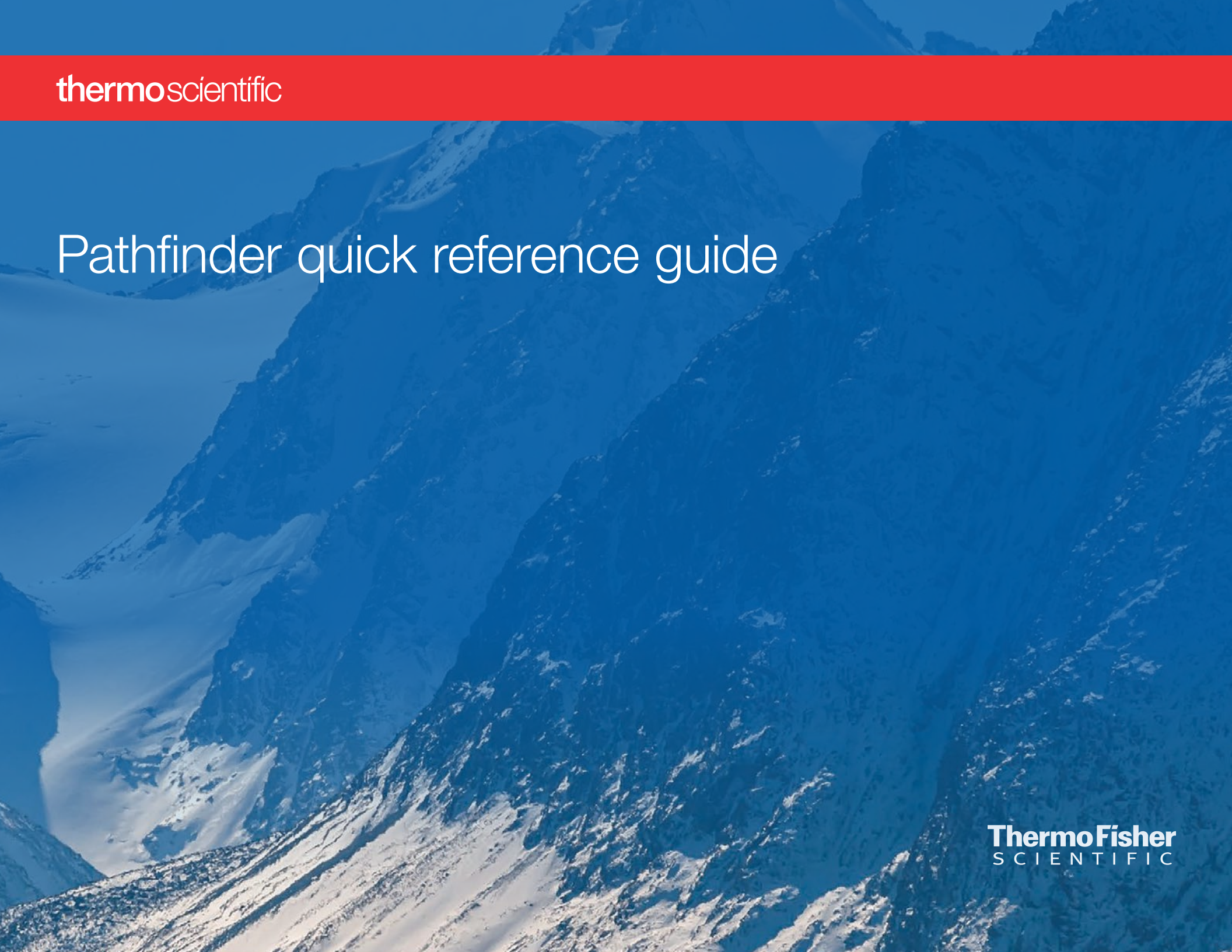
thermoscientific

Pathfinder quick reference guide



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Preface

This is a quick reference guide. It is not intended to replace the Thermo Scientific™ Pathfinder™ Software manual. Once you have learned a technique, the time may come when you wish to perform an operation, but the details don't quite come perfectly to mind. The purpose of this short document is to provide brief prompts to jog your memory and speed you on your way.

Therefore, this document doesn't cover every feature in Pathfinder Software nor does it provide a detailed explanation of any feature.

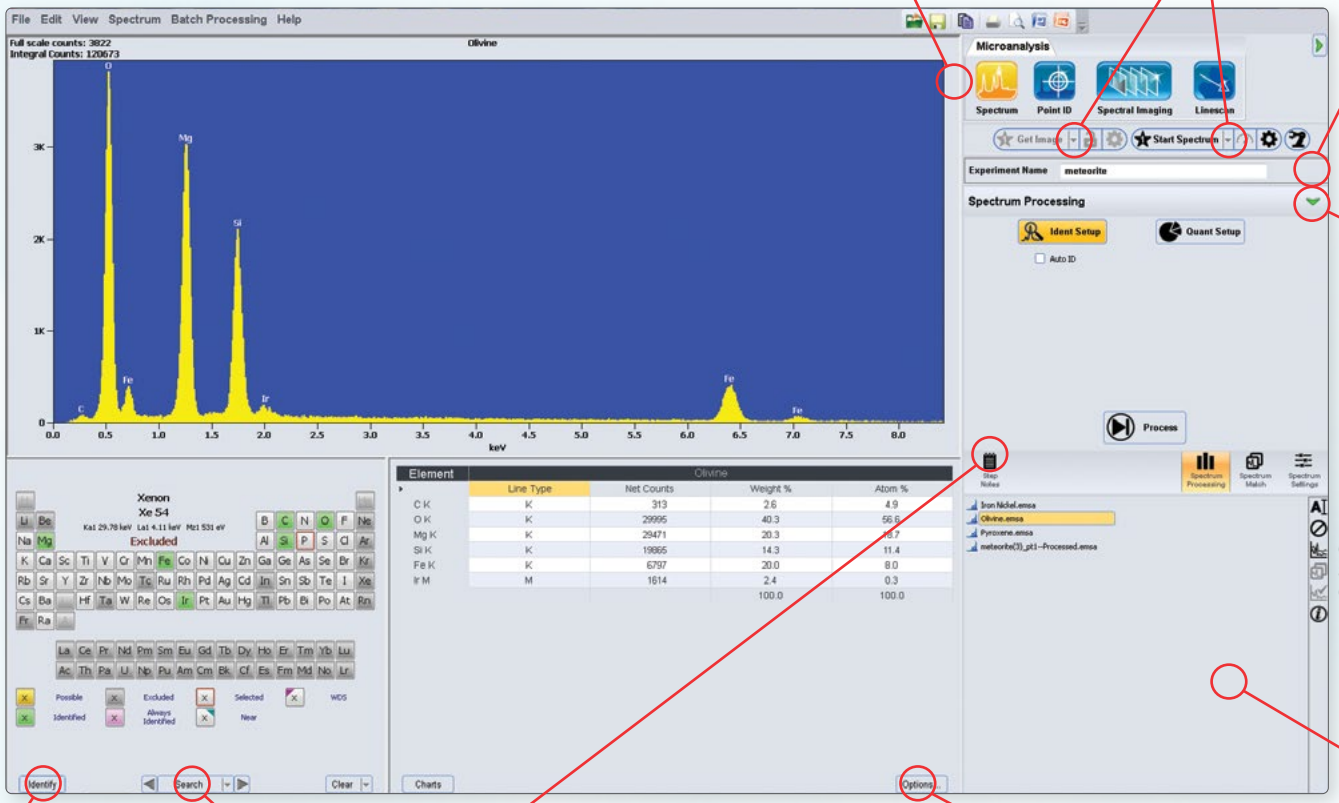
The format of this document is such that one topic will be covered in no more than two facing pages.

Hopefully, this document will help analysts make better use of their time by aiding their mental recall of their training.

If there are still questions, then please contact us. We are happy to help.

Contents

General information



Click on Rollovers in upper right to view an expanded view of any panel. Click again to return to the original view.

Click this icon to get a popup menu for selecting factory or user acquisition presets.

Use View/Preferences to make the experiment name always visible.

Click the green triangle to show/hide the advanced view of this panel.

Rename
Delete
Compare (No longer used)
Spectra
Check (part of Compare)
Information for selected file

Stored data files are listed in this panel. Click to open.

Click the Identify button to automatically identify the X-ray peaks in this spectrum.

Click the Search button for quick access to the Cursor and KLM marker options.

Click the Step Notes icon for some instructional notes for the current application. Click again to hide the notes.

Click to see options for kinds of quantitative results that can be displayed.

All spectra are stored in what is known as EMSA format. This is a human friendly, text format. You can open any spectrum and view its contents in a text editor or spread sheet.

File extensions identify different sources of data, but the file formats are the same.

- .emsa…Spectrum
- .psmsa…Point ID
- .lsmsa…Line Scan

All images are TIFF images though the extension may vary depending on the application that created it. Use the export command to get an image with the micron marker included.

Project explorer

File/Project Explorer

- Open a different project
- Create a new project
- Apply a template to a project

Right click on a locked project to find an option to unlock it.

Right click on a project and select **Open in Windows Explorer** to find the project on the mass storage device.

Temporary data

When first acquired, data are stored in a temporary folder. Some Batch operations cannot be performed on temporary data. Close a project to make data permanent. Close the project with:

- File/Close Project – then click the open project icon to quickly reopen the same project.

Menu commands	
Configure all report options	File/Page Setup
Close existing project, open Project Explorer	File/Close Project
Open the Project Explorer	File/Project Explorer
Option to always display the experiment name	View/Preferences
View the license key for this site *Double click on "License Key" to see a list of installed options.*	Help/About Pathfinder
Make a snapshot of current system settings *This template is used to configure a project from the Project Explorer.*	File/Create Template
Compress SI map files *Close and open the project if this is greyed out. Pathfinder uses SI maps in the compressed state. There is no uncompress command. This is a lossless compression.*	File/Compress SI File
Access the Electron Imaging app	View/Electron Imaging
Access the Service Mode	View/Service Mode
Access various export options	File/Import/Export

The following are accessed from the **Spectrum App**

Table of x-ray line energies	Spectrum/Element X-ray Lines
Tool to subtract references	Spectrum/Reference Subtract
Tool to perform math with spectra	Spectrum/Spectrum Math
Tool to monitor regions of the spectrum	Spectrum/Region Tool

Electron image setup

The image setup panel is used in many places in Pathfinder.

For normal work set these conditions:

- Resolution: 1024 x n (varies with the installation)
- Frame time: 10s
- Number of frames: 1

With some microscopes collecting an image faster than this may induce some image shift causing a misalignment of the x-ray data and the image. Experiment with a faster frame time if needed, but be aware of this effect.

A slower frame time will produce a less noisy image.

After setting these values click on the User Defined button and save the settings as desired (user 1 or 2). In the future simply make sure that value is showing when collecting an image.

