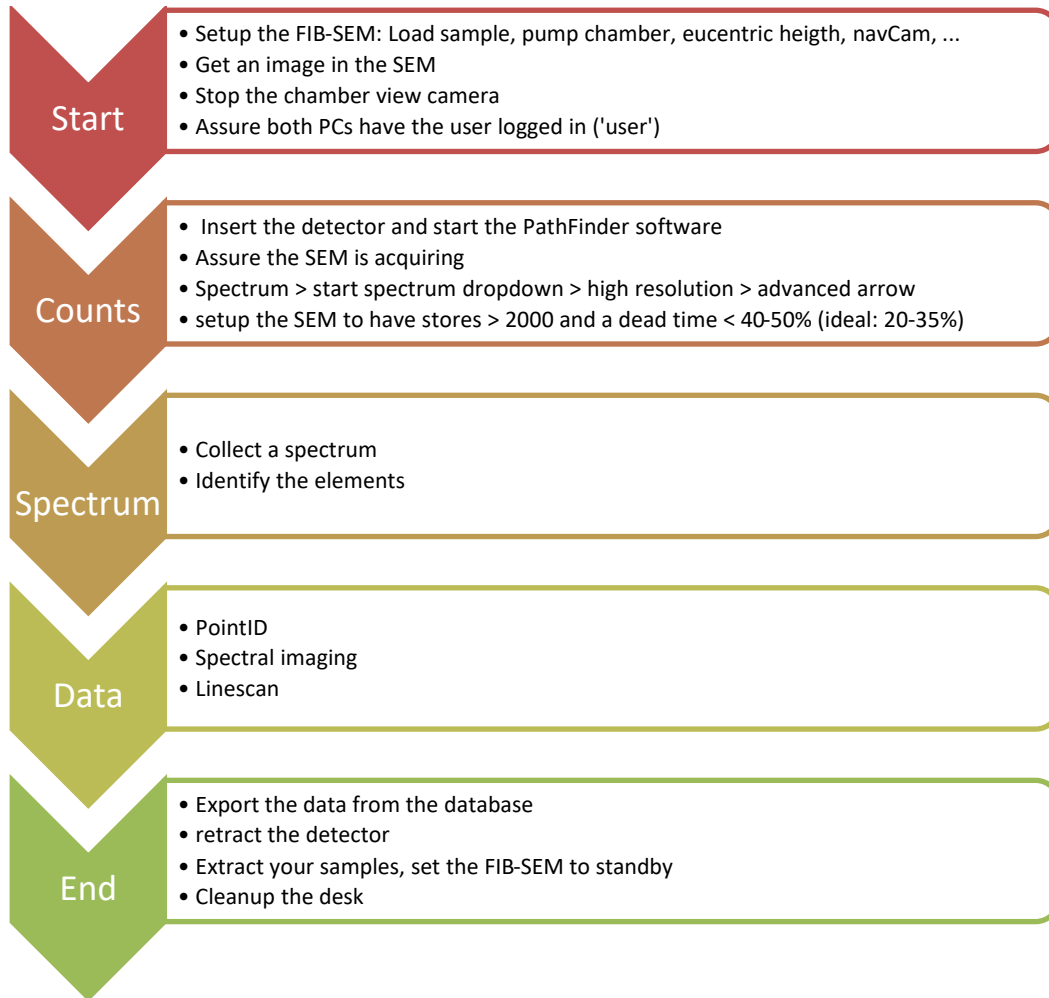


Quick summary



adolphe merkle institute
excellence in pure and applied nanoscience

UNIVERSITY
OF FRIBOURG
SWITZERLAND

Focused ion beam

Introduction

Version 3 – May 2026

FIB-SEM EDX



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Universal rules

Rule 1: don't touch a control if you are not sure of the outcome of that action

Rule 2: never, ever force beyond finger strength

Rule 3: wear gloves when touching anything that goes into the chamber

Rule 4: if in doubt, ask for help

Demonstration: Ending your session

Prerequisites:

Data recorded and exported

Ready to extract your data from the database

Experiment: end the EDX session

1. Switch on the chamber view

2. **Retract the detector entirely** (must not be visible anymore in live chamber view)

3. Close the Pathfinder software

4. Stop the SEM beam and put the FIB-SEM in standby mode

Demonstration: Saving your data

Prerequisites:

Data recorded

Ready to extract your data from the database

The data is automatically saved in the database. To extract the data from the database:

1. Export full field spectrum

- Look into your folder where you saved your database.
- There will be **an .emsa file** for every full spectrum you recorded⁶.

2. Point ID spectra

- Look into your folder where you saved your database.
- There will be **a folder** with the base name of your recording.
- Inside the folder you will find a .psmsa file. This is equivalent to the .emsa files.

3. Extract spectral imaging maps

- Save the maps by File > save map files.
- You will be asked to give the map a type (e.g. counts)
- A new entry will appear in the data list (e.g. filename.counts).
- The maps of all elements can be found in the database root folder as tif files (using the color code as setup in Pathfinder).

3. Extract line scans

- Select your line scan
- Save as CSV or tiff by File > import / export

⁶ .emsa files are text files with the spectrum and metadata.

