AZtec® User Manual

OXFORD INSTRUMENTS

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Contents

Getting Started

The unique features of the user interface are described in the Application over view followed by the Guided tour of the Application. The details about the software licensing are covered in the frequently asked questions:

Application overview

There is a great deal of flexibility in the user interface. You can configure the workspace the way you wish to work and save a custom configuration (layout) to come back to every time.

The main application consists of the workspace in the middle area. It is supported by a side panel on the right containing Project Data, Mini View and Step Notes. You can remove each of these components from the view if you wish.

Dockable and Floating Window Panes

The window panes are docked as the default configuration of the user interface. You can un-dock and free float them. Click and drag them wherever you want them in the interface or to a second monitor.

Re-sizable Windows and Dialogs

Windows and dialogs can be resized by clicking and dragging their edges. The main application window can also be re-sized.

Global Menu Bar

There is a Menu bar near the top of the application window. It has the common menu items that you can access wherever you are in the application.

EXAMPLE

Configurable Status Bar

The Status Bar is located at the bottom of the application window. You can choose which hardware parameters you wish to display in there. A progress bar also shows up in the Status bar when you are importing or saving a project.

Tool Bars

Various useful tools are available in local tool bars where appropriate.

EXAMPLE

'Pan', 'Normalize', 'Annotations', 'Show Data Values' and 'Show Candidate Elements' tools are available in a local tool bar in the Confirm Elements and in the

Acquire & Confirm windows in Point & ID on the right of the application window.

EXAMPLE


This tool bar is available in the Acquire and Confirm window in the Custom Map navigator. You can toggle on/off the user interface components from the display to your preferred layout.

Context Menus

Many useful menu items are available on the right click of the mouse in the application.

EXAMPLE

Image, Spectrum and Map viewers have many useful menu items. For example you can email a spectrum, image or map or append it to your report.

There are two modes of operation, Guided and Custom:

Guided Mode

The user interface components are laid out in Navigators that take you through your analysis from the Specimen through to the Report. You can navigate backwards and forwards as you wish. Each step has associated F1 (context sensitive) help and Step Notes to assist you at each stage of your analysis.

Custom Mode

In this mode, the key components are provided in one window. It allows you to perform the analysis in one workspace without having to move away from it. Each component can be undocked to have it free floating or dragged to another monitor to view it in full screen.

To provide you with more workspace, the Navigator area can be collapsed by pressing  in the top right of the application window. Press  to restore the Navigator.

Navigators

The software has Navigators to guide the user through the analysis process. There are the following navigators in **AZtecEnergy**:

- Analyzer - Guided on page 61
- Analyzer - Custom on page 86
- Point & ID - Guided on page 90
- Point & ID - Custom on page 154
- Optimize on page 194
- Map - Guided on page 161
- Map - Custom on page 175
- Linescan - Guided on page 178
- Linescan - Custom on page 190
- EBSD - Map on page 202
- Phase ID on page 237

Menu Bar

There is a menu bar at the top of the application window containing several menu options. Each menu has several items which are described below.

File on next page

View Menu on page 7

Technique selector on page 7

Tools Menu on page 8

Help on page 10

File Menu

Menu	Description
New Project	Removes any existing Projects, prompts to save and then opens a new Project as Project 1.
Open Project...	Removes any existing Projects from the data tree, then opens an existing Project, prompts to save any existing Projects if required.
Add	▪ **New Project**: Adds a new Project and leaves any open Projects in the data tree. ▪ **New Specimen**: Adds a new Specimen in the Project that has focus. ▪ **Existing Project...** adds an existing Project and leaves any open Projects in the data tree.
Remove Project	Removes the highlighted Project. If there is only one Project in the data tree, the Remove Project menu is disabled.
Save Project	Saves the highlighted Project.
Save Project As...	Makes a copy of the highlighted Project, prompts to enter a name and then opens it in the data tree and closes the existing Project.
Import INCA Project...	Imports an INCA Project, adds it to the Project list if existing Projects contain data otherwise replaces an existing "new Project".

Menu	Description
Save As INCA Project....	Saves the highlighted project as an INCA Project.
Export to CHANNEL5 Project	Exports the currently selected EBSD data as a CHANNEL5 project file.
Recent Projects	Allows to load from the recent Projects that you have been working on.
Close AZtec	Shuts down the application.

View Menu

Menu	Description
Data View	It has the Current Site and Data Tree tabs.
Mini View	It has various views such as a live spectrum, image or acquisition progress bar.
Step Notes	Provides a brief description of the main features of each screen. Users can write and edit their standard operating procedures (SOPs) for future reference.
Application Zoom Level	Available options are Largest, Large, Medium, Small and Smallest.

Technique Selector

The techniques available are EDS and EBSD. Select the technique you wish to use by pressing the appropriate selector button on the top left of the main screen.

Tools Menu

Menu	Description
Themes	Accessible Theme Oxford Instruments Theme Light Blue Theme Blue Theme
Languages	Default English French German Russian Chinese Simplified Japanese
User Profile...	Settings available to create a user profile are: EDS Acquire Line Data Settings EDS Acquire Map Data Settings EDS Element Settings EDS Peak Label Setting EDS Quant Settings Scan Image Settings Specimen Tilt Settings

Menu	Description
Preferences...	Preferences are saved per user. Make your selection for the following: Auto Save Image Viewer INCA Image Export Reports Spectrum Viewer Status Bar Welcome Screen
Status Messages	

Help Menu

Menu	Description
Show Help Home Page	Launches the Help Viewer with table of contents in the left pane and useful links to internal and external sites in the right pane.
Show NanoAnalysis Advice (F1)	Opens the Help Viewer. Pressing F1 on the keyboard loads the help page relevant to the active step of the navigator.
Launch User Manual	Opens the user manual as a PDF file.
Launch NanoAnalysis Encyclopedia	Opens the Encyclopedia in the Windows Explorer.
Oxford Instruments Website	Launches Oxford Instruments's home page.
About AZtec	Provides access to License Manager, System Info, Assembly Info and Credits.

Preferences

The Preferences dialog allows to choose the miscellaneous settings for display:

Auto Save

This option allows you to periodically auto-save the current Project.

Check, 'Save project after elapsed time' check box and specify the number of minutes that should elapse between each auto-save. The current Project will be saved at specified intervals.

EBSD 3D Phase Viewer

EBSD Image Viewer

EDS Layered Image Settings

There are two options:

- New X-ray map layers are visible in the EDS Layered Image.
- Apply automatic sorting to new X-ray maps.

EDS Linescan Viewer

The line thickness (in pixels) for the linescans can be selected from the drop down list. The default Line Thickness is Normal. If you select the 'User defined' option, you can specify the thickness using the slider bar.

The five available options are tabulated below:

	Thickness in Pixels
Thin	0.5
Normal	1.0
Thick	2.0
Thicker	4.0
User defined...	

Spectrum Viewer

You can make your selection how you wish to display the Spectrum Viewer.

- Vertical Scale Type - Choose from Linear and Logarithmic

Check the options you wish to have in the Spectrum Viewer display:

- Show Vertical Scale
- Show Horizontal Scale
- Lock Vertical Scale
- Lock Horizontal Scale
- Smooth Spectrum
- Expand Mini Quant

Image Viewer

The various settings that you can choose for the Image Viewer are:

Rescale Image Mode

Choose how you wish to rescale the image from the two following options:

- Fit Image to Display
- Fill Display with Image

Show Acquisition Areas

Choose one of the following three options how you wish to display the acquisition areas:

- Show All
- Show Selected
- Show None

More display settings are as below:

- Show Short Names -The labels for the acquisition areas are shortened to prevent them from overlapping and masking the text.
- Show Header - The label for the image is displayed in the header.
- Show Color Bar - The Color Bar is displayed below the Image Viewer.
- Show Scale Bar - The micron marker is displayed below the Image Viewer.

- Show Contrast/Brightness Buttons - The Auto and Manual buttons are displayed at the bottom right of the workspace.
- Show Annotations - Annotations are displayed on the image.
- Show Color Key - The color key is displayed in the bottom left part of the Layer Image in the Map application.
- Use Image Smoothing -

INCA Image Export

You may have SE and BSE images in your Project. When you save your Project as INCA Project, you can choose to export either SE or BSE image.

Check SE or BSE check box to make your selection.

Report

The various options available are described below:

- Report Image Scaling (Pixels Per Inch)

The Image scaling can be set to 96, 150 or 220 Pixels Per Inch

- Show Acquisition Areas in Reports

Choose one of the three options available, Show All, Show Selected, Show None

- Package Templates

A number of templates are available for each package. Two file formats available are Microsoft® Word or Microsoft® Excel.

Note that the reports can be viewed and saved with the Microsoft® Viewer supplied with the system. You can only edit reports if Microsoft® Office 2007 or higher is installed on your system.

A selection of templates are available in each of the following packages:

- EDS Point & ID Template
- EDS Map Template
- EDS Linescan Template
- EDS Analyzer Template
- Other Templates
    - Batch Templates - a number of templates are available for batch exporting data. Select a template from the drop-down list.

Status Bar on page 15

Make your selection of the parameters that you wish to display in the Status Bar from the Preferences dialog.

Welcome Screen

Check this option if you wish to display the Welcome Screen at the start up.

When you have selected your settings, press the Save button to save them. Press the Close button to close the Preferences dialog.

Note that the Preferences are saved per user.

Status Bar

The Status Bar displays the hardware status. It also allows the access to the Microscope Control, EDS detector and EBSD detector. A progress bar appears in the Status bar when you import, load or save projects.

The user selected parameters are displayed in the Status Bar at the bottom of main application screen. You can choose the parameters you wish to display on the Status Bar tab in the Preferences dialog. To access the Preferences dialog go to the Tools menu on the main tool bar and select Preferences:

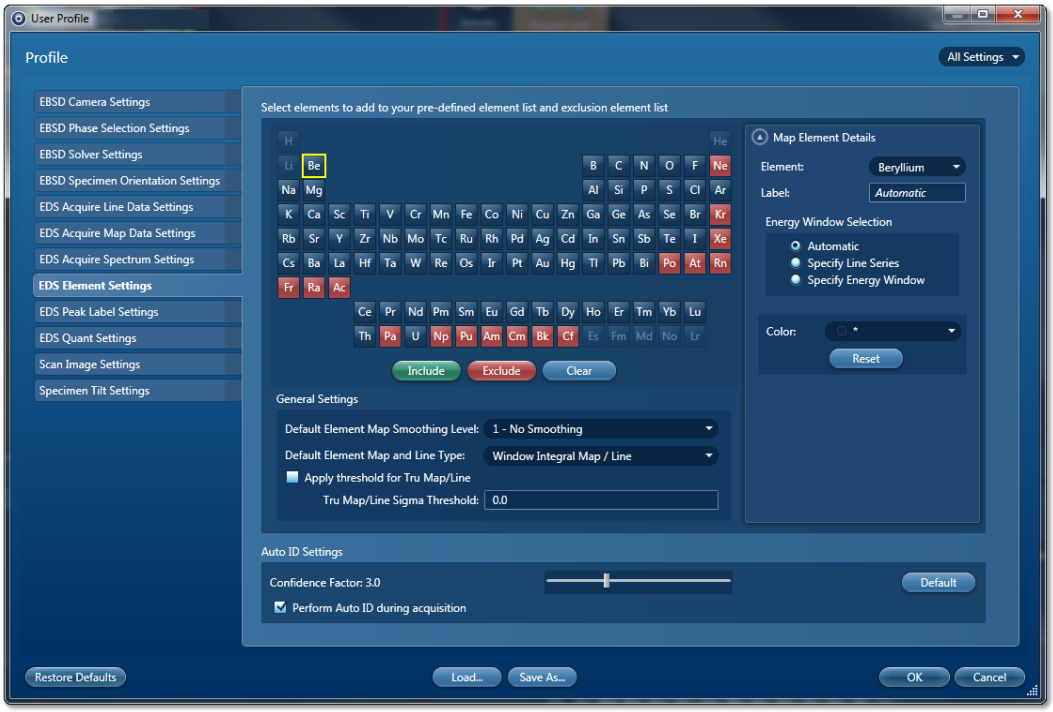
Check the relevant check boxes to make your selection and press the Save button. The selected parameters will be displayed in the Status Bar.

You can access the Microscope Control by pressing  located on the right end of the Status Bar.

See Also:

User Profile

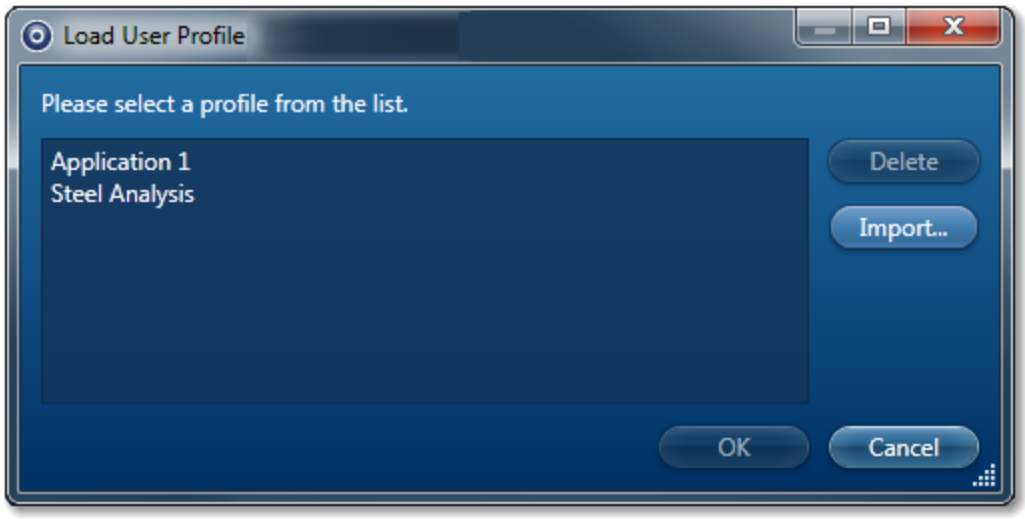
A user 'Profile' contains all the settings needed to reproduce analytical results obtained on a previous date or by another user. The User Profile dialog is launched from the Tools menu on the main application menu bar:



EXAMPLE

"I am in charge of a service lab and have a number of users reporting to me. We perform many different types of analysis that we carry out, but do not have the luxury of assigning one person to do the same analysis all the time. So it is important that we have a way of reducing the variability in analytical results between different users. At the moment I make sure I check the users' settings before they start "

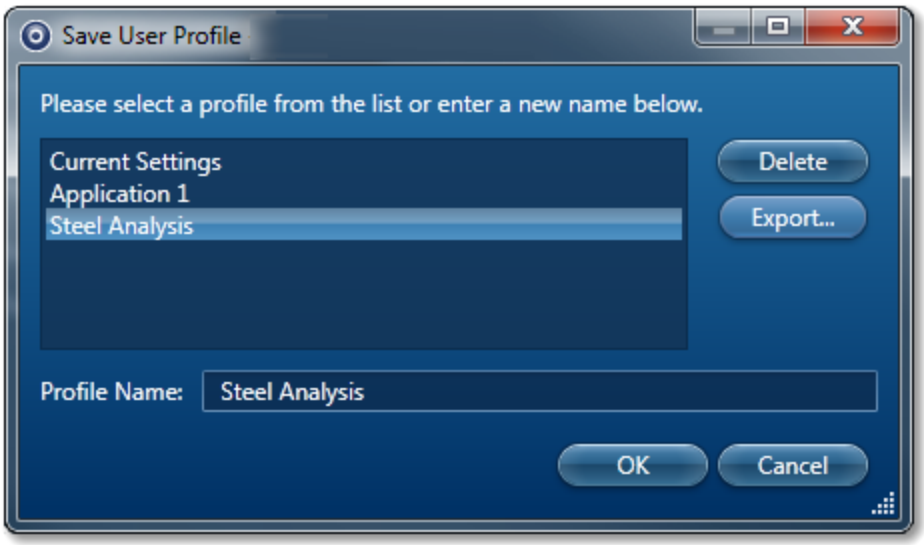
For each analysis type, all the relevant parameters can be saved in a profile, along with personalized step notes to instruct the users on the analysis. Subsequently anytime a user wishes to perform a particular type of analysis, all they have to do is load the relevant profile and all the appropriate settings will be changed and associated step notes will be loaded.



EXAMPLE

"My company has several sites all over the world, performing similar types of analysis. We need to ensure that each site carries out the same type of analysis in the same way, so we can compare results" ……."I need some help interpreting recently acquired data….if I send a project to Oxford Instruments Customer Support, how do I ensure that they see what I do?"

For both these cases the user profile can be exported via the user profile window:



The profile will be saved as a .config file and there will be user standards file (with .ois extension) if selected for use. See Managing Standardizations on page 199

Both files must be given to the person who you want to repeat or look at your data. The recipient will have to go to the Load Profile window and import the supplied profile.

EXAMPLE

For spectrum acquisition, you can specify the Number of Channels, Energy Range (keV), Process Time, Acquisition Mode and Acquisition Time (s) and save them in the

User Profile.

When the User Profile dialog is opened, it stores the backup copy of the current settings.

Press 

in the User Profile dialog to load a profile.

Press 

in the User Profile dialog to save a profile.

Press 

in the User Profile dialog to save the settings. This action will close the dialog and remove the backup copy.

Press 

to close the dialog. This action will restore the current settings from the backup copy.

There are separate tabs for different settings in the Use Profile dialog. The details of the settings in each tab are described in the topics which can be accessed from the links below.

See Also:

Scan Image - Settings on page 209

Acquire Line Data - Settings on page 185

Acquire Map Data - Settings on page 168

Acquire Spectra - Settings on page 112

Element Settings on next page

Peak Labels on page 116

Quant Settings on page 143

EDS Element Settings

The Element Settings tab in the User Profile dialog is provided with a periodic table. It enables you to define a list of Pre-defined Elements present in the specimen and the elements you wish to exclude from the AutoID routine.

When you press an element symbol in the periodic table, three buttons are enabled which are colored coded:

Include

Exclude

Clear

Defining an element from the periodic table is a cyclical process. Double-clicking on an element symbol will include this element. It will be colored green. Double-clicking it again will exclude this from the list and it will be colored red. Double-clicking on the symbol third time will clear this element from the list.

TIP!

For multiple element selection, hold down the Ctrl key, press on each element in the periodic table that you wish to select and then press the Include, Exclude or Clear button.

AutoID Settings

You can enable or disable AutoID during acquisition by checking or un-checking the 'Perform AutoID during acquisition' checkbox.

AutoID Confidence Factor

The default value for the Confidence Factor is set at 3. You can use the slider to set the value. The Confidence Factor is used to determine how AutoID behaves with regard to the sources of error.

Map Element Details

The 'Map Element Details' dialog allows you to configure the element maps. The default X-ray lines are used for element mapping unless you specify them. You can select the X-ray line for each element that you wish to map from the Map Element Details in the Element Settings tab or in the Construct Maps step.

You can define the energy window width for each element rather than using the default value.

You can select which elements to map and which ones to exclude.

See Also:

Auto ID Confidence Factor on the facing page

Auto ID Confidence Factor

If the Confidence Factor is set to a high value, AutoID will find the most significant peaks but may miss small peaks that are close to the noise level. If the Confidence Factor is set to a low value, AutoID will detect small peaks but may pick up false positive identifications that are due to statistics or systematic errors.

By default, we set the Confidence Factor to 3 which corresponds to the "3-sigma" confidence level for a normal statistical error distribution.

The Confidence Factor is used to determine how AutoID behaves with regard to the sources of error. AutoID is designed to find a good combination of peak profiles that matches the spectrum and thus identifies the elements present in the specimen. When peaks overlap, the proportion of constituent profiles is determined by least squares fitting to the sum of peak profiles. Counting statistics introduce fluctuations into the spectrum that are sometimes difficult to distinguish from genuine peaks. The statistical fluctuations introduce "random" errors that are equally likely to be positive or negative. When there are severe peak overlaps, it is even more difficult to distinguish genuine peaks from noise fluctuations.

In addition, chemical bonding effects and inaccuracies in peak profiles may mean that there is no combination of peak profiles that is an exact match to the spectrum, even when there is no statistical noise. If the peak profile is not perfect, this introduces bias or "systematic" error into the results.

If a fitted peak profile is much larger than the random or systematic errors, it is likely that the corresponding element is present in the specimen.

N o t e

To access the AutoID Confidence Factor, select User Profile from the Tools menu and then select the Element Settings tab. AutoID Confidence Factor is available in the AutoID Settings.

Support Panel

The Support Panel is present on the right side of the application window. It has three components, Data View, Mini View and Step Notes. You can add or remove any of these components from the display by selecting the View menu on the Menu bar. You can also minimize, maximize or close each component from the display by pressing the relevant button present at the top right corner of each component.

To increase your work area you may wish to collapse the Support Panel by pressing the arrow button in the top right corner of the application. Pressing this again will restore the Support Panel.

Data View

Data View has two tabs, one for the Current Site and one for the Data Tree. For details see the Data View topic from the link at the end of this topic.

Mini View

In the Mini View you can choose to display a number of different views such as Electron Image, Spectrum Monitor, the Ratemeter or many others depending on the step.

Step Notes

Step Notes provides the first time user of a navigator with simple instructions on how to complete a typical work flow. It also provides a site administrator or user with the ability to write a standard operating procedure (SOP).

See Also:

Data View on page 1

Mini View on page 78

Step Notes on page 79

Data View

The Data View panel is located on the right of the main application window, By default, it is always displayed. If it has been taken off the view, it can be restored by choosing the Data View from the View menu on the main menu bar.

Data is archived in a logical manner and can be directly viewed via easily recognizable icons.

Acquired data is automatically saved at the end of an acquisition. An auto save option can be enabled from the Auto Save tab of the Preferences on page 11 dialog on the Tools menu.

The Data View panel has two tabs, Current Site and Data Tree.

See Also:

Current Site on next page

Data Tree on page 71

Current Site

The Current Site shows the data for the currently selected Site in the Data Tree, plus the current acquisition and any pending acquisitions. The ordering of items in the Current Site is different to the Data Tree. The new data items are added to the end in the Current Site where as the Data Tree sorts the items under the Site by spectra, electron images and then maps.

The Current Site has some extra features:

Electron Image

Electron image has a lock/unlock icon. Click once to lock, then again to unlock:

If unlocked, subsequent electron image acquisitions in the same Site will replace the existing electron image.

Locking the Electron Image will prevent the image from being recycled.

Current Acquisition

Both Spectrum and Map acquisitions show a progress bar and a stop icon:

When acquiring EBSD data, pause/resume and restart icons are also shown. Progress information is also shown in the tool tip.

Pending Acquisitions

Spectrum shows a cancel icon:

Note spectra and map acquisitions can be queued.

See Also:

Data Tree on page 71

Data Tree Menus on page 32

Importing INCA Data

Data Tree

Data is archived in a logical manner and can be directly viewed via easily recognizable icons on the Data Tree. To access the Data Tree, select the Data Tree tab on the Data View panel.

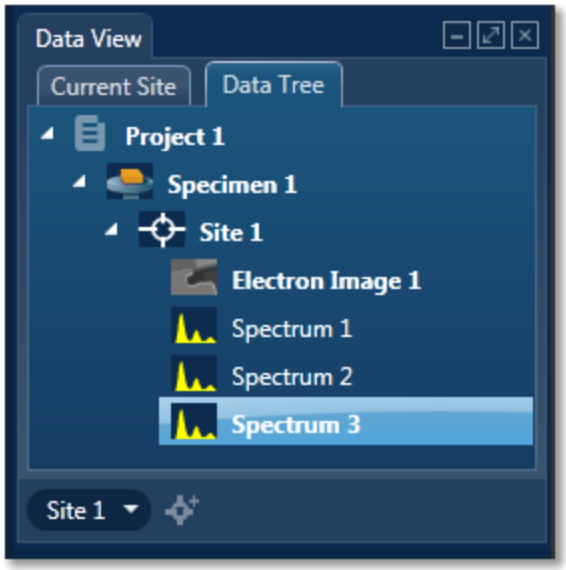
All open Projects and their contents are displayed in the Data Tree. Multiple Projects can be opened and shown in the Data Tree at the same time. If you have multiple Projects, Specimens or Multiple Sites in the Data Tree, you can easily get to your current site by pressing the Current Site tab.

When the application is started a default Project containing a Specimen and a Site is shown. As you acquire data, items are added to the Data Tree. The current items in the Data Tree are shown in bold.

Click on an item on the Data Tree to make it current.

Items on the Data Tree

The screen shot below shows an example of the main items in the Data Tree. Each item is described along with their icons below:



Project

Project is a top level container for data. Each Project is associated with a folder on the file system. The name of the folder is the same as the Project name. The Project folder contains a single file with an .oip extension and optional Data and Reports sub folders.

N o t e

When moving or copying project data ensure that the root project folder is moved/copied, not just the .oip file. The folder can be zipped using the standard

Windows compression utilities if required.

Specimen

Specimen represents the real specimen that you analyze and collect the data from, including images, maps and spectra. There may be many Specimens in a single Project. A Specimen may contain more than one Site.

Site

Site represents an area on the Specimen from where you acquire data such as images, spectra and maps. Site can hold multiple images, for example SE and BSE plus any imported images.

The analytical conditions such as kV, Magnification and Calibration are stored with the data.

Electron Image

Electron Image on each Site can be an SE or BSE image. You can acquire SE and BSE images simultaneously provided the suitable hardware is available.

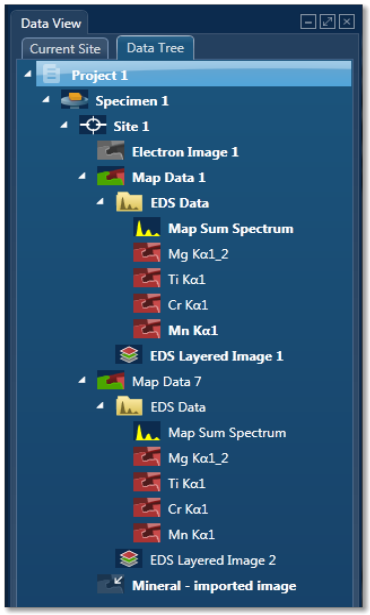
Imported Image

Any standard Windows Picture files can be imported into the Project for comparison or reporting. The file formats available are JPG, JPEG, BMP, PNG, WDP, GIF, TIF and TIFF. You can import an image using the context menu available from the Site.

Spectrum

Spectra are acquired from the areas defined on an electron image. Sum Spectra and Reconstructed Spectra are shown under the Map in the Data Tree.

You will see the following items in the Data Tree if you are acquiring element maps in the EDS application:



Map Data

Map Data is the container for a mapped area(s) in a Site. It can hold EDS Data, EBSD Data or both. One Site can contain more than one Map Data items. In the example above there are two items, Map Data 1 and Map Data 2.

EDS Data

EDS Data is the container for Map Sum Spectrum, Reconstructed Spectra and X-ray element maps.

Map Sum Spectrum

The sum spectrum is calculated from the data acquired from all the pixels in the electron image.

Reconstructed Spectrum

You can reconstruct spectra from areas selected on the Layered Image in the Map application.

X-ray Element Maps

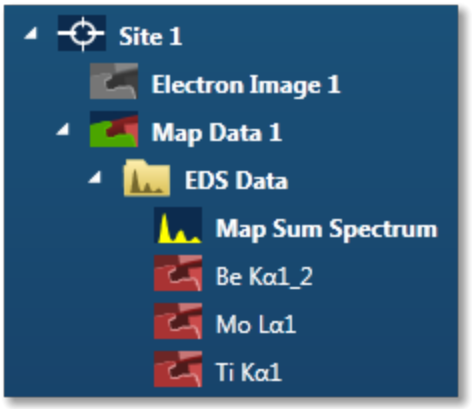
The data can be processed as Windows Integral Maps or TruMaps (FLS maps). The Data Tree is populated with the appropriate maps on selection of the map processing option:

Windows Integral Maps

The standard element maps obtained from the counts in the element energy window including the background.

TruMap

The maps are corrected for peak overlaps and any false variations due to X-ray background.

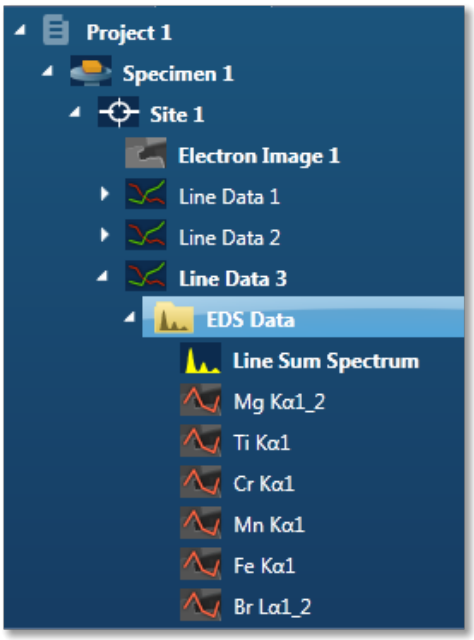


Layered Image

Layered Image is a composite image created from electron and X-ray map images.

Linescan Data

The data tree contains a Line item under the Site; this is the container for the line data. By default, this is labeled as 'Line #' where # is an auto-increasing number under the current site(Site 1) as shown below:



The Line item is the container for EDS Data. All linescans and the sum spectrum are contained within the EDS Data.

The Linescans can be processed as Windows Integral Linescans or TruLines. The Data Tree is populated with the appropriate Linescans on selection of the processing option:

Windows Integral Linescan

The standard element linescans obtained from the counts in the element energy windows including the background.

TruLine

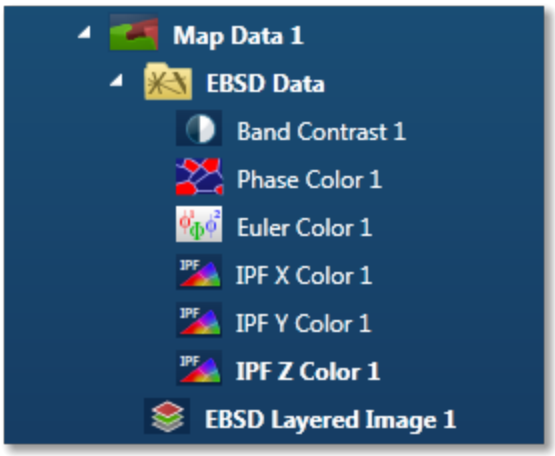
The Linescans are corrected for peak overlaps and any false variations due to X-ray background.

The label of the element linescan is composed of the element symbol followed by the lines series used for TruLine/Window Integral data analysis. For example Cr Kα1 is the label for a Chromium Linescan obtained from the Kα1 line.

The sum spectrum is called Line Sum Spectrum. The region the spectrum comes from is visible on the electron image. This is the same region as where the linescan data is acquired from.

EBSD Data Folder

The EBSD Data folder is the container for the six Map components as shown in the screen shot below:



These components are described briefly with their respective icons:

Band Contrast

Band Contrast is an EBSP quality number, higher the number more contrast there is in the EBSP.

Phase Color

This component colors the pixels in the map based on which phase was identified. The color for each phase is defined in 'Phases for Acquisition'.

Euler Color

The Map component colors the map based on the Euler color scheme and will help to show different orientations within the map.