It is a good idea to set a second user setting to a higher resolution such as this:

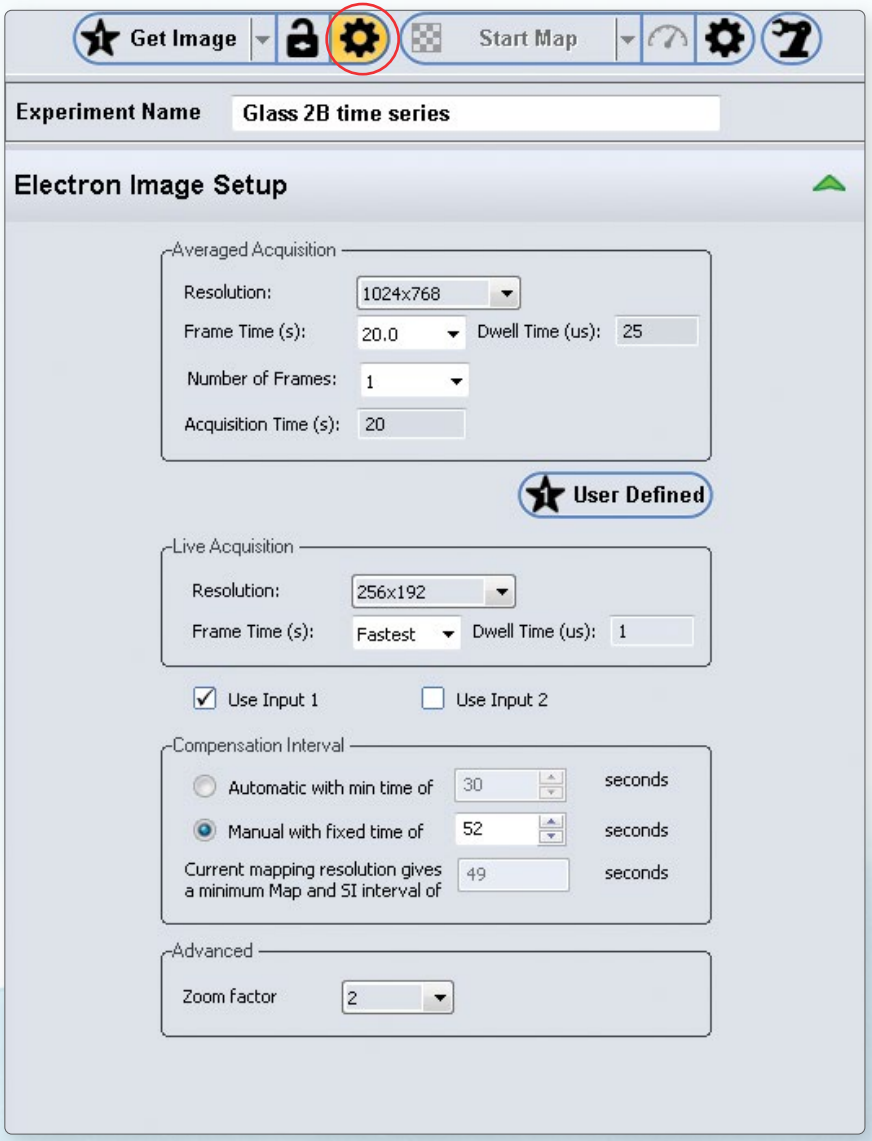
- Resolution: 2048 x n (varies with the installation)
- Frame time: 60s
- Number of frames: 1

It can be helpful to collect some high resolution images of a sample while collecting x-ray data. Of course, the best quality images will come directly from the microscope. However, images collected by Pathfinder will travel with the x-ray data in the project folder making these much easier to find a week or two or three or four later when a report is being written.

For drift compensation, a recommended starting condition is Manual with a fixed time about 50% longer than the frame time. Set the Zoom factor to 2 initially. Set this to 4 if needed.

Click the lock icon to see a popup menu enabling drift compensation.

Click Get Image to collect an image and invoke Drift Compensation if it was selected.



Click Gear icon next to Get Image, then click thedisclosure triangle to view this data.

Experiment setup

Settings for collecting x-rays in a spectrum

Set all of the termination criteria to zero to collect an indefinite amount of data. In this case, the system will keep collecting data until you press the Stop button.

If you are not sure about how much data to collect start with this:

- Live Time: 0s
- Max Peak Counts: 10,000
- Low Energy Cutoff: 0
- High Energy Cutoff: Auto
- Time Constant: Auto

This will collect data till the full scale reaches 10,000 counts. This will produce a consistent set of high quality spectra. The Auto setting for the Time Constant will cause the system to adapt to the microscope settings.

To set values not provided by the popup menu click in the field and enter the number with the keyboard.

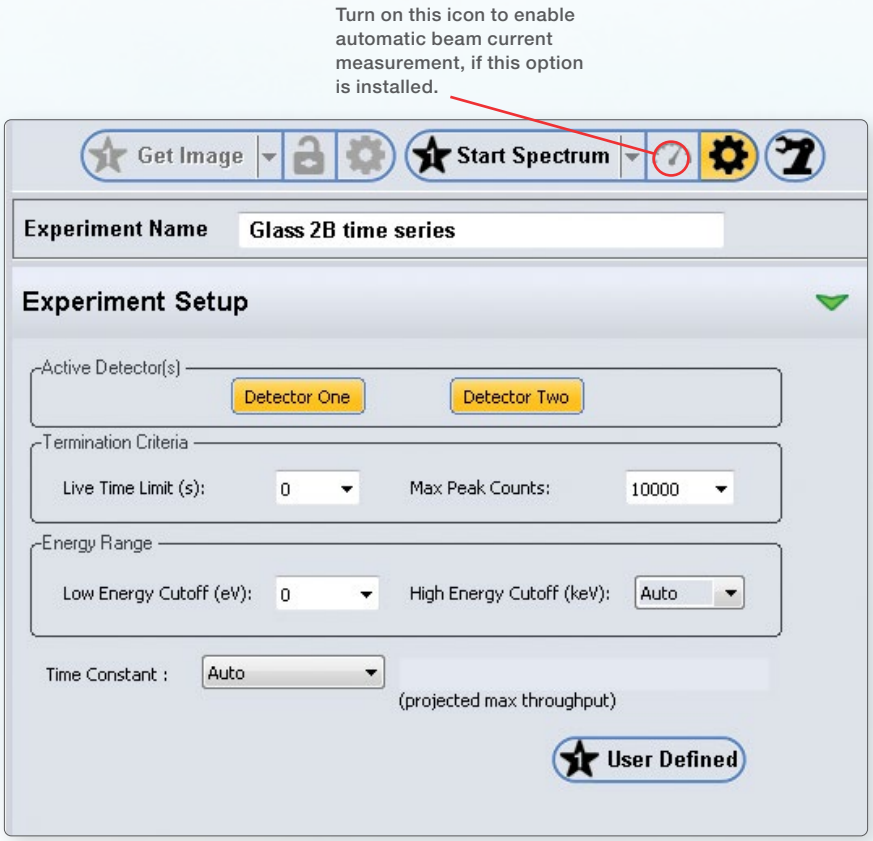
X-ray production is directly proportional to the beam current. Raise or lower the beam current to change the count rate.

Keep the dead time below 50%. Change the Time Constant or the SEM beam current to change the dead time.

To collect better peak shapes, use Time Constant 1 or 2. To collect data faster, such as when mapping, use Time Constant 3, 4 or 5.

In a two detector system click on one or both detector icons to choose which configuration to use to collect data. The various settings must be made individually for each detector.

After changing the settings click the **User Defined** button and save the settings.



Click the gear icon next to Start Spectrum to obtain this view.

Spectrum application

Acquire a spectrum

Set the experiment name. Set the experiment conditions as described on page 7. Click on Start Spectrum. A green progress bar will appear. Wait for acquisition to finish or click Stop Spectrum.

Identify peaks in a spectrum

Click the **Spectrum Processing** tool icon. Under **Ident Setup** click the Auto ID button. Once set, all newly acquired spectra will automatically have their peaks identified.

Alternatively, click the Identify button at the lower right of the periodic table to force the identification of peaks in the currently displayed spectrum.

To manually identify a peak, right click on an element symbol in the periodic table and choose **Identified** or **Always Identified**.

Click the **Spectrum Settings** tool icon then turn on **Show KLMs** to see the KLM markers.

Click on a symbol in the periodic table to see markers for that element. Click once anywhere in the spectrum panel then the left-right cursor keys will drive the KLM markers.

In Spectrum Settings turn on **Cursor** to see the energy cursor. Click in the spectrum to set the cursor to that energy.

Manipulate the spectrum

Click and drag in the spectrum to move it right-left or to expand it vertically.

After clicking in the spectrum the mouse scroll wheel will expand or contract the spectrum about that energy. Pg Up and Pg Dn keys do the same.

On the key pad, the arrow keys (4,6,2,8) will expand or move the spectrum

Double click the spectrum to reset its size and position.

Spectrum display

At the lower right of the screen is the list of spectrum names. Click on a file name to view it.

Once a file is selected, the icons to the right of the file name become active. See image on page 4.

The top icon is **Rename**.

The next will **Delete** a file.

The next enters **Compare** mode. Click this then other file names to overlay them in the display.

The next is for Match but this is deprecated in favor of using the Match tool panel.

The next is **Spectra Check**. First click Compare then click this to get a synthetic spectrum based on the elements set in the periodic table.

The last is **Information**. Click this then the Details button to see all stored information for a spectrum.

Spectrum match

Match compares the current spectrum to stored spectra and ranks them by similarity.

Click the **Spectrum Match** tool icon then **Match** to invoke this.

Click the **Database Manager** and under **New Match File** select **From Spectrum** to add the current spectrum to the set of available files in the top part of this panel.

Create a new database or select an existing one.

Select one or more files from the available files and click **Add** to **Database** to populate the lower panel. These are the possible matches. Close this panel.

Click the disclosure triangle next to the Match button.

Set the Low and High cutoffs to restrict matching to a selected region of the spectrum. It may be helpful to set the low end cutoff high enough to exclude carbon if this is a contaminant.

Set the Chi-square cutoff to a large value at first. 100 is a good value. If this value is too small then no matches might be found.

Batch export of quantitative results

Click **Options** under the quant results to select the desired data types (see page 4).

Choose the menu option Batch Processing/Spectrum Analysis…

Choose the desired options from the panel that appears.

Next choose the spectra to include in the result.

Next choose the name and location of the output file. Click OK.

All the spectra are processed and a .csv file is produced containing the result as a table.

Quantify a spectrum, standardless method

Click on the **Spectrum Processing** tool icon, then click **Quant Setup**. Click the Process button to obtain a result. Set the Auto Quant button to obtain a result each time a new spectrum is obtained.

Click the green triangle to reveal the advanced view. Set **Filter Fit** for the **Peak Fit Method**. For the **Correction Method** set Proza when working with bulk samples in an SEM and select **Cliff-Lorimer** when working with thin samples in a STEM.

Select **Calculate all elements as compounds** to obtain some results (usually for oxygen) from the oxidation state rather than using the peak intensity. Right click on an element symbol in the periodic table, choose **Advanced** then choose the oxidation state to use for that element.

Right click on an element in the periodic table and choose Quant Lines/Absent to keep an element peak identified and to process that peak but to exclude it from the results.

Results appear under the spectrum. Click the **Options** button to choose which kinds of data to view.

Export a report

From the menu bar choose:

- File/Page Setup
  then **Spectrum** to select options for the report.
- Click on the **Print Preview**, **Word** or **PowerPoint** icon to export the data. Word is installed on all systems. Powerpoint is recognized if installed. It may be convenient to install a PDF printer to obtain PDF reports via the printer icon.

Point ID application

Acquire data

Click the **Point ID** application icon. Confirm the experiment name. Confirm the Image and Spectrum setups (pages 6 and 7). Click the Get Image button to collect an image.

After the image is collected, under the image choose the desired state for the **Instant** icon. When set, it will cause the software to collect data as soon as a point in the image has been defined. When not set, more than one data point may be defined and acquisition starts when the **Start Spectrum** icon is clicked.

Click the disclosure triangle next to the first icon under the image and choose one of the area tools:

- Point
- Rectangle
- Spot
- Polygon
- Magic Wand

Point holds the electron beam steady at a single point while X-rays are acquired.

For **Rectangle** and **Spot**, click and drag to define an area. The beam scans through this area while a spectrum is acquired. The beam always scans a complete set of transitions across the rectangle.

