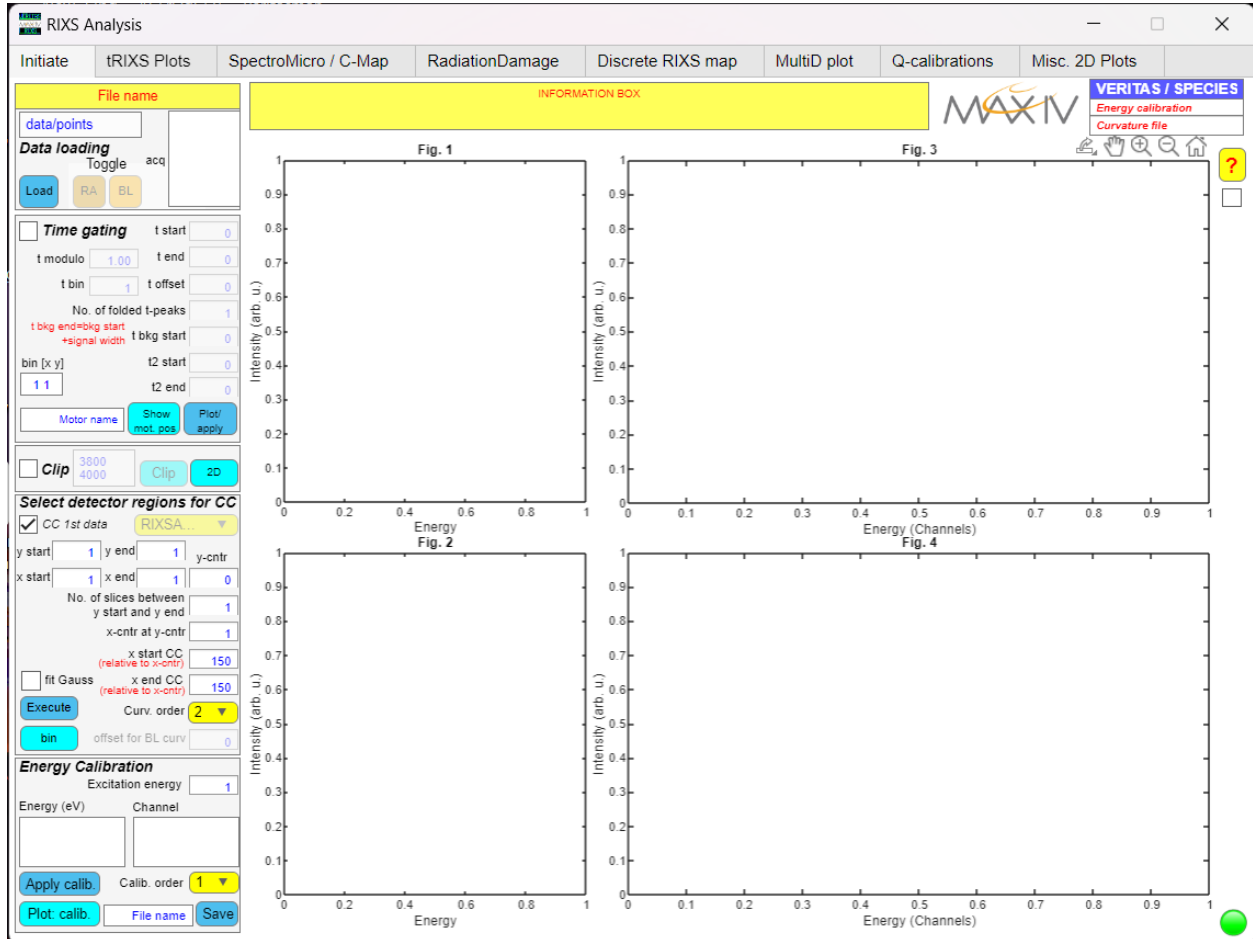


Fig. 3: RIXS Analysis interface.

Here is a brief introduction to all these tabs and their functionalities:

1. **Initiate** → start working with raw data. Apply the following filters: time gating, time gating background, start and end global time, mask out detector artifacts (is any), curvature correction (generate new or use the parameters from beamline), and energy callibration.
2. **tRIXS Plots** → slice the spectrum in time from nano-seconds (bunch clock) to seconds (global clock), correct the energy drift in time (if any), plot continuous RIXS maps (without reconstructions of energy steps) and extract PFY from it.
3. **Spectromicroscopy / C-map** → spatially scan the sample with $1 \times 5 \text{ um}^2$ spatial resolution and extract the RIXS spectrum of individual 5 um^2 pixels. Understand the inhomogeneity in electronic structure corresponding to a particular RIXS excitation feature. Also plots continuous RIXS maps.
4. **RadiationDamage** → study the effect and evolution of radiation damage in samples. Selectively extracts RIXS spectra within the initial and end of exposure time at a particular spot. In this way you can do step resolved or step integarted beam damage analysis. Plots continuous RIXS maps with reconstruction of energy steps (more precise than the other two).