Euler 1= R

Euler 2= G

Euler 3= B

The IPF color components color the pixels based on the orientation of the unit cell and chosen reference direction; x, y or z.

Note that the color key depends on the structure type so it is not always the easiest map to interpret.

IPF X Color

IPF Y Color

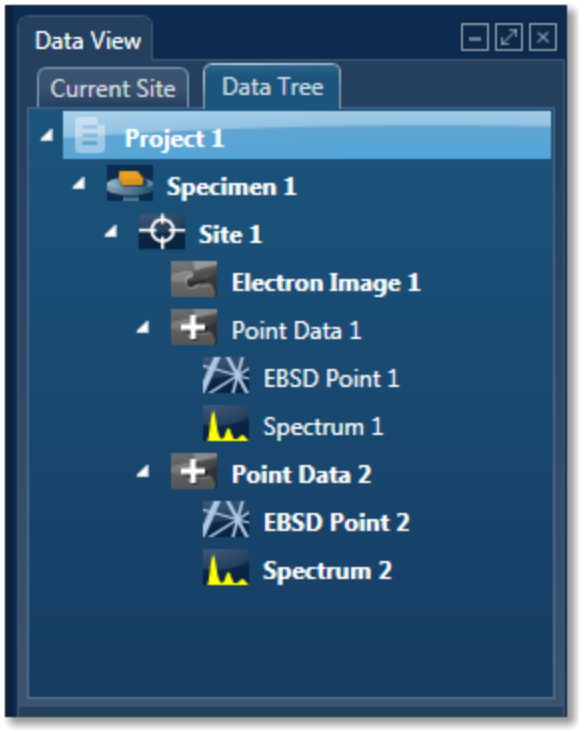
IPF Z Color

EBSD Layered Image

A Layered Image is a composite image created from electron and EBSD map images or element maps if EDS is present as shown in the screenshot above.

Point Data

In Phase ID, a Point Data node appears in the Data tree when spectra and EBSP are acquired from the points defined on the image:



Reanalyze Data

If you have acquired an EBSD Map with stored EBSPs it is also possible to reanalyze a map region with new settings such as new solver settings or even solving by including different phases. Re analyzed map data is stored in the data tree as shown in the screen shot below:

See Also:

Current Site on page 24

Data Tree Menus below

Importing INCA Data

Moving data to another PC on page 46

Data Tree Menus

Each item such as Project, Specimen and Site in the Data Tree has its own menu items. Right click with the mouse on a particular item to access the menu entries.

The menu entries for each item on the Data Tree are described below:

Project

There are two menu items for the Project, **Remove** and **Edit Notes**.

- Remove - removes the project from the Data Tree. This option is disabled if only one Project is in the Data Tree.
- Edit Notes - opens a dialog for editing Project notes.
- Details - opens a dialog showing the Project label and Date/time when the Project was created.

TIP!

To rename a Project select Save Project As... from the File menu.

Specimen

There are four menu items for the Specimen, **Rename, Delete, Edit Notes** and **Details**.

- Rename - allows to rename a Specimen.
- Delete - deletes the Specimen from the Project.
- Edit notes - opens a dialog for editing Specimen notes.

- Details - Opens a dialog showing the Specimen Label, Specimen Orientation and Pre-tilted Specimen Holder. The Details dialog will also include the specimen coating information if you have selected it in the Describe Specimen step.

Site

There are six menu items for the Site, **Rename, Delete**, **Report**, **Print, Email** and **Import Image**

- Rename - allows to rename a Site.
- Delete - deletes the Site from the Project.
- Report - this saves the Microsoft® Word or Excel report of all the data in the Site. It uses the report Batch Template selected in the Preferences dialog accessed from the Tools menu.
- Print - this prints the Microsoft® Word or Excel report of the data associated with the Site.
- Email - this helps to send the report via Email.
- Import Image - imports any standard Windows picture file for comparison or reporting.

Electron Image

There are seven menu items for the Electron Image, **Rename, Delete , Add Electron Image to Layered Image, Save As**, **Print**, **Email** and **Details**

- Rename - this renames the Electron Image.
- Delete - this deletes the Electron Image.
- Add Electron Image to Layered Image - this adds an electron image to the current Layered Image.
- Save As - Saves the current electron image in Microsoft® Word or Excel report.
- Print - prints the current electron image in Microsoft® Word or Excel report.
- Email - sends the image via Email.
- Details - opens the dialog showing the image details.

N o t e

You can view reports with the Microsoft® Word/Excel viewers supplied with your system. However, Microsoft® Office need to be installed for editing your reports.

Spectrum

There are six menu items for each spectrum on the Data Tree**, Rename,Delete, Save As, Print, Email** and **Details.**

- Rename- this renames the spectrum.
- Delete - this deletes each spectrum.
- Save As - saves the current spectrum in a user selected picture file format.
- Print - prints the current spectrum as an image.

- Email - sends the spectrum via Email.
- Details - opens the dialog showing the spectrum details.

N o t e

Hold **Ctrl** and click on items one by one on the Data Tree for multi -select / de-select. Hold **Shift** and click on children one by one in a branch on the Data Tree for multi-select/de-select.

Map

There are six menu items for Map on the Data Tree, **Rename**, **Delete**, **Save As**, **Print**, **Email** and **Details**.

- Rename - this renames the current map.
- Delete - this deletes the current map.
- Save As - saves the current map in a user selected picture file format.
- Print - prints the current map.
- Email - sends the current map via Email.
- Print - prints the current spectrum as an image.
- Details - opens the dialog showing the map details.

Layered Image

There are six menu items for the Layer Image, **Rename**, **Delete**, **Save As**, **Print**, **Email** and **Details:**

- Rename - this renames the Layered Image.
- Delete - this deletes the Layered Image.
- Save As - saves the current Layered Image in Microsoft® Word or Excel report.
- Print - prints the current Layered Image in Microsoft® Word or Excel report.
- Email - sends the Layered Image via Email.
- Details - opens the dialog showing the Layered Image details.

EDS Data

There are two menu entries for the EDS Data, **Rename** and **Delete**

- Rename - this renames the EDS Data.
- Delete - this deletes the EDS Data.

X-ray Map

There are six menu items for each X-ray Map, **Rename**, **Delete**, **Save As**, **Print**, **Email** and **Details:**

- Rename - this renames the X-ray Map.
- Delete - this deletes the X-ray Map.
- Save As - saves the current X-ray map in Microsoft® Word or Excel report.
- Print - prints the current X-ray map in Microsoft® Word or Excel report.

- Email - sends the map via Email.
- Details - opens the dialog showing the Layered Image details.

EBSD Data

There are four menu items for EBSD Data, **Rename**, **Delete**, **Export...** and **Details...**

- Rename - this renames the EBSD Data.
- Delete - this deletes the EBSD Data.
- Export - this exports the Map Data to CHANNEL5 format to allow processing.
- Details - opens the dialog showing EBSD Data Details.

Each map components (Band Contrast, Phase Color, Eulor Color, IPF X, IPF Y and IPF Z) has six menu items:

- Rename - this renames the selected component.
- Delete - this deletes the selected component.
- Save As - this saves the selected component as an image file.
- Print - prints the selected component.
- Email - sends the selected components via email.
- Details - opens the dialog showing details of the selected component.

Point Data

There are two menu items for the Point Data , Rename and Delete.

EBSD Point n

There are six menu items for each EBSD Point as in the case of each map component described earlier.

Spectrum n

There are six menu items for each Spectrum as in the case of each map component.

There is a **Delete All** menu for when multiple items are selected.

Mini View

The Mini View is an area of the Support Panel dedicated to the display of a number of different views which you can select depending on what data you wish to view. Views containing the current Electron Image , Spectrum Monitor or EDS Ratemeter are examples of such views.

Electron Image

The full field of view of the currently selected electron image is displayed here. It is often useful to refer to this image in steps where your application area is dedicated to displaying spectra or maps. For example you can view the electron image in the Mini View if you wish to view full size spectrum in the Acquire Spectra step.

The features of the electron image in the Mini View are:

The default state is full image with no Color Bar and no Scale Bar. You can display the Color Bar and Scale Bar (micron marker) by selecting them from the image context menu.

The Context menu items are:

Show Acquisition Areas	Show All
	Show Selected
	Show None
Show Scale Bar	

Features such as Pan, Zoom and User Annotations are not available in the Mini View.

Spectrum Monitor

It provide a means for the user to see what X-rays are being detected at any given moment. It is useful for a quick survey of the specimen to find an area of interest for analysis. Spectrum Monitor uses the current spectrum acquisition settings with the additional setting of the refresh rate for monitoring the spectrum. This refresh time is referred to as the Buffer Size. The default is 20 but can be changed under the Settings for Spectrum Monitor in the Miniview. Increasing the Buffer Size corresponds to a longer refresh rate.

The settings in the Spectrum Monitor are:

Buffer Size: The default value is 20.

Number of Channels: 1024, 2048 or 4096

Energy Range (keV): 0-10, 0-20 or 0-40

The settings can be selected from the Acquire Spectrum step or Mini View. If you make a change in the setting in one place it is automatically updated in the other.

Ratemeter

It is very useful for setting up the microscope beam current while viewing the X-ray acquisition parameters:

Input Count Rate (cps)

Output Count Rate (cps)

Dead Time (%)

Ratemeter also displays the current Process Time and the Recommended WD (mm).

Step Notes

Step Notes provide the first time user of a navigator with simple instructions on how to complete a typical work flow. It also provides a site administrator or user with the ability to write an SOP (Standard operating procedure).

A default editable set of notes are provided for each navigator step. The user can then overwrite these or add notes as required. A reset to default settings is available.

The notes are saved with the current user profile.

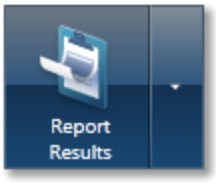
See Also:

Step Notes Editor below

Step Notes Editor

The editor allows you to format text as you would using a word processor. You can cut, paste and copy text, left, right and central align the text, change the font size and style, undo and redo, select bulleted list or numbered list and paste in a picture.

Report Results



You can quickly and easily generate reports from the data in your project.

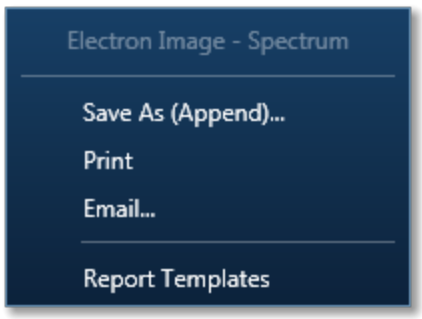
To produce a Microsoft® Word or Excel based report, simply click the Report Results button on the main navigation bar. This will give you a choice of where to save your new report. The default location for your new report is in the Reports sub-directory of your current project.

Once generated, the software automatically displays the new report so you can view, edit or print it.

Each navigator has a default report template. A report is generated from this template when you click the Report Results button. You can change the default report template by selecting it from the Report Preferences or accessing the Report Templates from the down arrow on the Report Results button.

Printing & Emailing Reports

You can Print or Email a report by clicking on the down arrow on the Report Results button and selecting the 'Print' or 'Email' option respectively.

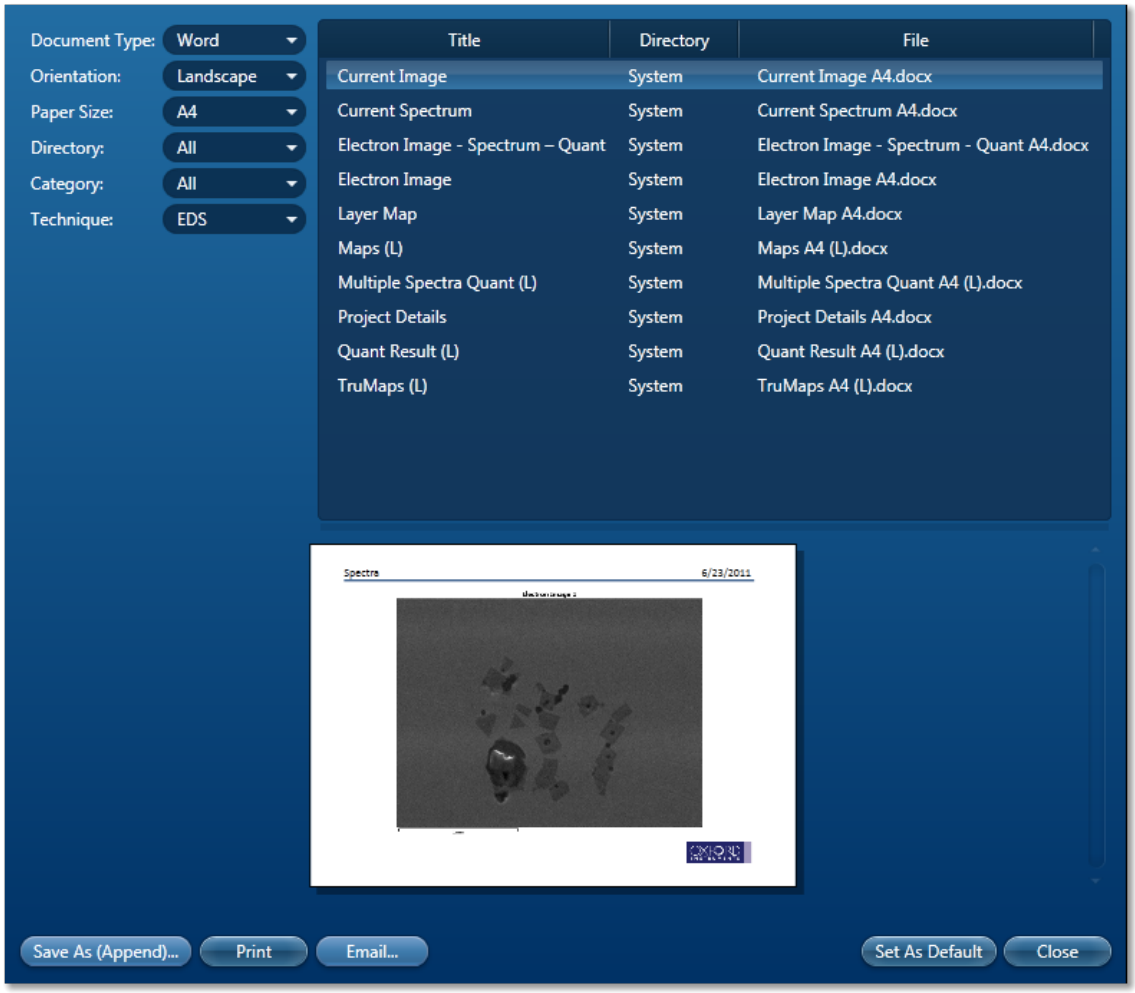


You can view the default report template currently selected for the current navigator for example it is Electron Image - Multiple Spectra in the above screen shot. You can also view the available templates by selecting the Report Templates menu.

Clicking on the Report Results button always performs the last action selected by the user. This allows you to generate reports in quick succession.

Report Templates

Reports are generated from the templates. These templates determine the look and feel of the final report. A set of templates are provided with the software. These templates include items which you might like to save, print or email, for example Quant Results and Spectra. You can view the complete set of templates by selecting the 'Report Templates' option by clicking the down arrow on the Report Results button:



By clicking the 'Set As Default' button you can set the highlighted template in the list as the default template for the current navigator. You can also change the default template by viewing the Report Preferences from the Tools menu.

You can also generate a report by selecting the 'Save As' button or double clicking a template. Preview of the selected template is displayed in the Selected Report Template dialog. If you have Microsoft® Word or Excel installed on your system computer, you will be asked to select name for the file. Subsequent reports will be appended to the open report.

N o t e :

If you have a Microsoft® Word or Excel file open, the Save As option will append your report to the open file.

The 'Print' and 'Email' buttons allow you to generate a report and additionally send it to the default printer or email the report using the default email package installed on your system computer.

Report Preferences

The preferences used for generating reports are accessed via the Tools menu on the main application screen and then selecting Reports. They allow you to specify how your images will look in your final reports and which Report Template is associated with each navigator.

The resolution of images in your reports can be specified by setting the Dots per Inch (DPI) option. You can specify whether the graduated color bars associated with a Map or an Electron Image is included and whether the area selections are shown in the Electron Images.

The Report Preferences also allow you to specify which Report Template is associated with Batch Reporting mode.

Advanced Reporting - Batch Reporting

The software has a Batch reporting feature which allows you to generate a report for Site. The Report Template used for this operation can be specified in the Report Preferences. Using this feature you can produce complex reports for one or more Sites. Batch reporting often includes items which occur many times, for example, Spectra or Maps.

To generate a Batch report, go to the Data Tree, select the Site and select the ‘Report’ option. Select the location of where you want the report to be saved, and a report will be generated giving

items from the entire Site. In this way you can select multiple Sites and generate a report for each.

The Report Template used for this operation can be specified in the Report Preferences by specifying the Batch Template.

Compile a report on the fly

You can prepare your report as you acquire data.The image, spectrum and map viewers have a range of context menus which allow you to export live or stored data. You can copy images, spectra or maps to the clipboard and paste them into Microsoft® Word or Excel. You can manipulate images, spectra and maps using various settings such as width, height, aspect ratio and zoom before exporting to a third party reporting application. You can email or print an image, spectrum or map from the respective viewer.

TIPS

Want to produce a report for a Site? Go to the Data Tree, select the Site and select the 'Save As' option. Select the location of where you want the report to be saved, and a report will be generated giving items from the entire Site. The Report Template used for this operation can be specified in the Report Preferences by specifying the Batch Template.

Want to change the Report Template for the current navigator? Go to the Tools menu on the main application screen and select Preferences. Click on Reports in the Preferences dialog. Select the navigator you wish to change, and select the new Report Template and click the 'Save' button to save your changes.

See Also

Context Menus - Image on page 115

Themes

There are four different themes i.e., color schemes available to choose to display the User Interface:

Accessible Theme

Light Blue Theme

Blue Theme

Search Tool

Enter one or more keywords in the Search Help field near the top right corner of the application window or Help Home Viewer and press  . The Help Viewer is displayed with links to a list of topics containing the keywords. When you click a topic link, the topic is displayed in the Help Viewer. You can go back to the list of topics by pressing the back arrow near the top left corner of the Help Viewer.

FAQs about Software Licensing

How can I activate my License Code?

You will need Internet access to Activate your License Codes. If the OI software is installed on a computer with Internet access you can simply enter the License Code into the License Manager and press the Activate button. The Licence Manager will then automatically send your License Code number to the remote licence server and, provided your License Code is valid, an Unlock Code number will be returned to the Licence Manager that will unlock the software you have purchased. Once Activated you will not need to do this again unless you want to Deactivate a License Code. Each software platform has its own separate License Code so you will need to do this for each platform.

My OI system computer does not have Internet access so how can I activate my License Code?

If your system does not have direct access to the Internet you can still Activate your License Code using any other computer with Internet access.

See NLS Getting Started Card and User Guide for details.

Can I install the OI software on more than one computer (PC or Laptop) at a time?

Yes you can. The terms of the license allow you to install the software on any number of PCs within your organization, but you will only be able to use the software on computers which have a valid License Code installed and Activated.

What is a single license?

Unless you specifically ordered multiple licenses when you purchased your OI system, you will have a single licence which means you can Activate your OI software only on one computer at a time. (If you need to run the software on more computers you can Deactivate one computer and Activate another or you can buy additional licenses.)

What is a multiple license?

If you purchased multiple licenses you will be able to run the OI software on the corresponding number of computers at the same time. For example, if you purchased five licenses you can Activate the OI software on a maximum of five computers, then if you try Activating a sixth computer you will be advised that all of your licenses are in use. Unless you specifically ordered multiple licenses when you purchased your OI system, you will have a single licence which means your OI software can only be Activated on one computer at a time. (If you need to run the software on more computers you can of course Deactivate one computer and Activate another or buy additional licenses.)

I ordered multiple licenses so why have I only got one License Code?

The License Code contains details of the software you have purchased and are entitled to use and the number of licenses (computers) you are entitled to Activate at the same time. So if you purchased five licenses you will only receive one License Code but it will allow you to Activate five computers at the same time using the same License Code.

What is a License Code?

A License Code is a unique 18-digit number which you will have received with your system. It contains encrypted details of the OI software you have purchased including the modules (functionality) and the number of licenses. When this number is entered into the software Licence Manager and the code is Activated the software functionality you purchased and are entitled to use is unlocked.

Can I use my single OI software on a different PC or Laptop?

Yes, you can. If you have your OI software installed on another computer you will need to Deactivate the license on the existing computer, and then Activate the license on the other computer. Transferring the Active license to the second PC does of course mean that your OI software will no longer run on the first (Deactivated) computer (because you only have a single license). Each software platform has its own separate License Code so you will need to do this for each platform.

Can I transfer my (single) license between computers more than once?

Yes, you can transfer (Deactivate and Activate) a license any number of times, but remember you can only Activate a single license on one computer at a time.

Can I use my OI software on more than one PC or Laptop at the same time?

Although you can install your OI software on more than one computer at the same time, if you have a single license you can only activate it on one of them at a time. If you have a multiple licenses you can activate the license on as many computers as your license allows. If you want to use your software on more computer than you currently have licenses for you can easily buy additional licenses as required from your OI representative.

N o t e

You can access the License Manager from Tools in Oxford Instruments NanoAnalysis group of programs.

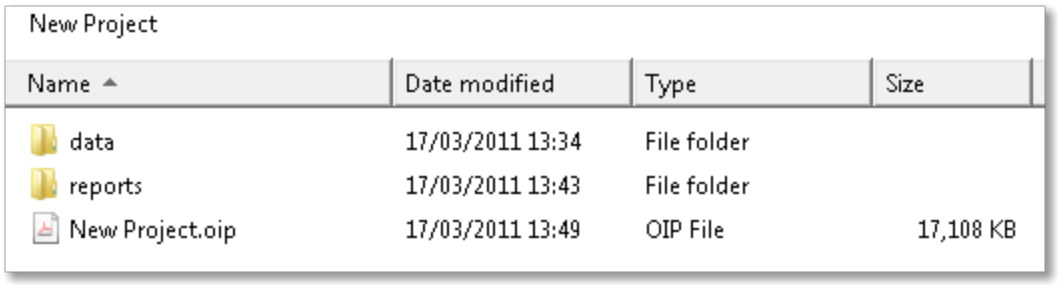
Moving data to another PC

When you start a new Project in AZtec, a Project folder is created. The Project folder contains a Project file with an '.oip' (Oxford Instruments Project) extension. By default the Project folder and Project file use the same project name, however it is possible to rename either of these provided the project is not open in AZtec.

A Project folder may contain two sub folders, 'data' and 'reports'. Acquired data is either stored in the '.oip' file or in the 'data' folder if additional data files are required. It is possible for a Project to not have a 'data' sub folder.

The 'reports' folder is the default location for saving any reports generated from the Project by the user. Reports can be saved in other locations where necessary. Before moving a project, please close any reports saved in the 'reports' subfolder.

An example of a project folder is shown in the screen shot below:



To move the project, either copy or move the Project folder to it's new location. This will maintain the folder structure, and allow the project to be opened from it's new location.

The Project can be opened on a second PC provided the AZtec software and an appropriate license are installed.

To open the Project:

- Launch the AZtec software either from the shortcut on the desktop or from the Oxford Instruments NanoAnalysis folder in All Programs on the Windows Start menu.
- Select Open Project from the File menu on the AZtec menu bar.
- Browse to the Project folder.
- Select the Project file with .oip extension and press Open.
- The Project is loaded in AZtec and the data items are populated in the Data Tree.

Getting Help

Various elements of Help available in the software are described below:

- **Context Sensitive Help (F1)**

  The active workspace in the application has an associated help topic. Press F1 to access the help topic. Each help topic has useful links for further information.

- **Step Notes**

  A default editable set of notes are provided for each navigator step. The user can then overwrite these or add notes as required. A reset to default settings is available.

- **On-Line Help**

  There are six options available from the Help menu on the application menu bar:

  A. Show Help (F1)

  This opens the Help Viewer with TOC in the left pane and the help topic on the right.

  You can also launch the Help Home Page by pressing  in the top right corner of the application window. The Home Page has the facility for searching the Help by entering the key words in the search field. It has links to the following four help items:

  - **Getting Started**

    This opens a page with links to topics to give you information about the main features of the user interface and Frequently asked questions about the software licensing.

  - **Oxford Instruments Website**

    This opens the Oxford Instruments Website.

  - **Support**

    This links to Oxford Instruments Support Website.

- **NanoAnalysis Encyclopedia**

This opens the Encyclopedia that contains help topics with interactive diagrams and movies. It provides the background information, theory and instrumentation of Micro-analysis techniques.

- **Show Nano Analysis Advice**

  It has a number of topics which provide step by step advice on most frequently performed tasks.

- **Launch User Manual**

  This opens the User Manual in PDF format. The manual is supplied with a table of content and a comprehensive Index.

- **Launch Nano Analysis Encyclopedia**

  This is another way of launching the Encyclopedia.

E. Visit Oxford Instruments Website

This launches Oxford Instruments website.

- **About AZtec**

  The About dialog opens. It has Software version number and Copyright statement. You can access License information, System information, Assembly information and Credits.

- **Search Help**

  Enter one or more keywords in the Search Help field near the top right corner of the application window and press  . The Help Viewer is displayed with links to a list of topics containing the keywords. When you click a topic link, the topic is displayed in the Help Viewer. You can go back to the list of topics by pressing the back arrow near the top left corner of the Help Viewer.

AZtecEnergy

Setup for EDS

There are two calibration routines available in the Calibrate step of Optimize navigator, Energy Calibration and Beam Measurement. To ensure that you understand when to calibrate your system and which calibration routine to use, read the comprehensive details below:

Beam Measurement- Settings

Calibrate

Two calibration routines available are Energy Calibration and Beam Measurement. For qualitative and normalized quantitative analyses, you will need to perform only the Energy Calibration part. However, if you are interested in accurate quantitative analysis with un-normalized results, you will need to perform the Beam Measurement routine too.

N o t e

You can access the Calibration routines from the Calibrate step in the Optimize navigator.

Energy Calibration

For accurate identification of peaks, you need to perform the Energy Calibration. Energy Calibration measures the shift in the position of the spectral peaks and resolution of the system. As the system has very stable electronics, you may only need to calibrate the system once in several months, provided the environmental temperature of the laboratory is fairly stable. A few degrees change in the environmental temperature can cause a small shift in the position of peaks.

The Energy Calibration routine is performed for representative Process times, available energy ranges and number of channels in one operation. This means if you change any of these settings soon after you perform the Energy Calibration, you will not need to re-calibrate the system.

See details on how to perform the routine below.

Beam Measurement

If you are an expert user, and you need more than relative concentrations and require accurate un-normalized quantitative analysis results, you must perform the Beam Measurement routine. Any change in the microscope settings such as accelerating voltage or lens control will lead to the change in the beam current. Under these circumstances you must perform the Beam Measurement routine before you do accurate quantitative analysis.

Note that you do not need to perform the Beam Measurement routine if you are only interested in:

- Qualitative Analysis
- Normalized Quantitative Analysis

See details on how to perform the routine below.

Details on Energy Calibration

Why Do We Need To Perform Energy Calibration?

- Ambient temperature changes will alter the gain of the system and this will affect where peaks appear in the spectrum. The exact peak positions and the resolution of the system are needed to precisely identify individual peak components in the spectrum.
- If peaks overlap, the relative sizes of individual peaks can only be calculated accurately if the width and position of each peak is accurately known. By measuring the position of one known peak, the system can be optimized to determine the position of all other peaks.

How Often Should I Perform Energy Calibration?

The electronics used is carefully designed to provide good temperature stability. Since a change of 10°C produces only a 1 eV shift in peak position, most routine analysis can be performed without re-optimizing peak position. However, if you need the software to resolve very closely overlapped peaks, you should perform Energy Calibration and re -optimize if the ambient temperature changes by a few degrees. With a good laboratory temperature control you may not need to optimize for many months.

How To Perform Energy Calibration

Energy Calibration requires the acquisition of a high quality spectrum from a suitable element from which details of the spectrometer gain are calculated and stored. One element can be used for both the Energy Calibration and Beam Measurement or you can use two different elements if you wish.

You can use an element as an energy calibration standard as long as the calibration peak is not overlapped by other peaks. There should not be any peaks within 100 eV of the calibration peak.

To perform Energy Calibration follow the steps:

- Select Energy Calibration from the Calibration Routine drop-down list.
- Select an element from the Calibration Element drop-down list.
- Get the element standard in the field of view of the microscope. Adjust the working distance to the recommended value and the beam current to achieve an optimum count rate.
- Press 

to start acquisition of the calibration spectrum. The current settings will be used to acquire the spectrum. A window will be painted across the peaks of the element X-ray line series.
- A progress bar near the top of the Calibrate window displays the estimated time for the completion of calibration spectrum acquisition.
- On completion of spectrum acquisition, a message is displayed asking you if you wish to perform the Energy Calibration. Press Yes if you wish to perform the Energy Calibration.

Note that the details of the Energy Calibration can be found in the Spectrum Details dialog in the Calculate Composition step when a spectrum has been quantified.

Details on Beam Measurement

For Beam Measurement, you must use a pure element standard and it must be stable under the beam. See Calibration Element.

Note that the acquisition settings chosen in the Acquire Spectra step are carried across to the Optimize Navigator and vice versa. Changing the settings in one will automatically change the settings in the other.

Why Do We Need To Perform Beam Measurement?

- The microscope beam current may vary with time. If we want to measure absolute concentrations, we need to make a comparison of intensity of a peak with that from a known material. If we measure a known material, we can then make accurate intensity measurements on unknowns, provided the beam current doesn't alter after the optimization.

How Often Should I Perform Beam Measurement?

- If you wish to calculate un-normalized totals, the frequency with which you perform the optimization will depend on the stability of the beam current. Repeated measurement of a known standard will indicate whether the beam current is varying. The variation in the analysis total will be in direct proportion to the change in current since the last optimization.

How To Perform Beam Measurement

The Beam Measurement routine requires the acquisition of a high quality spectrum from a suitable element from which details of the beam current is calculated and stored. One element can be used for both the Beam Measurement and Energy Calibration or you can use two different elements if you wish.

To perform Beam Measurement follow the steps:

- Select a calibration routine from the drop-down list of Energy Calibration and Beam Measurement.
- Select an element from the Calibration Element drop-down list.
- Choose the spectrum acquisition parameters from the Settings cog. For details see Beam Measurement- Settings.
- Get the element standard in the field of view of the microscope. Adjust the working distance to the recommended value and the beam current to achieve an optimum count rate.
- Press 

to start acquisition of the calibration spectrum. The current settings will be used to acquire the spectrum. A window will be painted across the peaks of the element X-ray line series.
- A progress bar near the top of the Calibrate window displays the estimated time for the completion of Beam Measurement routine. The progress is also displayed in the Current Site tab of Data View in the Support Panel.
- On completion of the Beam Measurement routine, a message is displayed to save it if you wish. If you decide to save it, the calibration spectrum is saved in your Project.

Note that the details of Beam Measurement can be found in the Spectrum Details dialog in the Calculate Composition step when a spectrum has been quantified.

See also:

Calibration Element on the facing page

Calibrate for Beam Measurement- Settings on page 56

Calibration Element

Select the element you are using for the Calibration from the drop down list. The choice of element depends on the type of calibration you are doing.