Polygon works two ways. Click multiple times in the image to define the vertices of a polygon. Right click to close the curve. Click and drag to define a smooth curve. Right click to close the curve.

Magic Wand uses grey levels in the image to automatically define a shape. For example, click on a bright feature in the image, then adjust the tolerance to include more or fewer of similar grey levels.

If a mistake was made in selecting an area, use the Select tool to select it then press the Delete key on the keyboard to delete it.

Suggestion: A useful application for Point ID is to create a **time series**. Set the spectrum acquisition time for a relatively short period such as 5s. Deselect the **Instant** icon. Use the Spot tool and define many areas at the exact same location. Once the size of the spot has been set you can click at a location to make a duplicate spot. Now click Start Spectrum to collect the data. The result will be a series of spectra from the same location acquired at different points in time. Quantify these and report the data and copy the results into a spread sheet and make charts from the results. This will show the behavior of the sample over time.

In some cases this will reveal samples which decay due to the electron beam, samples with mobile elements such as Na in glass.

Display stored data

Click on the Point ID icon. In the lower right panel are displayed the names of the stored Point ID data.

Click on a name to display that data. Under the selected name there will be a list of the spectra in this data set. Click on one of these names to display that spectrum. When selected areas are heavily overlapped this is the only way to view every spectrum.

Beneath the electron image is the Select tool. Click this icon then click any selected area drawn in the image to view that spectrum.

Click the Select icon again to deselect it when finished.

Most of the tools available for manipulating spectra in the Spectrum application can be used with Point ID.

Compare spectra

To compare spectra in Point ID open a data set and click on one of the spectra listed under the file name. The default will be the first spectrum. This will be the foreground spectrum in the compare view.

Click the Compare tool then click on one or more other spectra in this data set. As each name is clicked this spectrum will be added to the display. Each background spectrum is displayed in outline form. A legend is displayed next to the spectrum display. The color for each compared spectrum is also displayed next to its name in the file name panel.

Under the spectra a table of quantitative results for all of the selected spectra is displayed.

Spectra Check does not work in this mode.

Report spectra

In the menu bar choose File/Page Setup and select the **Point and Shoot** tab. Set the desired options and click OK.

In the Colors section **Printer Friendly** will change all of the solid colors to outlines. Historically, this reduced the amount of ink used by an ink jet printer. **Screen Colors** will reproduce the colors as shown on the display.

Batch export

Batch export sends a table of quantitative results from a Point ID data set to a .csv file.

The dialog is different from batch export in Spectrum.

Batch Processing/Point ID does not prompt for how to calculate the results. Instead, it follows the settings in **Spectrum Processing**.

If both **Auto ID** and **Auto Quant** are deselected then the Batch option is greyed out.

If only **Auto ID** is selected then all spectra will be identified but no result file is provided.

Suggestion: turn off **Auto ID** then identify the peaks in each spectrum as desired. Close the project and re-open it to make these changes permanent.

Set the quant display options to include the desired data types.

Set **Escape Peak** and **Sum Peak** removal as desired. (Spectrum Processing, click the green triangle to reveal these.)

Turn on **Auto Quant** then invoke Batch Processing/Point ID.

From the first panel select the file name, from the next panel provide an output name and destination and click OK.

Spectral imaging application

Prepare for SI map acquisition

Click the gear to the right of Start Map then click the green disclosure triangle to see the panel at left.

Select one or both detectors as desired, if this option is available. If two detectors are used settings for both need to be selected.

Set the resolution from the popup menu and the frame time. If there is any distortion or horizontal shift in the image and map try a frame time longer than 10 or 20s. Some microscopes don't behave well when driven at higher scan rates.

For termination, if the sample is an unknown then turn off all of the automatic terminations and stop the map manually. Set the number of frames to infinite. **Set Average Counts per Pixel Limit** and the **Element Map Vertical Full Scale** both to **No Limit**.

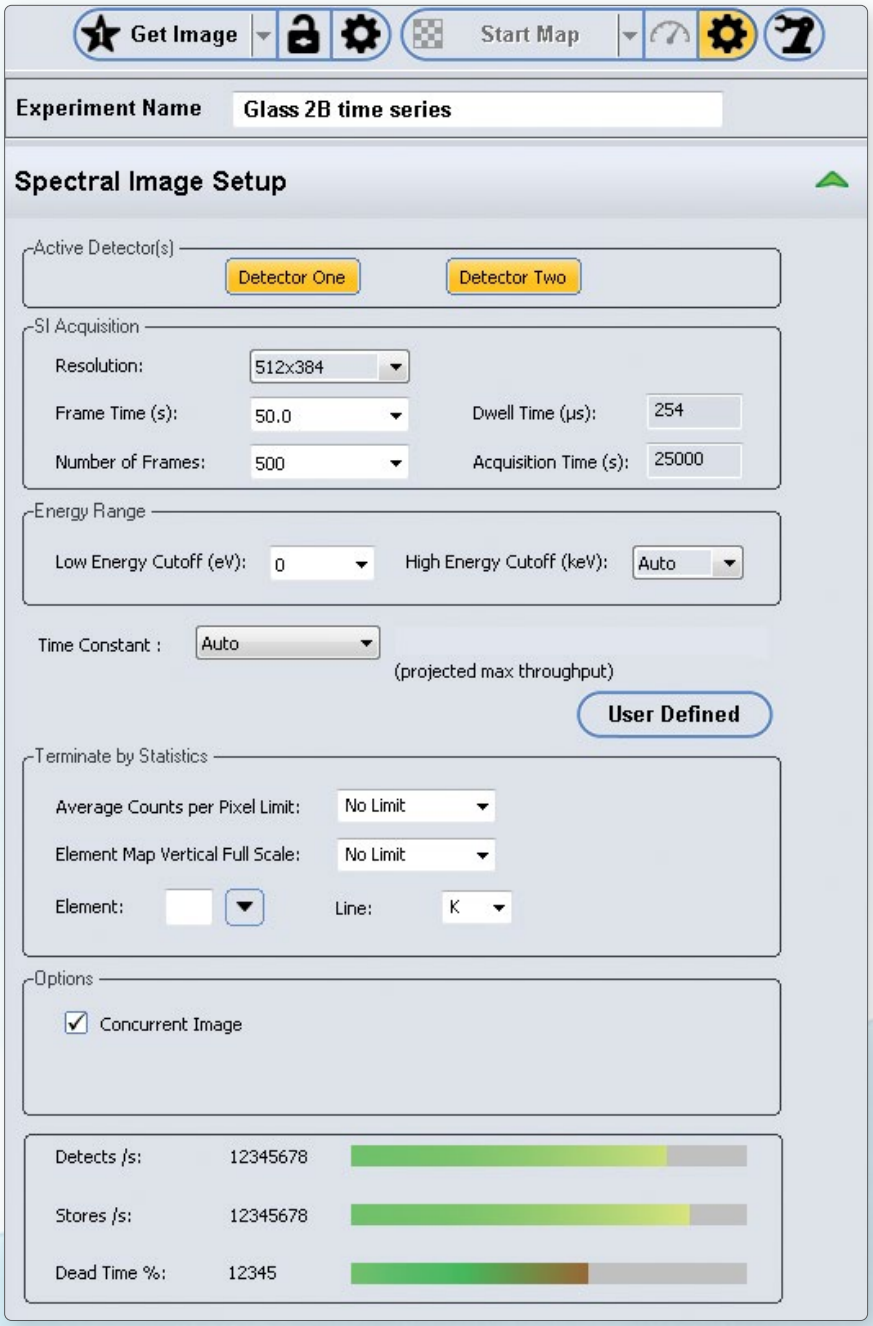
Use specific Termination Criteria when using stage automation or to obtain consistency among many maps.

Use the Average Counts per Pixel Limit to measure the average total X-rays in a pixel. Adjust to your own needs. Set this to 200 as a first test.

Set the Element Map Vertical Full Scale to terminate on the counts measured for a specific element. Select the element and line in the popup.

Set the **Time Constant** to **Auto**. If you wish to override this then set this to 1 or 2 for the best resolution. For faster acquisition in maps choose TC 3, 4 or 5. X-ray count rates are directly proportional to the electron beam current. Increase the beam current to get more counts. Keep the dead time under 50%.

Set the **Low Energy Cutoff** as desired, it is not bad to set it to 0eV. Set the **High Energy Cutoff** to Auto in order to match the electron beam keV. To get a smaller file size set this to 10 (keV). This value limits the size of the spectra stored in the map file.



Extract a spectrum from SI map

Acquiring a map

Confirm that the image settings are as desired (see page 6). If Drift Compensation will be used click the lock icon and choose **Drift On** then click **Get Image**.

After the image is acquired click **Start Map**. If Drift Compensation is enabled a feedback tool will appear showing the amount of drift occurring. A second tool will appear showing map progress.

If no Termination Criteria has been set then stop the map when sufficient data has been acquired.

One way to judge this is simply to look at the maps. If the maps provide the information needed then stop the acquisition.

Another method is to gauge the termination numerically. Look at the number appearing at the upper right of each map. If not seen expand the view. The number is not written if the display is overly compressed. Stop when one or more maps show a full scale of 100 or more. This is roughly comparable to setting the average counts per pixel to about 200. This is useful because it provides enough data for post acquisition calculations. Try different levels to see what works best for your case.

Fewer counts are sufficient for differentiating areas of high concentration. More data is useful for detecting trace elements.

A related consideration is setting the array resolution. Choosing a lower resolution may be advantageous because counts per pixel will grow more quickly in a lower resolution map and the quality of the data in each pixel is often more important than collecting a larger array of data.

Each step up in resolution results in four times more pixels requiring four times as many x-rays to achieve the same precision.

Extract spectra from an SI map

When an SI map is displayed, click the popup menu under the image to select an extraction tool.

Rectangle: Click and drag to define an area. The spectrum appears at lower right. Click the small icon at the upper right of the rectangle to make the rectangle cover the full image. Click it again to reduce its size.

Spot: Click to locate the spot. The spot size is fixed. To change the spot size select Edit/Parameters, then click the **Image Extract** tab and change the value in the **Spot** field.

Polygon: Click multiple points to define an area then right click to close the curve. Click and drag to make a smooth curve and right click to close the curve.

Magic Wand: This selects a shape based on grey level.

Export a Report

Use File/Page Setup, click on the Spectral Imaging tab. For colors select **Screen Colors** so that the report will look like the screen.

Click on the Word or PowerPoint icon to export the report. New pages are added each time these icons are clicked. Select the report and close it when finished making reports.

Displaying a spectral image

The general method of displaying a map is the same, regardless of the data type produced. Acquire a map or click on a file name to display a stored map. Identify the desired elements in the periodic table. Use **Auto ID** to select elements or turn off **Auto ID** and select elements manually. Set the elements as **Always Identified**.

Click the **Process** button shown at right to obtain a result.

Counts

In this case nothing more needs to be done. Counts data are produced by simply adding up the x-ray counts in an energy range covering an elemental peak. This is very quick and simple, but it includes background counts and counts from overlapped peaks.

Quant

Quant maps are calculated results obtained by subtracting the x-ray background from a spectrum and performing peak fitting to resolve peak overlaps. This is extremely powerful, but it requires that a few decisions be made.

As shown in the panel at right, choose the desired data type from the popup menu. **Net Counts** are simply counts after removing artifacts. The other values are calculated from **Net Counts** using the algorithm selected in **Spectrum Processing**.

Output Resolution selects a level of binning. It is suggested to use **High Detail** always unless you have reason not to.