5. **Discrete RIXS map** -> plots RIXS maps from previously analysed files or the calibrated files available in the .h5 RIXS file. Extract PFY.
6. **MultiD plot** -> not available yet.
7. **Q calibrations** -> it allows you to calibrate the manipulator angles and estimate the relation among Q, scattering angles and manipulator angles.
8. **Misc. 2D plots** -> for testing.

You may download and install the latest version of RIXS Analysis software for [Windows](#) and [MAC](#) using the link
The figure shows an overview of all the tabs and salient functionalities.

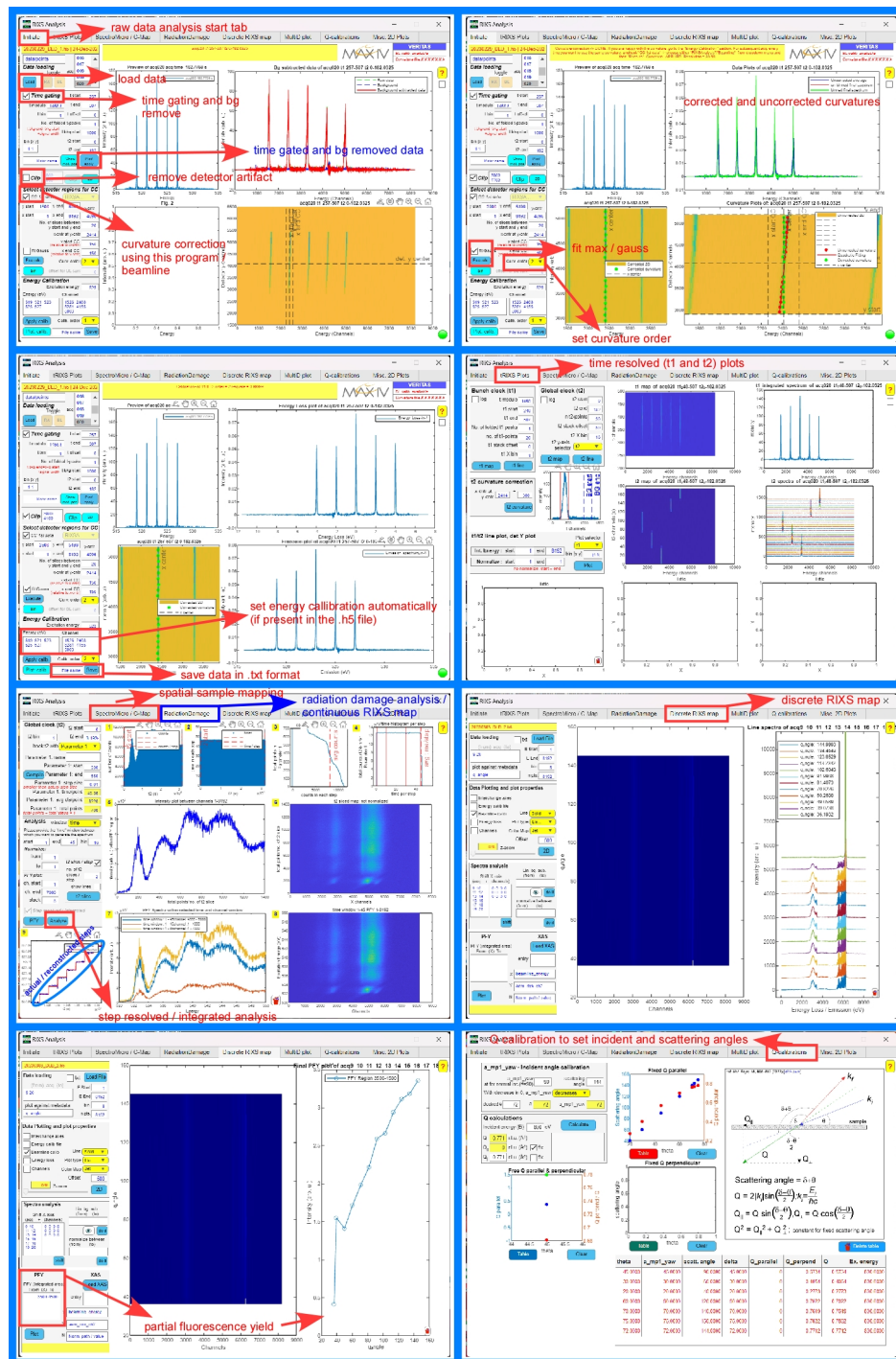


Fig. 4: RIXS Analysis tabs and functionalities

TROUBLESHOOTING

These are the most common issues that an user might encounter during the beamtime. If the issue is not present here, please pen down in the elogy so that we have updated information to deal with the specific issue effectively. You may also consult the floor coordinator to help you.

6.1 There is no beam!

- **Was there a beamdump?** First make sure there is current in the ring <http://status.maxiv.lu.se/>
- **Is the frontend closed?** Make sure the Veritas frontend is open. The text behind Veritas on the statuswebpage will be green if the frontend is open
- **Is anything blocking the beam?** In the synoptic, follow the path of the beam make sure that the valves are green.
- **Light at the slit?** We have a camera at the monochromator exit slit, a viewer can be launched from the synoptic, click “Start...” on the top right of the viewer to get an image. If you can see beam here, then you know you have light through the mono.