Demonstration: setup the microscope	6
Demonstration: setup the beam.....	7
Demonstration: Start the pathfinder software.....	8
Demonstration: optimizing X-ray counts	10
Demonstration: Record a spectrum	14
Demonstration: Identify using the periodic system	15
Demonstration: Point ID mode	17
Demonstration: Spectral imaging	18
Demonstration: Adjusting the spectral maps	19
Demonstration: Extracting spectra from maps	21
Demonstration: Map quantification	23
Demonstration: Multivariate statistical analysis with COMPASS	24
Demonstration: Phase maps.....	25
Demonstration: X-ray topography.....	26
Demonstration: Line scan	27
Demonstration: Saving your data	28
Demonstration: Ending your session	29

Demonstration: setup the microscope

Prerequisites:

Functional FIB-SEM

Starting your session

You do not need the FIB beam; the Ga ion beam does not produce X-rays.

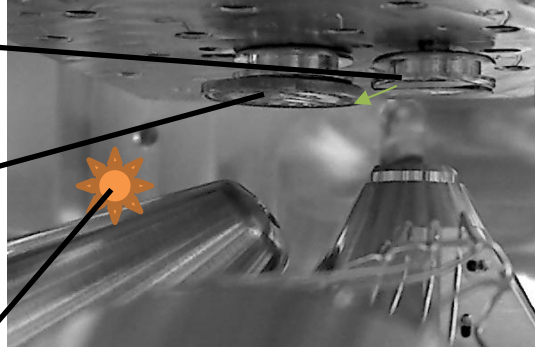
Experiment

Make sure you are logged in with username **'user', both** on the FIB-SEM microscope & support PC

Setup the basics at the FIB-SEM/SEM imaging

- Load your sample
- Home the stage
- Put the sample in eucentric height / 7 mm
- Make a Nav-Cam picture
- Use the ETD for imaging

Assure that no large sample is blocking the way to right side of the chamber (in chamber view). Below: suboptimal: the sample on the right might block the path



Where the detector will be

Taller object in path of X-rays

Object of interest

Demonstration: Line scan

Prerequisites:

Detector inserted

Stores / s optimized

Record a line scan at high signal to noise

The functionality of the linescan is similar to the line scan extraction by spectral imaging. However, by only scanning the points along the line (and not the entire map), a longer integration time can be achieved and thus a much better signal to noise ratio.

Experiment: carry out a line scan



- In the microanalysis tab: click Linescan
- Similar to the spectral imaging, record a SEM image and then record a linescan.
- Adjust the resolution of the scan if needed

Bug alert

You must save your file (File > Close Project) and reopen the database to adjust the output.

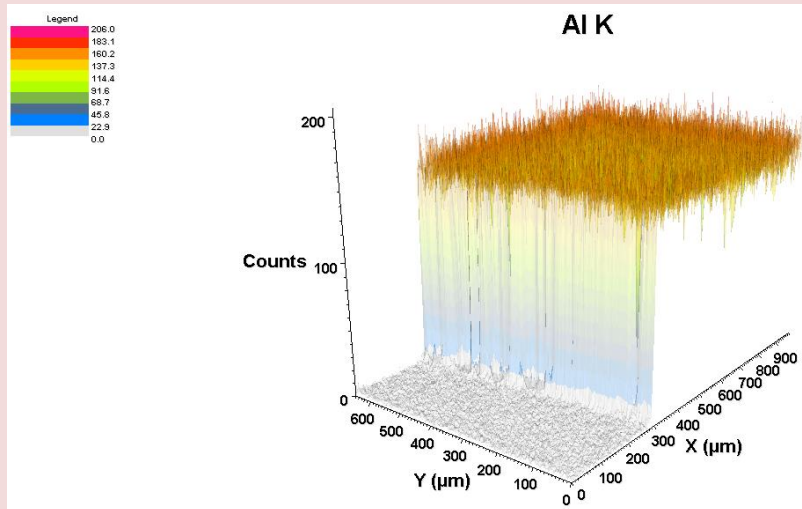
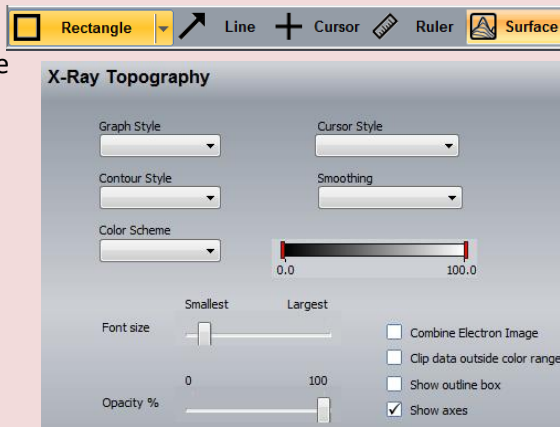
Demonstration: X-ray topography

Prerequisites:
Spectral maps recorded

3D graphs of the X-ray distribution

Experiment: X-ray topography plots

- Select surface in the cursor tab
- The workspace changes. A large white field appears on the top left.
- Select an element in the maps
- Choose your settings in the X-ray topography tab