In **Processing Accuracy**, **High Speed** is faster but may produce slight artifacts for neighboring peaks such as a trace of P in the presence of a large S peak. **High Precision** produces excellent results but will take longer.

Kernel Size integrates neighboring pixel data for the calculation. A larger value produces better data quality, but the result appears blurrier. 3x3 is a good compromise.

Modifying map appearance

Click on the element symbol above a map to overlay it on the image. Click it again to remove it. Overlay as many maps as desired on the image. Shift click to add or remove all maps.

Select the **Image Settings** tool to modify the appearance of the image or maps.

Click in one of the maps to select it. Then click on the radio button **Selected Map** to modify that map's appearance. In the example at right Mg was selected.

Change the color from the popup menu.

In the **Mode** menu, **Auto** is a simple auto brightness and contrast. **Hot Pixel Suppression** ignores the brightest 1% of the map then performs an auto brightness and contrast. This can be useful to enhance areas of lower concentrations in maps that have a few anomalously bright pixels.

In **Mode**, **Contour** is a special case. Click the green disclosure triangle to expand the panel and see the settings for this. For atomic percent or weight percent data set the Low value to 0 and the High value to 10000. This produces contours of 10%.

Select **All Maps** to set the **Mode** for all maps at once.

The **Electron** Image radio button modifies the electron image.

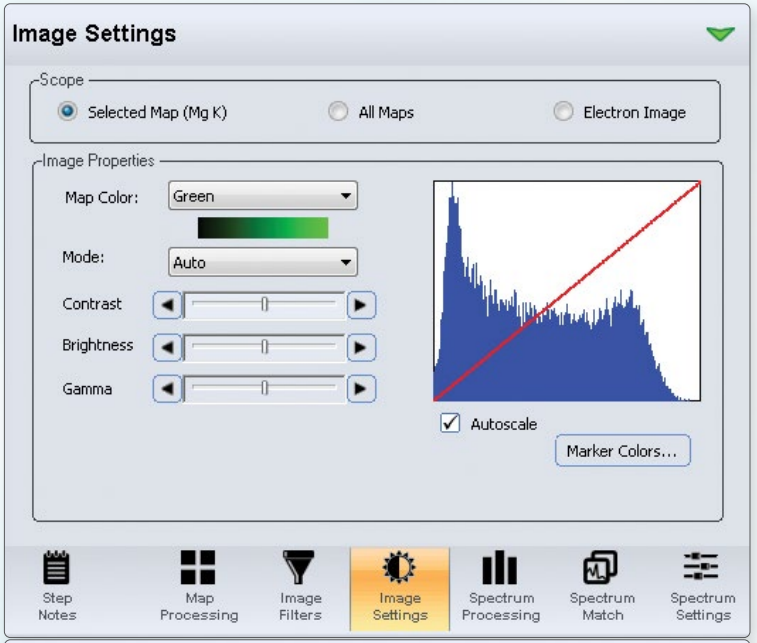
Set the location of the **Micron Bar** from the popup. Note that when exporting tiff images the micron marker is not included if it is in the header.

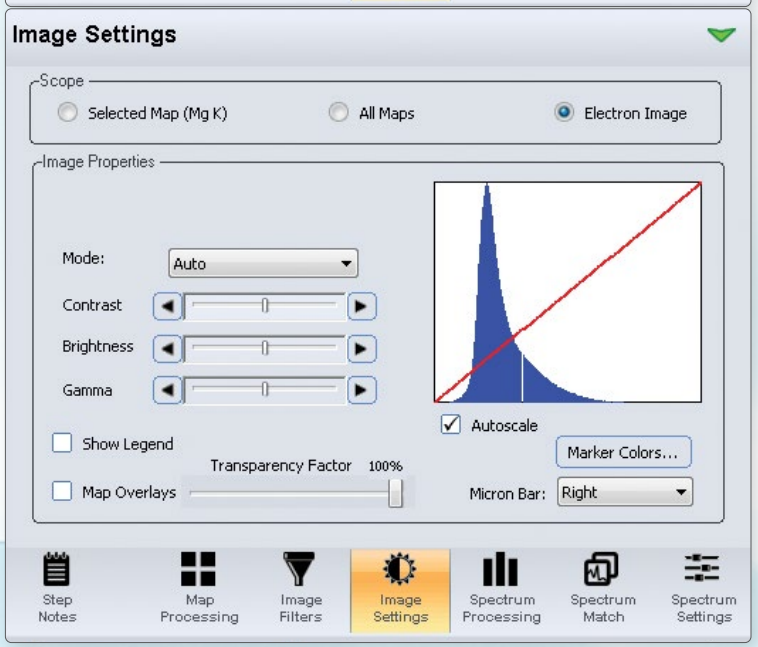
Show Legend displays a legend next to the electron image providing a key to identify maps overlaid on the image. In the case of contours it provides a full scale contour key.

Transparency Factor changes the opacity of the overlaid maps.

Saving the map images

Use File/Save Map File to save a snap shot of the current elemental maps. These are images only. No x-ray data is attached to them.





Extract a line profile from a map

Extracting Line Profiles from SI maps is a very powerful technique for viewing one dimensional trends in elemental compositions in samples. Instead of a line of points this tool creates a line profile from a row of rectangles. The rectangle width and length can be changed. The area of the rectangle affects the precision of each point in the result.

Under the image click on the **Line** icon to use this feature. The display reconfigures as shown on the next page. Click and drag in the image to create a new line. Click on the line and drag to reposition it.

Identify elements in the periodic table to produce a line profile for those elements.

When the feature launches, a new tool appears and is selected: **Linescan Processing**.

Modify the size of each rectangle with **Thickness** and **Number of Points**. Data is extracted from the map by integrating counts for an element within each rectangle. **Thickness** widens the line by widening the rectangles. This produces better precision because it includes more counts and because it covers more area which smooths the results from inhomogeneous samples. **Number of Points** doesn't add more data. It provides a smoothing effect by changing the number of rectangles along the line. Fewer rectangles means more data in each rectangle producing a smoother result. More rectangles produces better spatial resolution.

In samples that have a one dimensional component such as platings or coatings or layered samples it is very helpful to widen the line as much as possible.

Change the **Data Type** from the popup as desired. The chart refreshes immediately when the data type is selected.

Data Options change the appearance of the chart without changing the actual data.

Line Profiles provides for overlaying line profiles on the image. Click on an element symbol in the Chart to overlay that line profile on the image. Select different options to see how that affects the appearance of this overlay.

Right click on an element label in the chart key to see options for changing the color and line style for that element.

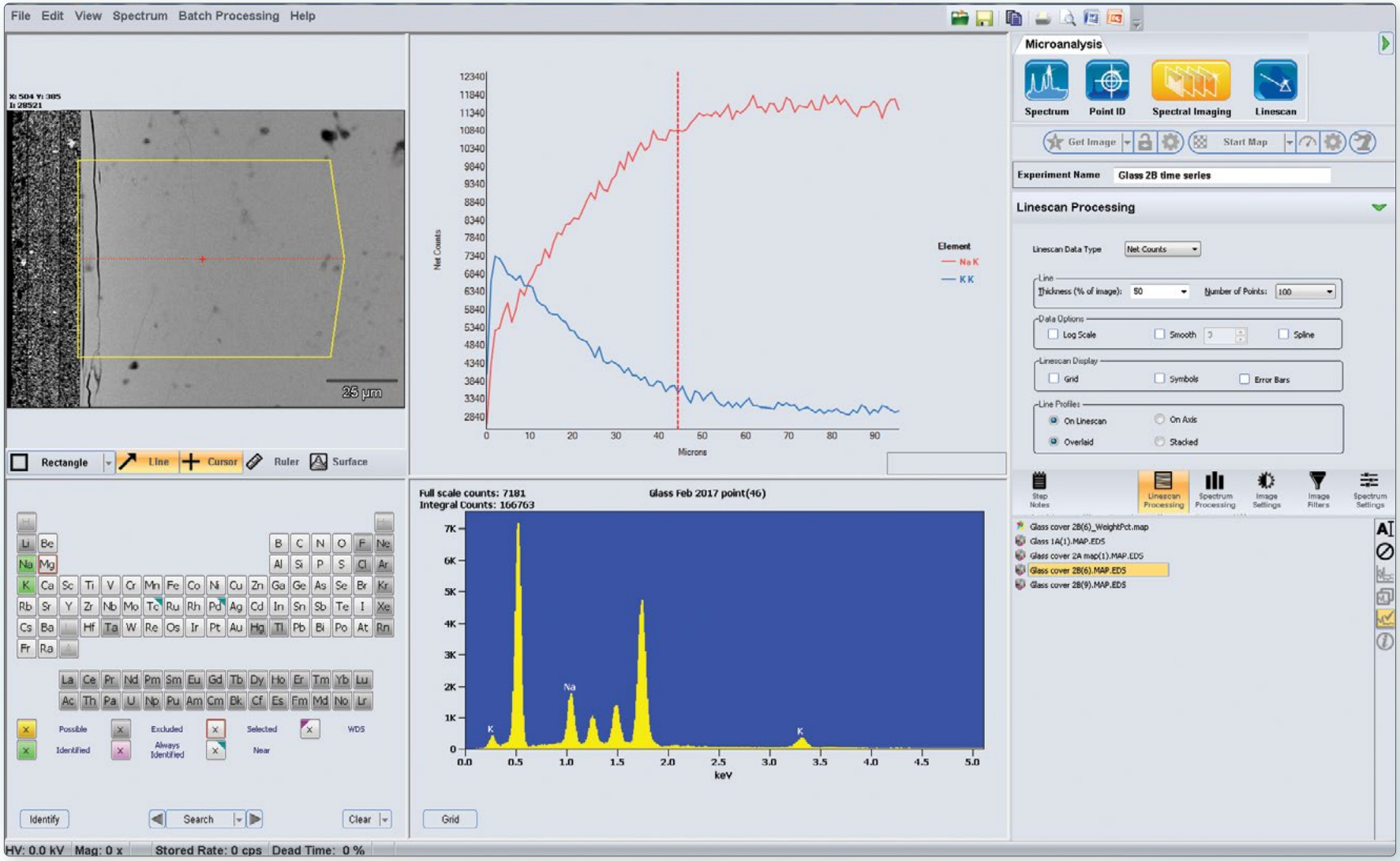
Click the **Cursor** button under the image to obtain two cursors. One line is drawn over the line profiles and a small red cross is drawn on the image. These cursors are linked. Moving either cursor moves both. They relate a position in the image with a position in the line profile. Turn off the cursor in order to move or redraw the line.

Each time the cursor is moved the spectrum used to generate that point is displayed below the chart.