6.2 Fault in RIXS Client

This is how the RIXS gui will look like when it is at fault. If you get this fault, you need to restart RIXS server.

What should you do to restart RIXS server ?

- open *terminal*
- type and enter *astor* (servers repository)
- Under *Veritas servers*, double click *b-316a:a101630-ctl-dcu-01 (Rixsaq Arm computer)*
- right click *Rixsaq/b316a* and select *Restart server*

Here is the pictorial representation:

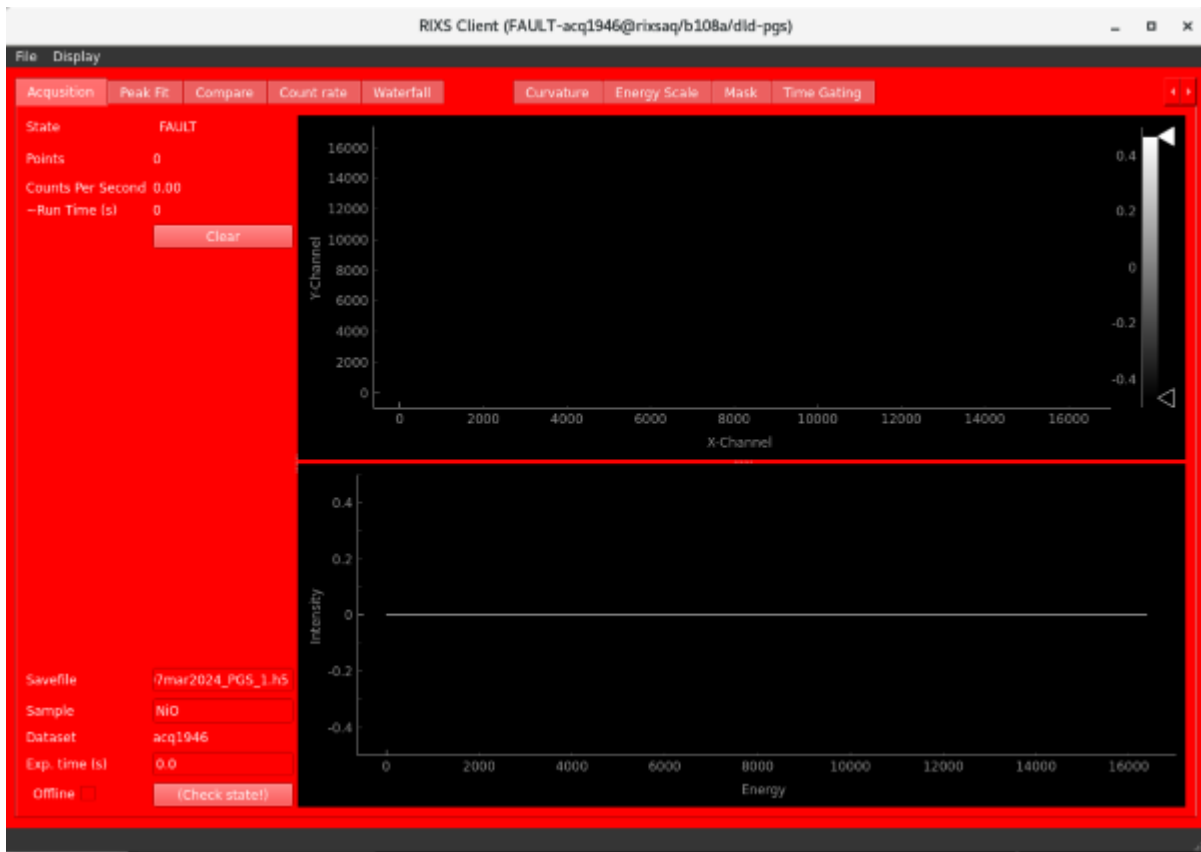


Fig. 1: RIXS Client at fault state

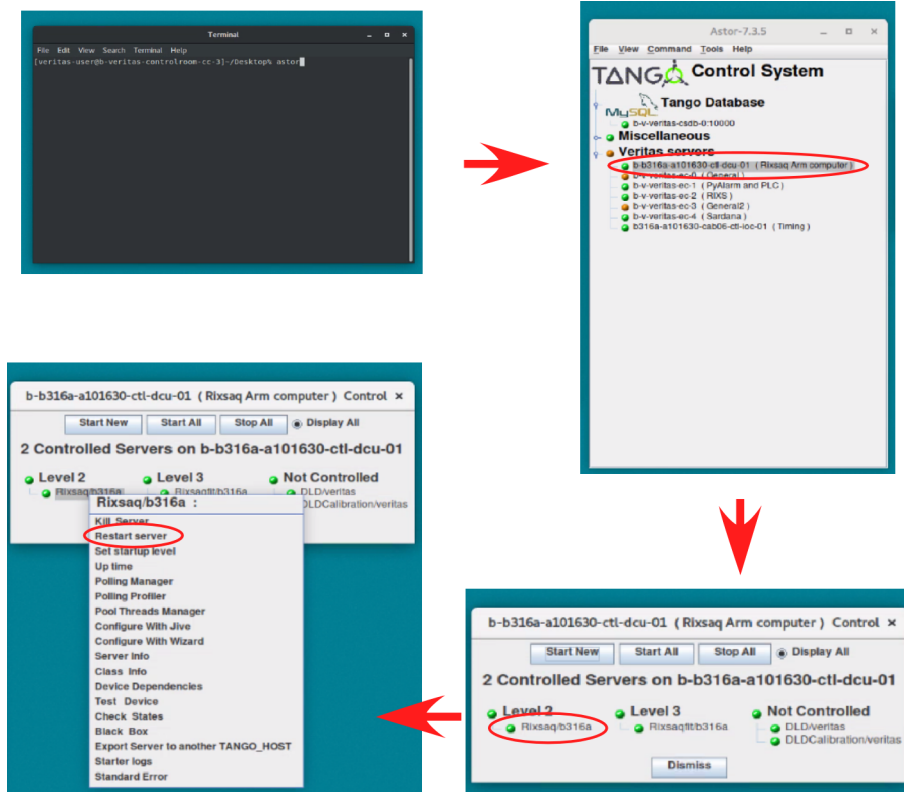


Fig. 2: How to restart RIXS server

6.3 Manipulator Motor axis is not moving at all

1. First, please check it is not physically hit something. Generally, this should not be the case unless the hardware limit switch is hit.
2. If the hardware limit switch is not hit, yet the motor not moving then try esync it. In terminal, run 'spock'. run 'ipap_esync' followed by the name of axis: a_mp1_x, a_mp1_y, a_mp1_z, a_mp1_yaw. Eg.: to esync 'a_mp1_x' axis, run 'ipap_esync a_mp1_x'
3. If the motor is still not moving, reset icepap by enable/disable "physical" switch. hold toggle to disable until LED indicator change (around 2sec). Hold toggle switch to enable side for around 4 sec. and if status LED indicator becomes green it is recovered. This was required once for a_mp1_y axis which has brake on it.