Demonstration: setup the beam

Prerequisites:
Sample(s) loaded
SEM bean on

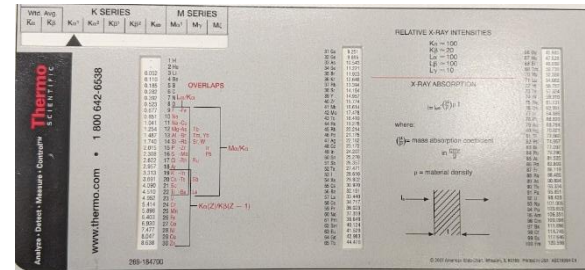
Starting your session

Over-voltage

The choice of the high voltage must be seen in the light of the elements you want to detect. As a rule of thumb:

$$HV \geq \frac{E_{x-ray}}{0.5 \text{ to } 0.7}$$

Or at 30 kV (the maximum on the FIB-SEM), you can detect up to 21 keV edges. Use the Slider tool to extract the information. For example, it Au is the goal:



- The K_{α} edge of Au is at 68.794 keV (= undetectable)
- The M_{α} edge of Au is at 2.123 keV (= detectable)
- The L_{α} edge of Au is at 9.711 keV (= detectable if HV > 13.9 kV).

Therefore, 15-20 kV is a good setting to detect Au.

Beam current

For now, the beam current can be set to standard values, e.g 0.4-0.8 nA.

Magnification

Do not zoom in too much to start. 500-1000X

Demonstration: Start the pathfinder software

Prerequisites:

Proper image under the SEM

Logged in under the username **'user'** on the Suppoer (EDX) PC

It is absolutely crucial that both PC are logged in with the same username: 'user'

Before you start: On the right side of the table, check the LED's on the SSD controller. All four LED's must be green.



Experiment: Insert the detector

- Insert the Detector using the EDX switch on the table. Press insert for 2-3 seconds until you see the detector extended into the chamber view. The LED on the switch will turn red.

EDX detector retracted



EDX detector inserted



Demonstration: Phase maps

Prerequisites:

Spectral maps recorded

Extract compositionally distinct binary phases

Phase maps in EDX data use principal component analysis (PCA) to decompose multi-elemental maps into distinct chemical phases, automatically segmenting regions with similar compositions without manual thresholding. Use case examples are distinguishing quartz and feldspar in geological samples or mapping precipitates, inclusions, or grain boundary phases in alloys.

Experiment: use Phases

In Map processing, find phases. You get a list of the elements (uncalculated phases)

Phase map type

Maximum intensity: Uses MI in each pixel to create the phase maps
 X Phase: proprietary algorithm
 No user input needed

Manual

Allows to set threshold

Demonstration: Multivariate statistical analysis⁵ with COMPASS

Prerequisites:

Spectral maps recorded

Extract compositionally distinct components without user input

This tool can objectively separate mixed pixel signals into distinct endmember spectra and identify phases without prior elemental assumptions. Some examples of use cases are Peak overlay mitigation in complex alloys, reduction of Ga noise in FIB lamellae and statistical denoising in poor signal-to-noise maps (e.g. after short acquisition time).

Experiment: use COMPASS**Method**

Area: weight by nearest neighbor, Recommended for most sample types

Spectral: No NN. Intended for samples with many small phases

Background

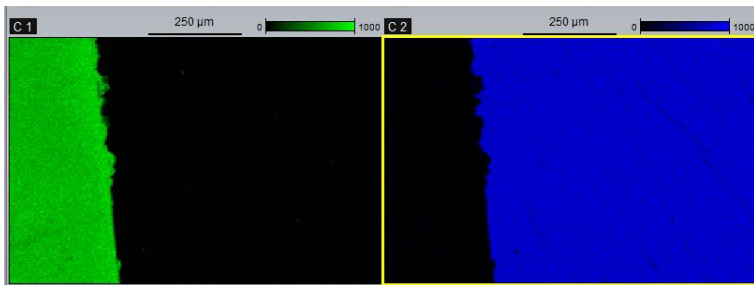
Using data: for data with a sufficiently high signal-to-noise

Using model: for noisy data

Number of components

0 (auto) recommended as pilot

1-15 optimization options

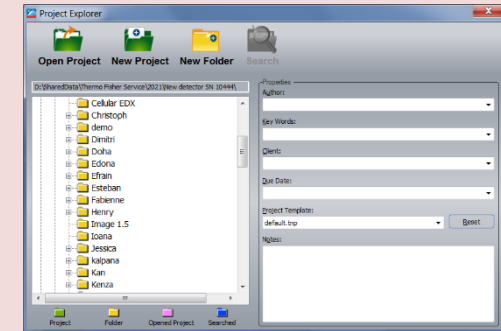
⁵ Based on principal component analysis

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Experiment: start the Pathfinder software and login onto a database- Start the Pathfinder (icon on the desktop) on the **Support PC**

- A splash screen is visible for 10-15 seconds.

- You are asked to use a database. Use an existing one or create your own in your user folder.

- **You do not have to actively start a cooling**

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Demonstration: optimizing X-ray counts

Prerequisites:

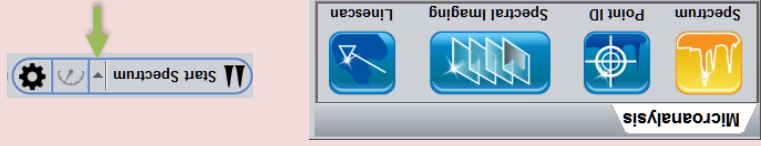
Detector inserted

This important setting is very hidden in the software

Before you start recording data, you should optimize the X-ray counts.