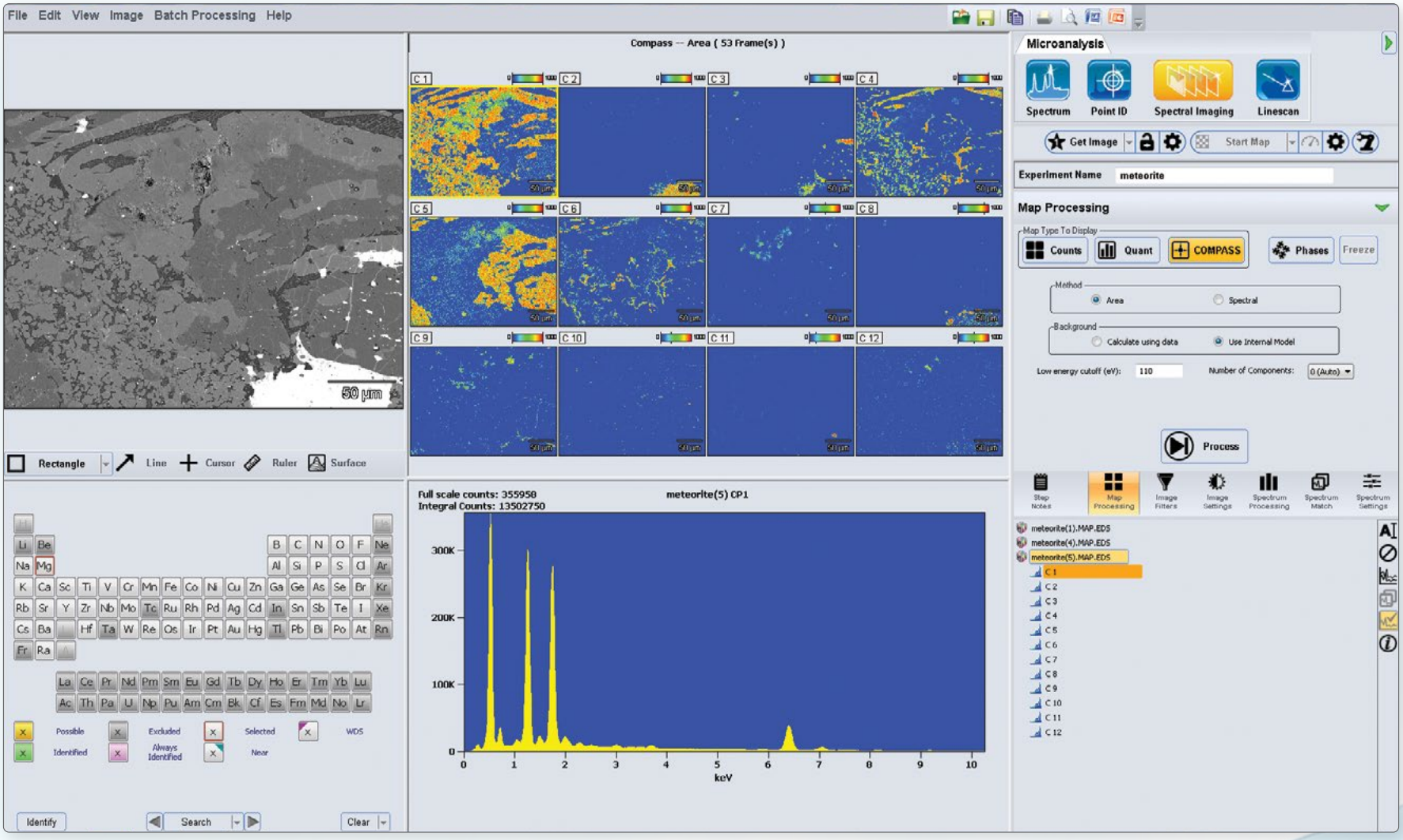
In the menu bar choose

File/Import /Export → Export Linescan as CSV

to obtain a file containing all of the numbers used to make the chart. This file can easily be opened in a spreadsheet for further processing or custom charting.


File Edit View Spectrum Batch Processing Help
25 µm
Rectangle
Line
Cursor
Ruler
Surface
Net Counts
Microns
Element
Na K
K K
Microanalysis
Spectrum
Point ID
Spectral Imaging
Linescan
Get Image
Start Map
Experiment Name
Glass 2B time series
Linescan Processing
Linescan Data Type
Net Counts
Thickness (% of image):
Number of Points:
Log Scale
Smooth
Spline
Grid
Symbols
Error Bars
On Linescan
On Axis
Overlaid
Stacked
Step Notes
Linescan Processing
Spectrum Processing
Image Settings
Image Filters
Spectrum Settings
Glass cover 2B(6)_WeightPct.map
Glass 1A(1).MAP.EDS
Glass cover 2A map(1).MAP.EDS
Glass cover 2B(6).MAP.EDS
Glass cover 2B(9).MAP.EDS
Full scale counts: 7181
Integral Counts: 166763
Glass Feb 2017 point(46)
keV
Possible
Identified
Excluded
Always Identified
Selected
Near
WDS
Identify
Search
Clear
Grid
HV: 0.0 kV
Mag: 0 x
Stored Rate: 0 cps
Dead Time: 0 %

COMPASS and Phase



In **Map** Processing select the **COMPASS** button as shown above. Set the Method option to Area. Set the **Number of Components** to **Auto**.

The Low Energy Cutoff excludes data below this limit. It may be useful to exclude the zero energy peak which might change in unpredictable ways. Set this limit above the carbon peak energy if carbon is only present as a contaminant.

Click Process to perform the calculation.

Click in any image to see the corresponding component below that. Strictly speaking, these are not spectra so they are not automatically identified. Identification is possible which may be helpful to interpret the results.

Calculate phase results

In the panel shown at lower right, click the **Phase** button, set the **Phase Map Type** to **Maximum Intensity**. Set the **Minimum Phase Area %** to about 0.05. Raise or lower this limit as desired. Click Auto to calculate the result. Higher values eliminate small phases.

To recalculate phases using different settings, first recalculate the COMPASS results.

Modify phase results

Click inside any phase image to see the associated spectrum below it. These are true spectra. The peaks can be identified. Quantitative results can be produced.

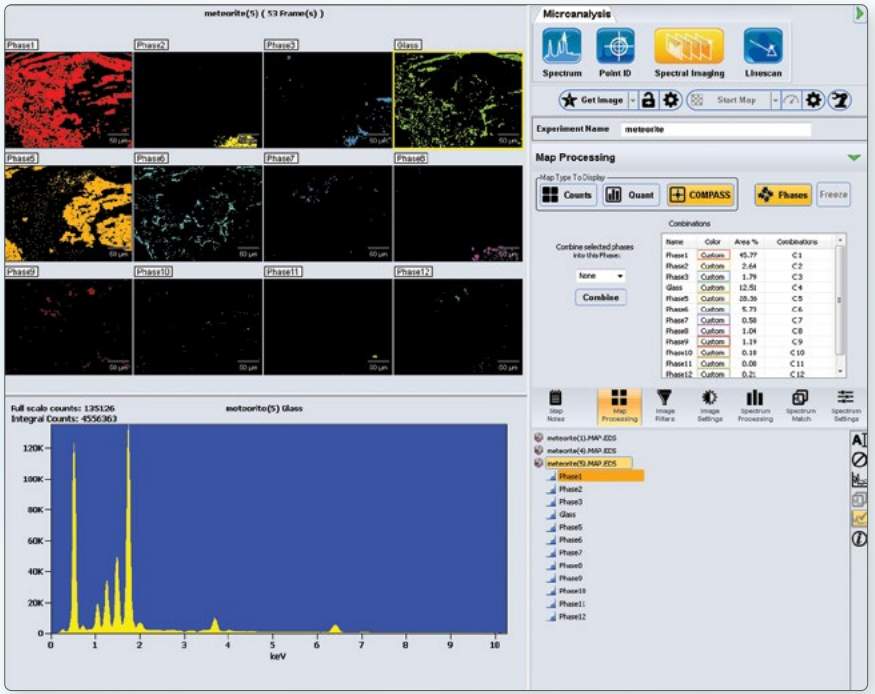
Click on the name of a phase to overlay it on the image. Shift click on a name to overlay all phases at once.

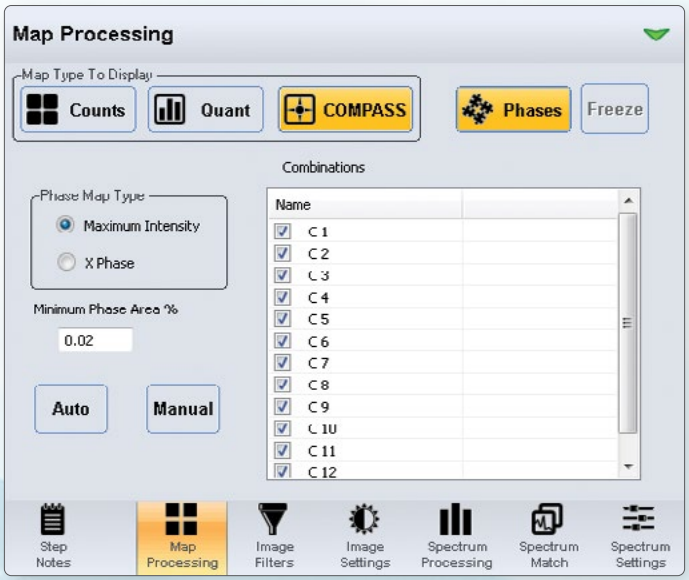
Sometimes the edges of the found phases overlap the adjacent regions. To obtain a better result use the extraction tool and extract a spectrum from the center of a found region.

Double click a phase's name to rename it. In the example at right Phase 4 was renamed to Glass.

To merge two or more phases into one phase click on their names in the list in the panel then choose the destination from the popup and click **Combine**.

To change the color of a phase use the **Image Settings** tool.





Line scan application

Setup to Acquire

Click on the gear icon next to the Start Linescan button then click the green disclosure triangle to see the panel shown at right.

The Linescan app steps the electron beam in a straight line. At each point in the line the beam pauses and a spectrum is acquired and saved. If desired, multiple passes are made along the line as the data is integrated. This can be used for producing a long, effective dwell time per pixel but without the beam remaining at one point for long stretches of time. This can be useful when analyzing beam sensitive samples. A chart is drawn depicting element concentration along the line.

In the panel at right select the **Number of Points**, **Dwell Time per Pixel** and **Number of Scans** from the popup menu or click in the field and type in any desired value.

The Acquisition Time is the product of these three values. It is a read only value.

Because a relatively small number of points are acquired, it is practical to set a relatively long dwell time per point. For this reason, LineScans, though restricted in area, can produce data with high precision.

Energy Range describes which part of the spectrum is saved.

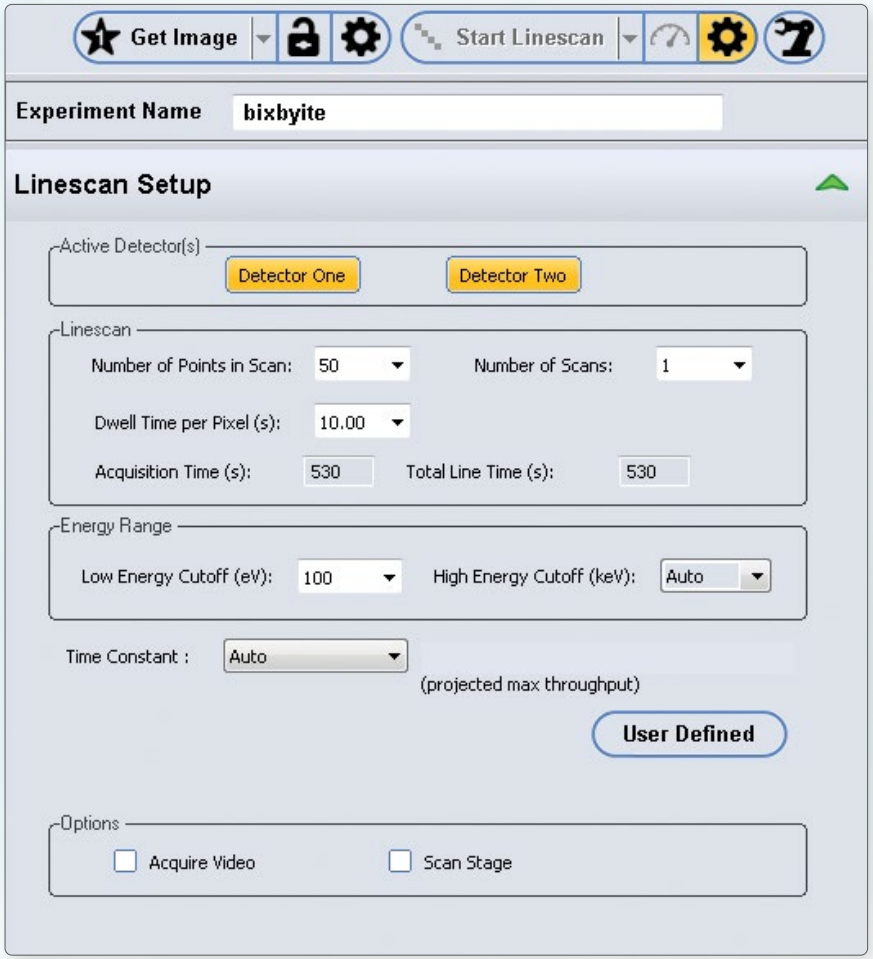
Acquire Video, when selected, causes a chart to be made of the video signal alongside the x-ray data. This can be especially useful when the signal is BSE which is proportional to atomic number.