If the problem persists, reach out to the floor coordinator or the local contact.

Note: this axis is not connected to PLC, so emergency stop for q-angle doesn't stop this axis.

OTHER IMPORTANT THINGS

7.1 Data transfers

If you want to access to your data from your home network you can do so using your DUO credentials. Please visit the site for detailed information: <https://www.maxiv.lu.se/beamlines-accelerators/controls-it/it-services/>

7.2 Wifi for users

Users on site can connect to the wifi network called maxiv_user. From that network it is possible to reach e.g. the elogy and jupyterhub.

7.3 OTP for Reaching jupyterhub

To also be able to access jupyterhub you must pass the two factor authentication, you will find the instructions here: https://wiki.maxiv.lu.se/index.php?title=Self-activation_of_OTP_token_application

Windows 10 wifi configuration at MAX IV

Windows does not detect the correct settings for our Enterprise-level network.

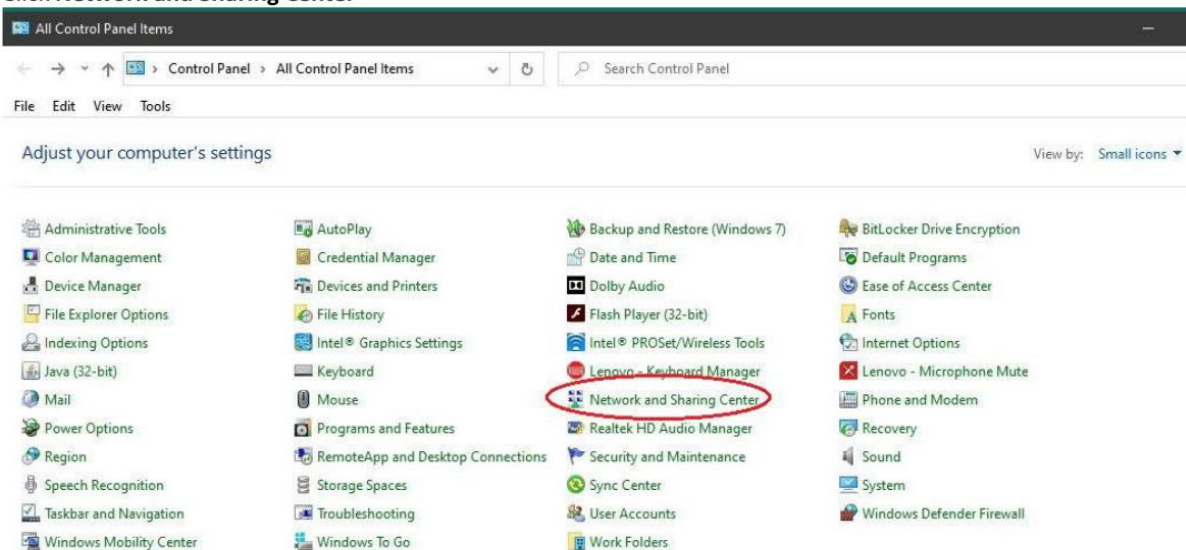
DUO-users can *only* connect to **maxiv_user**