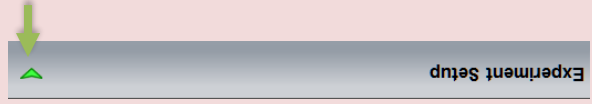
Experiment: finding the X-ray counts

- On the top right, in the microanalysis tab, choose spectrum:



- Then, click the down arrow next to 'Start spectrum' (Do not start a spectrum!) and choose any setting (e.g. High resolution).

- Then, in the top right of the experiment setup, click the green down arrow



- Now, the counts and stores are at the bottom of the experiment setup.



In chamber imaging

Infrared in-chamber imaging generates **soft photoelectrons** from detector surfaces and chamber walls that create a **low-energy noise continuum** (~0-200 eV) in EDX spectra, elevating background and suppressing true X-ray peak counts.

Converting counts into atomic %

Spectral maps recorded

Prerequisites:

Demonstration: Map quantification

- Select QUANT in map processing

- Deselect 'threshold' to assure you process all maps

- Set the endpoints you want to achieve:

- time you want to invest (with 256px

maps, it is a matter of seconds)

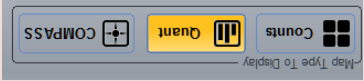
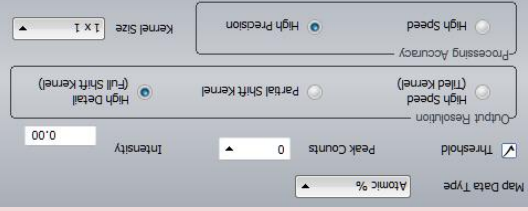
- kernel will apply a mean filter, increasing

the signal-to-noise at the cost of

resolution.

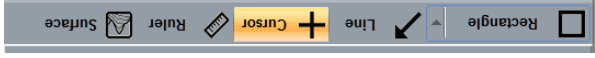
- Click process

The result are maps with a dynamic range of 100 (from 0% to 100% atomic or weight %)



Intensity cursor

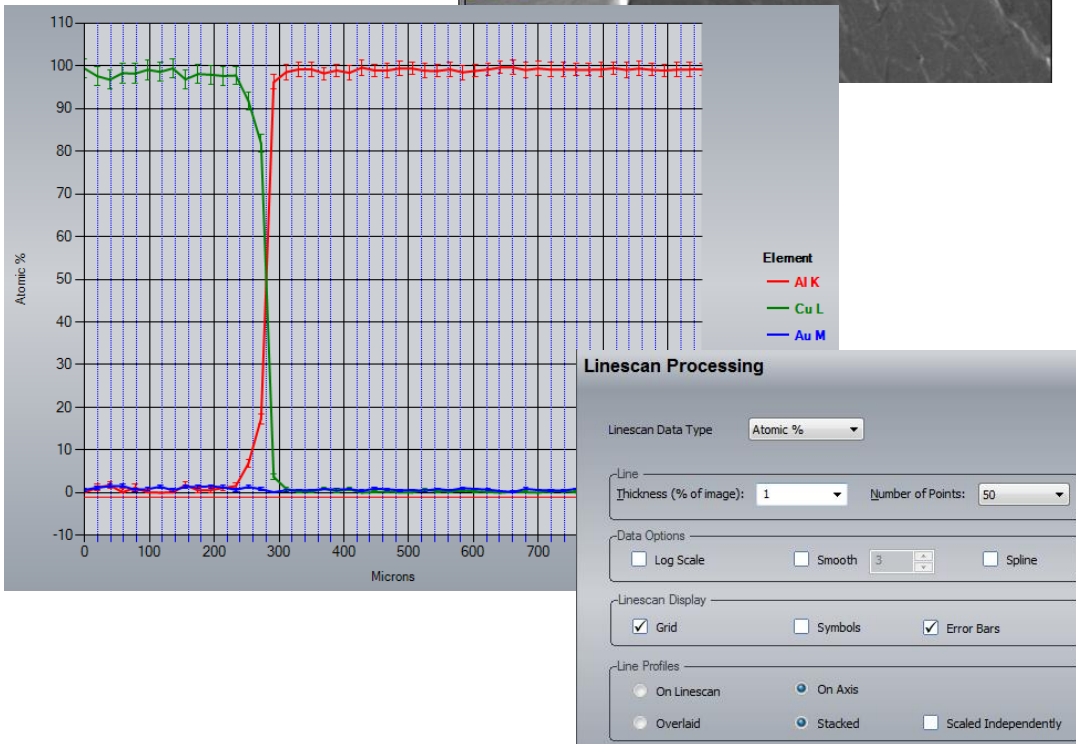
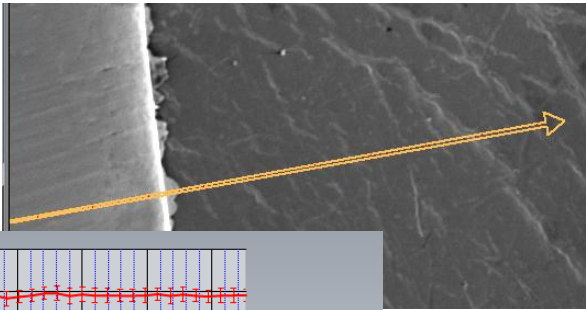
Now, use intensity cursor ('+ cursor') to output the atomic % for each element at a specific map (xy) position.