Scan Stage, when selected, causes the beam to be held steady and the stage to move under the beam instead of scanning the beam. This is potentially useful at very low magnifications.

The stage automation option (Analysis Automation) is required to use this option.

If Analysis Automation is installed it provides for acquiring very long line scans up to the limit of the allowed stage travel.

Set the Time Constant as desired. See Page 7.

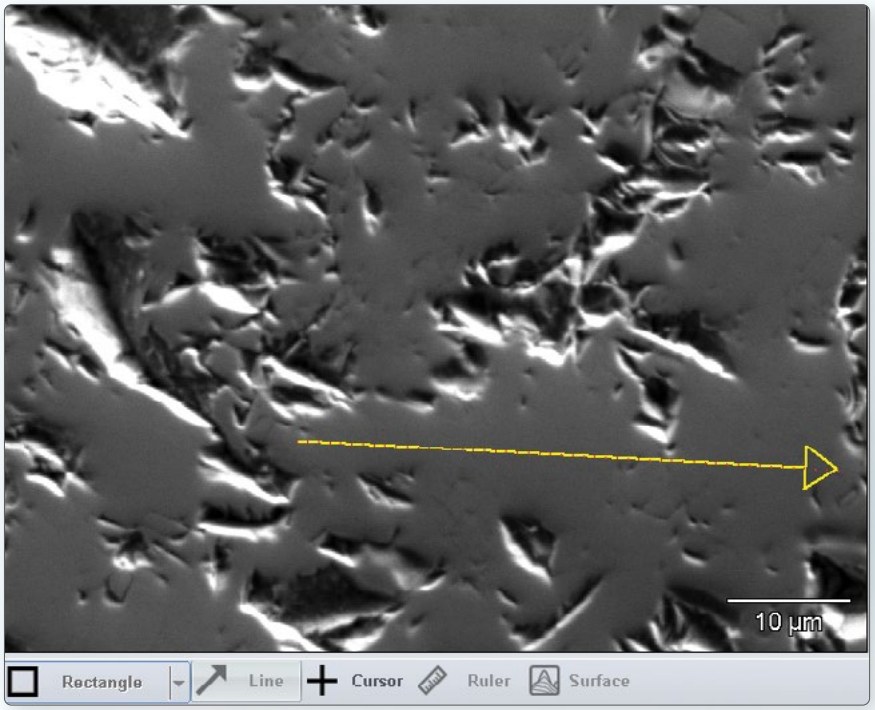


Acquire a linescan

Set the image settings as desired (see page 6) then click **Get Image**. If Drift Compensation has been enabled then during the acquisition the software will stop EDS acquisition when needed to acquire a fresh image to check for drift. Because of this it is better to set a longer time between these acquisitions as long as the compensation is still effective.

Set the desired elements to analyze in the periodic table. Regardless of the elements set, a full spectrum is stored at each point in the scan. If no spectrum is currently visible it will not be possible to set elements as **Identified**. In this case set them as **Always Identified**.

In the image, as shown at left, click and drag a line. Refresh the image to draw a new line. When satisfied with the line length and position click **Start Linescan**.



Modify the appearance of the linescan

After acquisition select the Linescan Processing tool to modify the appearance of the chart. See the discussion on page 16 regarding display options for extracted linescans. Most of that information applies. It is not possible to change the width of the line or the number of points along the line for this kind of linescan.

To change the elements displayed in the chart first select **Quant Setup** in **Spectrum Processing** and select **Auto Quant**. Change the identified elements as needed in the periodic table using **Always Identified**. Under Batch Processing choose Linescan Analysis. From the selector choose the name of the linescan and click Open. If this is a newly acquired linescan first close the project and reopen it to make the data permanent.

Energy calibration

Energy Calibration calibrates the energy scale for the spectra. This feature can be performed as often as desired. It keeps a record of the date of the last calibration.

To access this feature first select **View/Service Mode** as shown at right. Then select the EDS application icon as shown at right.

In the Experiment Setup field choose one the detectors if more than one is available.

Below the spectrum display choose the **Fine Gain Calibration** tab as shown at right.

Load a copper sample in the SEM. Set the kV to 15kV or higher; 20 or 25kV is suggested. Adjust the beam current so that the dead time is below 50% at TC 1.

In the **Setup** box (shown at right) choose Cu from the **Atomic Symbol** field, K line from the Line field. Leave the **Maximum Iterations** at the default of 30.

In the **Time Constant** popup menu choose Calibration Point #8.

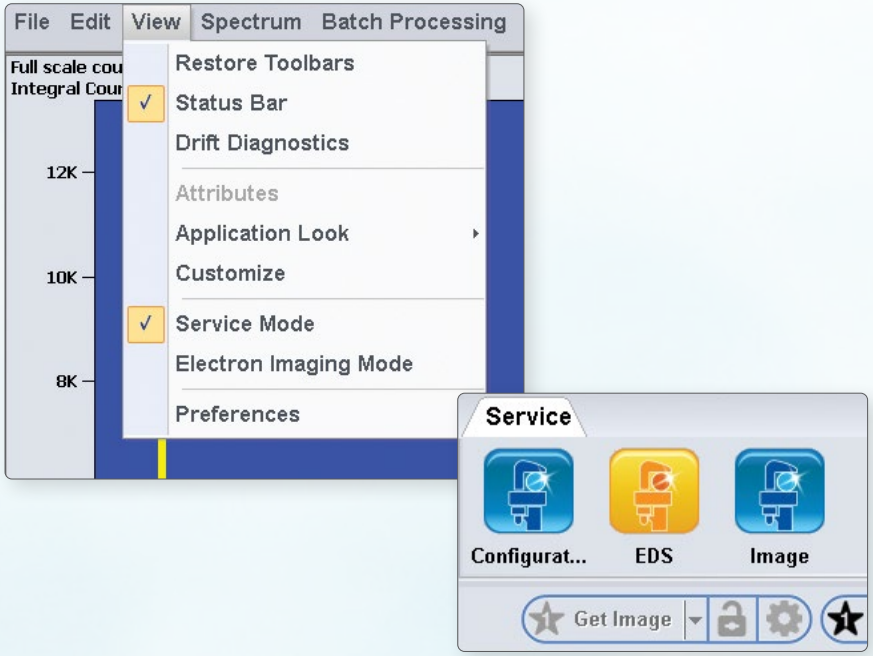
Click the **Start** button at the upper right of the screen.

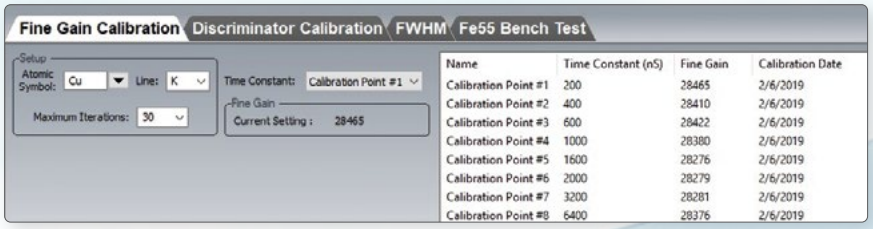
The software will acquire a spectrum for a short time then ask you to identify the copper peak. Place the cursor on the Cu K alpha peak in the spectrum and click OK. This is done to confirm that the system calibrates on the correct line. If the cursor is not showing, select **Spectrum Settings** to turn it on.

The software will collect several spectra automatically and complete the calibration. When done select the next **Time Constant**, click Start and calibrate that point. Repeat for the remaining six time constants.

It may be useful to keep a record of the **Fine Gain** values and **Calibration Dates** to show to your service representative in case these values suddenly deviate by a large amount.

Select **View/Service Mode** again to return to the EDS analysis software.





Using user generated reference shapes

Reference shapes are measured spectrum peak shapes used to measure peak intensities for each element in a spectrum. Pathfinder contains measured lines for every element and line commonly encountered. In some cases, it may be useful to measure a shape with the particular detector and electronics on hand. This is especially true for soft x-ray lines (below about 1 keV) or for cases of severe overlaps such as Al/Br or Ta/W/Si.

When a shape is needed the system first checks for a user generated shape, if none is found the factory supplied shape is used.

Almost any sample can be used for this purpose as long as the peak is isolated from other peaks. See the example for Cu at left. It makes no difference if this is a pure element or compound as long as the desired line is free of nearby peaks as shown here.

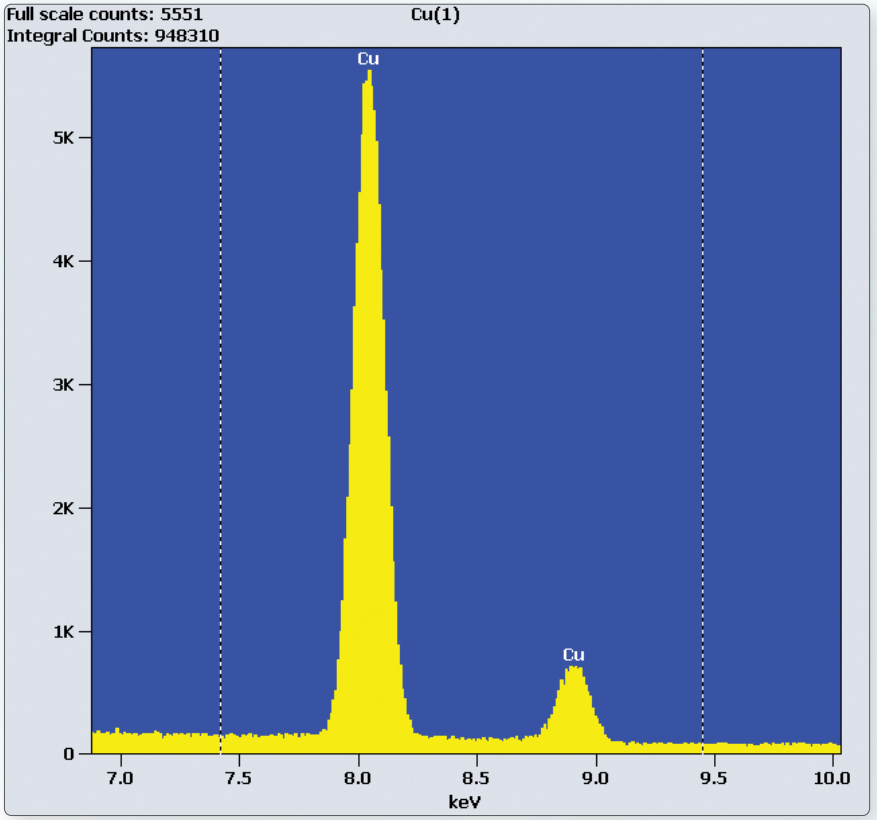
Collect the spectrum using the time constant that will be used to analyze unknowns. Collect at least 10,000 counts full scale. Keep the dead time well below 50%.