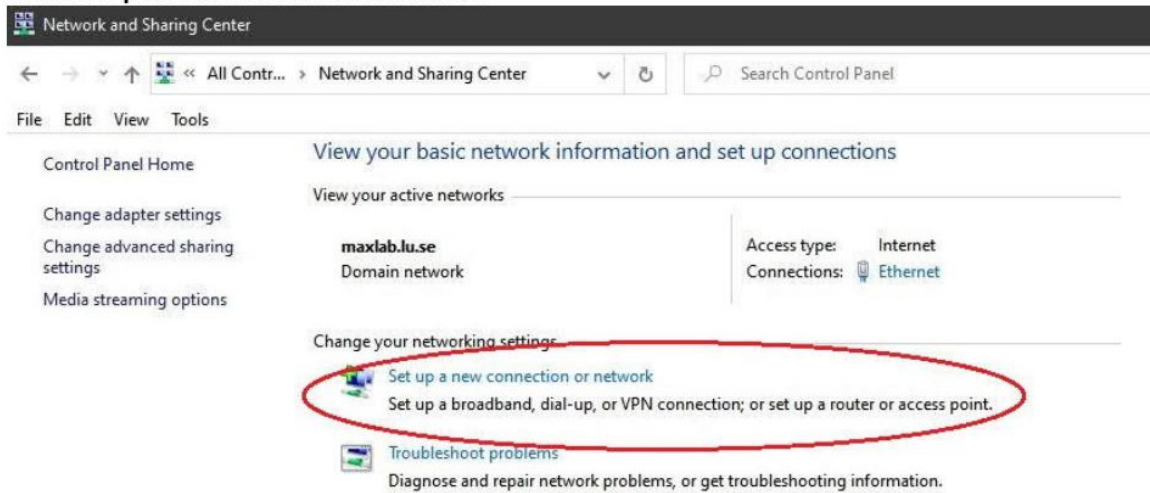
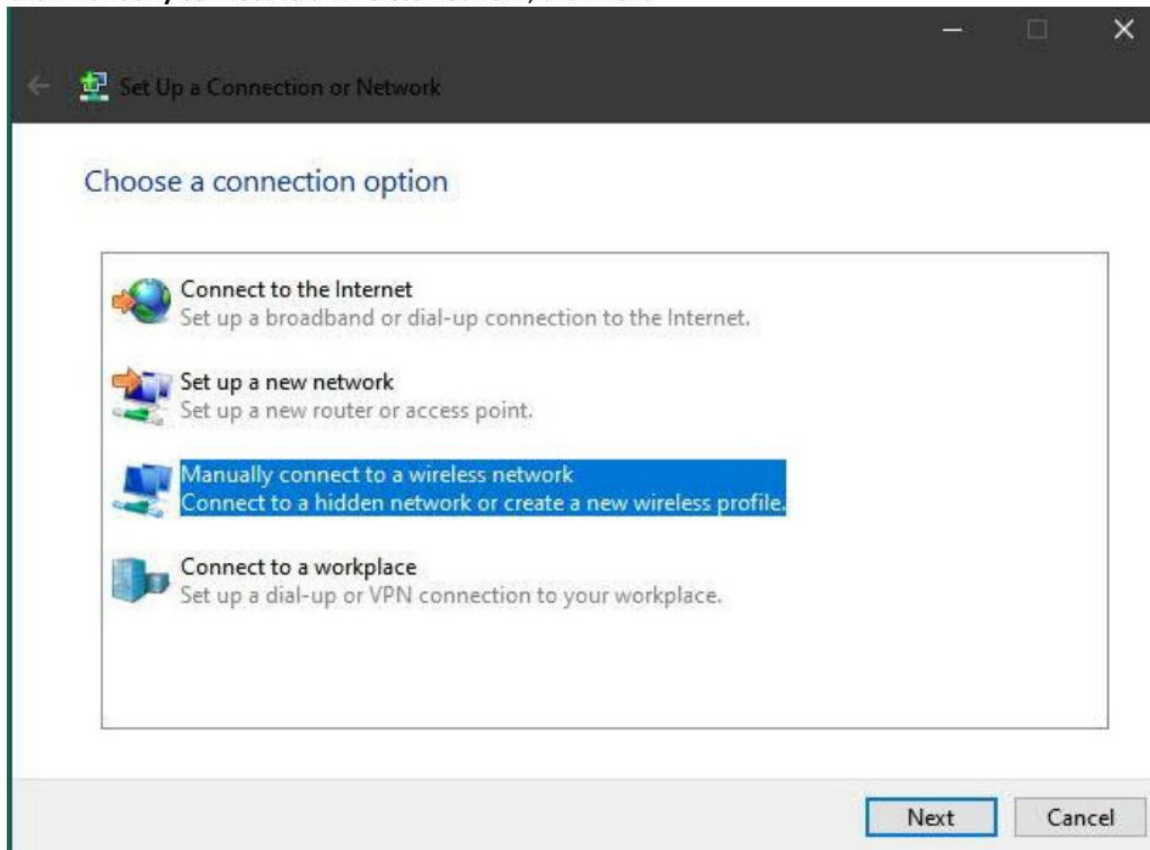
Staff and consultants can *only* connect to **maxiv_staff**