Grey:	1.34%
C:	0.00%
O:	2.24%
F:	0.00%
Mg:	5.37%
Al:	92.08%
Cl:	0.00%
Co:	0.00%
Cu:	0.00%
Pd:	0.31%
Au:	0.00%

2. Extract line plots

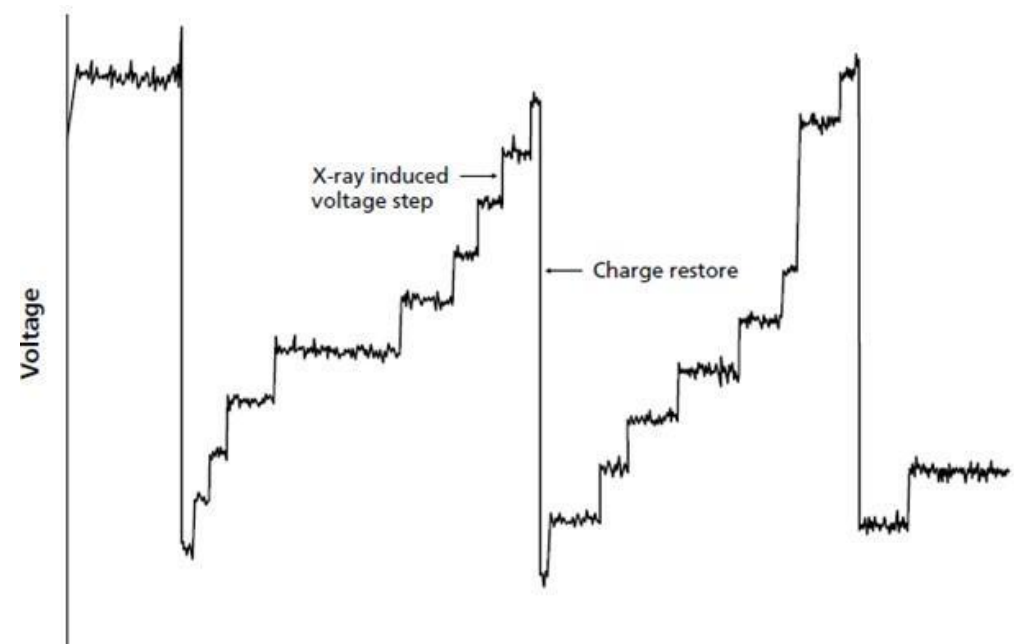
- Select 'Line'. An orange line overlay appears in the image.
- Adjust the line (grab the edges)
- On the right: linescan processing becomes available. Adjust if needed.



Experiment: optimizing the X-ray counts

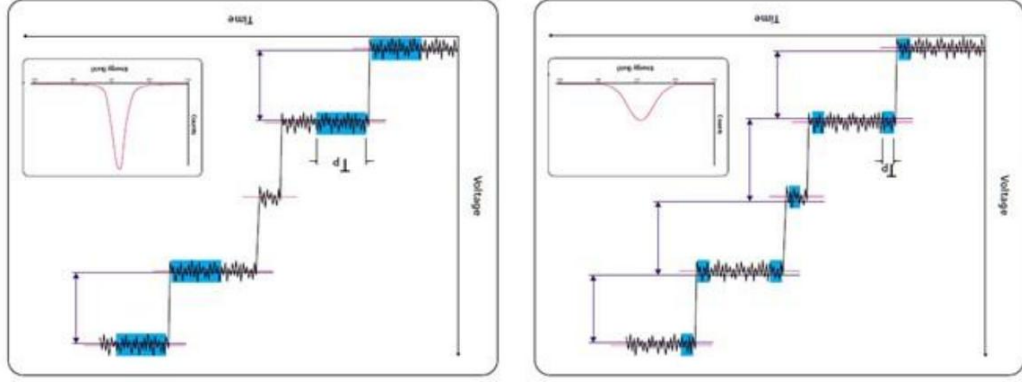
1. Switch off the chamber view. Click the lower right quadrant and press F6. Make sure the topleft corner has this symbol:
2. Start the SEM scanning (i.e. there is NOT the symbol on the top right quadrant)¹
 - Image size: e.g. 768 x 512
 - Scan speed for good imaging: 5-10 $\mu\text{s}/\text{pixel}$ (depends on the image size)
 - Detector: ETD
3. Adjust the Beam current until you have
 - high stores count (> 2000, better > 10 000)
 - not too high dead times (15 > dead time < 40)

Process time, dead time and stores /s



¹ At some point, the software can activate the scanheads, but not at the first scan.

The EDS detector detects X-rays and converts them into voltage steps on a linearly increasing voltage ramp. Each step on the voltage signal corresponds to a single X-ray detection. The role of the Pulse Processor is to remove the noise from each voltage step and to accurately measure the energy of each X-ray.



To remove the noise, it needs to average the signal before and after the voltage step, over a period of time known as the **Process Time (Tp)**.

The longer the T_p , the more the noise is reduced, resulting in a better X-ray peak resolution. However, this means no other X-rays can be processed during that time.