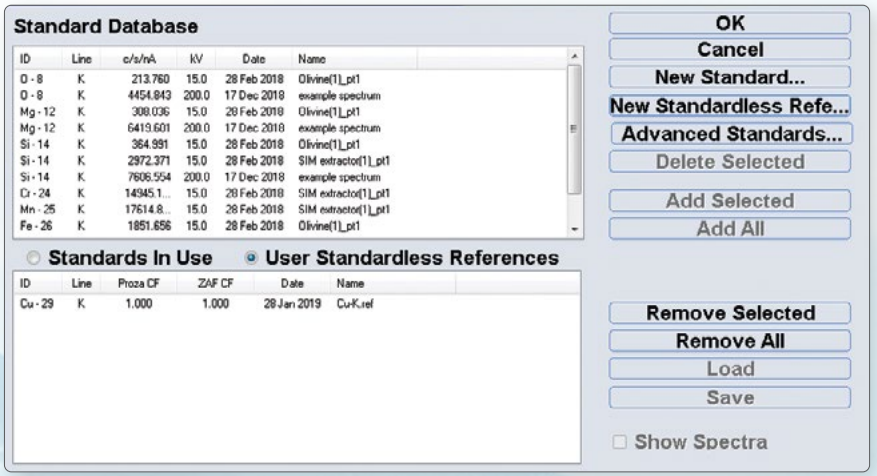
In the **Spectrum Processing** tool choose **Quant Setup** then click **Standards Manager**. This brings up the panel at left. Click the radio button **User Standardless References** to see which standards have already been saved. Click one one and click the **Remove Selected** button if needed.

Click **New Standardless Reference** to add a new reference. When done the new shape file will be shown in the panel as shown at left.

Advanced Topic

For some lines, such as the oxygen K line, it may be almost impossible to obtain a spectrum without carbon contamination. In this case you can edit the .emsa file to remove the carbon peak.





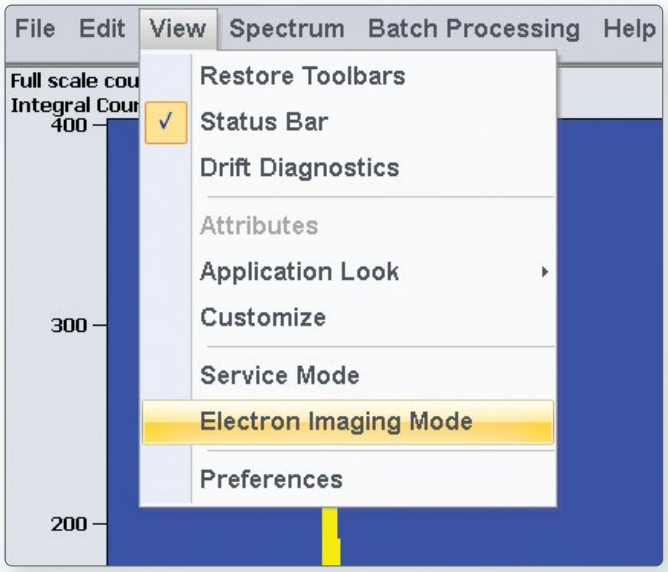
Electron image application

The Electron Image application is used to acquire a digital image from an electron microscope and to view digital images already stored in the current project.

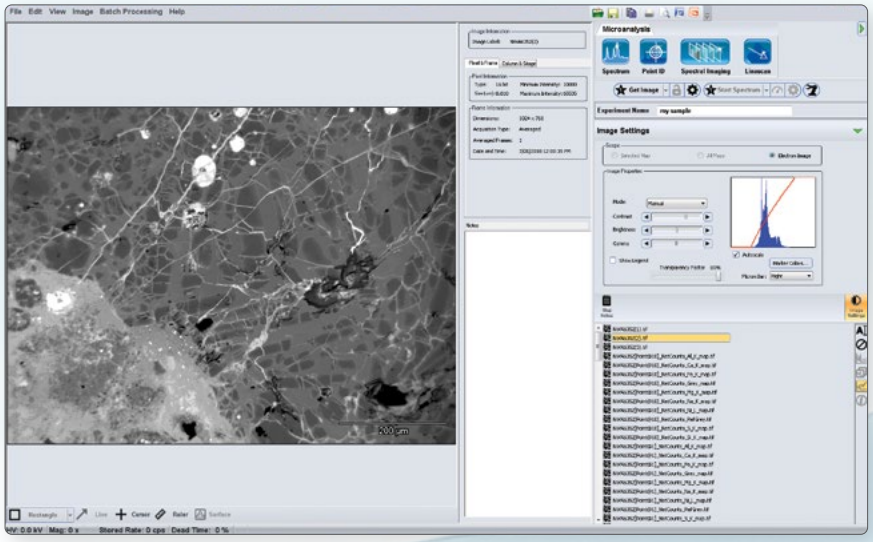
This application is launched from anyplace in Pathfinder by selecting

View/Electron Image Mode

as shown at right.



The full screen appearance of the application is shown at right.



To acquire an image set the image presets as shown on page 8 and confirm the **Experiment Name**. Click **Get Image** to acquire the image.

Click on the name of an image from the list at lower right to open it.

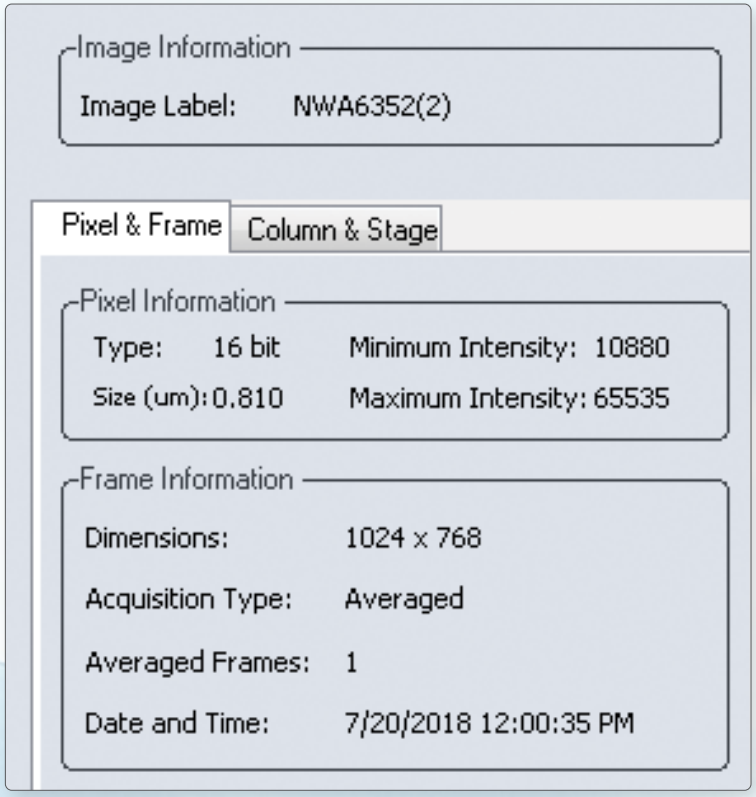
This application automatically opens the Image Settings tool used to adjust the brightness and contrast of the image.

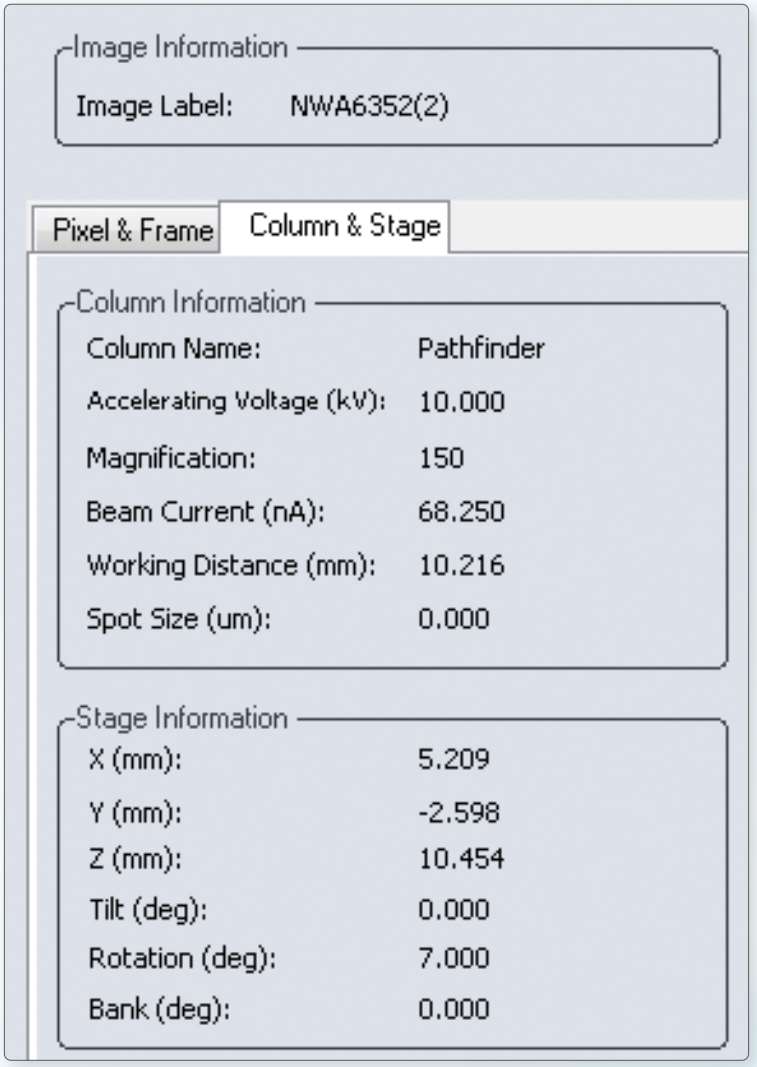
It can be helpful to acquire some high resolution images of each sample as part of an analysis. Because these images are stored in the project folder with the EDS data they will be easily accessible at a future time perhaps weeks or months after the analysis, regardless of onto which device the project was copied.

Select **View/Electron Image** a second time to close this application and return to the application previously in use.

Two tabs to the right of the image provide detailed information about the image. The **Pixel and Frame** tab shows information about the image itself such as array size and date and time of acquisition.

The **Column and Stage** tab shows information about the conditions of the electron microscope when the image was acquired such as accelerating voltage and magnification. Different details rely on different options in the software in order to be part of the image. If this information is not automatically supplied it can be entered manually in the Edit/Microscope Parameters panel. This must be done before the image is acquired.





User generated K-factors for Cliff-Lorimer

After having calculated a set of K-factors by hand, follow these instructions to enter them into the software.

Open for display a spectrum that has the ratio element and some candidate elements. Calculate K-factors by hand.

First, select the ratio element in the periodic table. Click once to obtain a red highlight around that symbol.

In the **Spectrum Processing** tool choose **Quant Setup** then click the green disclosure triangle to enlarge the panel. Ensure that Cliff-Lorimer is selected as the **Correction** method. Click the Standards radio button then the **Standards Manager** button.

The Standards Database panel appears. Choose Advanced Standards.