Configure the network:

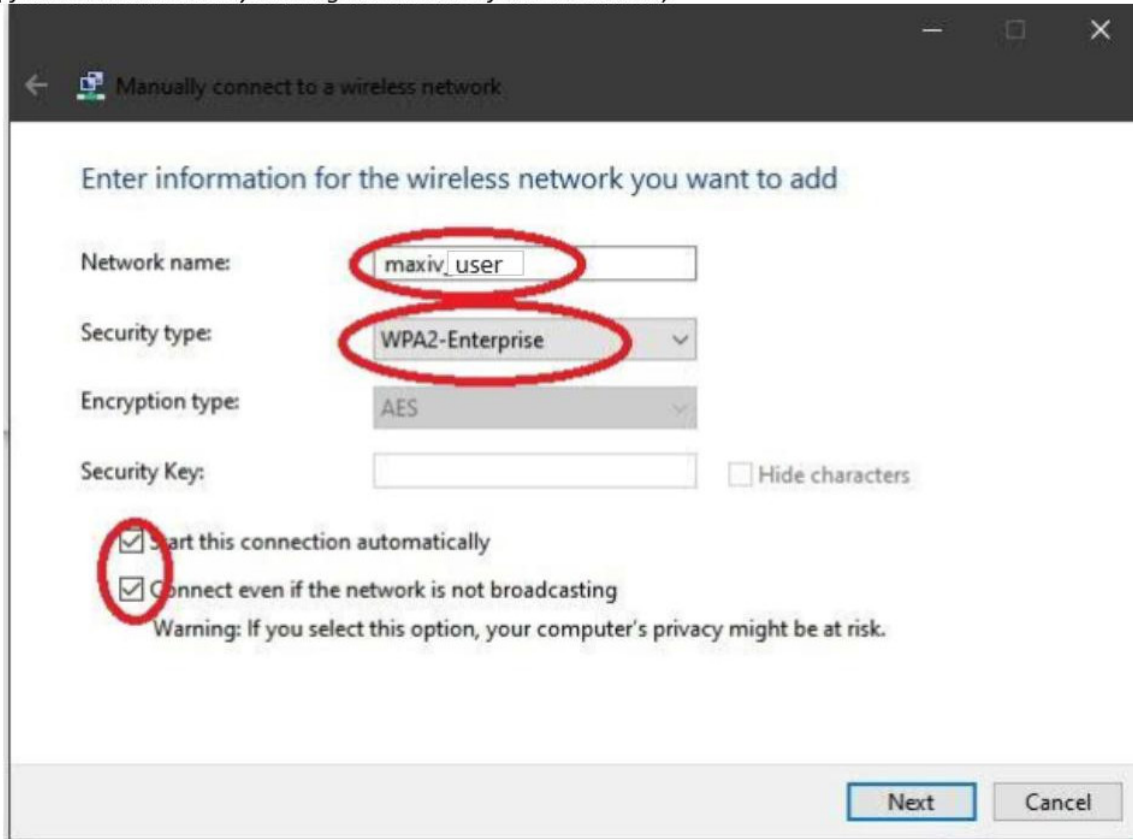
Right-click Windows **Start-button** and **Search** for "control panel"

Click **Network and Sharing Center**

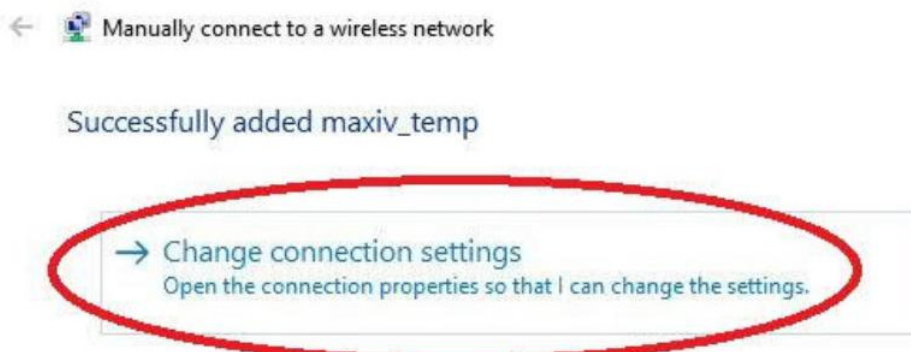


Click **Set up a new connection or network**Click **Manually connect to a wireless network**, click **Next**