For Energy Calibration

- X-ray peaks involve multiple lines and accurate calibration requires a large peak with well-known line energies and intensities. Therefore, you should choose a pure element with K series lines that are strongly excited at the kV you are using. Higher energy lines are less strongly excited but can give more accurate Energy Calibration provided the statistical precision is not compromised by poor excitation of the line. The following pure elements can be used for Energy Calibration: Si, Ti, V, Cr, Mn, Fe, Co, Ni, Cu and Zn.
- For example, if an accelerating voltage of 5 kV is used, then pure Si (not SiO2 or CaSiO3) would be a suitable Calibration Element. For 10kV, pure Ti is good choice. For a 20 kV accelerating voltage, pure Co would be suitable as the Calibration Element.

For Beam Measurement

- The system standards were calibrated using Co as an optimization element. Pure cobalt resists oxidation and polishes well and is therefore the most suitable choice to monitor beam current when you want to obtain accurate un-normalized or "absolute" estimates of composition. However, below 15kV, cobalt K is weakly excited and it is better to choose another pure element for monitoring. The system will make suitable corrections to allow the following pure elements to be used: Si, Ti, V, Cr, Mn, Fe, Co, Ni, Cu and Zn. If the optimization standard is oxidized, contaminated or has a rough surface, then this will have a direct effect on analysis totals. This is the reason why Al is not included in the list of available elements for calibration in the Optimize navigator.

Calibrate For Beam Measurement- Settings

When you select Beam Measurement, the Settings icon is enabled. These are the same X-ray acquisition parameters currently selected in the Acquire Spectra step. You can change the settings here if you wish. The parameters selected in the Optimize navigator will be used when you start acquiring spectra from your specimen.

Energy Range (keV)

The appropriate energy range should be selected in conjunction with the current microscope accelerating voltage. If the accelerating voltage is above 10 kV, in order to view lines which may be excited above 10 keV, the 20 keV range should be chosen. Below 10 kV, it may be more appropriate to choose the 10 keV range since no lines above 10 keV will be excited.

In Auto mode, the software checks for the accelerating voltage selected on the microscope and sets a suitable energy range in the software.

Number of Channels

Select the number of channels from the drop down list of 1024, 2048 and 4096 with which you display the spectrum. The number of eV/channel will depend on both the energy range and the number of channels you select.

In Auto mode, the software checks for the energy range selected and sets the appropriate number of channels.

Process Time

Select the Process Time from the drop-down list of 1 to 6. The Process Time is the length of time spent reducing noise from the X-ray signal coming from the EDS detector during processing. By selecting different Process Times it is possible to reduce differing amounts of noise. The longer the Process Time, the lower the noise. If noise is minimized, the resolution of the peak displayed in the spectrum is improved, in other words, the peak is narrower and it becomes easier to separate or resolve, from another peak that may be close by in energy.

If Default is selected, the Process Time is automatically set to a suitable value. There is a trade off between the Process Time that is used, and the speed at which data can be acquired into the X-ray spectrum.

Total counts in spectrum

The default value for 'Total number of counts in spectrum' is displayed here. This value is used to acquire a spectrum before the Beam Measurement Calibration is performed. You can enter the value that you wish to use.

The default value for the total number of counts is 600,000. It is the total number of counts in a Co spectrum acquired at 20 kV.

See Also:

Acquire Spectra - Settings on page 112

Nano Analysis Advice

In this section users are provided step by step advice on the most frequently performed tasks. The following tasks are described in details:

EDS Qualitative Analysis

In EDS, the qualitative analysis is the process of identifying elements present in a specimen. It involves acquiring a spectrum from the specimen and then identifying the peaks in the spectrum. Peaks can be manually identified to confirm elements using sophisticated tools available in the software. Once you have identified all the elements you can produce a Microsoft® Word or Excel report. You can email the spectrum to your customer directly from the spectrum viewer provided your system is connected to the network and it has appropriate software installed.

You can use the confirmed elements list for elemental maps and quantitative analysis.

Below is step by step guide for qualitative analysis to get the most accurate results out of your system with minimal effort:

- If you know what elements are present in your specimen and you only want to see peak labels or X-ray maps or X-ray linescans for those elements, then you can select them in the Pre-defined Elements tab in the Describe Specimen step of Point & ID, Map or Linescan navigator.
- If you are interested in seeing what other elements might be present, then select the AutoID option by checking the 'Perform AutoID During Acquisition' check box.

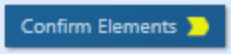
N o t e

Check the EDS Element Settings in the User Profile dialog (available from the Tools menu) to ensure that the elements that you have pre-defined in the Describe Specimen step are not in the Exclusion Elements List. Users can have different exclusion lists.

- Acquire an electron image from an area on your specimen in the Scan Image step available in the Point & ID, Map and Linescan navigators.
- Navigate to the Acquire Spectra step. Press to acquire a spectrum from the entire image. If you wish to acquire a spectrum from a point or an area on the image, select the appropriate tool from the toolbar on the left side of the screen. For details see How to acquire spectra on page 107
- For details of spectrum manipulation and annotation see Acquire Spectra - Toolbar on page 110
- You can see your MiniQuant results in a table or a bar chart during analysis. Real time Compare and instant MiniQuant options are available in the Acquire Spectra, Confirm Elements and Calculate Composition (Comparison of Results - Two Spectra template) steps. You can compare your current spectrum to a control spectrum during acquisition. For further details see Compare Spectra & MiniQuant Results on page 150
- Peaks in the spectrum are identified and labeled automatically using the AutoID and Pre-defined elements lists. If too many peaks are close together, you can move the peak labels for clarity. Select the Annotation tool available in the toolbar on the left of user interface in Acquire Spectra and Confirm Elements steps. Click on the label to select it and then drag it to a new position. For details of configuring peak labels see Peak Labels on page 116

- Navigate to the Confirm Elements step to manually confirm the elements identified by AutoID (if selected). Extensive tools including Show Markers, Show Peak Shapes, Show Fitted Spectrum, Show Theoretical Spectrum (from the Settings) and Show Candidate Elements (from the toolbar on the left) are available to assist you in confirming elements manually. For details see Confirm Elements - Tools on page 131
- Once all elements in the spectrum have been identified and confirmed, you can email the spectrum to your customer or generate a Microsoft® Word or Microsoft® Excel report using the Export option available on the context menu on the Spectrum viewer. For further details of context menus available on the Spectrum viewer see Context Menus - Spectrum Viewer
- You can use the confirmed element lists to acquire element maps and linescans and perform quantitative analysis.

N o t e

You can navigate to the Confirm Elements step from a quick link, 

within the Construct Maps and Construct Linescans steps to confirm an element for map and linescan acquisitions.

Analyzer - Guided

Analyzer is a microscope centric application. X-ray spectra are acquired from the regions on the specimen scanned by the microscope beam. There are two modes of operation in the Analyzer application, Guided and Custom.

In the Guided mode, the Analyzer navigator has four following steps:

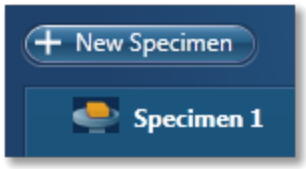
Describe Specimen

In this step there are two tabs, Summary and Pre-defined Elements.

Summary

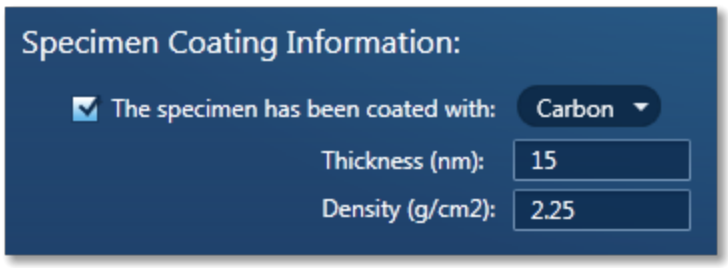
In the Summary view you can write notes on the Project and the Specimen present in the Project. (For convenience you can also copy images/diagrams and text from other documents/emails and paste into these windows). Notes are saved with the Project and you are allowed to edit notes in any step of the Navigator. It helps to capture the important information during the analysis. Click with the right mouse button on the Project or Specimen in the Data Tree and then select Edit Notes to write/modify the relevant notes.

You can add new Specimens to the current Project by pressing the New Specimen button:



Click on the Specimen in the Project Overview dialog. This action displays the ' Specimen Notes for Specimen 1' text box. Here you are provided with the text formatting tools. You are allowed to write notes about each Specimen and save them.

You can add coating information for each specimen (This information is used for the calculation of the quantitative results):



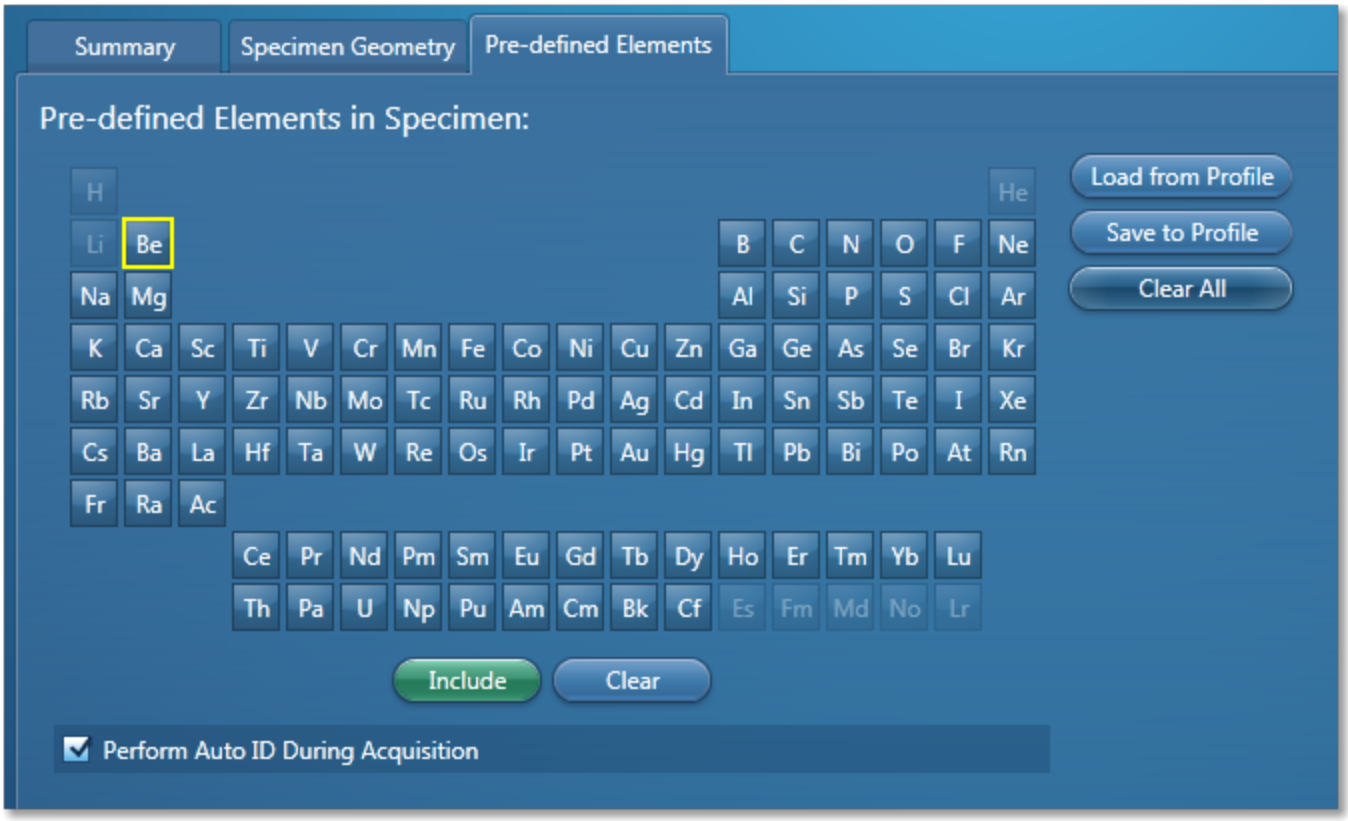
You have access to the periodic table for choosing the coating element for each Specimen. Two parameters, coating density and thickness exist which are required for a full coating correction to be applied for the calculation of the quantitative results. The default element is carbon, the defaults for thickness and density are 10 nm and 2.25 g/cm^3 respectively. Note that where appropriate the default density is that of the element at room temperature and pressure. The thickness and density may then be modified if required.

Pre-defined Elements

If you know what elements are present in your Specimen and you only want to see peak labels or X-ray maps for those elements, then you can select them in the “Pre-defined Elements”tab.

Press the Pre-defined Elements tab to access the periodic table:

If you wish to enable the AutoID option check the 'Perform AutoID During Acquisition' option.



Double-click on the element symbols that you wish to include in the analysis. All the included elements will be marked with the green color key in the periodic table. To save the Pre-defined Elements in the current User Profile press 

. It means when you load the User Profile next time these elements will be included in the analysis.

If you have already created a User Profile with the Pre-defined Elements in the User Profile dialog press 

.

Pressing 

will deselect the Pre-defined Elements from the periodic table and they will not be included in the current analysis.

The peaks for the Pre-defined Elements if included in the analysis are labeled in the Acquire Spectra step. MiniQuant will display the quant results for these elements as Wt% or a bar chart.

The Pre-defined Elements will be marked as Pre-defined in the Confirm Elements list box in the Confirm Elements Step. There may be other elements in the Specimen which are identified by AutoID routine if the 'Perform AutoID during acquisition' option has been checked in the User Profile dialog.

T i p

Right click on the Project or Specimen in the Data Tree and select Edit Notes to write or edit notes in any step of the Navigator.

See also:

Why are specimen coated? on the facing page

Coating Techniques on page 66

Element Lists on page 146

Data Tree on page 71

Mini View on page 78

Step Notes on page 79

Why Are Specimen Coated?

- Samples are sometimes coated with a thin conductive layer prior to observation in the SEM to ensure that there is a good electrical path to ground. This prevents non-conducting specimens, as well as the oxides which are present on the surface of many samples, from charging under the electron beam.

- Carbon is generally the preferred coating material for microanalysis applications because of its minimal effect on the X-ray intensities.

- Gold is also commonly used for coating specimens since it increases the secondary electron yield providing improved SEM image quality. However, the number of peaks produced by the gold coating can cause overlap problems with the peaks of interest.

- A guide for the desirable thickness range of coatings is of the order of 5-30 nm.

- To minimize the effect of your coatings aim to make them as thin as is practically possible. Thick coatings will, for some samples, result in poor analysis.

Effect of the Coating on the X-ray spectrum

The coating will have three main effects:

1. Energy loss of the primary electron beam as it passes through the coating.

2. Attenuation of the emerging X-rays.

3. The contribution of characteristic peaks to the X-ray spectrum. Thus, carbon coated samples will always display a carbon peak in the spectrum.

In the software, you can specify a coating element for a particular sample. During spectrum processing any X-ray peaks arising from this element are automatically **deconvolved** in addition to two other corrections (loss of X-ray intensity due to absorption of the emergent X-rays, reduction of primary keV). Application of these corrections is particularly important for low kV spectra in particular (~ 5 keV). The final quantitative results could have significant errors if no such corrections were applied.

- Sample step - input of additional parameters : coating density and thickness
- Standardization - here the normalized area of the standard (I(std) / I(optimization)) is corrected for the coating.
- Full calculations - the quantitative results are corrected for the coating.

Described below are the expected modes of operation for the locations described above.

Describe Specimen step

In the Describe Specimen step, two parameters exist which are required for a full coating correction to be applied: coating density and thickness. This part of the program behaves in the following way:

- **New project/specimen** - For example, select coating correction, the default element is carbon, the defaults for thickness and density are 15 nm and 2.25 g/cm3 respectively. Note that where appropriate the default density is that of the element at room temperature and pressure. The thickness and density may then be modified if required.
- **Existing specimen** - If a coating element was selected this will remain as before with the density set to the default value and the thickness set to zero. With these settings the coating element will be deconvolved as before but no coating correction will take place. The full coating correction will be enabled by setting the thickness to a non zero value.

Standardization

The value of the Standard Correction Factor is adjusted to take account of the selected coating. The adjusted value will be used in the quant calculations.

Quantification

During quantification for a coated specimen corrections will be made for the reduction in the effective kV for the primary beam when entering the specimen and the reduction in the emergent X-ray intensity due to the additional absorption of the coating layer. Thus for a particular specimen the values of the concentrations will increase when the coating correction is enabled and in general the effect will be most pronounced in the case of spectra acquired at low kV.

Coating Techniques

Unless you are working with a variable pressure or low vacuum microscope, it is important that the sample you are analyzing conducts sufficiently so that it does not charge under the electron beam. It also may not be a problem if you are using very low voltages. There are a number of ways to reduce charging including coating your sample with a conductive material prior to observation in the SEM. Coatings are usually applied by using a vacuum evaporator, or a sputtering device. For X-ray microanalysis, we recommend that you use carbon since it does not generally interfere with elements of interest in the sample. Gold, usually used when a good secondary electron image is required, is not recommended for X-ray microanalysis, because of the large number of lines in the gold X-ray spectrum which may overlap with the lines of interest from your sample.

Evaporation

The most common form of coating with carbon is using evaporation. A high current is passed through carbon rods, under vacuum. The heating effect causes the carbon to evaporate, and in turn, this is deposited as a thin film on the surface of the sample. The actual process of formation of a thin film is a complex process, and not fully discussed here.

- Ensure that one of the carbon rods is sharp. The end of one rod is usually flattened, while the other will be pointed.
- Place your sample in the evaporator.
- Evacuate the chamber.

- Once the desired vacuum has been achieved, usually about $1x10^{-5}$ Pa, it is important to out gas the rods. This is done by heating them until they glow a dull red.
- The pressure in the chamber will rise, and the pressure should then be restored before the evaporation process.
- Pass a high current through the carbon rods.
- The heating effect causes the carbon to evaporate and deposit a thin film on the surface of the sample.
- It is often useful to place a piece of white paper or filter paper beneath the sample to help you gauge the amount of carbon you deposit. Although the degree of coating you need will depend on the conductivity of the sample, as rule of thumb, when the paper appearance of the paper becomes light brown, this should be sufficient carbon.

Element Lists

Any list of elements in the **AZtec** software can be split into the following three categories:

- Pre-defined Elements - elements expected in specimen
- Identified Elements - typically based on automatic peak identification (Auto ID)
- Fixed List - used for Quantitative analysis

Pre-defined Elements

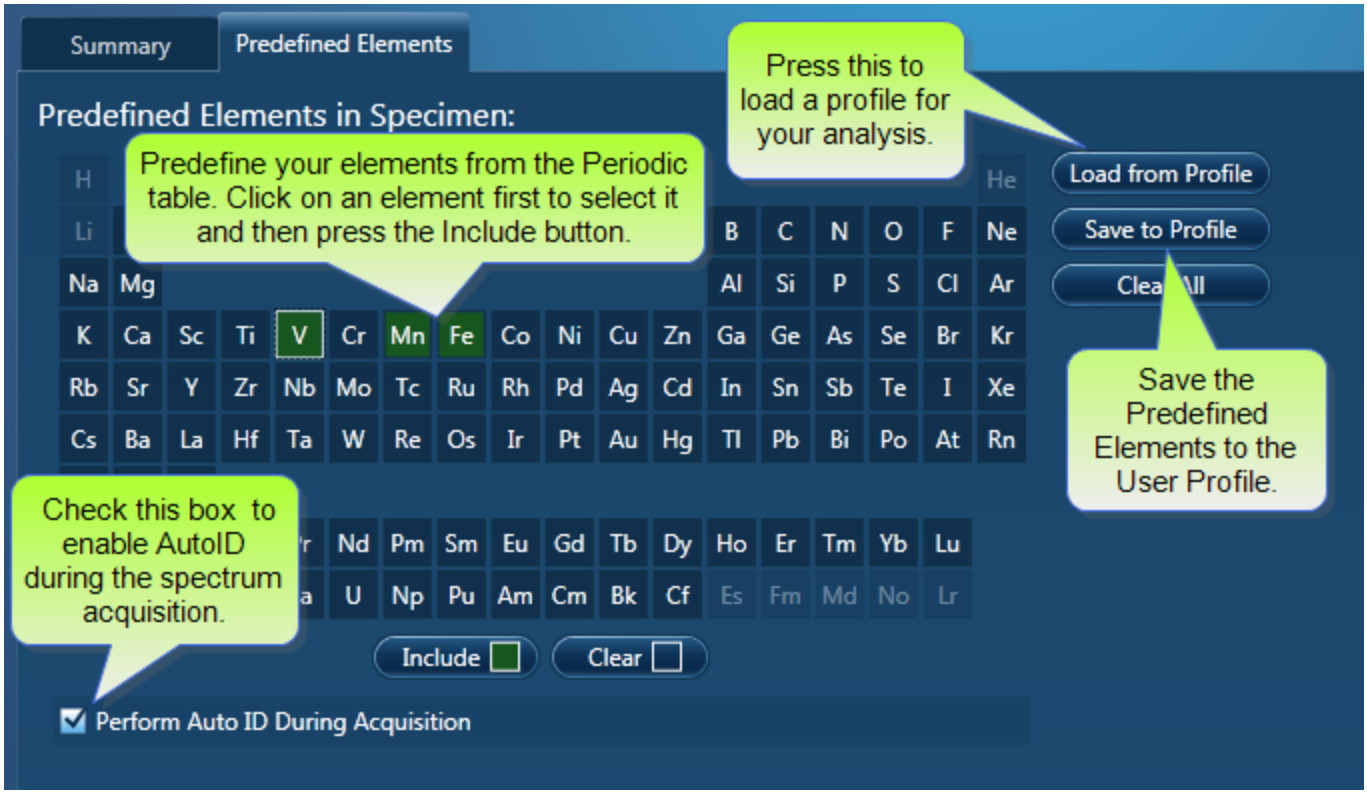
You may have prior knowledge of your Specimen and know what elements to look for.

Examples

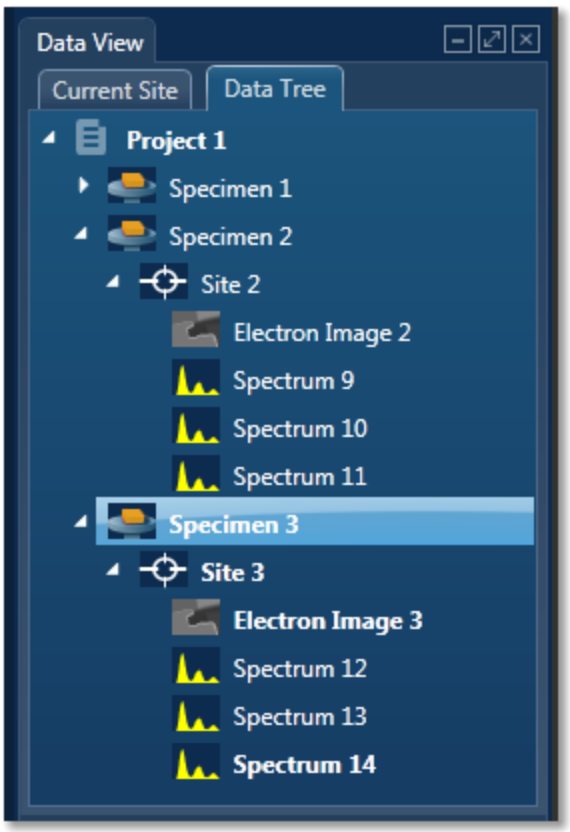
'I want to look for a particular list of elements. (I am not interested in any other elements)…I may want to see their labels on spectra, their X-ray maps or both….I want to see these even if the element is not present'.

' I know what's in my sample…. I want to look for a specific set of elements (I want to see these even if the element is not present.) …..but I would like to know if there is anything else in my sample too'.

You can define these elements' in the 'Pre-defined Elements' tab in the Describe Specimen step. If you want to save the Pre-defined Elements to a profile you must first press 'Save to Profile' button, then save the profile via the drop down menu. When you want to analyze your Specimen, you can load this profile or another profile by pressing the 'Load Profile' button in the Describe Specimen step as shown in the screen shot below:



Note that the 'Pre-defined Elements' are saved with the current Specimen. Changing the 'Predefined Elements' will only update the Pre-defined Elements in the current Specimen. It will not update any existing Specimens in the Project.



The current specimen is the one that you are presently analyzing/processing the data from. For example, in the screen shot above, Specimen 3 is the current specimen, Specimens 1 and 2 are the other specimens in the Project.

Identified Elements

The 'Identified Elements will include:

- Any Pre-defined Elements
- Elements identified by Auto ID
- Any additional Elements identified manually

If the 'Pre-defined Elements have been specified, these will be included for identifying and labeling peaks in the current spectrum automatically.

Note that the 'Identified Elements' are saved in the Spectrum.

'Perform Auto ID During Acquisition' option is enabled by default and can be deactivate by unchecking it in the Describe Specimen step as shown in the screen shot above. You can then AutoID at any time by pressing the button.

Additional peaks in the spectrum can be identified manually by using the 'Show Candidate Elements' tool in the Confirm Element step. Click on the question mark icon to select the Show Candidate Element tool. Position the cursor at the center of a peak by double-clicking with the mouse. The list of elements spectra corresponding to the energy at the cursor is displayed in the panel on the right. By highlighting an element in this list, you will see the markers showing all the lines for this element.

Note that the 'Identified Elements' will be quantified if you have selected the Current Spectrum, or the Fixed List and Current Spectrum Element List in the Quant Settings in the Calculate Composition step or EDS Quant Settings in the User Profile dialog.

N o t e

EDS Quant Settings are available in the User Profile Dialog accessed from the Tools menu. These settings are also available from the Calculate Composition step.

Fixed List

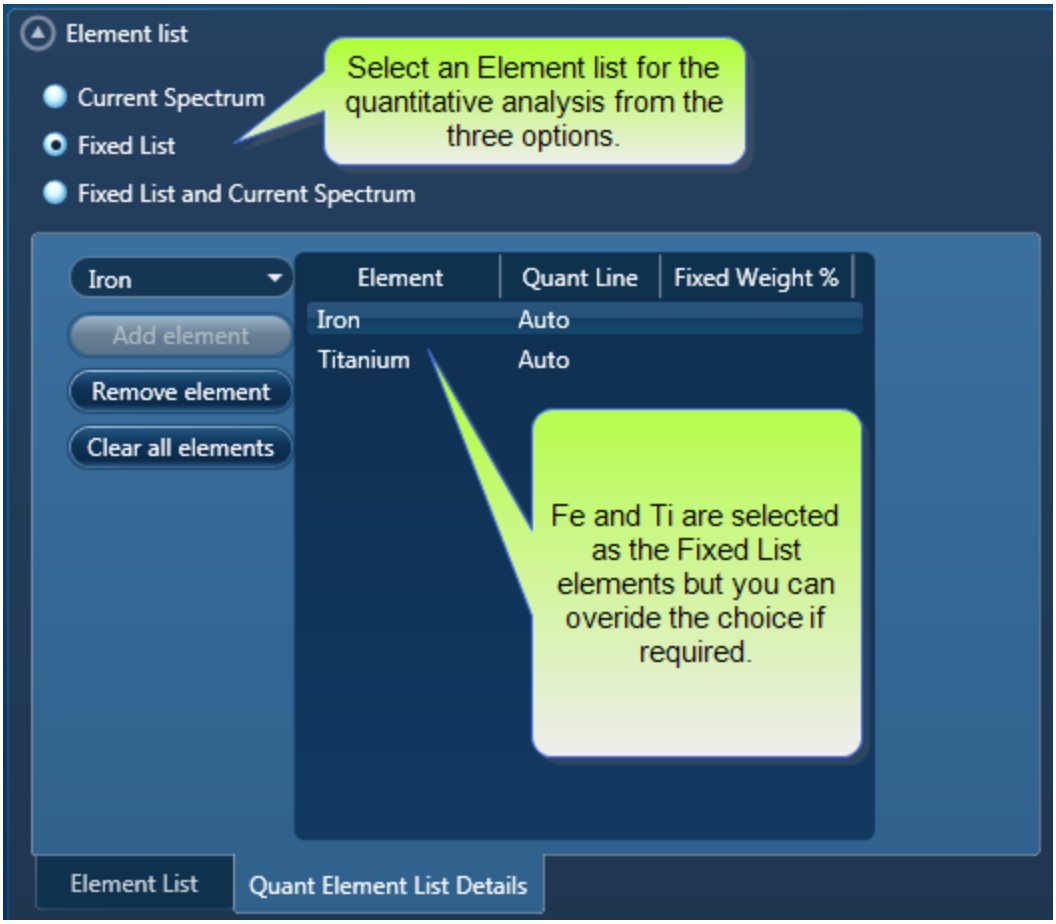
The elements in the 'Fixed List' are defined in the Quant Settings dialog which is available in the User Profile and the Calculate Composition window.

Note that the Fixed List is only used for calculating composition in quantitative analysis.

E x a m p l e

'I want to do quantitative analysis on my glass samples and want to compare results from one batch to another batch. I am always looking for the same specified list of elements'.

You can specify the Element List for Quant from the three available options in the Quant Settings dialog as shown in the screen shot below:



Current Spectrum

This list includes the Pre-defined Elements and elements identified by Auto ID and manually using the Candidate Element tool.

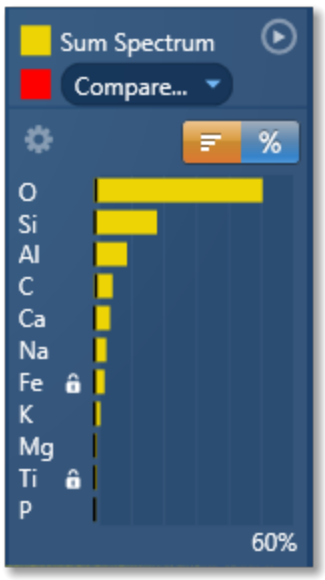
Fixed List

You select the Fixed List option if you know what elements you wish to quantify. Choose the elements from the drop-down list as shown in the screen shot above.

Fixed List and Current Spectrum

To quantify the elements in the above two lists, select the Fixed List and Current Spectrum option.

MiniQuant results table will clearly display which list is being used. A lock icon will be displayed against the 'Fixed List' elements as shown in the screen shot below:



In this example, Fe and Ti are selected in the Fixed List. The rest of the elements in the chart results are from the Current Spectrum because the Element List selected for quantification was 'Fixed List and Current Spectrum'.

Note that the 'Fixed List' is saved in a User Profile.

See also:

Describe Specimen on page 62

Acquire Spectra on page 105

Confirm Elements on page 129

Calculate Composition on page 141

User Profile on page 17

Data Tree

Data is archived in a logical manner and can be directly viewed via easily recognizable icons on the Data Tree. To access the Data Tree, select the Data Tree tab on the Data View panel.