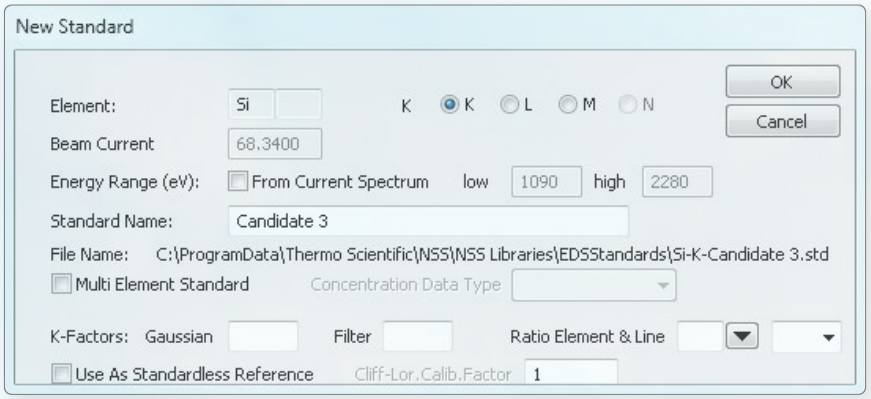
The **New Standard** panel (above right) appears. Select the Ratio Element & Line and enter the calculated K-factor for this element (presumably 1.0) in the **Filter** field. Simply enter 1.0 for **Gaussian**.

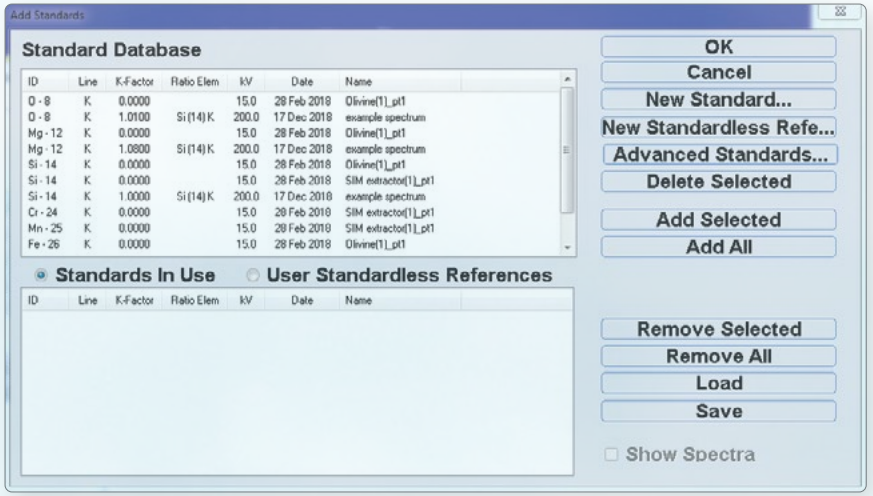
It is extremely important to uncheck the item labeled From **Current Spectrum**. Failing to do so will possibly produced very inaccurate results.

Click **OK**. Repeat this process for the other elements in the spectrum. Don't forget to enter the **ratio element** and **line**.

After saving the last element's K-factors return to the Standards Database. If there are any standards listed in the lower field, click **Remove All**.

Now find the newly created standards in the upper field, select them and click **Add Selected**.





Now click OK and proceed to calculate quantitative results.

The standards are saved at the root of the system so they are available to all users in all projects. If the project is copied to a second computer then the standards will have to be saved again on that machine.

Using standards with quantitative analysis

Before starting, have on hand the compositions of the standards that will be used. Acquire spectra from these standard samples. Make sure that beam current measurements are stored with the spectra. Make a note of the names of the spectra to be used as standards. Identify the elements in each spectrum.

In the **Spectrum Processing** tool choose **Quant Setup**. Click the button for **Standards Manager**. If there are already standards listed in the bottom panel click Remove All to clear this list.

Click **New Standard** and follow the dialog.

At the page that asks for standard composition click the popup menu next to each element to choose the file that contains the composition for the standard from which this element was acquired.

The first time using this application there will be no such file. At the bottom of this panel, click the option to **Create/Edit Compositions**. This will create a file which is simply a description of the standard including the concentration for each element in the standard sample. It contains no x-ray information.

You can create such files for all your standards in advance. You only need to create them once then they can be reused each time a spectrum is acquired from that standard.

After the last standard file has been created, select the newly created standards in the upper panel of the **Standards Database**. It may be necessary to scroll down to find them. Select these files and click **Add Selected**.

The names of the selected standard files should now be listed in the bottom panel called **Standards** in Use. Click OK to close this panel.

In the periodic table the elements for which standards are set should be colored in pink. Select a target spectrum. In the **Spectrum Processing** tool choose **Quant Setup** and click the **Process** button to calculate a result.

If there are elements identified in the periodic table for which standards were not saved Pathfinder will try to calculate a result for those elements by the standardless method. These will be identified in the result.

It can be very useful, when an artifact element is present to identify it in the periodic table, then right click on the symbol and for **Quant Lines** choose Absent. This will keep the peak identified and it will properly separate this peak from others in the spectrum, but no result is reported for this element.

Under the quantitative results table click the **Options** button. It is very helpful, when using standards, to include the **Standard Name** in the report as a check to confirm that the correct standard was used to obtain a result. This feature lists the name of each standard next to the element whose result relied on that standard.

Analysis Automation

Analysis Automation is an option for Pathfinder which is used to conduct multiple analyses at different stage locations. Select **Help/About Pathfinder** and double click on the phrase **"License Key"** to see if the option is installed.

Analysis Automation is available for every application in Pathfinder. It behaves differently in each application according to the character of that application.

To invoke **Analysis Automation** click the icon as indicated at right. This brings up the panel shown at right.

This panel accomplishes two things. First, it provides a way to choose locations on the sample for analysis. This set of points can be saved on the hard drive. Alternatively, a stored set of points can loaded from the hard drive.

Second, this panel launches an acquisition. Click **Start Automation** to begin an acquisition. Progress of the acquisition is seen here as well.

There are three patterns of stored locations: selected areas, grids and circular areas. Selected areas are arbitrary locations selected by the analyst. Grids are rectangular arrays of locations. Circular areas are similar to grids but covers a sample which is circular in shape such as filter paper.

To select new points set a name for the set of point in the **Sequence Name** field. Click on the popup menu labeled **Acquisition Type** as shown at right.

Selected Area: Move the sample stage to a new location. Click **Add Location**. The location appears in the list of locations. Select an existing location and **Remove** it or move the stage and click **Add (Change)** to modify the location.

Grid: Picture the grid of locations on the sample. Move the stage to the upper left corner of the grid. Focus the image electronically. Click to accept the first point. Move the stage to the lower right corner of the array. If the image is out of focus, correct the focus by moving the stage up or down. Click to accept this point. Move to a third location on the sample (not necessarily part of the grid. Again focus by moving the stage. Click to accept the third point. Pathfinder will calculate a plane from these three points.

There is an option to use the saved magnification. In this case the system uses the SEM magnification that is currently set while the points are being saved. Otherwise, Pathfinder will use the SEM magnification set at the time the acquisition starts. In either case, Pathfinder uses the magnification and the known size of the selected area to calculate a set of fields that covers the selected area.

Circle: Imagine a circle covering the sample. Move the stage to the top of the circle and accept that location. Move the stage to the 9 o'clock position on the circle and accept that location.

Once selected, it is a good idea to **Save** the points. Next click **Start Automation**. Click the green disclosure triangle to see a graphic indicating the progress of the acquisition. Click **Stop Acquisition** if there is some reason to cancel the acquisition early.

This is how Analysis Automation behaves in each application.

Spectrum: Pathfinder moves the stage to each location and acquires a spectrum according to the Spectrum presets. (See page 9). There is an option to either set the electron beam to a steady point in the center of the field of view or to scan the electron beam across the field of view while acquiring a spectrum. The result is a number of spectra.

Point ID: Preset locations in the image for each stage location. Pathfinder then moves to the location and acquires spectra for each desired point or area in the image. The result is a number of Point ID data sets.

LineScan: In this case the stage locations are selected as a start and end point. Pathfinder holds the electron beam steady while moving the SEM sample stage under the beam and acquiring spectra. The result is a data set consisting of spectra. LineScan will process these and display a chart but without an image.

To obtain an image save the points file before acquiring x-ray data. Then use the Electron Imaging application, recall the points file and collect images along the same path to obtain an image of the path.

Spectral Imaging: It is critical to set a termination criterion before starting the acquisition. (See page 12). The result is a number of SI maps. If this was a grid or circle, then there is information stored with these such that Montage can merge them into a large map.

Electron Image: An electron image is acquired at each SEM stage location according to the current image settings. (See page 6). If this was a grid or circle location, information is stored with the data such that Montage can merge these into one image.

Use **Electron Image** with a low resolution array and short frame time as a way to test the point selection. Use Montage and check that the image covers the desired area. Check that Pathfinder properly orders the images top to bottom and left to right. If this is not correct then contact service.

The images will likely not fit together perfectly. The stage and beam scanning devices have different calibrations. It may help to calibrate the beam to the stage. Using the same magnification as the intended analysis, locate a feature on a sample. Mark one end on the screen, note the stage location, then move the stage till the other end of the feature is at this mark. Note the difference in stage.

Batch processing and montage

Having acquired a set of spectra or maps, **Batch Processing** and **Montage** are used to process these rich data sets. Any randomly located data may be processed this way. In addition, if data were acquired at grid locations with **Analysis Automation** then **Montage** can tile this data. These features operate differently with the different applications.

Batch Processing/Spectrum Analysis

See page 9.

For Linescan spectra, for spectrum name enter *.lsmsa and Return and navigate in the project to find these in order to get .csv output files for this data type.

Batch Processing/Point ID

See page 11.

Batch Processing/LineScan

Set the desired elements in the periodic table and the quantitative result type in **Linescan Processing**. This processes each spectrum then produces a new chart.

Electron Image

If an array of images was acquired with Analysis Automation and the grid or circle option then select

Batch Processing/Create Montage merges these into one image.

Spectral Image Maps

There are two ways to process maps. Regardless of how the maps were acquired (manually or with **Analysis Automation**) it is possible to automatically process a number of SI maps to produce images of element distributions.

From the **Spectral Imaging** application choose

Batch Processing/Extract Quant Maps.

This presents a dialog for selecting the maps to process and the kinds of processing to perform. (See page 14).

The results are sets of images. These maps can be overlaid on the electron image, their colors and brightness and contrast can be changed. They are useful for reporting or sending image results to requestors. However, there is no x-ray data attached to these images so extractions cannot be performed. This is the same result as is obtained by invoking **File/Save Map File**.

If the set of maps was obtained with **Analysis Automation** using a grid or circle pattern then **Montage** can be used to merge them into one large map with a result image for each element.

To create a montage of maps, first select the **Map Processing** tool then choose the **Quant** button. Set the calculation as desired. A good starting point is to choose **High Detail**, **High Precision** and a kernel size of 3x3.

Set the desired elements to be **Always Identified**. Turn off **Auto ID**.

Select **Batch Processing/Create Montage**.

Click the **Process Quant** radio button. Select the data set from the list presented and click the arrow icon (→) to proceed. Click Close when done.

Site license

Site license

Every Pathfinder customer is welcome to make use of Pathfinder software on the desktop or laptop computers in the laboratory.

The target computer needs to be running the Microsoft Windows OS that is required for use with the version of Pathfinder being installed. It also requires at least an HD display.

With the delivery of the Pathfinder analyzer, a letter was included describing the site license and listing the installed options.

Use the supplied installation media to install the software. Contact Technical Support to obtain a link to download newer versions of the software.

On a workstation installation, first install Pathfinder software, but do not run it. Next, select “Configure my Pathfinder installation as an off-line viewer” from the software installer main menu.

thermo scientific

Find out more at **thermofisher.com/pathfinder**

ThermoFisher SCIENTIFIC