Detect/s is the total number of X-rays hitting the detector
Stores/s (or Throughput) is the number of processed X-rays

The Pulse Processor can process a limited number of X-rays per second and that number depends on the T_p ; the longer the T_p , the fewer X-rays can be processed per second. The dead time is a percentage that reflects the number of unprocessed X-rays.
Dead Time = (1 - Stores/Detects) x 100.

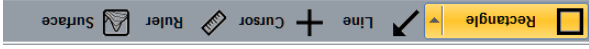
Demonstration: Extracting spectra from maps

Prerequisites:

Spectral maps recorded

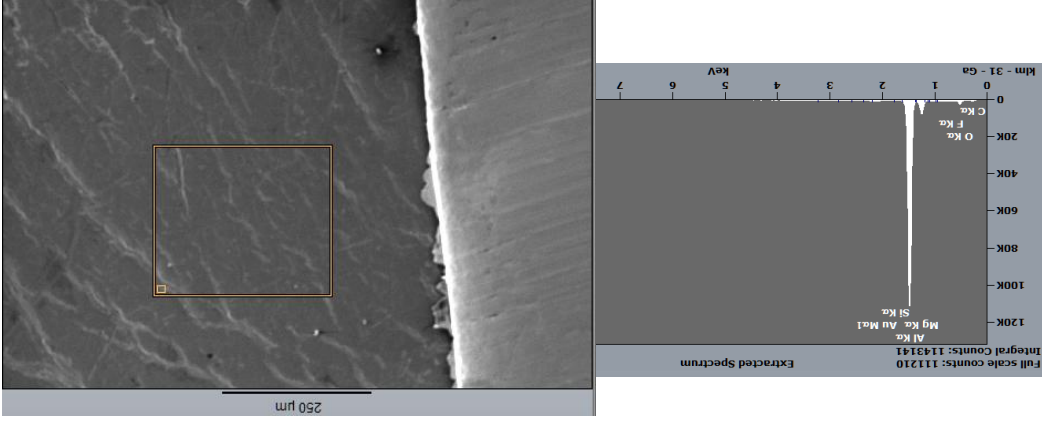
Browse through the data in the spectral maps

1. Extract data from points or region of interests



In the bar under the SEM image, select a cursor type (rectangle, spot,

...) and select a region in the SEM/Overlay image. The extracted spectrum will show up in the spectrum pane (make sure intensity cursor + cursor is switched off).



The spectral data is shown either as:

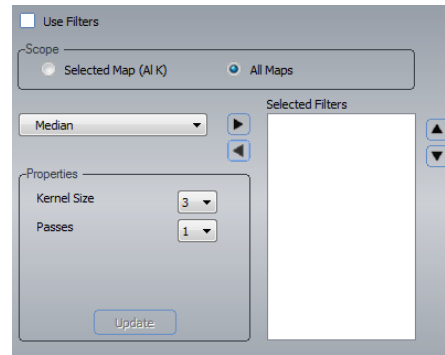
- Area integral Total X-ray counts from the selected area (default)
- Trace element search Maximum counts for each eV channel (useful for finding small concentrations of an element)

3. Image filters

The software allows to improve noise by filters (especially the smoothing filters).

- Filters will create severe artefacts in data with low dynamic range. Increase dynamic range by recording longer.

- In high dynamic range data, filters are not advisable.



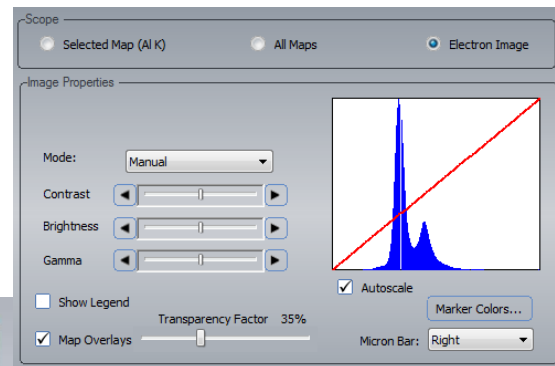
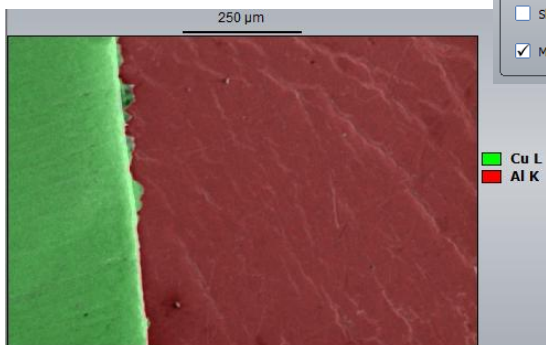
When you use filters, make sure you know what you are doing!

4. Change the transparency of the overlays

- In Image settings, choose Electron image.

- BUG ALERT: Click Image filters and then again on Image settings!!

- You can now change the transparency of the overlays



What process time to use?

Longer Process Times =

- better energy resolution
- but lower stores.

So, the choice of the Process Time depends on your application.

- ➔ measurement of overlapping elements or detection of light elements: long T_p
- ➔ high stores required (mapping, low concentration): low T_p

What Dead Time should I be using?

< 60%.

How many Stores /s should I have

This depends on the sample and your settings. Do not attempt to measure with less than 1000-2000 Stores/s. Good values are between 10 000 and 30 000 Stores /s. Above 50 000 stores /s it is good to be true (and then often not true).