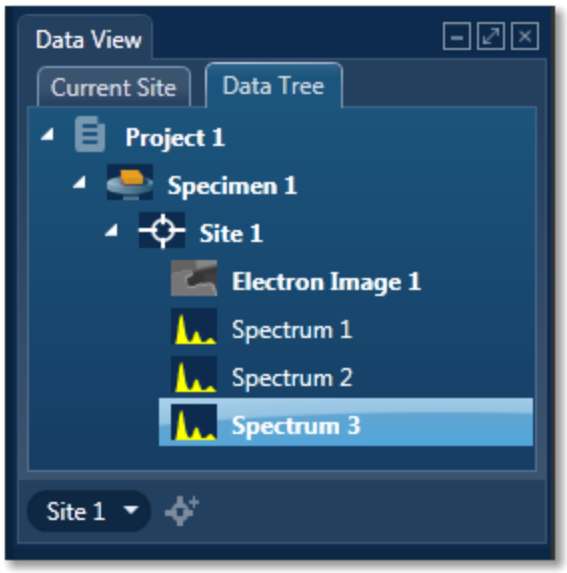
All open Projects and their contents are displayed in the Data Tree. Multiple Projects can be opened and shown in the Data Tree at the same time. If you have multiple Projects, Specimens or Multiple Sites in the Data Tree, you can easily get to your current site by pressing the Current Site tab.

When the application is started a default Project containing a Specimen and a Site is shown. As you acquire data, items are added to the Data Tree. The current items in the Data Tree are shown in bold.

Click on an item on the Data Tree to make it current.

Items on the Data Tree

The screen shot below shows an example of the main items in the Data Tree. Each item is described along with their icons below:



Project

Project is a top level container for data. Each Project is associated with a folder on the file system. The name of the folder is the same as the Project name. The Project folder contains a single file with an .oip extension and optional Data and Reports sub folders.

N o t e

When moving or copying project data ensure that the root project folder is moved/copied, not just the .oip file. The folder can be zipped using the standard Windows compression utilities if required.

Specimen

Specimen represents the real specimen that you analyze and collect the data from, including images, maps and spectra. There may be many Specimens in a single Project. A Specimen may contain more than one Site.

Site

Site represents an area on the Specimen from where you acquire data such as images, spectra and maps. Site can hold multiple images, for example SE and BSE plus any imported images.

The analytical conditions such as kV, Magnification and Calibration are stored with the data.

Electron Image

Electron Image on each Site can be an SE or BSE image. You can acquire SE and BSE images simultaneously provided the suitable hardware is available.

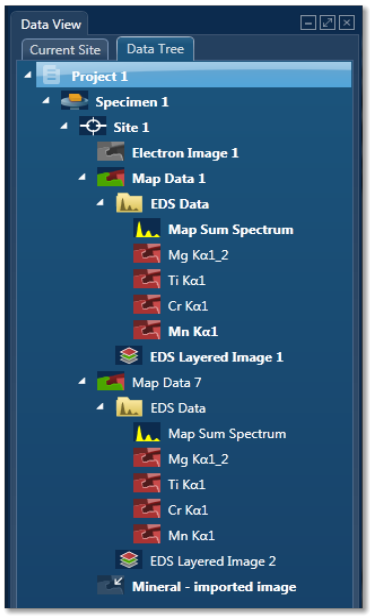
Imported Image

Any standard Windows Picture files can be imported into the Project for comparison or reporting. The file formats available are JPG, JPEG, BMP, PNG, WDP, GIF, TIF and TIFF. You can import an image using the context menu available from the Site.

Spectrum

Spectra are acquired from the areas defined on an electron image. Sum Spectra and Reconstructed Spectra are shown under the Map in the Data Tree.

You will see the following items in the Data Tree if you are acquiring element maps in the EDS application:



Map Data

Map Data is the container for a mapped area(s) in a Site. It can hold EDS Data, EBSD Data or both. One Site can contain more than one Map Data items. In the example above there are two items, Map Data 1 and Map Data 2.

EDS Data

EDS Data is the container for Map Sum Spectrum, Reconstructed Spectra and X-ray element maps.

Map Sum Spectrum

The sum spectrum is calculated from the data acquired from all the pixels in the electron image.

Reconstructed Spectrum

You can reconstruct spectra from areas selected on the Layered Image in the Map application.

X-ray Element Maps

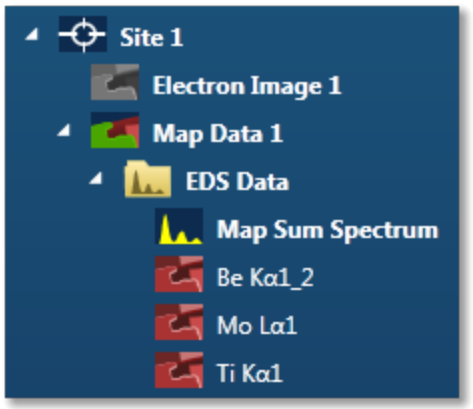
The data can be processed as Windows Integral Maps or TruMaps (FLS maps). The Data Tree is populated with the appropriate maps on selection of the map processing option:

Windows Integral Maps

The standard element maps obtained from the counts in the element energy window including the background.

TruMap

The maps are corrected for peak overlaps and any false variations due to X-ray background.

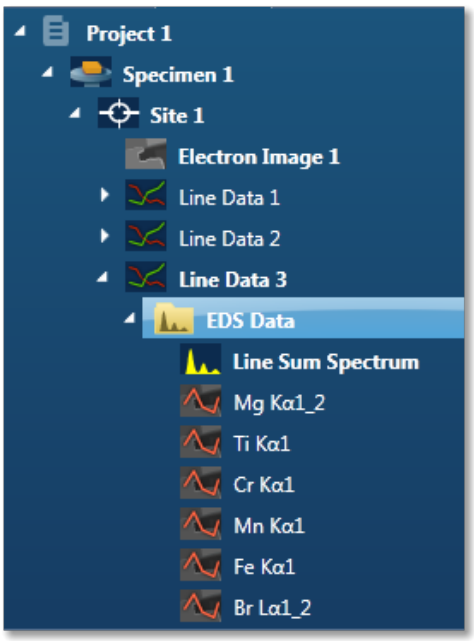


Layered Image

Layered Image is a composite image created from electron and X-ray map images.

Linescan Data

The data tree contains a Line item under the Site; this is the container for the line data. By default, this is labeled as 'Line #' where # is an auto-increasing number under the current site(Site 1) as shown below:



The Line item is the container for EDS Data. All linescans and the sum spectrum are contained within the EDS Data.

The Linescans can be processed as Windows Integral Linescans or TruLines. The Data Tree is populated with the appropriate Linescans on selection of the processing option:

Windows Integral Linescan

The standard element linescans obtained from the counts in the element energy windows including the background.

TruLine

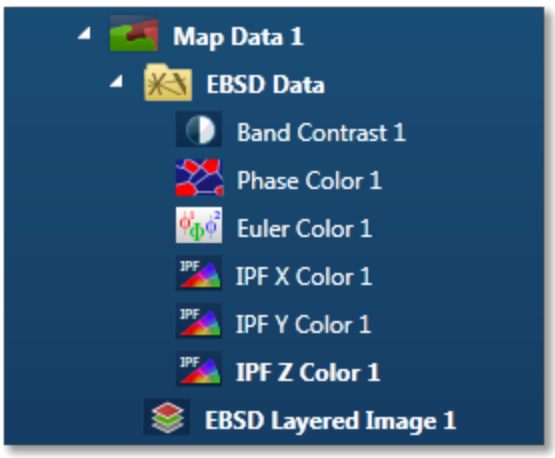
The Linescans are corrected for peak overlaps and any false variations due to X-ray background.

The label of the element linescan is composed of the element symbol followed by the lines series used for TruLine/Window Integral data analysis. For example Cr Kα1 is the label for a Chromium Linescan obtained from the Kα1 line.

The sum spectrum is called Line Sum Spectrum. The region the spectrum comes from is visible on the electron image. This is the same region as where the linescan data is acquired from.

EBSD Data Folder

The EBSD Data folder is the container for the six Map components as shown in the screen shot below:



These components are described briefly with their respective icons:

Band Contrast

Band Contrast is an EBSP quality number, higher the number more contrast there is in the EBSP.

Phase Color

This component colors the pixels in the map based on which phase was identified. The color for each phase is defined in 'Phases for Acquisition'.

Euler Color

The Map component colors the map based on the Euler color scheme and will help to show different orientations within the map.

Euler 1= R

Euler 2= G

Euler 3= B

The IPF color components color the pixels based on the orientation of the unit cell and chosen reference direction; x, y or z.

Note that the color key depends on the structure type so it is not always the easiest map to interpret.

IPF X Color

IPF Y Color

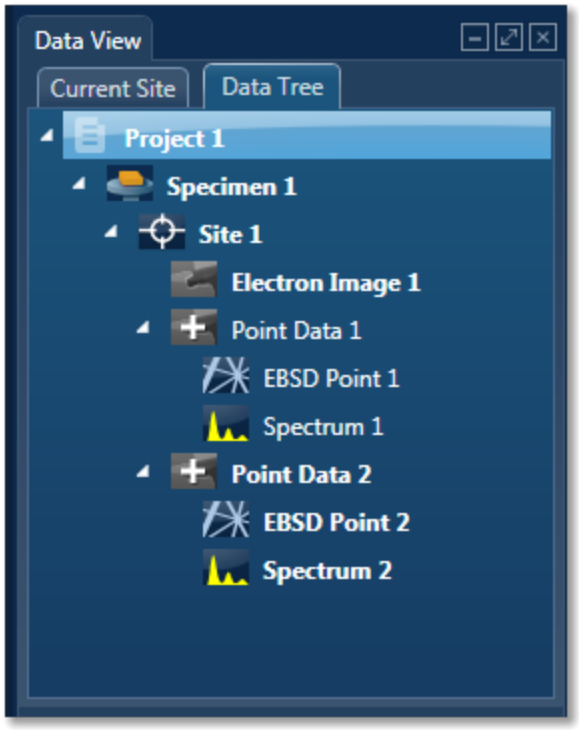
IPF Z Color

EBSD Layered Image

A Layered Image is a composite image created from electron and EBSD map images or element maps if EDS is present as shown in the screenshot above.

Point Data

In Phase ID, a Point Data node appears in the Data tree when spectra and EBSP are acquired from the points defined on the image:



Reanalyze Data

If you have acquired an EBSD Map with stored EBSPs it is also possible to reanalyze a map region with new settings such as new solver settings or even solving by including different phases. Re analyzed map data is stored in the data tree as shown in the screen shot below:

See Also:

Current Site on page 24

Data Tree Menus on page 32

Importing INCA Data

Moving data to another PC on page 46

Mini View

The Mini View is an area of the Support Panel dedicated to the display of a number of different views which you can select depending on what data you wish to view. Views containing the current Electron Image , Spectrum Monitor or EDS Ratemeter are examples of such views.

Electron Image

The full field of view of the currently selected electron image is displayed here. It is often useful to refer to this image in steps where your application area is dedicated to displaying spectra or maps. For example you can view the electron image in the Mini View if you wish to view full size spectrum in the Acquire Spectra step.

The features of the electron image in the Mini View are:

The default state is full image with no Color Bar and no Scale Bar. You can display the Color Bar and Scale Bar (micron marker) by selecting them from the image context menu.

The Context menu items are:

Show Acquisition Areas	Show All
	Show Selected
	Show None
Show Scale Bar	

Features such as Pan, Zoom and User Annotations are not available in the Mini View.

Spectrum Monitor

It provide a means for the user to see what X-rays are being detected at any given moment. It is useful for a quick survey of the specimen to find an area of interest for analysis. Spectrum Monitor uses the current spectrum acquisition settings with the additional setting of the refresh rate for monitoring the spectrum. This refresh time is referred to as the Buffer Size. The default is 20 but can be changed under the Settings for Spectrum Monitor in the Miniview. Increasing the Buffer Size corresponds to a longer refresh rate.

The settings in the Spectrum Monitor are:

Buffer Size: The default value is 20.

Number of Channels: 1024, 2048 or 4096

Energy Range (keV): 0-10, 0-20 or 0-40

The settings can be selected from the Acquire Spectrum step or Mini View. If you make a change in the setting in one place it is automatically updated in the other.

Ratemeter

It is very useful for setting up the microscope beam current while viewing the X-ray acquisition parameters:

Input Count Rate (cps)

Output Count Rate (cps)

Dead Time (%)

Ratemeter also displays the current Process Time and the Recommended WD (mm).

Step Notes

Step Notes provide the first time user of a navigator with simple instructions on how to complete a typical work flow. It also provides a site administrator or user with the ability to write an SOP (Standard operating procedure).

A default editable set of notes are provided for each navigator step. The user can then overwrite these or add notes as required. A reset to default settings is available.

The notes are saved with the current user profile.

See Also:

Step Notes Editor on page 37

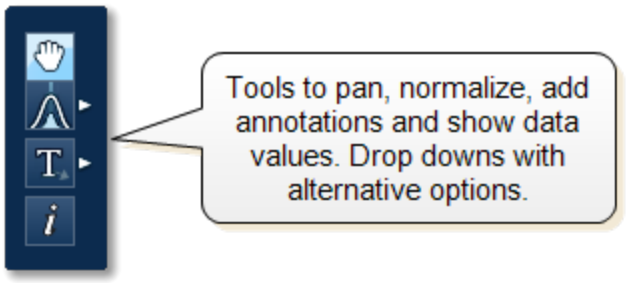
Acquire Spectra

Analyzer is microscope centric application. You can acquire a spectrum from a region on the specimen scanned by the electron beam.

There is an acquisition toolbar near the top of the workspace. It has controls for starting and stopping the spectrum acquisition.

There is a Settings cog for selecting the acquisition parameters. For details see Acquire Spectra - Settings on page 112.

The toolbar located on the left side of the workspace has various tools for spectrum manipulation and annotation as shown in the screen shot below:



For description of each tool, see Acquire Spectra - Toolbar on page 110

The Compare Spectra & MiniQuant Results on page 150 option is available in the top right corner of the Spectrum viewer. You can compare the current spectrum with any other spectrum from an opened Project on the Data Tree. Instant MiniQuant results can be viewed in a table or a bar chart.

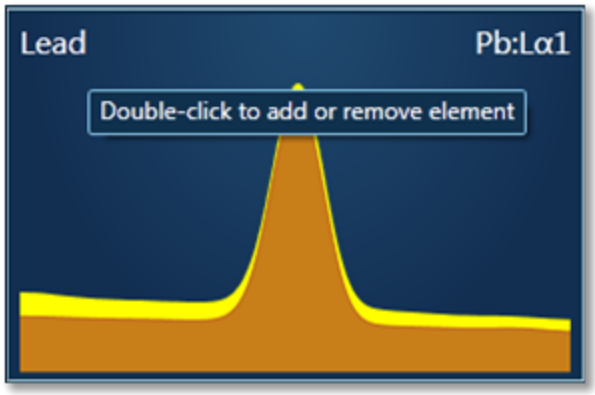
A number of useful shortcut menus are available as right mouse click in the spectrum viewer. For details see Context Menus - Spectrum Viewer.

Confirm Elements

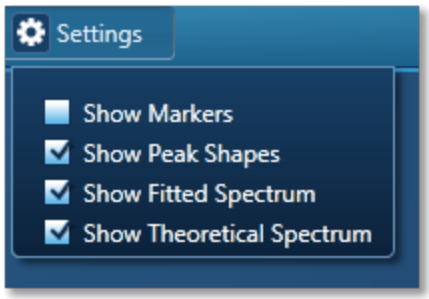
This step has been designed to help you confirm the elements that have been identified by AutoID in your spectrum. These elements are then used to create a confirmed elements list for qualitative and quantitative analyses. Extensive tools including Element Series Markers, Overlays, Element Profiles and Show Candidate Elements are available here to assist you in confirming elements manually.

How to confirm elements:

- Start with the largest peaks. Press the question mark icon to select the Show Candidate Elements tool from the tool bar on the left hand side of the interface, then double click on a peak in the spectrum viewer. The candidate elements are displayed in a stacked spectra view on the right hand side of the window (you can double click on any of these elements to add or remove it from the confirm elements list).



- You can control what overlays you see in the Spectrum viewer via the 'Confirm Elements Settings'. These overlays can be very useful in helping you to interrogate complex spectra.



- Press Include/Exclude once you are satisfied with the identification of each element to build your list of the confirmed elements.

See Also:

Confirm Elements - Settings on page 130

Confirm Elements - Tools on page 131

Element Lists on page 146

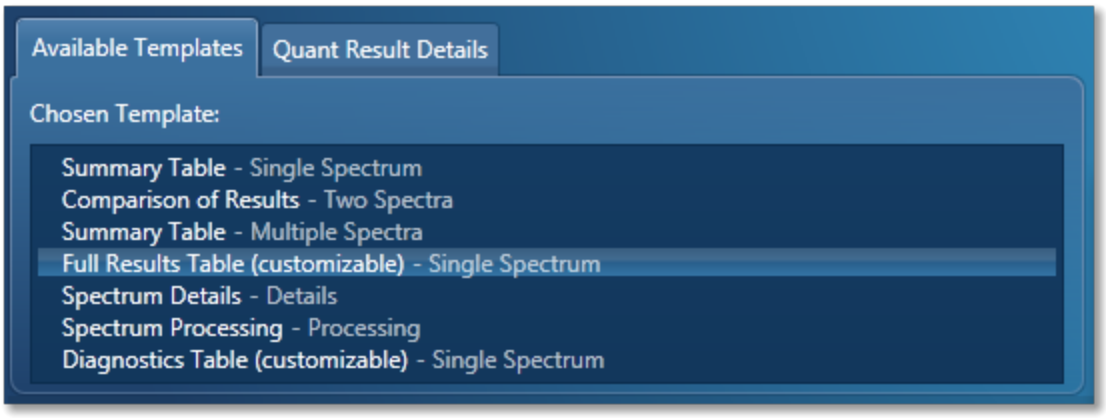
Peak Labels on page 116

Compare Spectra & MiniQuant Results on page 150

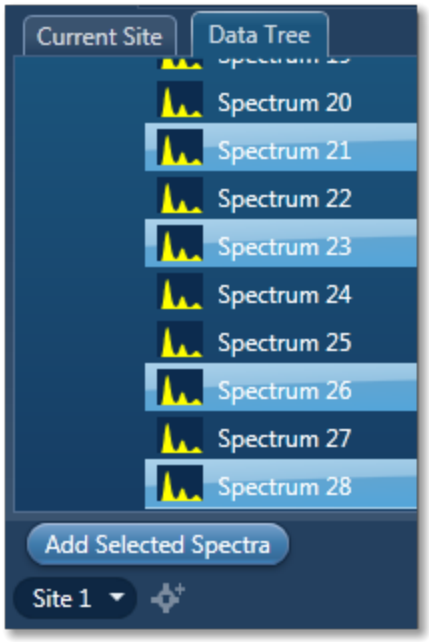
Calculate Composition

In this step you can view quant results in more detail using any of the 'Available Templates'.

To view result select the template that you wish to use:



- If you want to see a comprehensive set of results from a single spectrum, then choose the 'Full Results Table (customizable) - Single Spectrum' template and whichever spectrum is highlighted in the Data Tree will have its results shown in this template.
- To populate a multiple spectra template, hold the Ctrl key down while choosing spectra on the Data Tree and then press the 'Add Selected Spectra' button at the bottom of the Data Tree window.



- To compare quant results from two spectra, select 'Comparison of Results - Two Spectra' template. Then select the comparison spectrum from the Compare option in the 'Mini Quant and Compare' option. The compare spectrum will be overlaid on the current spectrum in the Spectrum Viewer. The quant results will be displayed in the table below.
- If you wish to change the Quant Settings press the Settings button to display the Quant Settings dialog. Apply the changes and close the dialog.
- Press the Requantify button to display the recalculated results.

Quant Results Details

You can see the settings used for calculating the composition in the Quant Results Details list box:

Parameter	Description
Label (Spectrum Label)	E.g., Spectrum 1
Element List Type	Current Spectrum, Fixed List or Combined List
Processing Options	All Elements, Element by Difference, Combined Element or Oxygen by Stoichiometry
Apply Coating Correction	Enabled or Disabled
Coating Element	E.g., Carbon
Coating Thickness	E.g., 15 nm
Coating Density	E.g., 2.25 g/cm3
Automatic Line Selection	Enabled or Disabled

Parameter	Description
Normalization	Enabled or Disabled
Thresholding	Enabled or Disabled
Deconvolution Elements	None/Selected
Factory Standards	Standardizations file supplied with the system
User Standards	Standardizations file defined by the user
Pulse Pile Up Correction	Enabled/Disabled
Detector File	Indicates file that has been used to characterize detector
Efficiency	Calculated/File based

Quant Results View

The information displayed in the Quant Results View depends on which template has been selected. You can view Spectrum Details, Spectrum Processing and Diagnostics table in addition to quant results.

See Also:

Quant Settings on page 143

Element Lists on page 146

Compare Spectra & MiniQuant Results on page 150

Analyzer - Custom

Analyzer is microscope centric application. X-ray spectra are acquired from the regions on the specimen scanned by the microscope beam. There are two modes of operation in the Analyzer application, Guided and Custom.

In the Custom mode, the Analyzer navigator has three steps. The Describe Specimen step is explained in the previous section. The two new steps are described below:

Acquire And Confirm

Acquire and Confirm is the main step of the Analyzer Navigator in the Custom mode. Three components are available in the single workspace. The Acquire Spectra component is located in the top half of the workspace, Quant Results in the bottom left and Confirm Elements in the bottom right.

The three components are combined in the Custom mode to give you a single workspace called Acquire and Confirm. It offers the convenience of working in one window without having to move away from it for acquiring a spectrum and obtaining the quant results.

You can choose which component you wish to display in the workspace by pressing the relevant button in the toolbar,  . You can toggle to switch on/off a component from the view.

Press  to un-dock a component as a free floating window located in the top right corner of the view. Press  to switch it into a full screen view.

To re-dock the free floating window back into the main workspace press  .

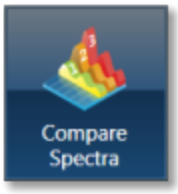
Each component has identical functionality as its counterpart in the Guided Navigator. To get help on each application follow the links below:

Acquire Spectra on page 80

Confirm Elements on page 129

Calculate Composition on page 141

Compare Spectra



This step in both the Point & ID and Analyzer Navigators allows you to compare spectra acquired from different sites of interest and specimens from the currently opened projects .

You can compare spectra acquired using different settings for example energy ranges (0-10, 0-20 or 0-40 keV) and number of channels (1024, 2048 or 4096).

Spectra associated with the current Site can be added to the Compare table by holding down the control key and pressing Add Selected Spectra. Note that if you have acquired the spectra in Point & ID, the positions of all the spectra associated with the current Site of Interest are displayed on the image. You can add spectra from any Project, Specimen and Site of Interest from the Data tree into this table.

Select which spectra you wish to compare by selecting them individually from the Data Tree, Press 'Add Selected Spectra'. This will add all the spectra you wish to compare into the 'Compare' table:

If you want to remove any spectra from the table, highlight the spectrum and press 

You can choose which of the available spectra you wish all the others to be compared to by selecting your reference spectrum from the compare table and pressing Select Reference Spectrum.

Settings

You can change the color of individual spectra by selecting the color from the drop down list in the compare table.

To change the line thickness of individual spectra, select it from the Line Thickness drop down list in the Compare table.

To apply the chosen line thickness globally, select it from the Compare Spectra Settings from

near the top of the Compare viewer.

Normalize

Normalize is a useful function for comparing spectra acquired using different input X-ray count rates such as spectra acquired with two different beam currents. Note that you can normalize spectra using a point or a region.

Normalize Spectra (Point)

• Select this option from the toolbar near the top left of the Compare Spectra screen.

• Double-click in the spectrum to set a normalization point along the X-axis.

• A window is drawn on either side of this point. The spectra in the Compare viewer are scaled to the average value of cps/eV (Y-axis) in the window.

Normalize Spectra (Region)

• Select this option from the toolbar near the top left of the Compare Spectra screen.

• Click and drag to set a normalization region along the X-axis.

• The spectra in the Compare viewer are scaled to the average value of cps/eV (Y-axis) in the normalization region selected in the previous step.

Smooth

The Smooth function is available from the context menus of the spectrum viewer. This is useful when comparing spectra where small differences may be obscured by statistical scatter.

The smooth function applies an energy-dependent filter to the spectrum. This has the effect of slightly broadening the peaks and also filtering out the rapid fluctuations due to statistics. Statistical fluctuations can sometimes appear like a real peak. When it is difficult to decide whether a peak is present or not, the smooth function substantially reduces the statistical fluctuation so that any real peak becomes more visible.

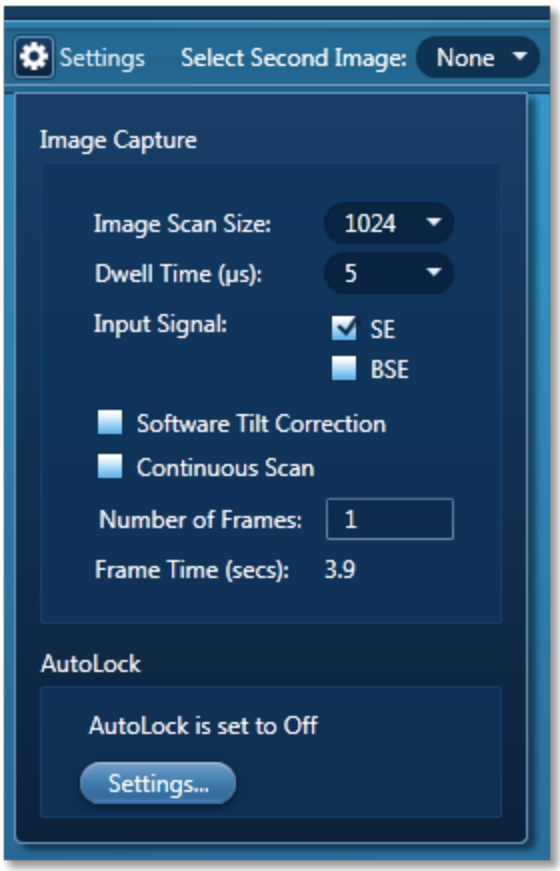
Point & ID - Guided

Scan Image

In the Scan Image step you can acquire an electron image into a 'Site'. A 'Site' is generally seen as a folder that contains images and analyses related to a particular area on a Specimen.

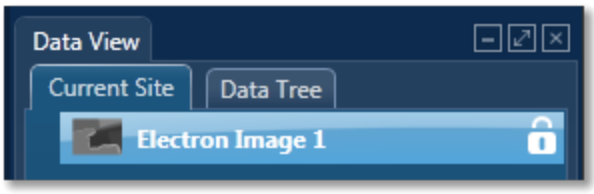
Press 

to start the image acquisition according to the current acquisition parameters. If you wish to change the acquisition parameters press the Settings cog on the Acquisition Toolbar. The Image Settings dialog is displayed:



You can select Image Scan Size, Dwell Time (µs), Input Signal (note that the label on the Input Signal will reflect whatever has been set during the system guided install for example SE, BSE or FSD), either Continuous Scan or Number of Frames and Frame Time (secs).

You are not restricted in the number of images you can have in a Site. Just ensure that the images you wish to keep are padlocked in the data tree to stop them being overwritten as shown in the screen shot below:



Toggle between saving or replacing the current image with successive image acquisition.

Press 

to stop image acquisition. Acquisition will stop at the end of the current frame. Click again to stop immediately. Note that when you navigate from the step acquisition will stop at the end of the frame.

Acquisition Toolbar

The acquisition toolbar is located near the top of the Scan Image screen under the Navigator. It has buttons for starting and stopping the image acquisition, the Settings cog for selecting the image acquisition parameters and a button to link/unlink images for manipulation:

Extensive tools are provided in the Scan Image screen to manipulate and enhance electron images.

There is a toolbar near the top left side of the screen. It has tools to pan and annotate the image. There are five different tools to add annotations as shown in the screen shot below. You can easily edit and delete annotations.

Selecting the Show Data Values tool from the toolbar and clicking anywhere on the image will display the Intensity value at that point.

T i p !

You can zoom in and out of the image using the mouse wheel.

Manual and Automatic Brightness, Contrast & Color Control Tools

Manual and Automatic brightness, contrast & color adjustment tools are located near the bottom right of the screen.

Context Menus

The Image viewer is provided with the Context menus for copying, exporting and printing images.

To find details about the Toolbars, Settings, Context Menus and Brightness & Contrast Adjustment tools follow the links below.

AutoLock

If your Specimen is drifting, then you can activate AutoLock from the Image Settings to ensure that any analysis you do corresponds to the true location on your image.

For EDS, if you do not want to collect an image and just want to acquire spectra, then you can skip this step and go straight to the Acquire Spectra step.

See Also:

Scan Image Toolbar on page 95

Scan Image - Settings on page 209

Context Menus - Image on page 115

Brightness, Contrast and Gamma Controls on page 170

AutoLock on page 96

Scan Image - Settings

The selectable parameters that control image acquisition (Image Scan Size, Dwell Time and Number of Frames) should be chosen according to your specific requirements. Both the time taken and the data storage size of the image are dependent on these parameters.

For a quick look at the specimen select the lowest image scan size and the fastest speed. This will enable you to decide whether you require either a higher pixel density, in order to observe finer detail such as small features, or a longer dwell time in order to improve the image quality by reducing the noise.

The available acquisition parameters are:

- Image Scan Size
- Dwell Time (µs)
- Mains Synchronize
- Input Signal
- Software Tilt Correction
- Continuous Scan
- Number of Frames
- Frame Time (secs)
- AutoLock

Image Scan Size

In general, the resolution of an image or Image Scan Size is defined as the number of picture points or pixels along the x and y axes e.g., 256 x 256, 512 x 512 or 1024 X 1024. The quality of the image improves as the resolution at which an image is acquired is increased. However, a microscope monitor/CRT is usually a rectangular display (rather than square), so the resolution is

displayed as a rectangle i.e., 256 x 200 in order to take into account the aspect ratio. The y dimension is set at installation, when imaging is calibrated. It will vary with each system.

Select the Image Scan Size for image acquisition from the following drop down options available:

64

128

256

512

1024

2048

4096

8192

Dwell Time (µs)

Images can be acquired using different speeds. The beam dwells on each pixel for a specified length of time while the signal is collected and then it moves to the next pixel. So the speed at which an image is acquired depends on the dwell time.

Speed	Dwell time
Fastest	1 µs
Fast	5 µs
Normal	10 µs
Medium	35 µs
Slow	65 µs
Slowest	400 µs

Mains Synchronize

Selecting Mains Synchronize on the Image Setup window, synchronizes the start of each scanned line to the mains supply. This will help to reduce mains borne interference in the image. Note that the acquisition time will be marginally longer than when mains synchronize is not selected.

Note that Mains Synchronize will only be visible if the appropriate hardware is installed.

Input Signal

For EDS, secondary electron imaging is generally most appropriate if you are imaging a sample which has topography whereas backscattered imaging is a very useful means of identifying areas of different composition on flat samples. Secondary electron imaging is the most common form of imaging and for a first look at your sample, choose this mode.

If you are analyzing a flat, polished sample and you can see weak contrast, switch to back-scattered imaging which will tend to enhance this contrast by showing up areas of different phases.

For EBSD, Forward Scattered Imaging is often used. A high proportion of the electrons scattered during EBSD carry imaging information. Because of the high angle of tilt dictated by the collection geometry required for EBSD, many electrons are scattered forward and down towards the bottom of the phosphor screen. These electrons carry similar information to the conventional backscattered electron signal. Using Forward Scattered Electron (FSE) imaging diffraction contrast is enhanced and the resultant signal makes the presence of individual grains easy to identify. The forward scattered electron signal produced is therefore ideal for EBSD investigations. However, the user may use any electron signal as required for the reference image.