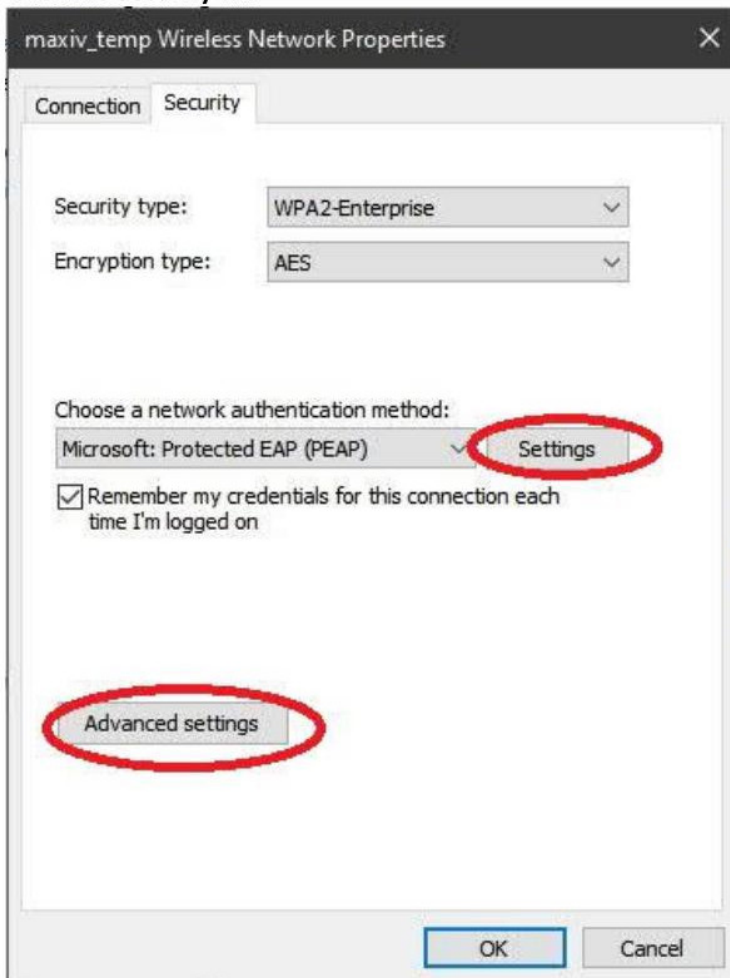
Network name: **maxiv_user**
Security type: **WPA-Enterprise**
Tick Start automatically and Connect even if not broadcasting
Click **Next**
(If the network already exists goto the end of this document)



Click **Change connection settings**,



Click the **Security** tab



Under **settings** (on the Security tab)