Example of a good setting

Detects /s:	18800	<div style="width: 100%; height: 10px; background-color: #ccc; position: relative;"><div style="width: 20%; height: 10px; background-color: #00ff00;"></div></div>
Stores /s:	13592	<div style="width: 100%; height: 10px; background-color: #ccc; position: relative;"><div style="width: 20%; height: 10px; background-color: #00ff00;"></div></div>
Dead Time %:	23	<div style="width: 100%; height: 10px; background-color: #ccc; position: relative;"><div style="width: 23%; height: 10px; background-color: #00ff00;"></div></div>

Demonstration: Record a spectrum

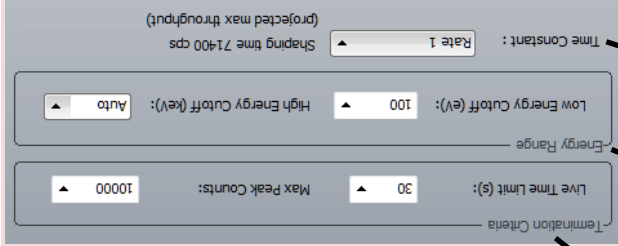
Prerequisites:

Detector inserted

Stores / s optimized

Record a spectrum of the entire field of view

Experiment



Stop the acquisition after e.g. 30 seconds, or a peak reaches e.g. 10 000 counts

Cut off artefacts/noise below 100 eV. Leave HEC to Auto

High throughput or high spectral resolution

Click start spectrum Start Spectrum

Result: Spectrum processing

- Assume that Auto ID is on & click the green arrow
- There are some options for the Auto ID
- Click process to repeat the analysis?



² Process will only start the identification of the peaks. Clicking Identify button in the bottom left will do the identification and the quantification.

Demonstration: Adjusting the spectral maps

Prerequisites:

Spectral maps recorded

Change the visuals of the maps

1. Change the selected elements

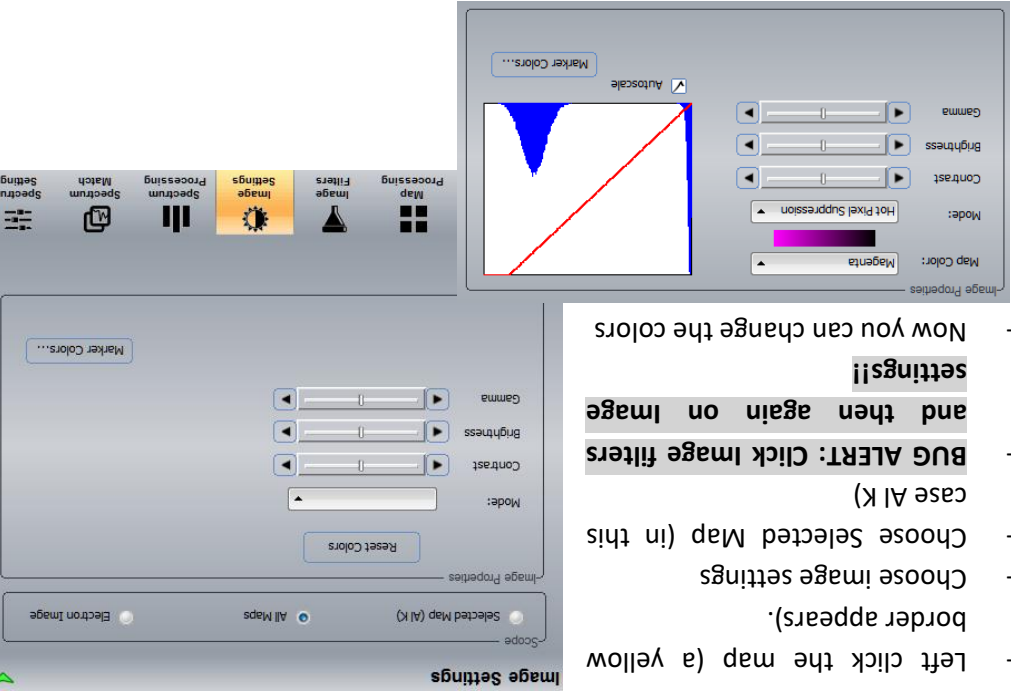
Use the periodic table, right-click on the wrong element and choose 'excluded' to remove elements.

2. Change the false color

- Left click the map (a yellow border appears).
- Choose image settings
- Choose Selected Map (in this case Al (K))

BUG ALERT: Click image filters and then again on Image settings!!