Continuous Scan

If the Continuous Scan option is checked, you will see the image start to scan down the window and it will continue to refresh after each frame. If there are any instabilities in your specimen (e.g., charging or drifting problems) then these will be apparent as the image may shift slightly after each scan.

In order to stop the continuous scan, press the Stop button.

• Click once and the scan will stop when the current frame is complete.

• Click twice and it will stop immediately.

Note that when navigating to a different step, the scan will stop at the end of a frame.

Number of Frames

Enter the number of times you wish the beam to scan the site of interest for image acquisition.

Frame Time (secs)

The frame time is displayed in seconds. The value of frame time depends on the resolution, speed and mains synchronize if available.

See Also:

AutoLock on next page

Scan Image Toolbar

The Toolbar is located near the top left side of the Scan Image window. Tools are provided to manipulate and annotate the image:

You can move the image using the Pan tool. Use the wheel mouse to zoom in and out.

There are five different tools to add annotations on the current image as shown in the screen shot below:

To edit an annotation double-click on it to select it, the editing handles will be displayed. Use the handles to edit the annotation.

To delete an annotation, select it by double-clicking on it and then press the Delete key on the keyboard.

To delete all annotations on an image, choose Select All from the Annotations context menu on the image viewer and then press the Delete key on the keyboard.

AutoLock

AutoLock is designed to increase the stability of data acquisition on SEMs and TEMs where the image may shift. This image shift can occur for a number of reasons, such as sample movement due to temperature changes at high magnifications or charging of the sample.

AutoLock works by acquiring an image, comparing it with the reference image acquired at that Site, determining the image shift and adjusting the scan position to compensate for the shift. AutoLock will correct for an image shift at the interval specified while acquisition is in progress.

N o t e

AutoLock is accessed from the Settings in the Scan Image step in the Guided mode and Acquire and Confirm step in the Custom mode of Point and ID navigator. In Map and Linescan, AutoLock is accessed from the Settings in the Scan Image step in the Guided mode and Acquire and Construct step in the Custom mode.

To display the status of AutoLock in the Status Bar (On, Off, Due, Acquiring) check the AutoLock Status check box in the Status Bar tab in the Preferences dialog. You can access Preferences from the Tools menu.

Setting up the AutoLock:

1. Enable the AutoLock from the Settings in the Scan Image screen. Set it to Auto or Custom mode using the slider bar.

There are three modes,

Off

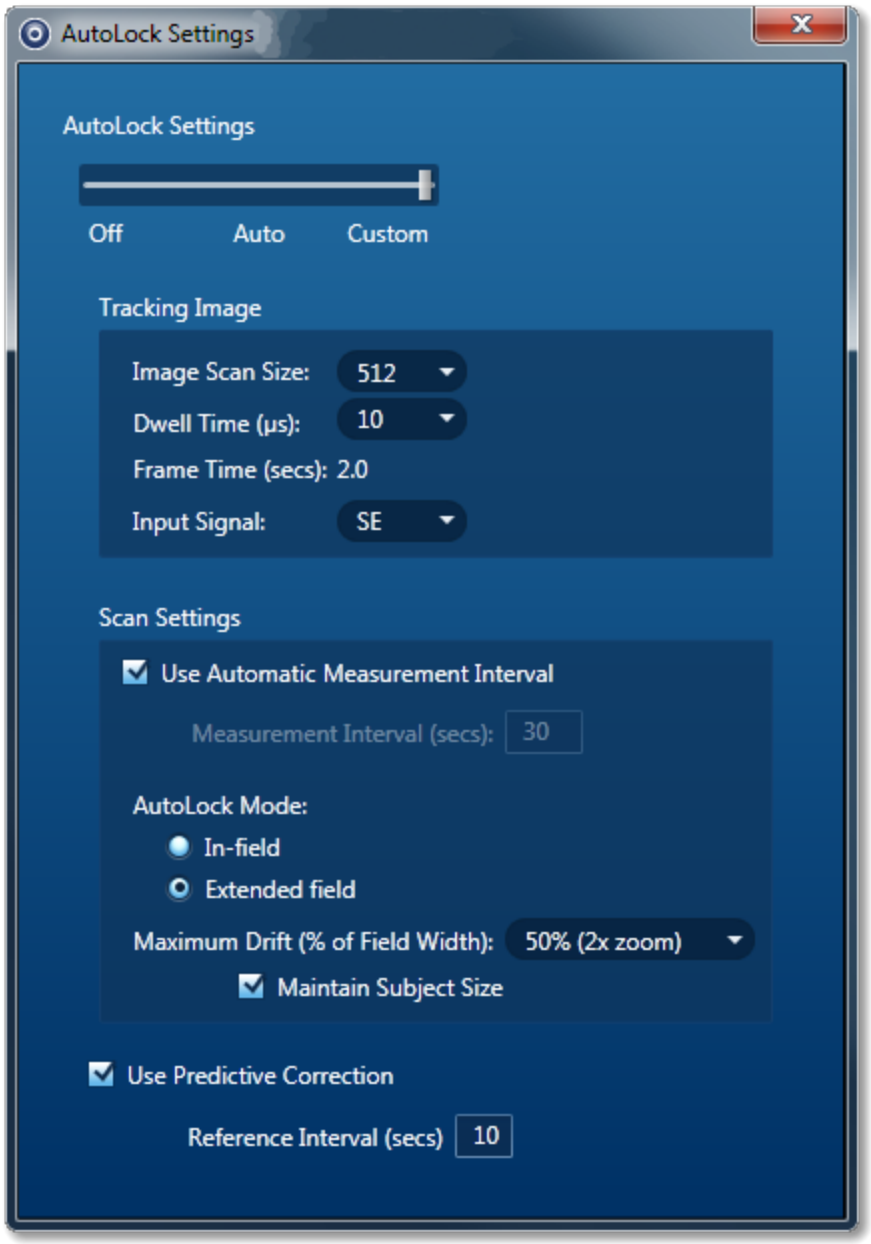
When the slider bar is set to Off position, the AutoLock is disabled.

Auto

In the Auto mode, the system chooses a set of default settings. This would typically use a 50% reduced scan at low resolution, providing AutoLock for a distance of half the scan area. If you require extra correction, use the Custom setting. The tracking image settings are displayed but the Scan Settings and Predictive Settings are hidden in the Auto mode.

Custom

In the Custom mode, you can define all AutoLock settings including Tracking Image, Scan Settings and Predictive Correction as shown in the screen shot below:



2. Start image acquisition by pressing the Start button. It will initialize the AutoLock and then acquire an electron image. The AutoLock Settings can only be changed if no data has been captured for a given electron image; in this case, an existing electron

image will be deleted and replaced unless you have locked the image in the Data Tree.

N o t e

If data has already been collected, changing the AutoLock Settings will require starting a new Site.

During data acquisition you can choose to display the status, history and diagnostic information of AutoLock in the Mini View:

Drift Progression

The drift profile is shown as snail trail (yellow). It represents the amount of drift that has occurred.

The full, dark area around the image represents the total imaging area, if a full 100% scan was captured. The sample image, as appears in the main user interface, is shown overlaid on this.

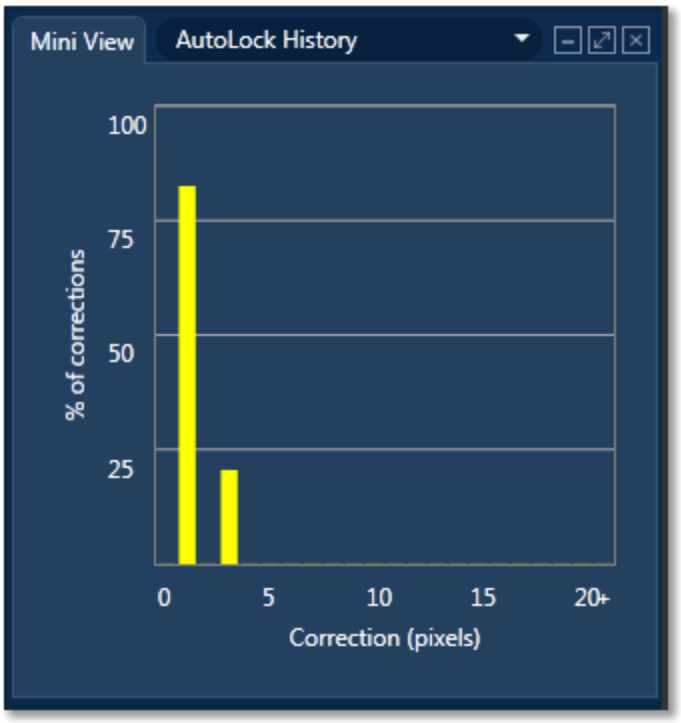
If the sample image reaches the edge of the dark surround, that indicates the limit of AutoLock has been reached. If drift continues in that manner, some parts of the sample will be outside the viewable area of the microscope. Note that Aztec will terminate the current experiment if the tracking area (or the scan region in In-field mode) reaches the edge. Any queued experiments will be immediately canceled if they are also outside the edge of the image.

The trail may extend outside the sample image but not outside the total imaging area. The trail will reset for each acquisition, i.e. it will only show the drift from the current acquisition.

Drift History

The AutoLock performance histogram, like the drift profile trail, also shows the amount of drift that has been applied during a single acquisition e.g., map acquisition. However, it provides a histogram view that allows rapid assessment of drift.

Consider the diagram below showing the histogram display:



The horizontal axis shows the amount of correction applied in image pixels and the vertical axis shows the percentage of the correction that had to be applied. For a stable sample, the amount of correction should be low – this will appear as very high values to the left of the histogram – maybe 100% across 1-2 pixels. For less stable samples, the histogram will spread to the right.

In the worst case, the histogram will show large peaks to the right hand side, indicating that large amounts of drift have been detected. In this case, you may want to stop the sample and take corrective action.

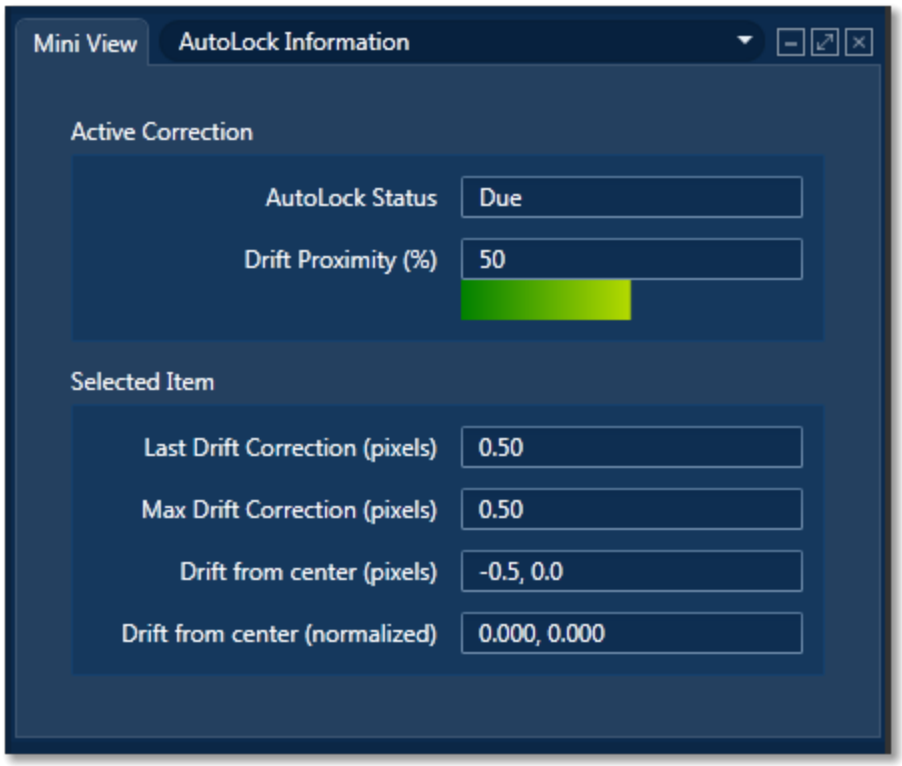
Very large drift values will be clamped to the right side of the histogram once they get beyond a certain value. The cut-off point will be based on the AutoLock Settings.

The histogram will reset for each acquisition, i.e., it will only show the drift from the current acquisition.

You can export the raw drift values (times and distances) as a CSV file, via the context menu on the Mini View.

AutoLock Information

The following diagnostic data is displayed if you select AutoLock Information in the Mini View:



Active Correction

AutoLock Status and Drift Proximity are displayed here:

AutoLock Status

The current status is displayed here.

Drift Proximity (%)

The remaining drift range (as a percentage of the field width) is displayed as Drift Proximity (%). The proximity display shows a colored bar that extends from green to yellow to red as the limits of AutoLock are reached. The bar will be full and in the red if AutoLock is exceeded (i.e., the scan region has drifted to the edge of the image).

Selected Item

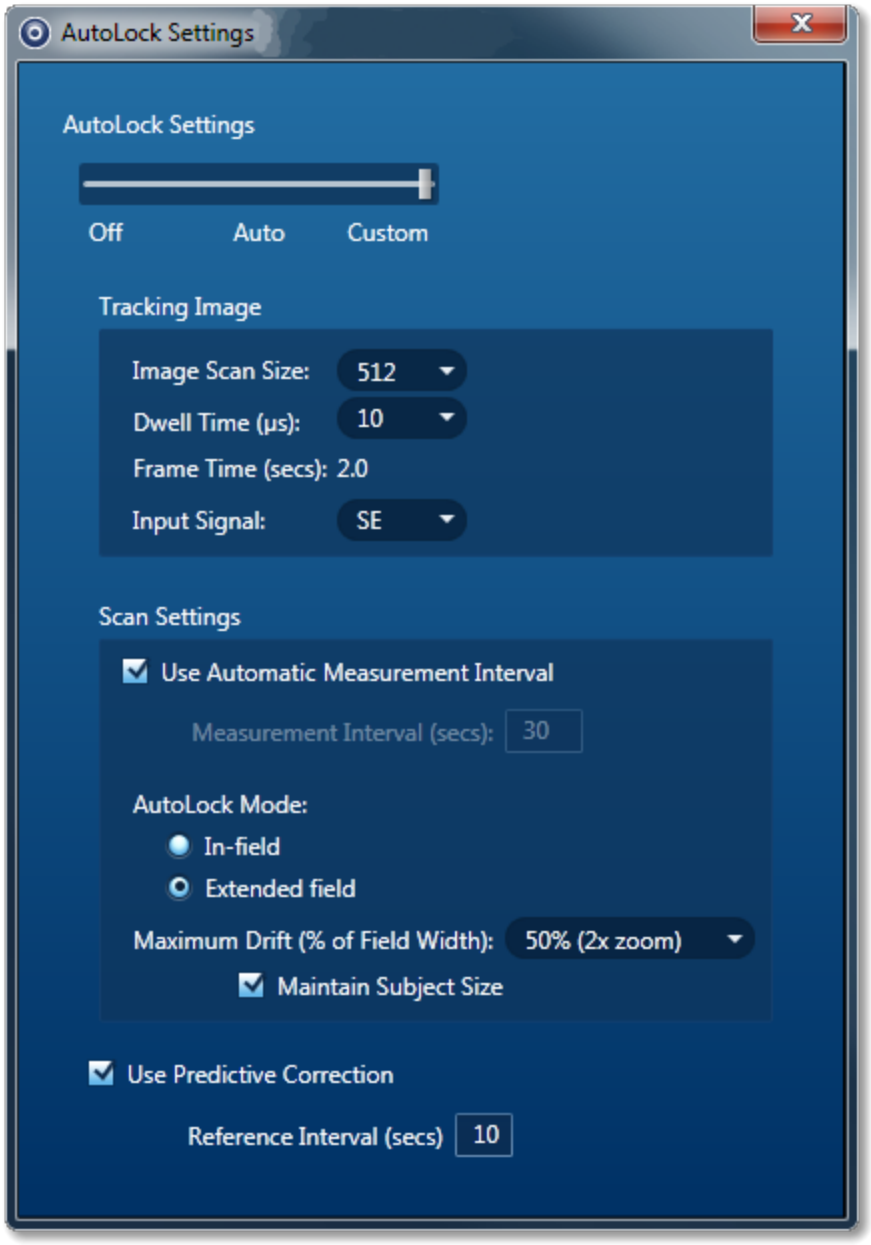
Details of the drift correction for an item selected on the Data Tree in the current Project are displayed here.

See Also:

AutoLock Settings below

AutoLock Settings

AutoLock is set to Off, Auto or Custom mode using the slider bar. In the Auto mode, the system chooses a set of default settings. In the Custom mode, you can specify the AutoLock settings shown in the screen shot below:



Tracking Image

You need to specify the tracking image settings to use, including the resolution (Image Scan Size), speed (Dwell time in µs) and Input Signal.

Image Scan Size

You can choose the size of the reference/tracking image from the Image Scan Size drop down list. The available options are 64 to 2048.

Scan Settings

You need to specify the drift measurement interval, the AutoLock mode and enable/disable 'Use Predictive Correction'.

Measurement Interval

Here you can specify the interval (in seconds) between tracking images. Drift correction is applied after each tracking image is collected. For slow drift, long intervals are acceptable. For fast drift or for drift that changes direction frequently, shorter intervals are more accurate (but will slow down acquisition). The default value is 30 seconds.

Use Automatic Measurement Interval

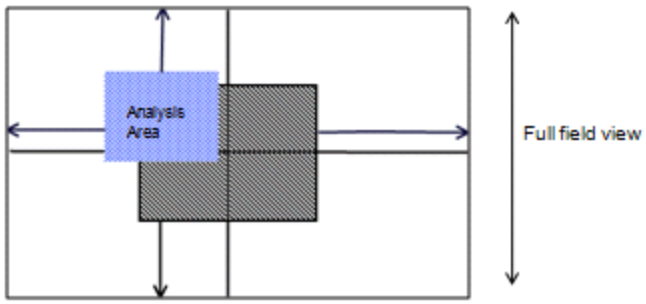
If you select this option, the program will determine the measurement interval for you. The interval is adaptive; as the speed of drift changes over time, the measurement interval will be increased or decreased accordingly. If Predictive Correction is also enabled, the automatic measurement interval will adjust to improve the quality of the predictive correction.

AutoLock Mode

There are two modes of operation, In-field and Extended field:

In-field

In this mode, the scanned area (field of view) is viewed in full all the time. It means that mapping or analysis is done on an area within this field. It also means that the drift correction is applied within this field. Digital zoom is not available in this mode. The In-field mode is illustrated in the figure below:



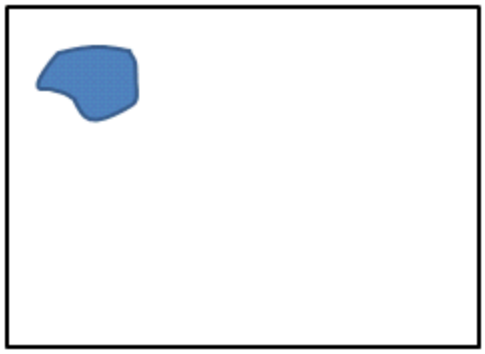
The amount of drift correction that can be applied is shown by the arrows from the analysis area/tracking area to the boundaries of the field of view.

Extended field

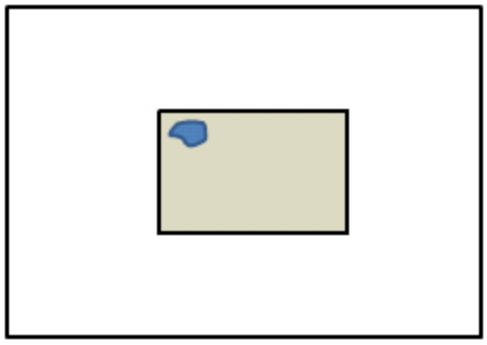
In this mode, the maximum drift available is 50% (2x zoom) and 150% (4x zoom). Setting the zoom level reduces the size of the captured area. If 2x zoom is selected only the middle 50% of the field of view is captured. The full field of view can be preserved by using the 'Maintain subject size' option described below.

Maintain subject size

You select an area you wish to map/analyze on the microscope, AutoLock preserves this area after the digital zoom is applied if you have checked the option, 'Maintain subject size' as illustrated in the screen shot below:



Before digital zoom is applied



After digital zoom is applied

This is done automatically by setting a new magnification on the microscope before acquisition starts. This value is determined by dividing the current magnification by 2 (2x digital zoom) or by 4 (4x digital zoom) if 25% is selected.

The Maintain subject size' option is not available in the In-field mode.

N o t e

If the microscope does not have column control then 'Maintain subject size' will not be available.

Use Predictive Correction

If 'Use Predictive Correction' is selected, a correction is applied periodically at selected intervals between tracking images. It is a useful option if your sample has a fairly consistent amount of drift. At the start two reference images are acquired. You can define the interval between the reference images. The Predictive correction will be updated when a tracking image is acquired.

Context Menus - Image

A number of useful shortcut menus available as right mouse click in the image viewer are shown in the table below:

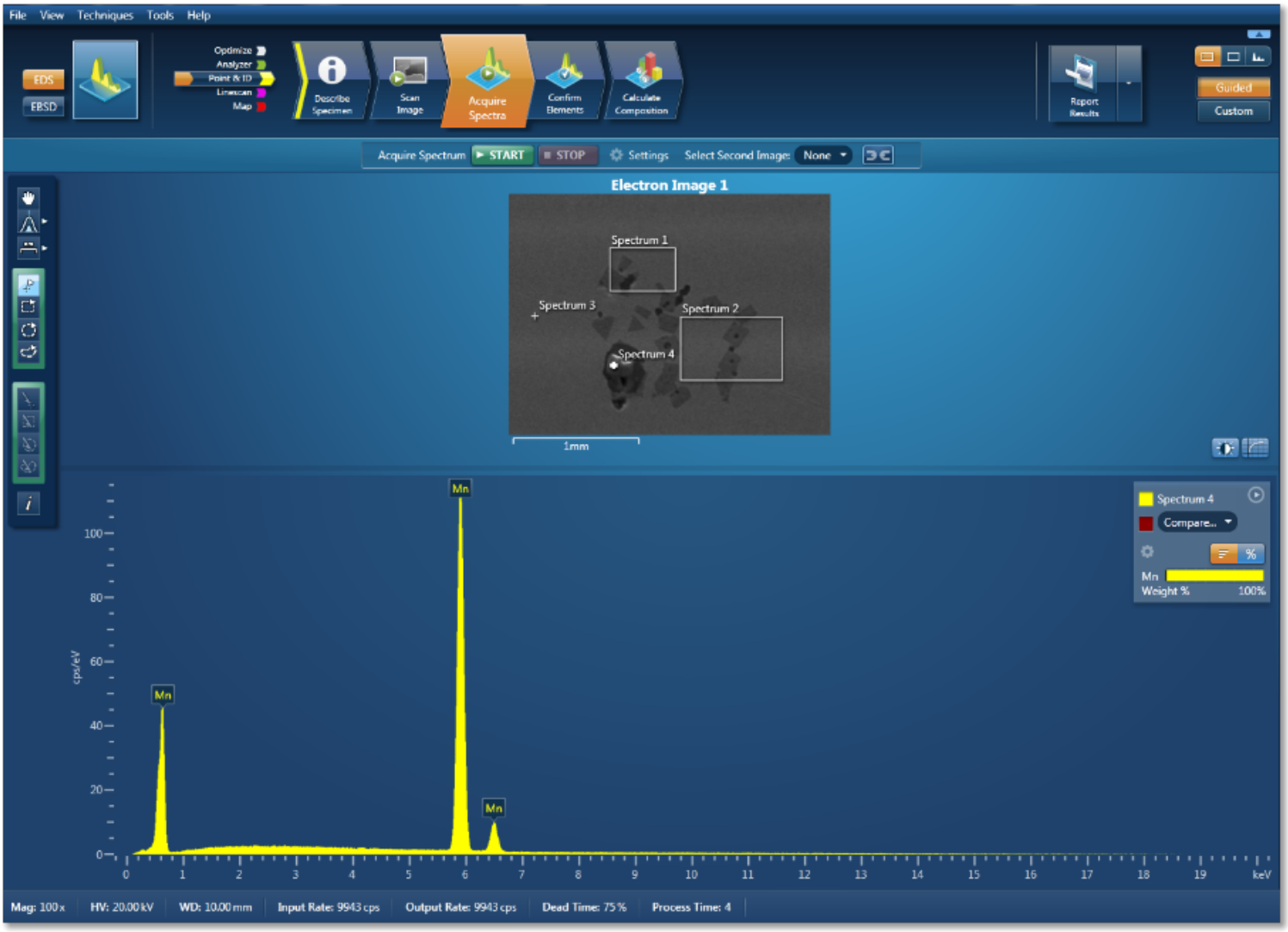
Context Menu Item	
Rescale Image	Fit Image to Display
	Fill Display with Image

Context Menu Item	
View	Color Bar
	Header
	Scale Bar
	Show Contrast/Brightness Buttons
	Color Key
Set Image Colors	
Export	Save As (Original Resolution)...
	Save As...
	Copy
	Print
	Email...
	Settings...
Annotations	Show
	Select All
	Style...
	Delete
Show Acquisition Areas	Show All
	Show Selected
	Show None
	Show Short Names
Details...	

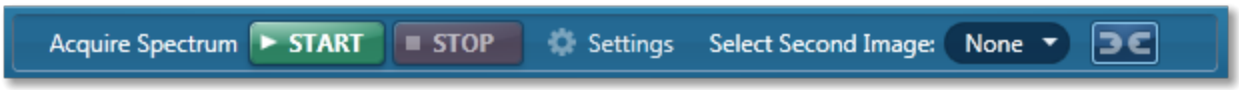
Acquire Spectra

In this step you acquire spectra from the current electron image (SE/BSE). You can also reconstruct spectra from a Layered Image or X-ray map if you have already acquired SmartMaps. Real time Compare and instant MiniQuant options are also available here.

You can display the components that you are working on such as image and spectrum using the controls on this toolbar  located in the top right side of the screen. You have choice of displaying image and spectrum as shown in the screen shot below or just an image or a spectrum full screen:



There is an acquisition toolbar near the top of the workspace:



It has controls for starting and stopping the spectrum acquisition. There is a Settings cog for selecting the acquisition parameters. For details see Acquire Spectra - Settings link below.

The toolbar located on the left side of the workspace has various tools for image and spectrum manipulation, enhancement, annotation and area selection. For details see Acquire Spectra - Toolbar topic from the link below.

There are manual and auto brightness, contrast and color controls available for the image view. You can use these controls to enhance and high light certain features in the image.

The Compare Spectra & MiniQuant Results option is available in the top right corner of the Spectrum viewer. You can compare the current spectrum with any other spectrum from an opened Project on the Data Tree. Instant MiniQuant results can be viewed in a table or a bar chart.

See also:

How to acquire spectra on the facing page

Modes of X-ray spectrum acquisition on page 109

Acquire Spectra - Toolbar on page 110

Acquire Spectra - Settings on page 112

Context Menus - Spectrum Viewer

Peak Labels on page 116

Element Lists on page 146

How To Acquire Spectra

You can acquire a spectrum from the entire image, a single point or area on an image. You can also acquire spectra from multiple points and/or areas on an image. Tools are provided to specify points and areas on the image, for detailed description read the topic, Modes of X-ray spectrum acquisition on page 109.

The screen shot below shows the defined points and areas on the image and the spectra being populated on the Data Tree:

Spectra have been acquired from the areas and points (white) labeled as Spectrum 1, 2, 3 and 4. Spectrum 5 is currently being acquired from the area (yellow) labeled as Spectrum 5. Spectrum 6 and 7 (blue) are in the queue.

For step by step guidance on how to acquire spectra see below:

Spectrum acquisition from a single point

- Having acquired an image in the Scan Image step, navigate to the Acquire Spectra step.
- Select the Point Tool from the Toolbar on the left of the window.
- Click on the image with the mouse to acquire spectrum from a point.

- Spectrum acquisition starts from that point. The position of the point is marked as a cross on the image and it is labeled as Spectrum 1. It is added to the Data Tree just below the image it is acquired from.
- The progress of spectrum 1 acquisition is displayed on the Current Site tab.

Spectrum acquisition from multiple points

- Having acquired an image in the Scan Image step, navigate to the Acquire Spectra step.
- Select the Point Tool from the toolbar on the left of the window.
- Click on different locations on the image to define multiple points.
- Spectrum acquisition starts from the first point as soon as you click on the image. The rest of the points are queued up for acquisition.
- The position of each point on the image is marked as a cross and it is labeled as Spectrum x (1, 2, 3...).
- As spectra are being acquired, they are added to the Data Tree just below the image they are acquired from.
- Status of each point is color coded i.e., current point from which a spectrum is being acquired is yellow, all queued up points are blue and post acquisition points are white.

Spectrum acquisition from an area

- Having acquired an image in the Scan Image step, navigate to the Acquire Spectra step.
- Select an area selection tool from the Rectangle, Ellipse and Freehand in the toolbar on the left of the window.
- Click and drag the mouse to outline a rectangular, ellipsoid or irregular shaped area on the image with the Rectangle, Ellipse or Freehand Tool respectively.
- Spectrum acquisition starts from the defined area as soon as you release the mouse. The position of the defined area is marked with the relevant shape and it is labeled as Spectrum 1.
- Spectrum 1 is added to the Data Tree just below the image it is acquired from.

Spectrum acquisition from multiple points and areas

- Having acquired an image in the Scan Image step, navigate to the Acquire Spectra step.
- Select the Point Tool from the toolbar on the left of the window.
- Click on different locations on the image to define multiple points.
- Select an area selection tool from the Rectangle, Ellipse and Freehand in the toolbar on the left of the window.
- Click and drag the mouse to outline a rectangular, ellipsoid or irregular shaped area on the image with the Rectangle, Ellipse or Freehand Tool respectively.
- Spectrum acquisition starts in the order you have defined the points and areas. Status of each point/area is color coded i.e., current point/area from which a spectrum is being acquired is yellow, all queued up points/areas are blue and post acquisition points/areas are white.
- All points and areas defined on the image are labeled as Spectrum x (1, 2, 3...).

- As spectra are being acquired, they are added to the Data Tree just below the image they are acquired from.