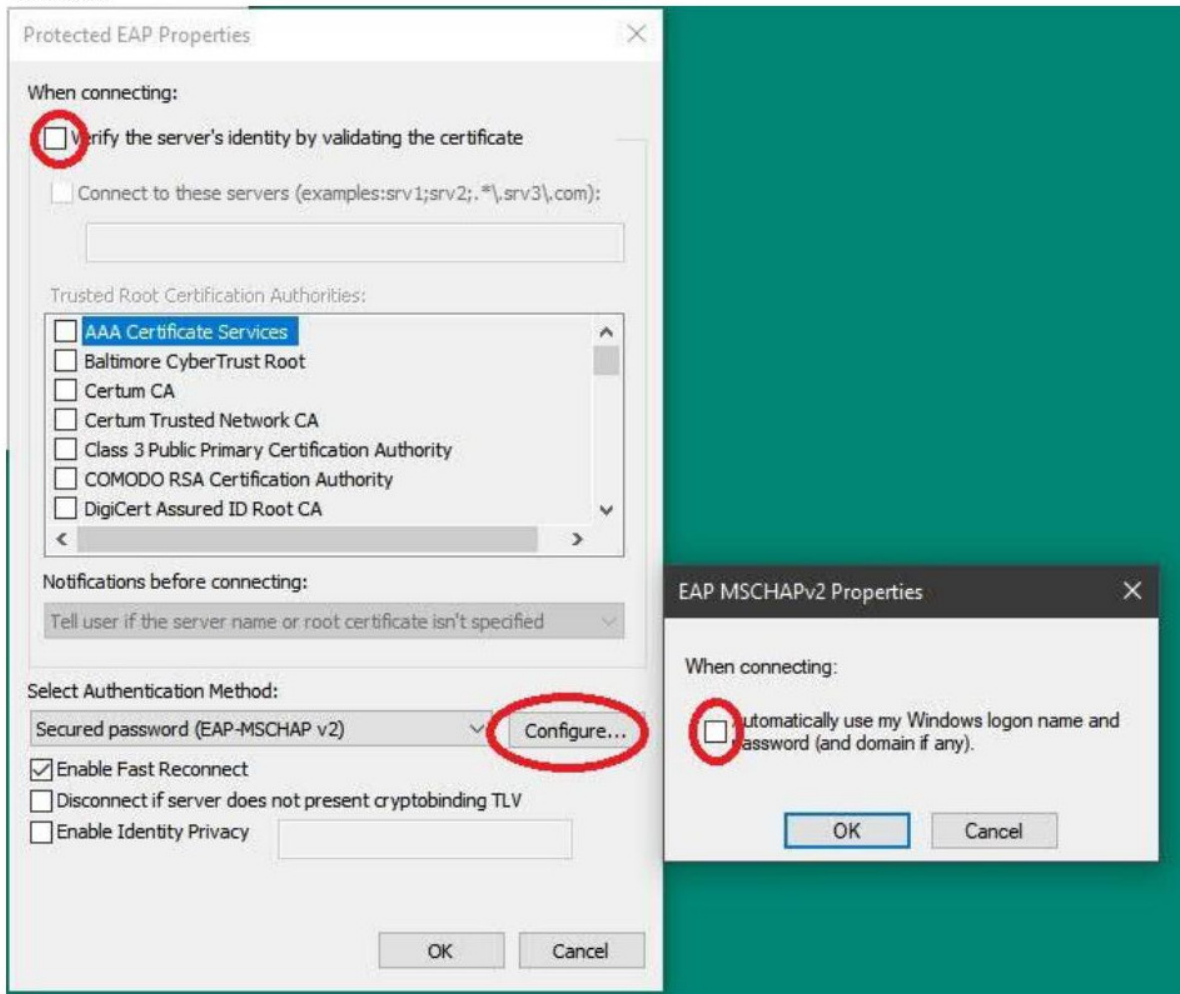
Untick **verify certificate**

under **Configure**

Untick use Windows logon

click **OK**

click **OK**



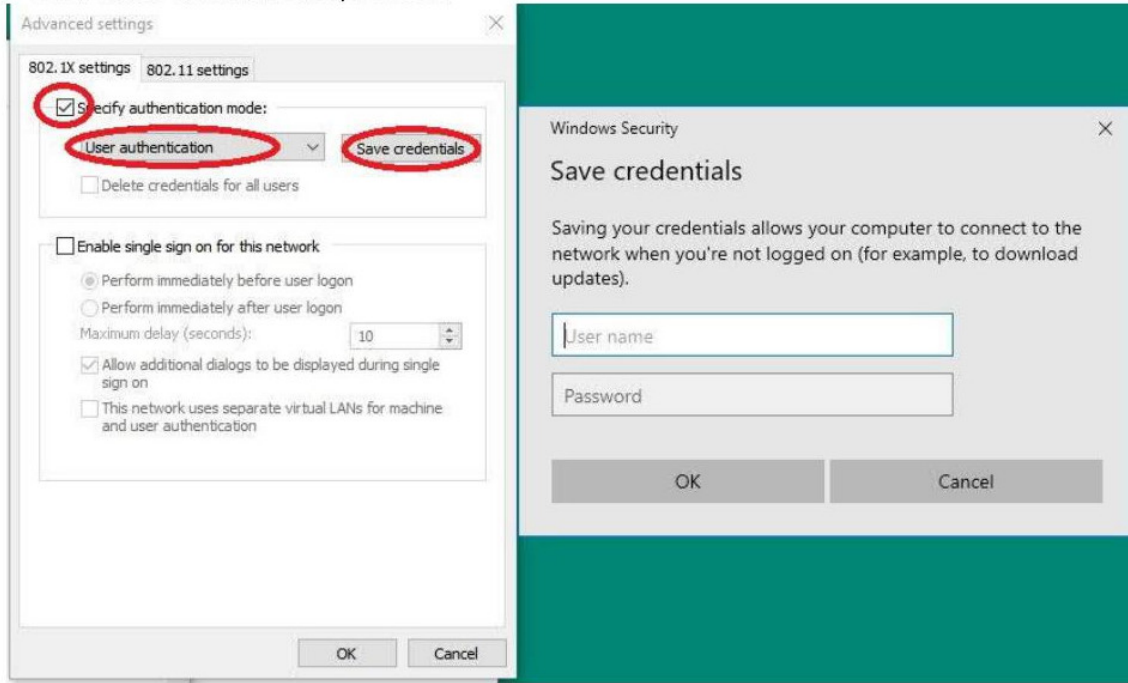
Under **Advanced settings** (on the Security tab)

Tick **specify authentication mode**

In drop-down list select **User authentication**

Under **Save credentials**

enter MaxIV username and password



click **OK**

Click **OK**

Click **OK**

Click **Close**

You should now be able to connect.

Reconfigure the network

To delete the network and start again you must "forget" it:

- Right-click Windows **start button**
- Click **Network connections**
- Click **Wi-Fi**
- Click **Manage known networks**
- Click network name (**maxiv_staff** or **maxiv_guest**)
- Click **Forget**
- Close the window

[Anders Holmström, IT support September 2020]

FEWQUENTLY ASKED QUESTIONS

INFORMATION FOR BEAMLINER STAFF

Here we can keep info that is generally only needed for the beamline staff

Source code for this manual can be found at <https://gitlab.maxiv.lu.se/veritas/veritasmanual>