- Now you can change the colors



Demonstration: Spectral imaging

Prerequisites:
 Detector inserted
 Stores / s optimized

Record an elemental map

Experiment: acquire a map

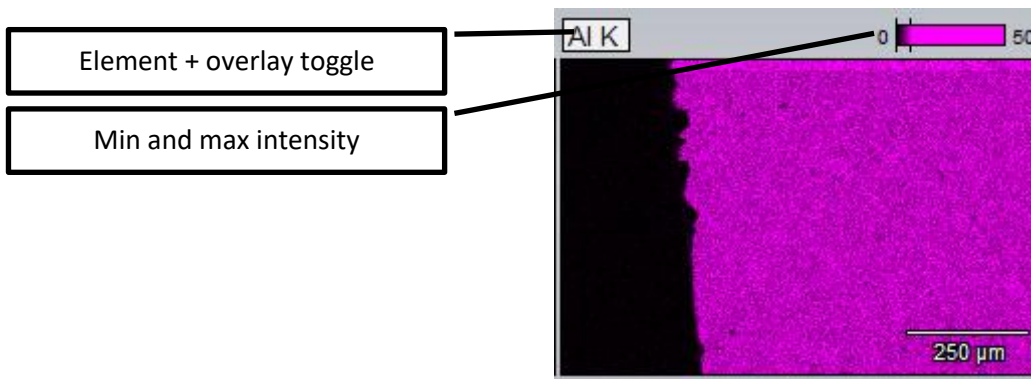
1. Acquire an SEM image (see before)
2. Setup the variables. Map scans can take a very long time, and map size is a key setting affecting the time. Do not overdo the map size. Usually, 256px is a good setting⁴.

- *Frame time*: Time scan 1 frame
- *Number of frames*: repetitions

SI Acquisition

Resolution:	256x170	Dwell Time (µs):	459
Frame Time (s):	20.0	Number of Frames:	60
Acquisition Time (s):	1200		

3. Start the scan. If the autoID is on (standard), the maps of the detected elements will be shown in the central pane.



⁴ It is advisable to have at least 50 values in the scan (this is the dynamic range). More is better.

Demonstration: Identify using the periodic system

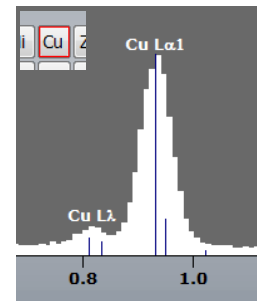
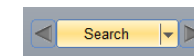
Prerequisites:
 Spectrum recorded

Record a spectrum of the entire field of view

KLM lines

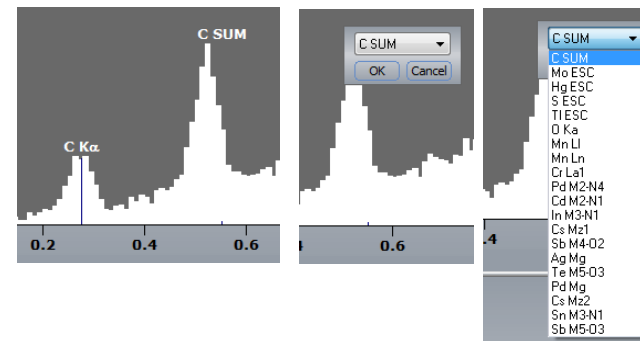
With no auto ID run (all peaks unknown), left click on an element and the peaks will be overlaid on the spectrum.

Click left/right on search to go through all elements.



Select the peak element

If the element was detected, double-click to see other available elements.



Compare with a synthetic curve

Comparing with a theoretical curve allows you to see if you missed any elements

Demonstration: Point ID mode

Prerequisites:

Detector inserted

Stores / s optimized

Record a spectrum of the entire field of view

Experiment: get a point spectrum

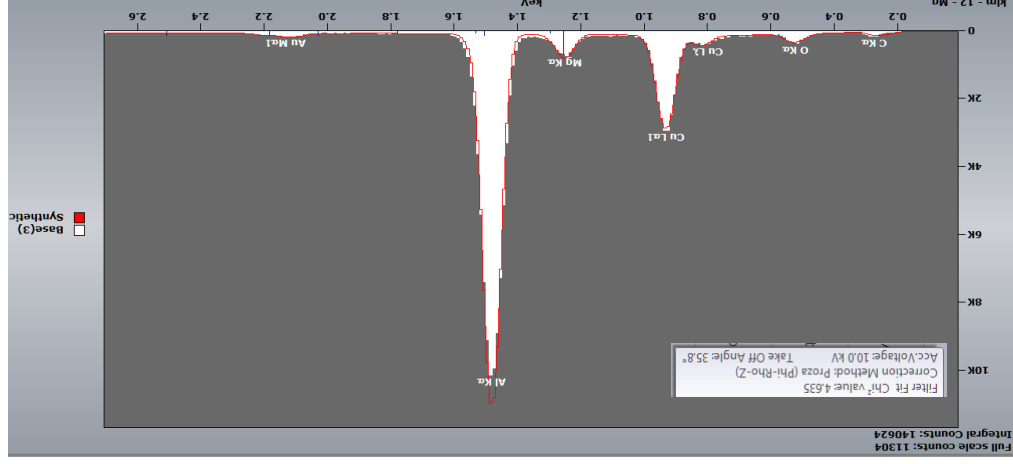
1. Record an SEM image: Click Get Image after setting up the imaging details.

2. In the SEM image pane, select the geometry (point, ...) And draw or place your ROI. If instant is selected The scan will start immediately. Otherwise, Click Start Spectrum



Select your data from the bottom right and click the compare icon³

- Leave normalization to none, but click the spectra check:
- 3 new entries become available in the list:
 - click "Synthetic Spectrum"
 - The goodness of fit is shown by hovering over the quantification pane title. The lower the better.



Bug alert

- If the spectral check buttons are grayed out: Click on any other of the Microanalysis modes
- Click back on the mode you were working in (e.g. Spectrum)



³ If this is grayed out: select another modality and then switch back
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