Spectrum Acquisition Tools

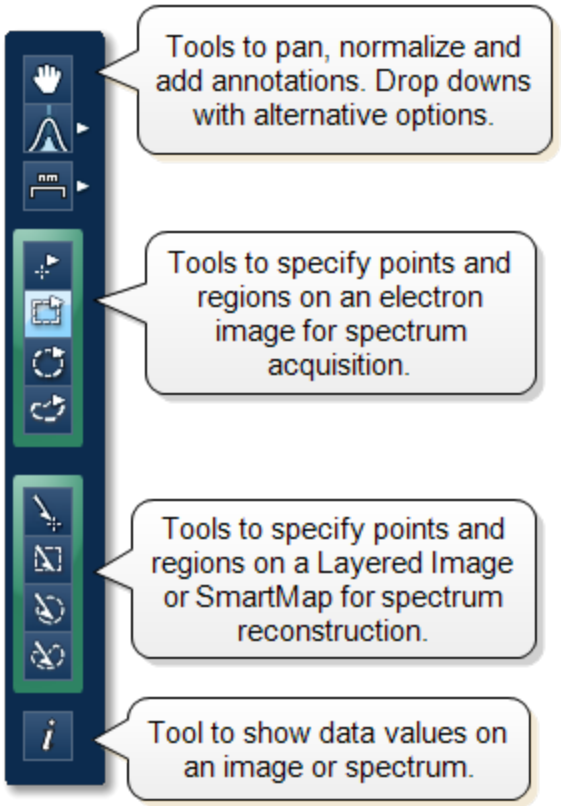
There is a toolbar on the left side of the Acquire Spectra and Acquire & Confirm windows that has four point and area selection tools. You can use these tools to define points and regions on an image to acquire spectra. See the table below for detailed description of each tool:

Spectrum Acquisition Tools	
	**Point** Click on this icon to select the Point Tool from the toolbar and then click on the image to start the spectrum acquisition from that point. This is a useful tool for quick survey of a homogenous specimen.
	**Rectangular** Click on this icon to select the Rectangular Tool. Click and drag the mouse on the image to outline a rectangular area. When you release the mouse button, an area will be outlined and a spectrum will be acquired from it. This is a useful tool for examining regular shaped features and areas on an image.

Spectrum Acquisition Tools	
	**Ellipse** Click on this icon if you wish to define an ellipsoid area on the image. Click and drag the mouse on the image to outline an area. When you release the mouse button, an area will be outlined and a spectrum will be acquired from it. This tool allows you the flexibility of outlining an oval or ellipsoid feature on an image.
	**Freehand** Click on this icon if you wish to acquire a spectrum from an irregular shaped feature on the image. Click and drag the mouse around the feature on the image. Once you have defined the feature release the mouse button. A spectrum will be acquired from it.

Acquire Spectra - Toolbar

The Acquire Spectra screen has a toolbar on the left side of the workspace shown in the screen shot below:



Pan

The Pan tool allows to expand the spectrum along the vertical axis and move the spectrum along the horizontal axis. To expand the spectrum along the horizontal axis with Pan tool selected, hold down the Ctrl key while dragging the spectrum with the left mouse.

Normalize Spectra

You can normalize two spectra over a selected point or a region.

Normalize Spectra (Point)

- You have the current spectrum in the spectrum viewer.
- Select the second spectrum using the Compare drop down. The second spectrum is overlaid on the current spectrum.
- Select the Normalize Spectra (Point) option from the toolbar. The cursor turns into an up down arrow ( ).
- Double-click in the spectrum to set a normalization point along the X-axis. A window is drawn on either side of this point. Both the spectra are scaled along the Y-axis to the average value (usually cps/eV) in the window.

Normalize Spectra (Region)

- You have the current spectrum in the spectrum viewer.
- Select the second spectrum using the Compare drop down. The second spectrum is overlaid on the current spectrum.
- Select the Normalize Spectra (Region) option from the toolbar. The cursor turns into a crosshair (+).
- Click in the spectrum viewer to select the start point of the energy window. A default window is displayed about this point. Drag the mouse to define your window and then release it. A window will be drawn between the first point and the end point where you release the mouse. Both spectra are scaled along the Y-axis to the average value (usually cps/eV) in the window.

Annotations

Five tools available to add annotations on the current spectrum and the image are Caliper, Angle, Text, Rectangle and Ellipse. Select the tool by clicking on it and then click on the spectrum/image to add annotation. For example to add text select the Text annotation tool, click on the spectrum where you wish to enter the text and then start typing the text. To delete annotation double click on it to select it and then press the Delete key on the keyboard.

Spectrum Acquisition Tools

There are four spectrum acquisition tools, Point, Rectangle, Ellipse and Freehand. Select a tool to acquire spectra from points and/or regions on the image. For details see Modes of X-ray spectrum acquisition on page 109

For step by step advice on spectrum acquisition see How to acquire spectra on page 107.

Spectrum Reconstruction Tools

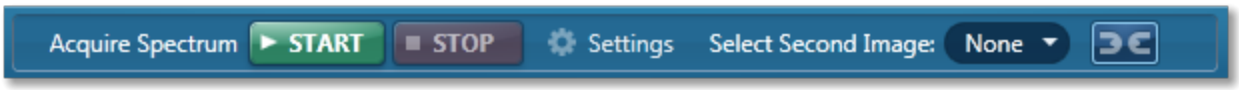
You can reconstruct spectra from SmartMaps using Point, Rectangle, Ellipse and Freehand tools. These tools are enabled on map acquisition.

Show Data Values

With this tool you can view the Energy (keV) and counts in any channel of the spectrum. Simply select the Show Data Values tool from the toolbar and then hover on spectrum. The values will be displayed as you move from channel to channel.

Acquisition and Settings Toolbar

Near the top of the Acquire Spectra window, there are buttons for starting and stopping acquisition as shown below:



Press the Start button to acquire a spectrum from a point or region specified on the electron image.

There is also a Settings cog in the toolbar. For details of settings see Acquire Spectra - Settings below.

You can choose to display two electron images (SE/BSE) side by side by selecting the second image from the drop down list in the toolbar. Images can be linked for manipulation using the Link button.

Acquire Spectra - Settings

The settings are described in detail below:

Energy Range (keV)

Select a spectrum energy range from the available options of Auto, 0-10, 0-20 or 0-40 keV from the Energy Range drop down list.

An appropriate energy range should be selected in conjunction with the current microscope accelerating voltage. If the accelerating voltage is above 10 kV, in order to view lines which may be excited above 10 keV, the 20 keV range should be chosen. Below 10 kV, it may be more appropriate to choose the 10 keV range since no lines above 10 keV will be excited.

In the Auto mode, the **AZtec** system checks for the accelerating voltage set on the microscope and selects a suitable energy range in the software.

Number of Channels

Select number of channels from the drop down list of Auto, 1024, 2048 or 4096 (4K) with which you wish to display the spectrum. The number of eV/channel will depend on both the energy range and the number of channels you select:

Energy Range (keV)	Number of Channels	eV/channel
0-10	4096	2.5
0-10	2048	5
0-10	1024	10
0-20	4096	5
0-20	2048	10
0-20	1024	20

Energy Range (keV)	Number of Channels	eV/channel
0-40	4096	10
0-40	2048	20
0-40	1024	40

In the Auto mode, the **AZtec** system checks for the energy range selected and sets the appropriate number of channels.

N o t e

The Energy Calibration routine is performed for all process times and for all available energy ranges and number of channels. It means if you change any of these settings soon after you had performed the Energy Calibration you do not need to re-optimize the system.

Process Time

Select the Process Time from the drop-down list of Process Times, Default and 1 to 6. The Process time is the length of time spent reducing noise from the X-ray signal coming from the ED detector during processing. By selecting different Process times it is possible to reduce differing amounts of noise. The longer the Process time, the lower the noise. If noise is minimized, the resolution of the peak displayed in the spectrum is improved, in other words, the peak is narrower and it becomes easier to separate or resolve, from another peak that may be close by in energy.

If Default is selected, the Process Time is automatically set to a suitable value.

There is a trade off between the Process time that is used, and the speed at which data can be acquired into the X-ray spectrum. Process time 1 is the shortest, and as such, gives the highest X-ray acquisition rates, but at some cost to resolution. Process time 6 is the longest, and gives the highest resolution, but at some cost to maximum acquisition rate. The longer the Process time, the slower data can be acquired, i.e. the higher the system Deadtime will be for a given input count rate. (The input rate is not affected by the pulse processor).

Which Process Time should I use?

When you start your application first time, the Process Time is set to Default. This is a suitable choice for many routine applications where you are looking for good resolution of peaks and fast acquisition.

For the first look at a specimen you should use a long process time (5 or 6) to start with in order that you do not miss any detail in your spectrum. For example, when identifying peaks particularly those closely spaced and overlapping, it is important to get good peak separation. Good resolution is also important for looking at a series of lines that are very closely spaced, like an L series and process times 4 to 6 should be chosen. Common overlaps include the Mo L and the S K lines.

If there are no closely spaced peaks then you can afford to use a shorter Process Time such as 1-3 which will enable you to increase the acquisition rate by increasing the beam current. A compromise between acquisition speed and resolution should be found if there are peak overlaps.

When acquiring SmartMap data you should choose your Process Time carefully.

1. You may have been working on a Specimen in either Analyzer or Point & ID where you have setup your acquisition parameters to optimize your quantitative analysis. If you now wish to acquire SmartMap data and you think you may wish to reconstruct spectra from your SmartMap data and then quantify these spectra, you should maintain these acquisition parameters. This means that you may have to acquire data with a long Process Time to maximize resolution but limit the maximum acquisition rate.
2. You may have been working in either Analyzer or Point & ID and you want to view the distribution of elements whose main peaks do not overlap as a map or a linescan. In this case you should use a shorter Process Time which will mean that you can work with higher acquisition rates and shorter acquisition times. The choice of Process Time will very much depend on your sample and what you wish to do with your SmartMap data once it has been acquired.
3. If you have started your Project in Map and you are analyzing an unknown sample, we recommend that you use a long Process Time in order that you do not miss any detail in your spectrum. However if you only wish to map certain elements whose main lines do not overlap, you can afford to shorten the Process Time and increase the acquisition rate by increasing the beam current.

Acquisition Mode

There are two options to terminate the acquisition, Auto and Live Time.

If Auto mode is selected, acquisition continues until enough counts are collected in the spectrum for quantification.

You can choose to terminate acquisition at the end of a preset Live Time. Enter the required time in seconds into the text box. This is the time for which the system is processing counts into the spectrum. The live time clock runs slower than the real time clock so that the acquisition for '100' live seconds takes longer than 100 real seconds. This time is extended to compensate for the output rate being less than the input rate by the degree of Deadtime.

Acquisition Time

Enter the Acquisition Time in seconds for acquiring spectra.

Pulse Pile Up Correction

Check Pulse Pileup Correction check box if you wish to automatically correct the spectrum for pulse pileup peaks. Uncheck the box if you wish to disable this correction.

Pileup peaks can occur when a second pulse arrives and triggers the measuring system during the time required to process a previous pulse. When this happens, neither pulse will appear in its correct position. The result being a peak at a higher energy equivalent to the sum of the energy of the two photons.

The largest pileup peaks will be seen at twice the energy of the main peaks - e.g. Fe Ka pile up peaks will be seen around 12.8 keV.

Notes

The pileup correction algorithm assumes that the count rate at every energy is constant throughout the analysis period. Therefore, the correction works best when analysis is performed on single pixels, points or areas of same composition. Bad results may be obtained if the beam is rastered over an area where composition is changing or if a spectrum is reconstructed from a SmartMap over a region where the composition is changing.

Context Menus - Image

A number of useful shortcut menus available as right mouse click in the image viewer are shown in the table below:

Context Menu Item	
Rescale Image	Fit Image to Display
	Fill Display with Image
View	Color Bar
	Header
	Scale Bar
	Show Contrast/Brightness Buttons
	Color Key
Set Image Colors	
Export	Save As (Original Res-olution)...
	Save As...
	Copy
	Print
	Email...
	Settings...
Annotations	Show
	Select All
	Style...
	Delete
Show Acquisition Areas	Show All

Context Menu Item	
	Show Selected
	Show None
	Show Short Names
Details...	

Peak Labels

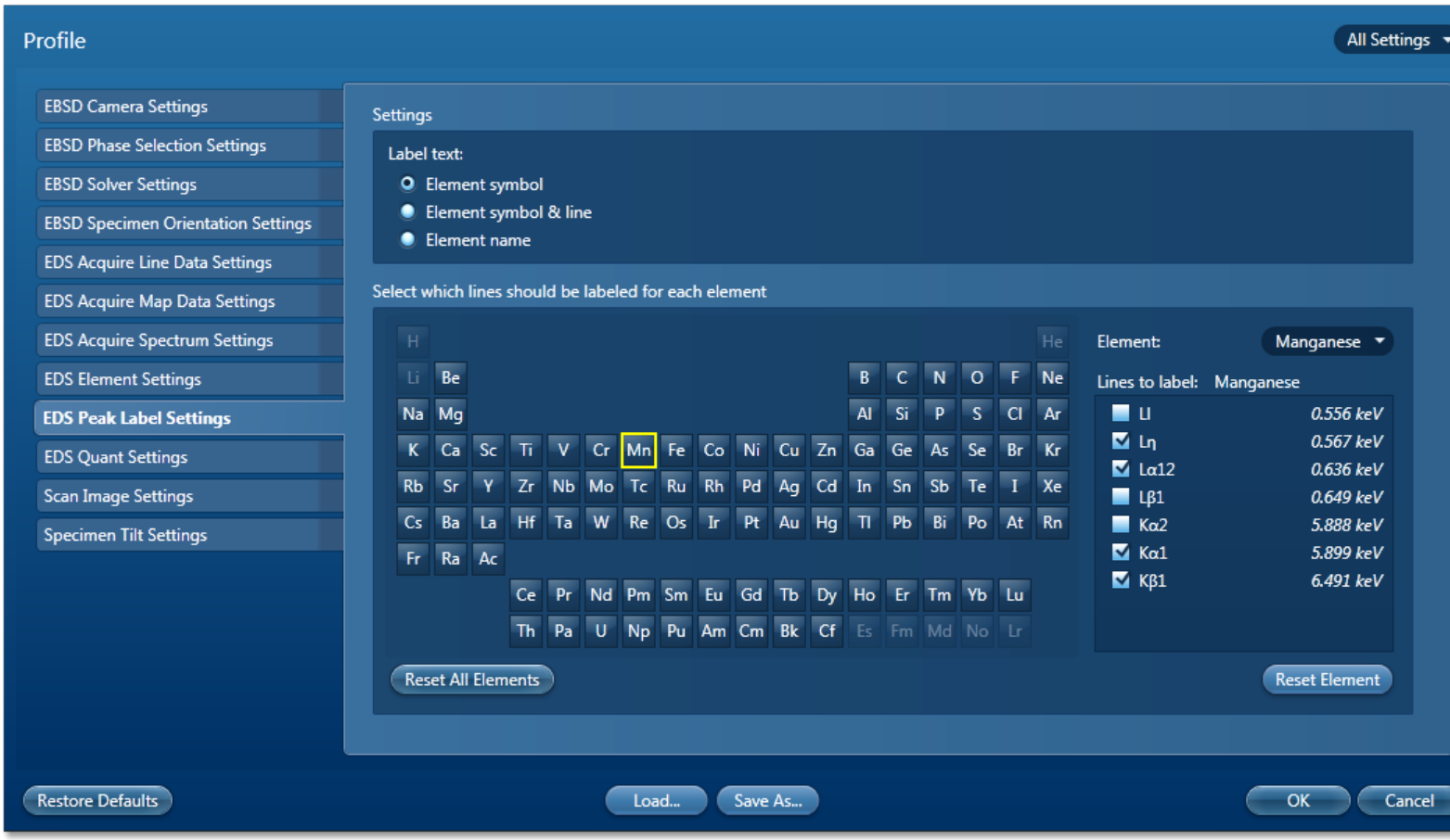
Peaks in the spectrum are automatically labeled during acquisition if AutoID is enabled in Predefined Elements tab in the Describe Specimen step.

You can configure peak labels from the Peak Labels tab available in two places in the software:

- User Profile
- Confirm Elements step

Default Peak Label Behavior

The default peak labeling behavior is controlled by the User Profile. You can access the User Profile screen from the Tools menu on the main application window. Select the Peak Labels tab from the User Profile screen:



You can select how you wish to display labels on the peaks from the following three options:

1. Element Symbols (e.g., Mn)
2. Element Symbol & Line (e.g., Mn Kα1)
3. Element name (e.g., Manganese)

Make your selection by checking the relevant radio button. This configuration is saved with the User Profile. Note that peaks will be labeled according to your new selection on the next spectrum acquisition. The labels on the current spectrum will not be automatically updated. To update the labels on an existing spectrum, use the 'Apply Profile' button on the Confirm Elements step shown in the screen shots later on in this topic.

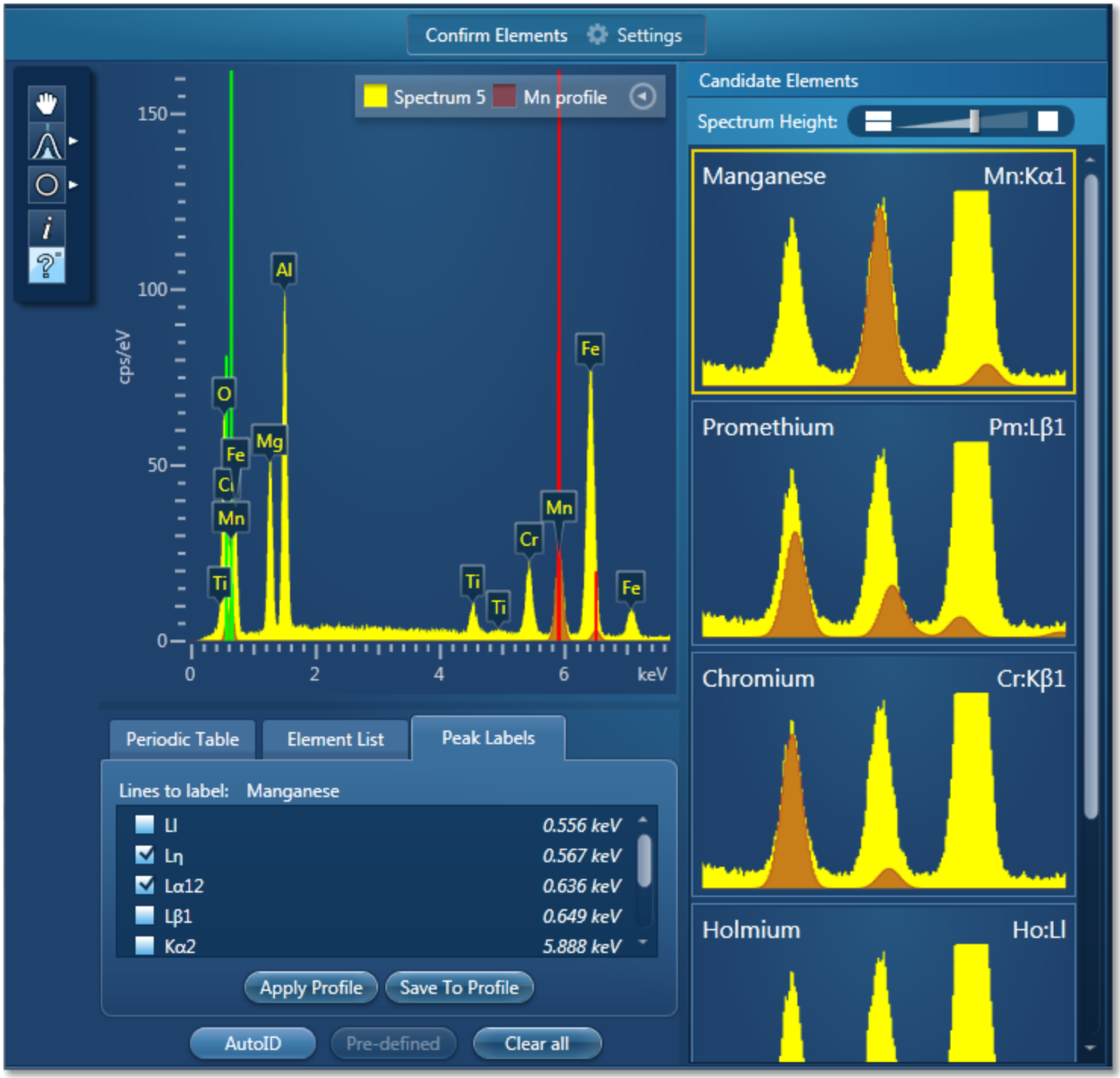
When you click on an element symbol on the Periodic table, a list of X-ray lines together with their energies is displayed. This list corresponds to those in the X-ray database. The lines which are checked are the ones used that will be used for labeling peaks. You can check or uncheck a line to select or deselect it for labeling. To restore the settings to the factory settings for this element press the  button.

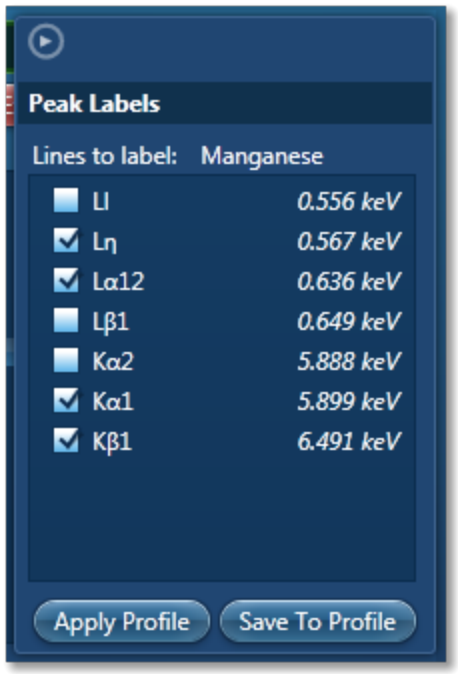
You may have configured lines for other elements. To restore them to the factory settings press the  button. This action will restore all the elements to the default settings.

Refining Peak Labels Manually

You can manually refine the peak labels for an existing spectrum in the Confirm Elements step.

You can configure which lines you wish to be labeled for each element from the Peak Labels tab or Peak Labels slide-out menu as shown the screen shots below:


Confirm Elements
Settings
Spectrum 5
Mn profile
cps/eV
keV
Al
O
Fe
Mg
Cl
Mn
Ti
Cr
Candidate Elements
Spectrum Height:
Manganese
Mn:Kα1
Promethium
Pm:Lβ1
Chromium
Cr:Kβ1
Holmium
Ho:Ll
Periodic Table
Element List
Peak Labels
Lines to label: Manganese
Ll 0.556 keV
Lη 0.567 keV
Lα12 0.636 keV
Lβ1 0.649 keV
Kα2 5.888 keV
Apply Profile
Save To Profile
AutoID
Pre-defined
Clear all



The lines which are checked are the ones used for labeling the peaks in the current spectrum. You can check or uncheck a line to add or remove the label. To save your labeling configuration for an element in the User Profile, press the Save to Profile button after checking the lines.

To use the labeling configuration saved in the User profile press the Apply Profile button. This action will remove all labels from the current spectrum and apply labels according to the scheme saved in the User Profile.

Moving Peak Labels Manually

Click on the peak label that you wish to move and drag it to a new position by holding the left mouse button.

After moving the peak labels on the current spectrum you can restore them to their original position by selecting 'Reset Positions' from the Peak Labels section of the context menu on the Spectrum viewer.

Notes

- If there are too many labels too close together only main peak labels are displayed. The hidden labels will reappear if you stretch the spectrum along the x-axis.
- You may find that previously hidden labels show up when labels are moved or deleted.
- All existing peak labels are removed and the spectrum is relabeled according to the User Profile whenever the Element List changes e.g., when an element is manually added or removed or when AutoID is used.

Element Lists

Any list of elements in the **AZtec** software can be split into the following three categories:

- Pre-defined Elements - elements expected in specimen
- Identified Elements - typically based on automatic peak identification (Auto ID)

- Fixed List - used for Quantitative analysis

Pre-defined Elements

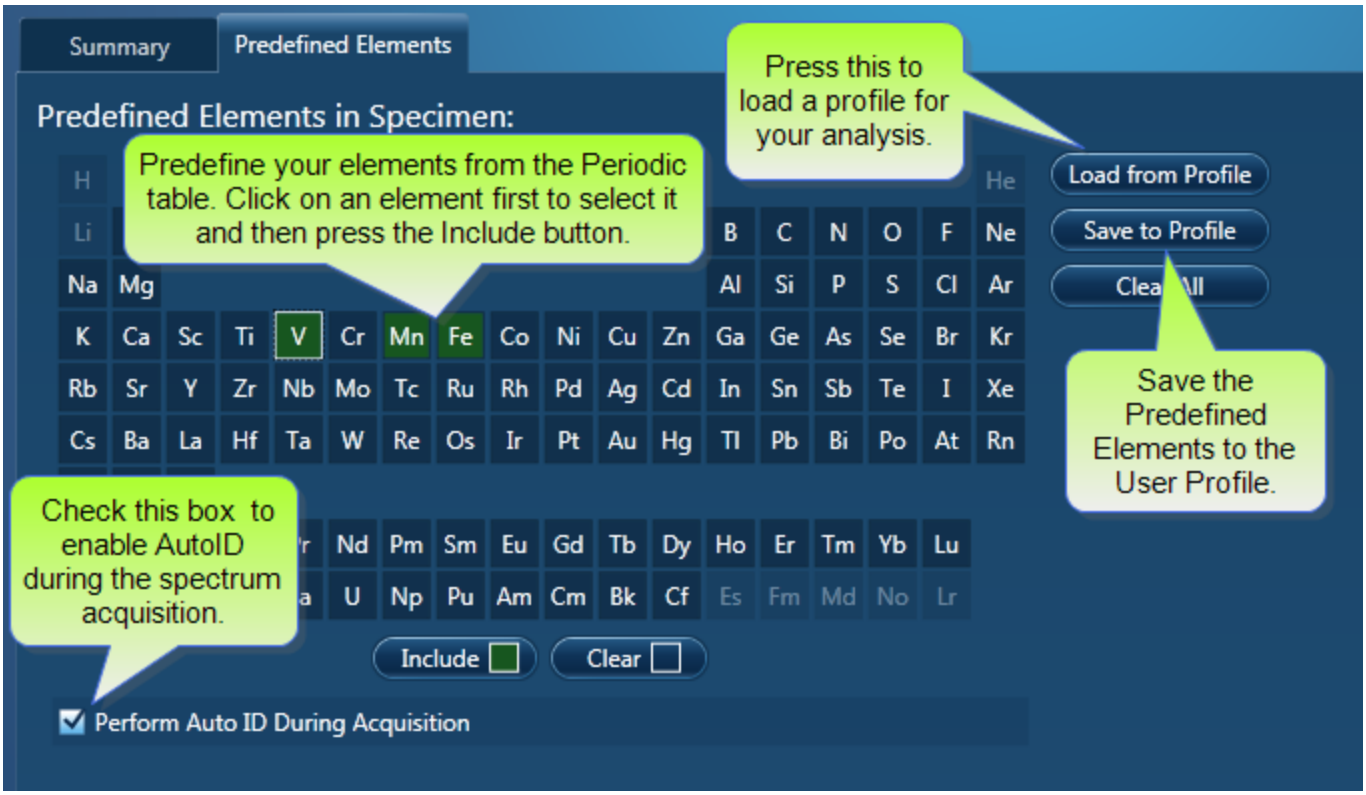
You may have prior knowledge of your Specimen and know what elements to look for.

Examples

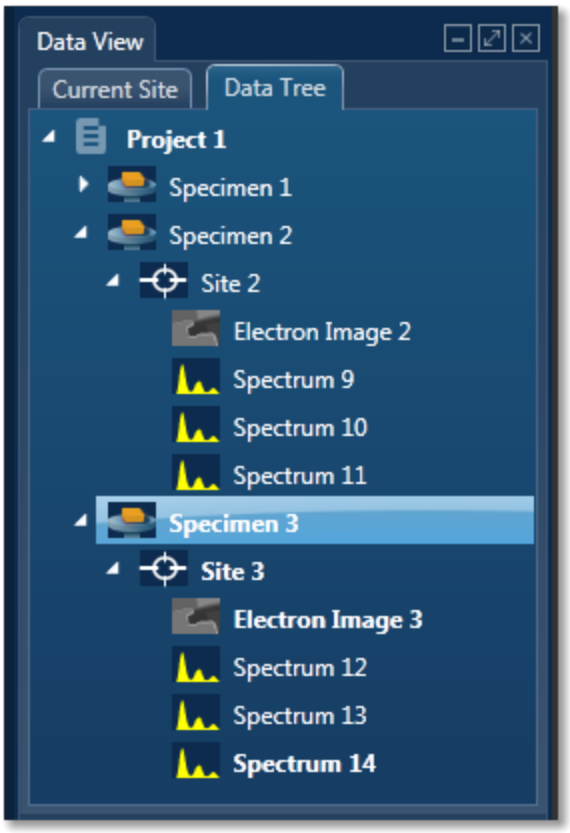
'I want to look for a particular list of elements. (I am not interested in any other elements)...I may want to see their labels on spectra, their X-ray maps or both....I want to see these even if the element is not present'.

' I know what's in my sample.... I want to look for a specific set of elements (I want to see these even if the element is not present.) .....but I would like to know if there is anything else in my sample too'.

You can define these elements' in the 'Pre-defined Elements' tab in the Describe Specimen step. If you want to save the Pre-defined Elements to a profile you must first press 'Save to Profile' button, then save the profile via the drop down menu. When you want to analyze your Specimen, you can load this profile or another profile by pressing the 'Load Profile' button in the Describe Specimen step as shown in the screen shot below:



Note that the 'Pre-defined Elements' are saved with the current Specimen. Changing the 'Predefined Elements' will only update the Pre-defined Elements in the current Specimen. It will not update any existing Specimens in the Project.



The current specimen is the one that you are presently analyzing/processing the data from. For example, in the screen shot above, Specimen 3 is the current specimen, Specimens 1 and 2 are the other specimens in the Project.

Identified Elements

The 'Identified Elements will include:

- Any Pre-defined Elements
- Elements identified by Auto ID
- Any additional Elements identified manually

If the 'Pre-defined Elements have been specified, these will be included for identifying and labeling peaks in the current spectrum automatically.

Note that the 'Identified Elements' are saved in the Spectrum.

'Perform Auto ID During Acquisition' option is enabled by default and can be deactivate by unchecking it in the Describe Specimen step as shown in the screen shot above. You can then AutoID at any time by pressing the button.

Additional peaks in the spectrum can be identified manually by using the 'Show Candidate Elements' tool in the Confirm Element step. Click on the question mark icon to select the Show Candidate Element tool. Position the cursor at the center of a peak by double-clicking with the mouse. The list of elements spectra corresponding to the energy at the cursor is displayed in the panel on the right. By highlighting an element in this list, you will see the markers showing all the lines for this element.

Note that the 'Identified Elements' will be quantified if you have selected the Current Spectrum, or the Fixed List and Current Spectrum Element List in the Quant Settings in the Calculate Composition step or EDS Quant Settings in the User Profile dialog.

Note

EDS Quant Settings are available in the User Profile Dialog accessed from the Tools menu. These settings are also available from the Calculate Composition step.

Fixed List

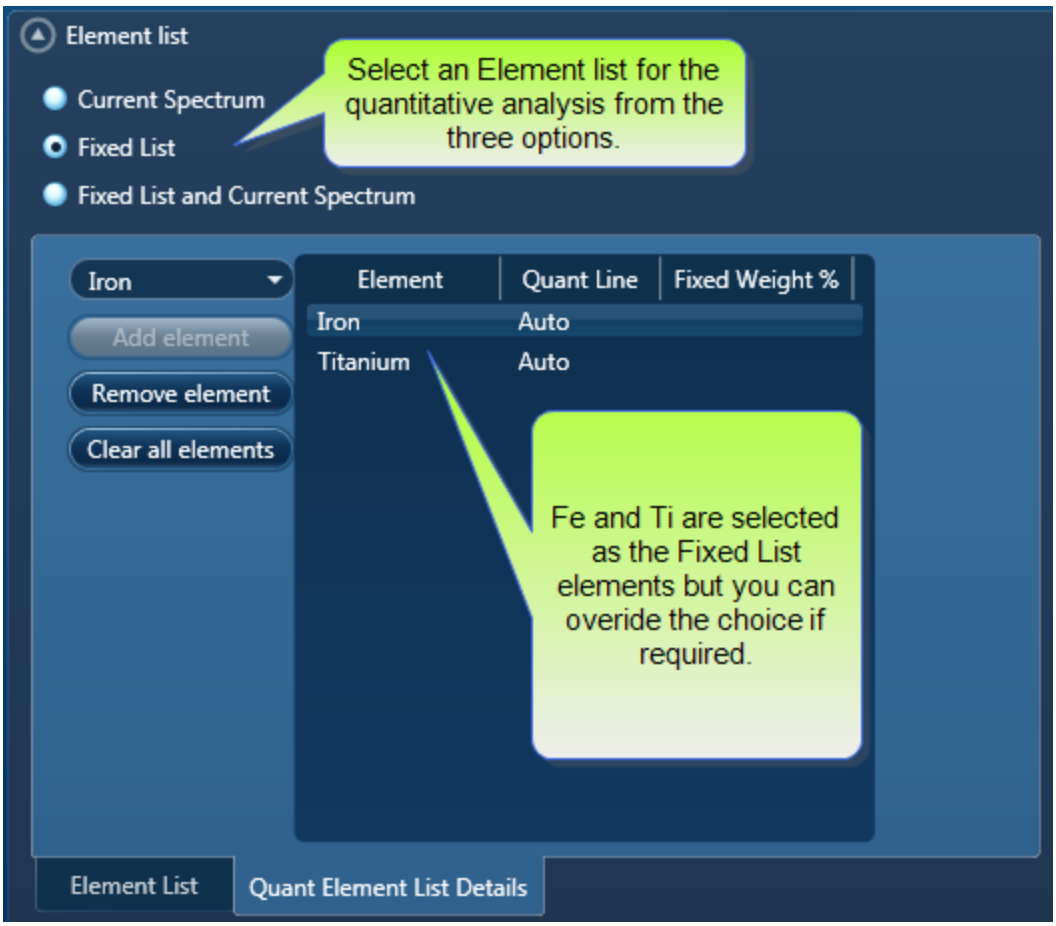
The elements in the 'Fixed List' are defined in the Quant Settings dialog which is available in the User Profile and the Calculate Composition window.

Note that the Fixed List is only used for calculating composition in quantitative analysis.

Example

'I want to do quantitative analysis on my glass samples and want to compare results from one batch to another batch. I am always looking for the same specified list of elements'.

You can specify the Element List for Quant from the three available options in the Quant Settings dialog as shown in the screen shot below:



Current Spectrum

This list includes the Pre-defined Elements and elements identified by Auto ID and manually using the Candidate Element tool.

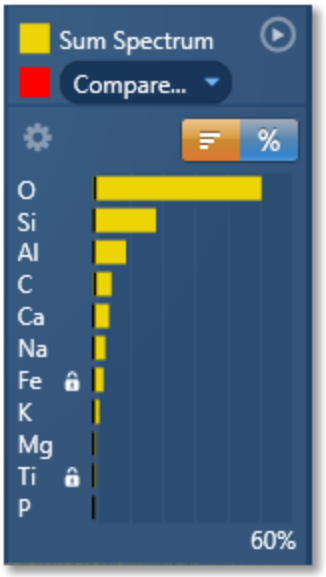
Fixed List

You select the Fixed List option if you know what elements you wish to quantify. Choose the elements from the drop-down list as shown in the screen shot above.

Fixed List and Current Spectrum

To quantify the elements in the above two lists, select the Fixed List and Current Spectrum option.

MiniQuant results table will clearly display which list is being used. A lock icon will be displayed against the 'Fixed List' elements as shown in the screen shot below:



In this example, Fe and Ti are selected in the Fixed List. The rest of the elements in the chart results are from the Current Spectrum because the Element List selected for quantification was 'Fixed List and Current Spectrum'.

Note that the 'Fixed List' is saved in a User Profile.

See also:

Describe Specimen on page 62

Acquire Spectra on page 105

Confirm Elements on page 129

Calculate Composition on page 141

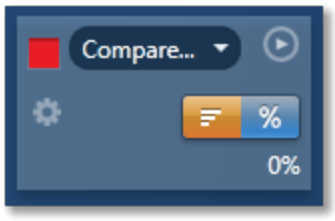
User Profile on page 17

Compare Spectra & MiniQuant Results

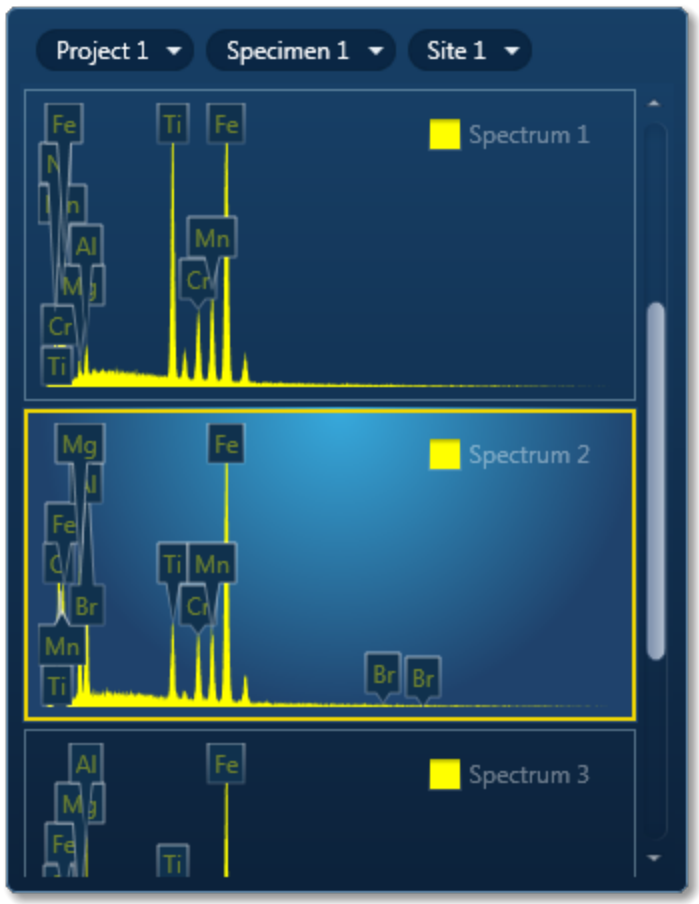
Real time Compare and instant MiniQuant options are available in the Acquire Spectra, Confirm Elements and Calculate Composition (Comparison of Results - Two Spectra template) steps. User can see results without having to move away from the acquisition mode. Using these options you can:

- See your results during analysis.
- Compare your current spectrum to a control spectrum during acquisition.
- View MiniQuant results in a table or a bar chart.

Click  in the top right corner of the Spectrum Viewer in Acquire Spectra, Confirm Elements or the Calculate Composition window to access the Compare & MiniQuant options:



In the above example, Spectrum 1 is the current spectrum and Spectrum 2 is the comparison spectrum. You can select the comparison spectrum from a Project currently available in the Data Tree. It can be from any Project, any Specimen and any Site of Interest currently available in the Data tree. To choose the comparison spectrum click on the down arrow (Spectrum 2 in the above example). Spectra available in the current Project, Specimen and Site of Interest are displayed as below:

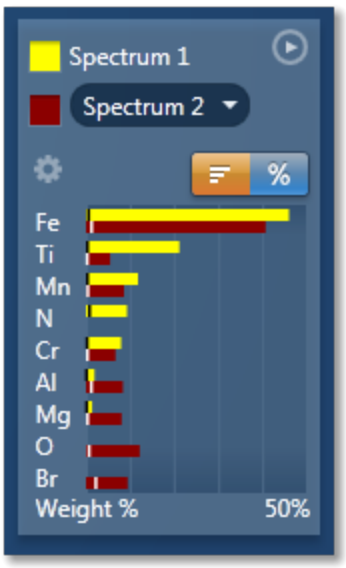


Click on the spectrum in the display to select it for comparison. The selected spectrum will be overlaid as a line spectrum over the current spectrum. The MiniQuant results are displayed in a table as shown in the example below:

The results are displayed as wt% (weight%).

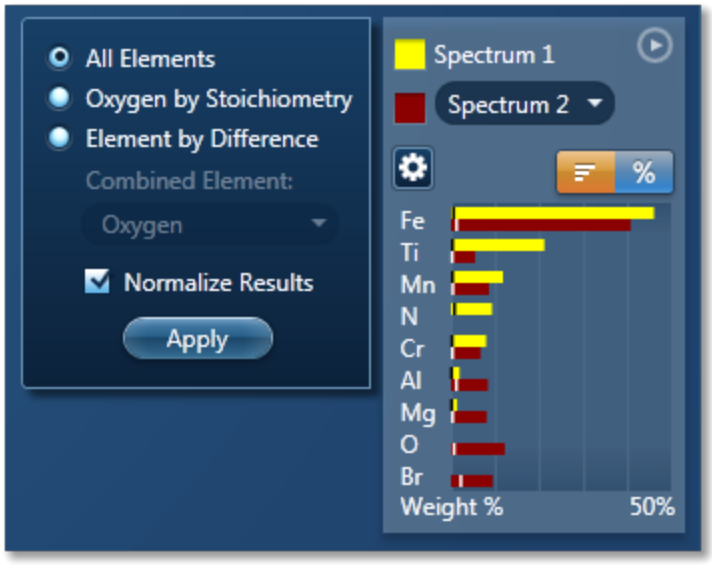
The statistical error is displayed as **σ** (weight% sigma) for the calculated wt%. It is the overall confidence figure for the analysis. You can use sigma to assess the results especially when an element is present at low concentration. For example, if an element concentration is 0.2 wt% and the **σ** is 0.12 wt%, the element might be detected at a statistically significant level if the acquisition time for the spectrum is extended. If the **σ** is 0.4 wt%, it is pointless to extend the acquisition time and it is safe to assume that the element if present, is at a level above the limit of detection for this technique.

Press  to display the results in a chart:



The sigma values are displayed as black or white vertical bands across the bars in the chart results as shown in the example above. In this case the full scale of the bar chart is 60%.

If you wish to change the MiniQuant Settings press  :



Make your selection by clicking on the radio button and then press the Apply button. The results will be updated immediately .

N o t e

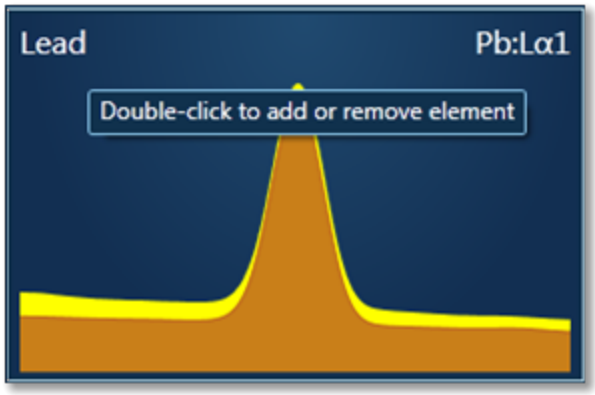
The Quant Settings in the MiniQuant and Calculate Composition are the same. Updating one updates the other and vice versa.

Confirm Elements

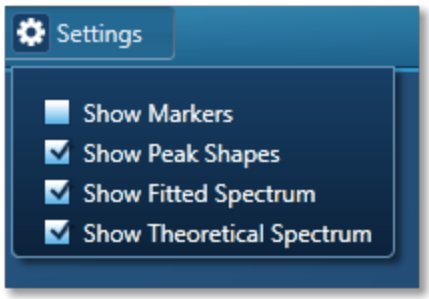
This step has been designed to help you confirm the elements that have been identified by AutoID in your spectrum. These elements are then used to create a confirmed elements list for qualitative and quantitative analyses. Extensive tools including Element Series Markers, Overlays, Element Profiles and Show Candidate Elements are available here to assist you in confirming elements manually.

How to confirm elements:

- Start with the largest peaks. Press the question mark icon to select the Show Candidate Elements tool from the tool bar on the left hand side of the interface, then double click on a peak in the spectrum viewer. The candidate elements are displayed in a stacked spectra view on the right hand side of the window (you can double click on any of these elements to add or remove it from the confirm elements list).



- You can control what overlays you see in the Spectrum viewer via the 'Confirm Elements Settings'. These overlays can be very useful in helping you to interrogate complex spectra.



- Press Include/Exclude once you are satisfied with the identification of each element to build your list of the confirmed elements.

See Also:

Confirm Elements - Settings below

Confirm Elements - Tools on the facing page

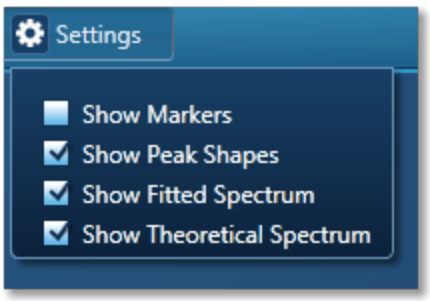
Element Lists on page 146

Peak Labels on page 116

Compare Spectra & MiniQuant Results on page 150

Confirm Elements - Settings

To display the Confirm Elements Settings, click on the cog icon near the top of the screen. The various option available are shown in the screen shot here:



To select any of these options simply check the associated check box.

Show Markers

Clicking on one of the elements in the confirmed elements list puts up the markers for that element. Lines series are color coded. K series lines are marked in red, L series lines are marked in green and M series lines are marked in purple.

Show Peak Shapes

Peak Shapes (one for each line series for each element) are fitted to the spectrum using the Filtered Least Squares, FLS approach. This effectively removes the effect of background and corrects for peak overlap. The Fitted Spectrum shows the fitted peak shapes superimposed on a close approximation to the background and this makes it easy to see if a particular element has been missed or a peak shape is a bad match to the observed peak shape.

Show Fitted Spectrum

This tool is very useful for checking for the presence of small amounts of elements whose peaks are heavily overlapped in the spectrum.

It overlays a fitted spectrum onto the current spectrum. The shape of the fitted spectrum is based on the elements labeled in the current spectrum (AutoID). If any peaks are incorrectly labeled, or any elements missed, then the fitted spectrum will not overlay correctly on your current spectrum. Use the Show Candidate Elements tool to identify elements on the part of the spectrum where the fitted spectrum and the current spectrum have their greatest discrepancy. Then add

the possible elements identified manually by double clicking on them individually in the stacked spectra view and test if they improve the overlay fit.

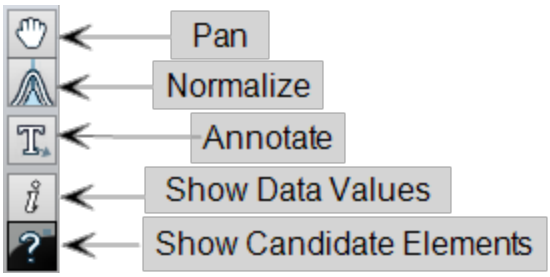
Show Theoretical Spectrum

This tool calculates a full x-ray spectrum from the analyzed composition. This calculation includes the efficiency of excitation of all lines, the effects of absorption and backscatter within the sample and calculates the relative intensity of both lines and bremsstrahlung background. Although the theory is not perfect, it normally predicts peaks and background within about 10% accuracy. If elements have been misidentified or element composition ratios are incorrect, then the Theoretical Spectrum will appear significantly different from the observed spectrum, either in terms of peak intensities or background. When the theoretical spectrum is a good match to the observed spectrum, this provides useful confirmation that the analysis results are sensible.

Note that the Theoretical Spectrum is calculated assuming that the specimen is flat and homogeneous. If the specimen shows a lot of topography or has composition that varies throughout the information volume, then the calculation will not be relevant. For example, if a spectrum is obtained from a point that is not directly visible by the detector, then the emitted x-rays will be absorbed on there way to the detector by an unknown amount or unknown material so the overall effect cannot be predicted.

Confirm Elements - Tools

A toolbar is located near the top left side of the Confirm Elements step. There are five different tools to manipulate the spectrum. These are Pan, Normalize, Annotations, Show Data Values and Show Candidate Elements:



Pan

The Pan tool allows to expand the spectrum along the vertical axis and move the spectrum along the horizontal axis. To expand the spectrum along the horizontal axis with Pan tool selected, hold down the Ctrl key while dragging the spectrum with the left mouse.

Normalize Spectra

You can normalize two spectra over a selected point or a region.

Normalize Spectra (Point)

- You have the current spectrum in the spectrum viewer.
- Select the second spectrum using the Compare drop down. The second spectrum is overlaid on the current spectrum.
- Select the Normalize Spectra (Point) option from the toolbar. The cursor turns into an up down arrow ( ).

- Double-click in the spectrum to set a normalization point along the X-axis. A window is drawn on either side of this point. Both spectra are scaled along the Y-axis to the average value (usually cps/eV) in the window.

Normalize Spectra (Region)

- You have the current spectrum in the spectrum viewer.
- Select the second spectrum using the Compare drop down. The second spectrum is overlaid on the current spectrum.
- Select the Normalize Spectra (Region) option from the toolbar. The cursor turns into a crosshair (+).
- Click in the spectrum viewer to select the start point of the energy window. A default window is displayed about this point. Drag the mouse to define your window and then release it. A window will be drawn between the first point and the end point where you release the mouse. Both spectra are scaled along the Y-axis to the average value (usually cps/eV) in the window.

Annotations

Three tools available to add annotations on the current spectrum are Text, Rectangle and Ellipse. Select the tool by clicking on it and then click on the spectrum to add annotation. For example to add text select the Text annotation tool, click on the spectrum where you wish to enter the text and then start typing the text. To delete annotation double click on it to select it and then press the Delete key on the keyboard.

TIP!

To delete all annotations at once go into the context menu on the spectrum viewer. Choose Select All from the Annotations menu and then select Delete from the Annotations menu. This operation will remove all the annotations from the current spectrum.

Show Data Values

With this tool you can view the Energy (keV) and counts in any channel of the spectrum. Simply select the Show Data Values tool from the toolbar and then hover on spectrum. The values will be displayed as you move from channel to channel.

Show Candidate Elements

Click on the question mark icon to select the Show Candidate Element tool. Position the cursor at the center of a peak by double-clicking with the mouse. Note, you may wish to expand the spectrum horizontally by holding down the control key and dragging the spectrum with the mouse. The list of elements spectra corresponding to the energy at the cursor is displayed in the panel on the right. By highlighting an element in this list, you will see the markers showing all the lines for this element.

The profile of each candidate element is overlaid on the current spectrum. The color of the profile is different from the current spectrum to enhance the display and assist you in identifying and confirming elements.

Spectrum Height

This tool aids in the manipulation of the height of each candidate element spectrum using the slider bar:

Display MiniQuant & Compare

Real time compare and instant MiniQuant options are available in Acquire Spectra, Confirm Elements and Calculate Composition steps. You can see results without having to move away from the acquisition mode. You can also compare the current spectrum to a control spectrum during acquisition. You can view MiniQuant results compared in a table or as a bar chart.

The element list is taken from the Quant Settings in the Calculate Composition step. The default Element List is Current Spectrum.

Element Lists

Any list of elements in the **AZtec** software can be split into the following three categories:

- Pre-defined Elements - elements expected in specimen
- Identified Elements - typically based on automatic peak identification (Auto ID)
- Fixed List - used for Quantitative analysis

Pre-defined Elements

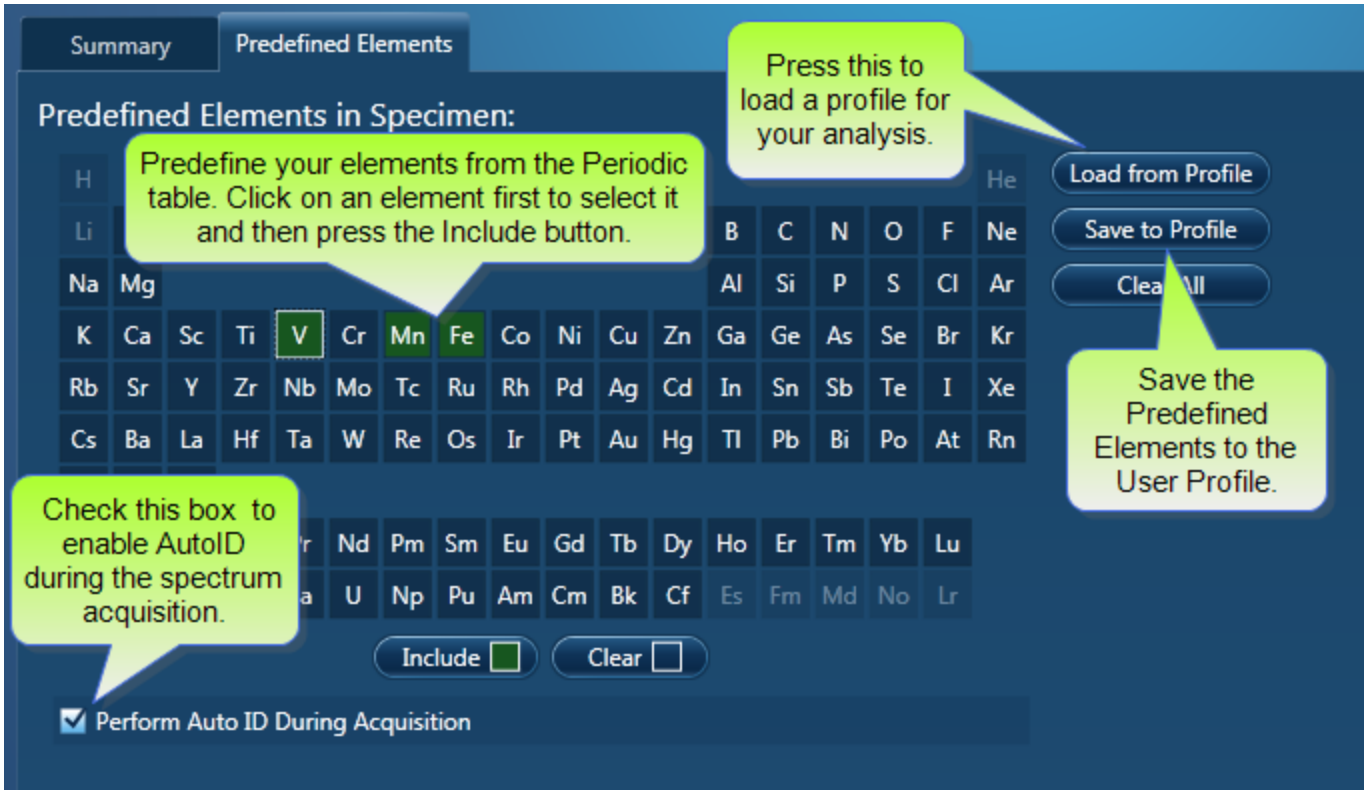
You may have prior knowledge of your Specimen and know what elements to look for.

Examples

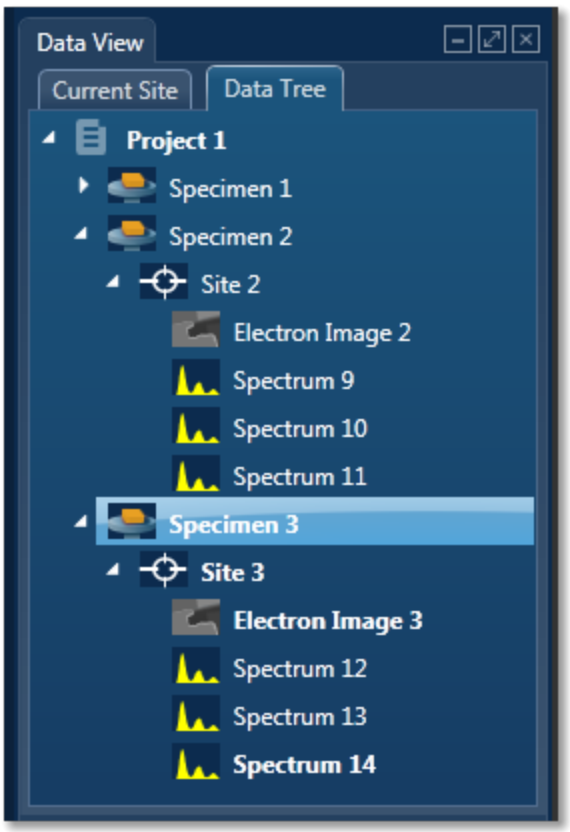
'I want to look for a particular list of elements. (I am not interested in any other elements)...I may want to see their labels on spectra, their X-ray maps or both....I want to see these even if the element is not present'.

' I know what's in my sample.... I want to look for a specific set of elements (I want to see these even if the element is not present.) .....but I would like to know if there is anything else in my sample too'.

You can define these elements' in the 'Pre-defined Elements' tab in the Describe Specimen step. If you want to save the Pre-defined Elements to a profile you must first press 'Save to Profile' button, then save the profile via the drop down menu. When you want to analyze your Specimen, you can load this profile or another profile by pressing the 'Load Profile' button in the Describe Specimen step as shown in the screen shot below:



Note that the 'Pre-defined Elements' are saved with the current Specimen. Changing the 'Predefined Elements' will only update the Pre-defined Elements in the current Specimen. It will not update any existing Specimens in the Project.



The current specimen is the one that you are presently analyzing/processing the data from. For example, in the screen shot above, Specimen 3 is the current specimen, Specimens 1 and 2 are the other specimens in the Project.

Identified Elements

The 'Identified Elements will include:

- Any Pre-defined Elements
- Elements identified by Auto ID
- Any additional Elements identified manually

If the 'Pre-defined Elements have been specified, these will be included for identifying and labeling peaks in the current spectrum automatically.

Note that the 'Identified Elements' are saved in the Spectrum.

'Perform Auto ID During Acquisition' option is enabled by default and can be deactivate by unchecking it in the Describe Specimen step as shown in the screen shot above. You can then AutoID at any time by pressing the button.

Additional peaks in the spectrum can be identified manually by using the 'Show Candidate Elements' tool in the Confirm Element step. Click on the question mark icon to select the Show Candidate Element tool. Position the cursor at the center of a peak by double-clicking with the mouse. The list of elements spectra corresponding to the energy at the cursor is displayed in the panel on the right. By highlighting an element in this list, you will see the markers showing all the lines for this element.

Note that the 'Identified Elements' will be quantified if you have selected the Current Spectrum, or the Fixed List and Current Spectrum Element List in the Quant Settings in the Calculate Composition step or EDS Quant Settings in the User Profile dialog.

N o t e

EDS Quant Settings are available in the User Profile Dialog accessed from the Tools menu. These settings are also available from the Calculate Composition step.

Fixed List

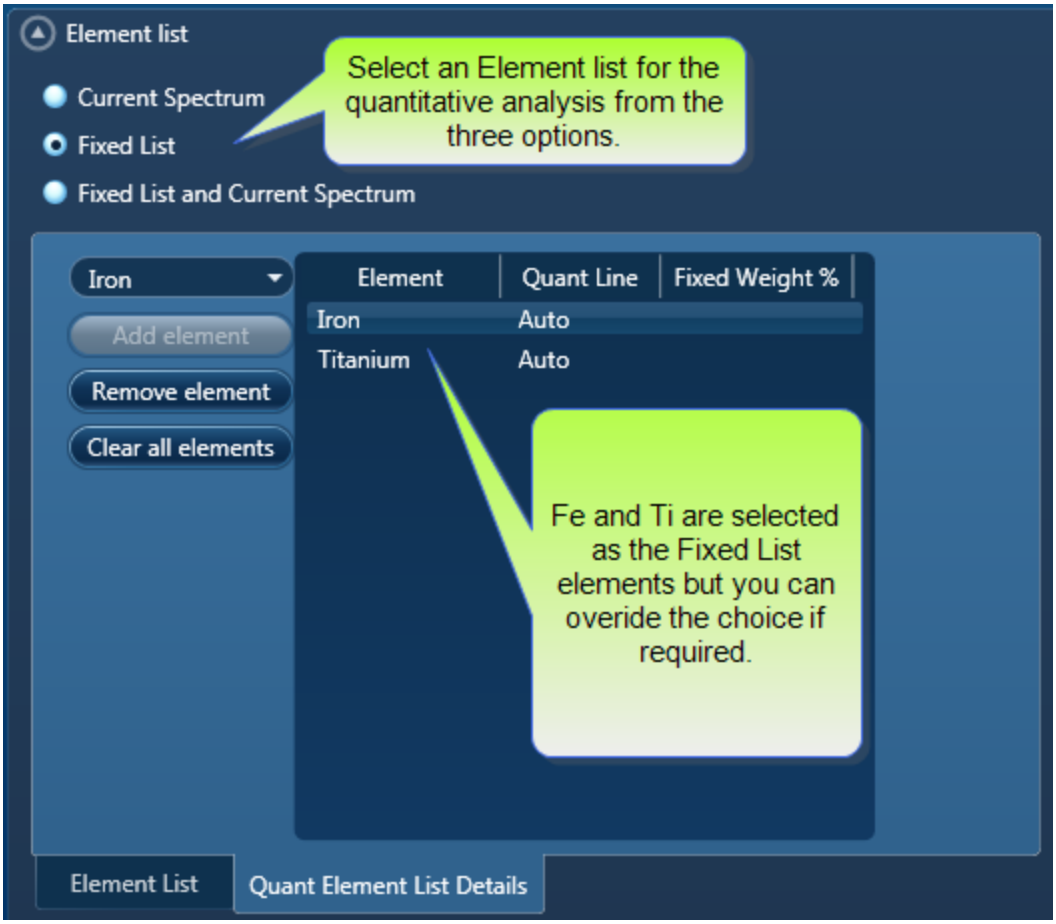
The elements in the 'Fixed List' are defined in the Quant Settings dialog which is available in the User Profile and the Calculate Composition window.

Note that the Fixed List is only used for calculating composition in quantitative analysis.

E x a m p l e

'I want to do quantitative analysis on my glass samples and want to compare results from one batch to another batch. I am always looking for the same specified list of elements'.

You can specify the Element List for Quant from the three available options in the Quant Settings dialog as shown in the screen shot below:



Current Spectrum

This list includes the Pre-defined Elements and elements identified by Auto ID and manually using the Candidate Element tool.

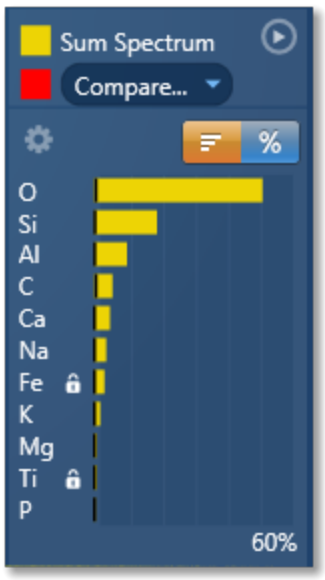
Fixed List

You select the Fixed List option if you know what elements you wish to quantify. Choose the elements from the drop-down list as shown in the screen shot above.

Fixed List and Current Spectrum

To quantify the elements in the above two lists, select the Fixed List and Current Spectrum option.

MiniQuant results table will clearly display which list is being used. A lock icon will be displayed against the 'Fixed List' elements as shown in the screen shot below:



In this example, Fe and Ti are selected in the Fixed List. The rest of the elements in the chart results are from the Current Spectrum because the Element List selected for quantification was 'Fixed List and Current Spectrum'.

Note that the 'Fixed List' is saved in a User Profile.

See also:

Describe Specimen on page 62

Acquire Spectra on page 105

Confirm Elements on page 129

Calculate Composition on page 141

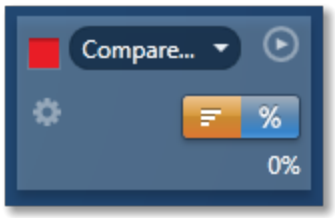
User Profile on page 17

Compare Spectra & MiniQuant Results

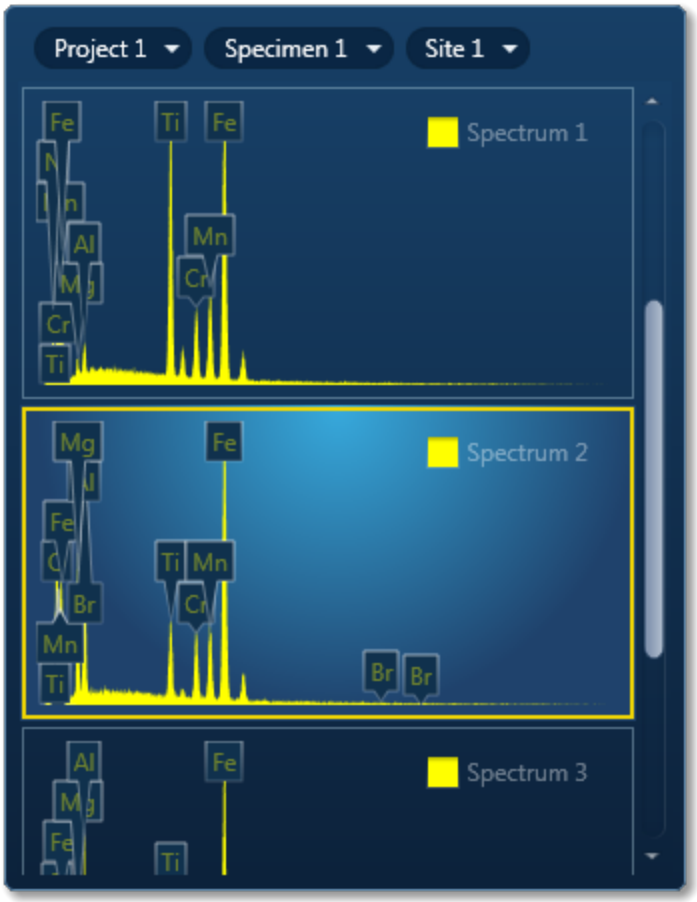
Real time Compare and instant MiniQuant options are available in the Acquire Spectra, Confirm Elements and Calculate Composition (Comparison of Results - Two Spectra template) steps. User can see results without having to move away from the acquisition mode. Using these options you can:

- See your results during analysis.
- Compare your current spectrum to a control spectrum during acquisition.
- View MiniQuant results in a table or a bar chart.

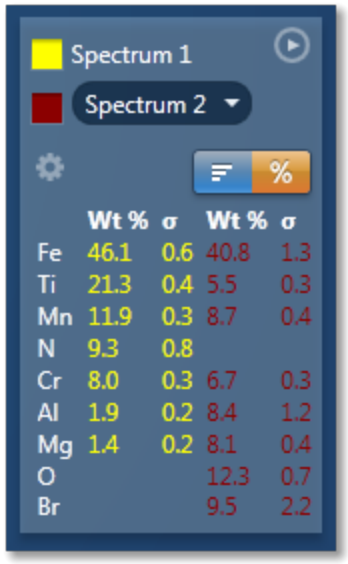
Click  in the top right corner of the Spectrum Viewer in Acquire Spectra, Confirm Elements or the Calculate Composition window to access the Compare & MiniQuant options:



In the above example, Spectrum 1 is the current spectrum and Spectrum 2 is the comparison spectrum. You can select the comparison spectrum from a Project currently available in the Data Tree. It can be from any Project, any Specimen and any Site of Interest currently available in the Data tree. To choose the comparison spectrum click on the down arrow (Spectrum 2 in the above example). Spectra available in the current Project, Specimen and Site of Interest are displayed as below:



Click on the spectrum in the display to select it for comparison. The selected spectrum will be overlaid as a line spectrum over the current spectrum. The MiniQuant results are displayed in a table as shown in the example below:

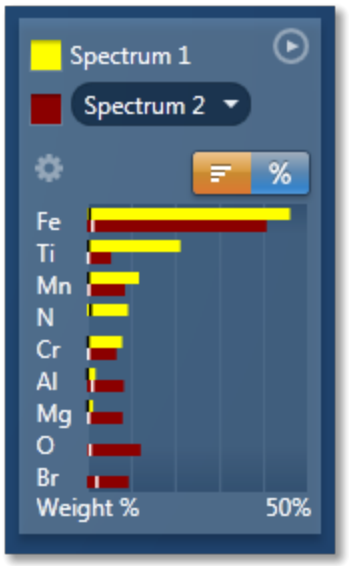


	Wt %	σ	Wt %	σ
Fe	46.1	0.6	40.8	1.3
Ti	21.3	0.4	5.5	0.3
Mn	11.9	0.3	8.7	0.4
N	9.3	0.8		
Cr	8.0	0.3	6.7	0.3
Al	1.9	0.2	8.4	1.2
Mg	1.4	0.2	8.1	0.4
O			12.3	0.7
Br			9.5	2.2

The results are displayed as wt% (weight%).

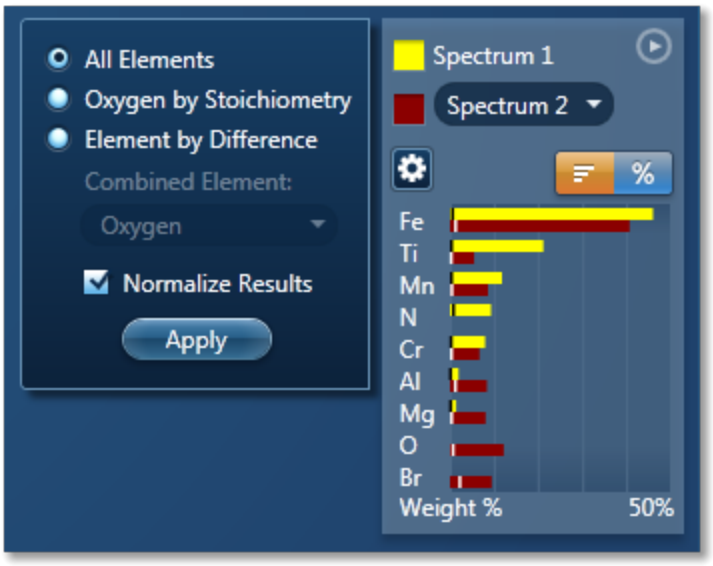
The statistical error is displayed as **σ** (weight% sigma) for the calculated wt%. It is the overall confidence figure for the analysis. You can use sigma to assess the results especially when an element is present at low concentration. For example, if an element concentration is 0.2 wt% and the **σ** is 0.12 wt%, the element might be detected at a statistically significant level if the acquisition time for the spectrum is extended. If the **σ** is 0.4 wt%, it is pointless to extend the acquisition time and it is safe to assume that the element if present, is at a level above the limit of detection for this technique.

Press  to display the results in a chart:



The sigma values are displayed as black or white vertical bands across the bars in the chart results as shown in the example above. In this case the full scale of the bar chart is 60%.

If you wish to change the MiniQuant Settings press  :



Make your selection by clicking on the radio button and then press the Apply button. The results will be updated immediately .

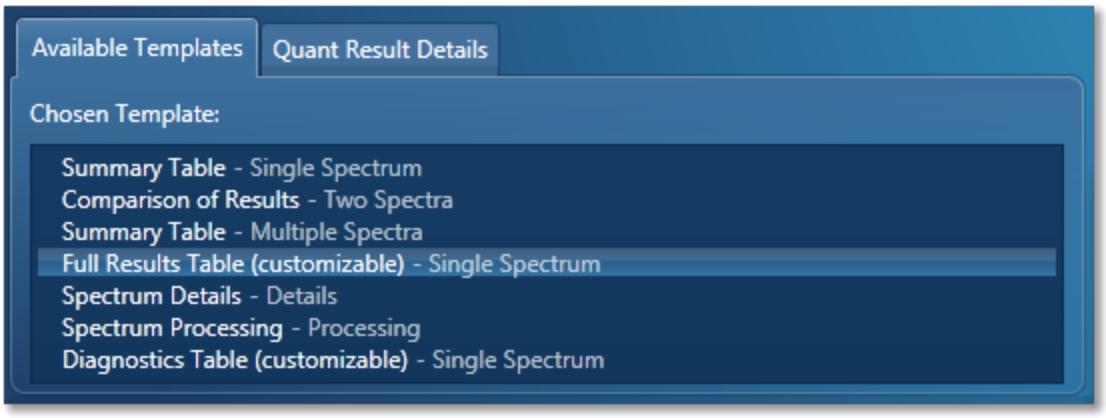
N o t e

The Quant Settings in the MiniQuant and Calculate Composition are the same. Updating one updates the other and vice versa.

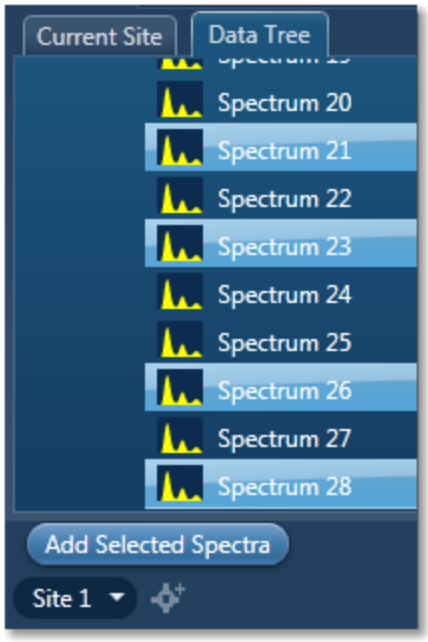
Calculate Composition

In this step you can view quant results in more detail using any of the 'Available Templates'.

To view result select the template that you wish to use:



- If you want to see a comprehensive set of results from a single spectrum, then choose the 'Full Results Table (customizable) - Single Spectrum' template and whichever spectrum is highlighted in the Data Tree will have its results shown in this template.
- To populate a multiple spectra template, hold the Ctrl key down while choosing spectra on the Data Tree and then press the 'Add Selected Spectra' button at the bottom of the Data Tree window.



- To compare quant results from two spectra, select 'Comparison of Results - Two Spectra' template. Then select the comparison spectrum from the Compare option in the 'Mini Quant and Compare' option. The compare spectrum will be overlaid on the current spectrum in the Spectrum Viewer. The quant results will be displayed in the table below.
- If you wish to change the Quant Settings press the Settings button to display the Quant Settings dialog. Apply the changes and close the dialog.
- Press the Requantify button to display the recalculated results.

Quant Results Details

You can see the settings used for calculating the composition in the Quant Results Details list box:

Parameter	Description
Label (Spectrum Label)	E.g., Spectrum 1
Element List Type	Current Spectrum, Fixed List or Combined List
Processing Options	All Elements, Element by Difference, Combined Element or Oxygen by Stoichiometry
Apply Coating Correction	Enabled or Disabled
Coating Element	E.g., Carbon
Coating Thickness	E.g., 15 nm
Coating Density	E.g., 2.25 g/cm3
Automatic Line Selection	Enabled or Disabled

Parameter	Description
Normalization	Enabled or Disabled
Thresholding	Enabled or Disabled
Deconvolution Elements	None/Selected
Factory Standards	Standardizations file supplied with the system
User Standards	Standardizations file defined by the user
Pulse Pile Up Correction	Enabled/Disabled
Detector File	Indicates file that has been used to characterize detector
Efficiency	Calculated/File based

Quant Results View

The information displayed in the Quant Results View depends on which template has been selected. You can view Spectrum Details, Spectrum Processing and Diagnostics table in addition to quant results.

See Also:

Quant Settings below

Element Lists on page 146

Compare Spectra & MiniQuant Results on page 150

Quant Settings

The Quant Settings are described below:

Processing Options

To make the correct selection, a little knowledge of the specimen is required. For example, can all elements in the specimen be detected and analyzed, or are you analyzing a mineral where it is more usual to calculate the oxygen present?

- **All Elements**

This option is used when processing spectra from specimens in which all elements yield X-rays which can be readily detected e.g., steels, alloys and other materials with insignificant amounts of elements lighter than sodium.

- **Element by Difference**

This option can be used if you can readily measure X-ray signal from all elements except one in the specimen. The omitted element is called the combined element. The concentration of the combined element is not measured, but it is calculated assuming that the difference between the analyzed total and 100% is due only to the presence of this element. Intensity corrections are calculated assuming the presence of this element. The total from this type of analysis is always 100%.

This option can be used when analyzing a specimen in which a significant quantity of a light element which cannot be detected, is known to be present. This method can also be used in cases where an element for which no standard is available is present.

- **Oxygen by Stoichiometry**

Use this option if you want the concentration of oxygen to be calculated assuming that it is bound by predefined stoichiometry to all the other analyzable elements. The stoichiometry is defined by the valency of the oxygen ions and the valencies of other measured elements:

  - **Number of Ions**

Enter the number of oxygen ions that are combined stoichiometrically to the other elements. The calculations are based on the number of oxygen ions and how many atoms there are in each unit cell.

  - **Valency**

When 'Oxygen by Stoichiometry' is selected, the option for choosing the valency for each analyzable element becomes available. The most common value for the valency of the element is displayed when you click on an element symbol on the periodic table. To use a different value, enter the new value in the Valency text box.

Normalize Results

When this option is selected the analytical total of an analysis carried out using All elements or Oxygen by Stoichiometry is forced to 100%.

Use of this needs care in interpreting the final result since if, for example, the element list is incomplete, there will be serious errors in the result, even though the total is 100%.

This is often used as an expedient where the beam current is unstable or the specimen is unpolished. With normalization, you need not worry about beam current fluctuations but you must take care not to omit any major elements from the element list because this will not be obvious in an analysis total which is forced to be 100%.

Element List

You can select a different type of element list depending on how you want your spectra/spectrum to be quantified:

- **Current Spectrum**

If this option is selected, each spectrum will be quantified using the elements confirmed in the Confirm Elements step for the current spectrum.

- **Fixed List**

Select this option if you wish to define a list of elements with which to quantify your spectra. For example you may only wish to quantify your spectra using certain elements if you are constantly quantifying similar spectra. Define your Fixed List using the Periodic Table. To include an ele-

ment in the list, click on the element symbol on the Periodic Table and press 

or double-click on the element symbol.

- **Fixed List and Current Spectrum**

Select this option when you know what elements there are in your specimen and you also wish to include any other element that may be present. You define your Fixed List using the Periodic Table as described in bullet number 2 above. The Confirmed Elements List is from the Current Spectrum. This list includes all the elements identified by AutoID and any other elements that may have been added to the Confirmed Element list manually. What elements are quantified when you select 'Fixed List and Current Spectrum' are shown in the examples below in a table:

	Fixed List	Current Spectrum	Combined List
Spectrum 1	Si, O	Si, O, Al, Ca	Si, O, Al, Ca
Spectrum 2	Si, O	B, N	Si, O, B, N

Quant Element List Details

From this tab you can view the details of each element in the list. The default setting is that the X-ray lines to be used for Quant are automatically selected. You can manually select the X-ray line for each element if you un-check the 'Automatic selection of line for all elements' option. You can check the 'Fixed weight %' option and enter the value.

Deconvolution Elements

Deconvolution elements may be used to select elements present in the spectrum that should not be quantified, but whose influence needs to be accounted for when processing the spectral data. For example elements present in an oxidation layer, or in a substrate layer.

If you wish to deconvolve elements from a spectrum, select the required element from the drop down list and press ‘Add element’. Further elements can be added or removed using Add element or Remove element respectively.

Selecting an element for deconvolution means the peaks will automatically be deconvolved from the spectrum but the element will normally not be quantified. The deconvolution element will only be quantified if its' composition is entered as fixed wt% or is calculated by stoichiometry or difference.

Threshold Quantitative Results

Quantitative results are displayed with +/- value which is one sigma (standard deviation) based on counting statistics. Typically, results which are less than 3 sigma have reduced significance and so it may be desirable to set them to zero. Thresholding may be applied so that results below

the selected sigmas are set to zero. Thresholding will also ensure that negative insignificant values, which sometimes result from trace element analysis, are set to zero.

To enable 'Threshold Quantitative Results', check this option in the Quant Settings.

The default value for Sigma is 3 which represents 99.7% confidence level.

Quant Standardizations

The system is supplied with factory standardizations. To use your own standards for quantitative analysis, you first need to acquire spectra from standards and perform at least one standardization using the Standardize step on the Optimize navigator. When you have done this your user file will be available to select for use by the "User" radio button under Quant standardizations in EDS Quant Settings. If the "Factory" button is selected, factory standardizations will be used for the calculation of quantitative results.

In the default "Quant Standardizations" file some low energy lines have been deliberately omitted because there are many potential sources of error for quantification (For example close overlaps, chemical shifts, anomalous excitation and absorption effects on individual lines, inaccurate absorption coefficients and presence of carbon and oxide layers that give large peaks at low kV) If you understand the issues you can still use your own standards to perform analysis for these lines. However, they have been omitted from the default file.

At low kV, fewer x-ray lines are excited and if the recommended line is not available, quantification is not possible. In this case the spectrum overlays cannot be calculated and will not appear in the Confirm Elements step. If you want to work at low kV the factory standardizations file “Quant Standardizations(Extended Set)” has additional low energy L and M lines that will allow you to obtain a concentration result and enable the spectrum overlays. You may find it convenient to use the same file at both high and low kV but it is important to realise that concentration estimates obtained using these extra low energy lines may sometimes be inaccurate.

Apply and Save

If you make a change to the Quant Settings and press 

, the settings are saved and the currently selected spectra are quantified. The quant results are updated immediately.

Save

If you make a change to the Quant Settings and press 

, the new settings are saved to be used when you do quantification next time.

Element Lists

Any list of elements in the **AZtec** software can be split into the following three categories:

- Pre-defined Elements - elements expected in specimen
- Identified Elements - typically based on automatic peak identification (Auto ID)
- Fixed List - used for Quantitative analysis

Pre-defined Elements

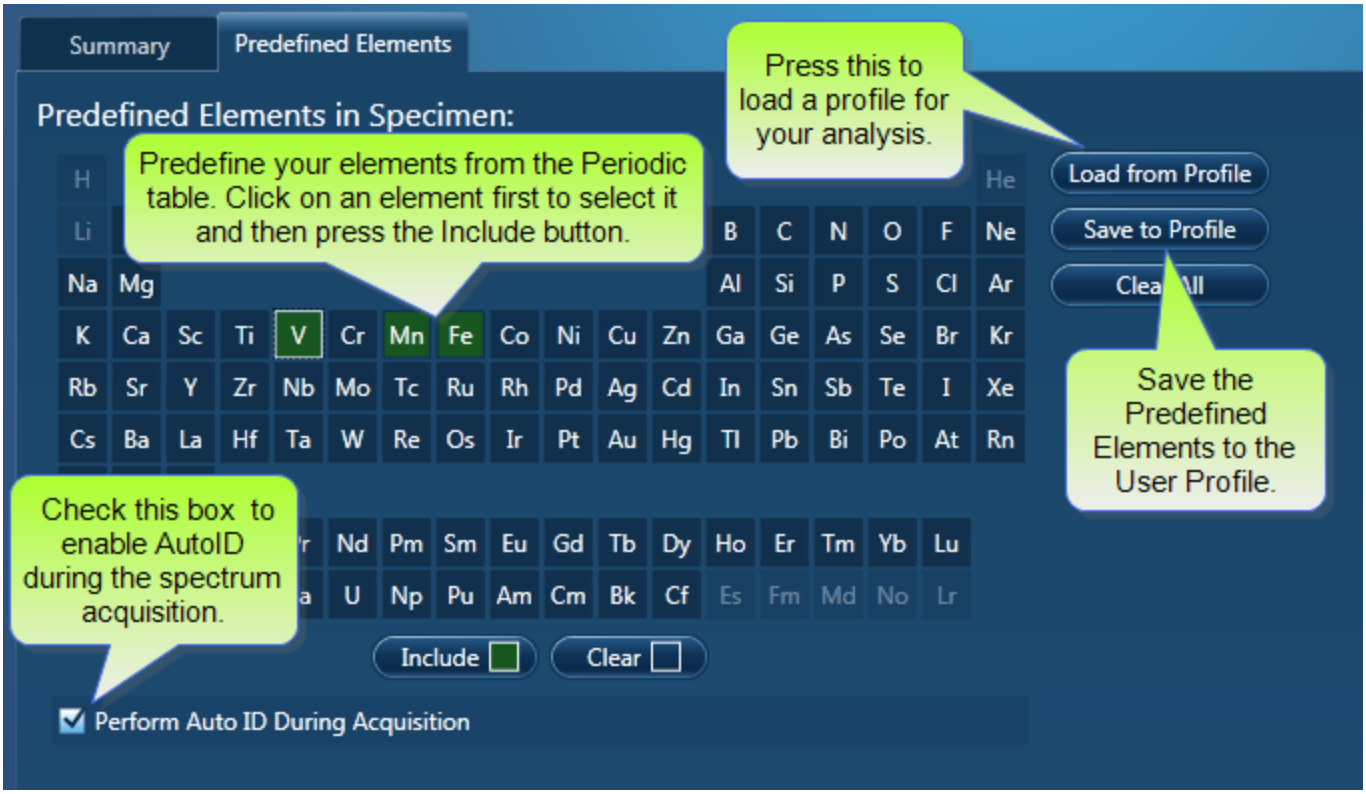
You may have prior knowledge of your Specimen and know what elements to look for.

Examples

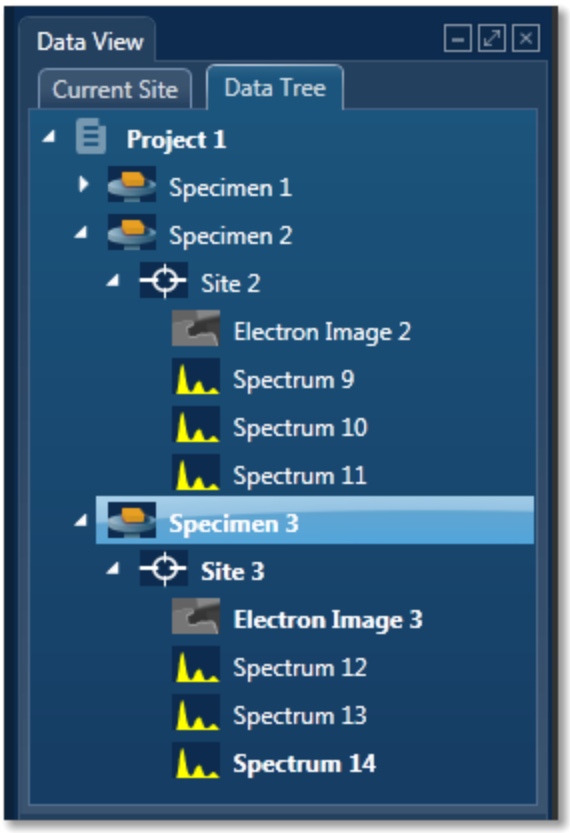
'I want to look for a particular list of elements. (I am not interested in any other elements)…I may want to see their labels on spectra, their X-ray maps or both….I want to see these even if the element is not present'.

' I know what's in my sample…. I want to look for a specific set of elements (I want to see these even if the element is not present.) …..but I would like to know if there is anything else in my sample too'.

You can define these elements' in the 'Pre-defined Elements' tab in the Describe Specimen step. If you want to save the Pre-defined Elements to a profile you must first press 'Save to Profile' button, then save the profile via the drop down menu. When you want to analyze your Specimen, you can load this profile or another profile by pressing the 'Load Profile' button in the Describe Specimen step as shown in the screen shot below:



Note that the 'Pre-defined Elements' are saved with the current Specimen. Changing the 'Predefined Elements' will only update the Pre-defined Elements in the current Specimen. It will not update any existing Specimens in the Project.



The current specimen is the one that you are presently analyzing/processing the data from. For example, in the screen shot above, Specimen 3 is the current specimen, Specimens 1 and 2 are the other specimens in the Project.

Identified Elements

The 'Identified Elements will include:

- Any Pre-defined Elements
- Elements identified by Auto ID
- Any additional Elements identified manually

If the 'Pre-defined Elements have been specified, these will be included for identifying and labeling peaks in the current spectrum automatically.

Note that the 'Identified Elements' are saved in the Spectrum.

'Perform Auto ID During Acquisition' option is enabled by default and can be deactivate by unchecking it in the Describe Specimen step as shown in the screen shot above. You can then AutoID at any time by pressing the button.

Additional peaks in the spectrum can be identified manually by using the 'Show Candidate Elements' tool in the Confirm Element step. Click on the question mark icon to select the Show Candidate Element tool. Position the cursor at the center of a peak by double-clicking with the mouse. The list of elements spectra corresponding to the energy at the cursor is displayed in the panel on the right. By highlighting an element in this list, you will see the markers showing all the lines for this element.

Note that the 'Identified Elements' will be quantified if you have selected the Current Spectrum, or the Fixed List and Current Spectrum Element List in the Quant Settings in the Calculate Composition step or EDS Quant Settings in the User Profile dialog.

Note

EDS Quant Settings are available in the User Profile Dialog accessed from the Tools menu. These settings are also available from the Calculate Composition step.

Fixed List

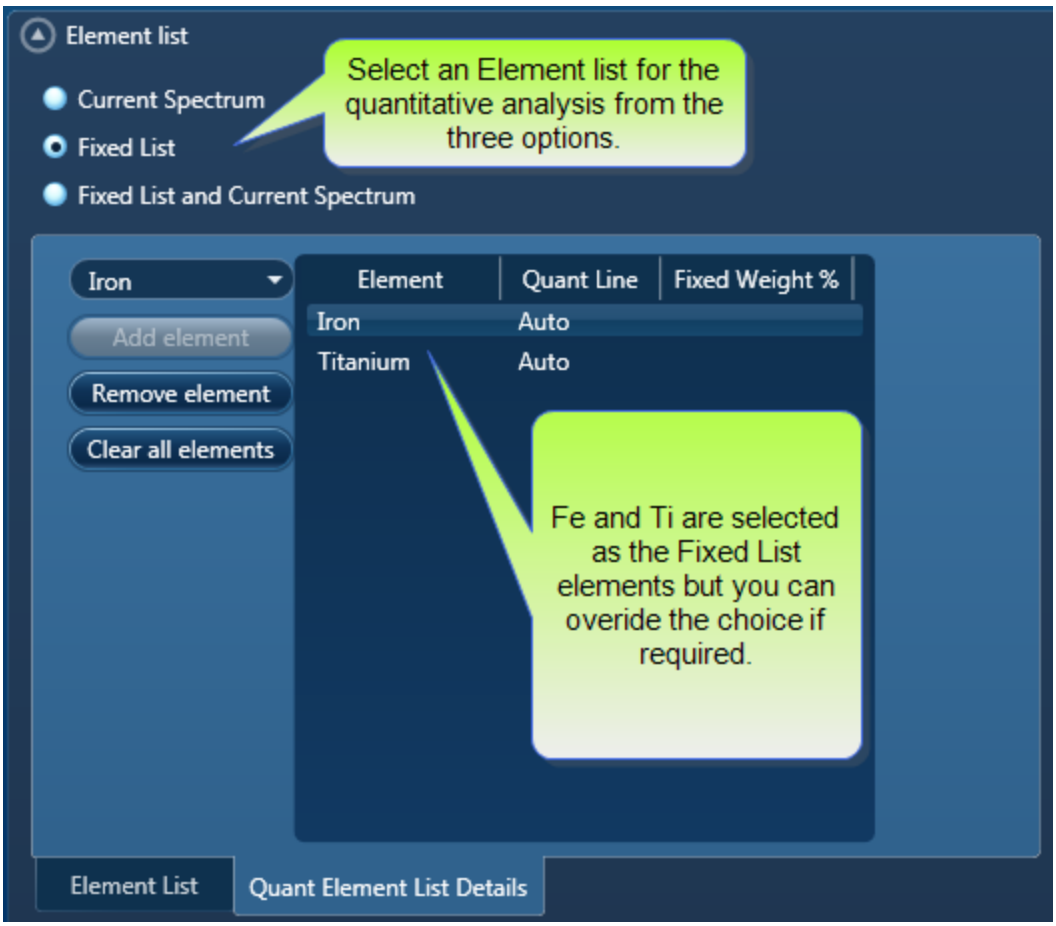
The elements in the 'Fixed List' are defined in the Quant Settings dialog which is available in the User Profile and the Calculate Composition window.

Note that the Fixed List is only used for calculating composition in quantitative analysis.

Example

'I want to do quantitative analysis on my glass samples and want to compare results from one batch to another batch. I am always looking for the same specified list of elements'.

You can specify the Element List for Quant from the three available options in the Quant Settings dialog as shown in the screen shot below:



Current Spectrum

This list includes the Pre-defined Elements and elements identified by Auto ID and manually using the Candidate Element tool.

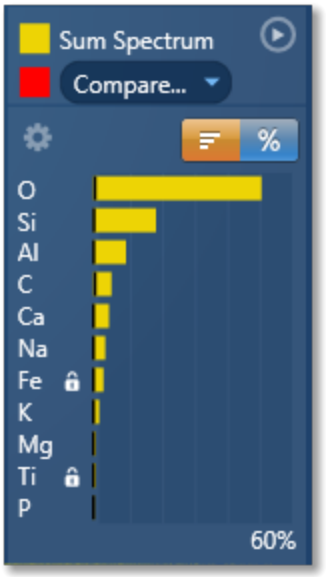
Fixed List

You select the Fixed List option if you know what elements you wish to quantify. Choose the elements from the drop-down list as shown in the screen shot above.

Fixed List and Current Spectrum

To quantify the elements in the above two lists, select the Fixed List and Current Spectrum option.

MiniQuant results table will clearly display which list is being used. A lock icon will be displayed against the 'Fixed List' elements as shown in the screen shot below:



In this example, Fe and Ti are selected in the Fixed List. The rest of the elements in the chart results are from the Current Spectrum because the Element List selected for quantification was 'Fixed List and Current Spectrum'.

Note that the 'Fixed List' is saved in a User Profile.

See also:

Describe Specimen on page 62

Acquire Spectra on page 105

Confirm Elements on page 129

Calculate Composition on page 141

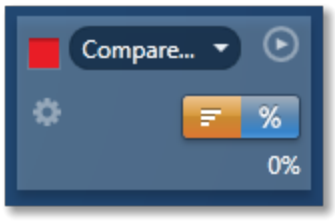
User Profile on page 17

Compare Spectra & MiniQuant Results

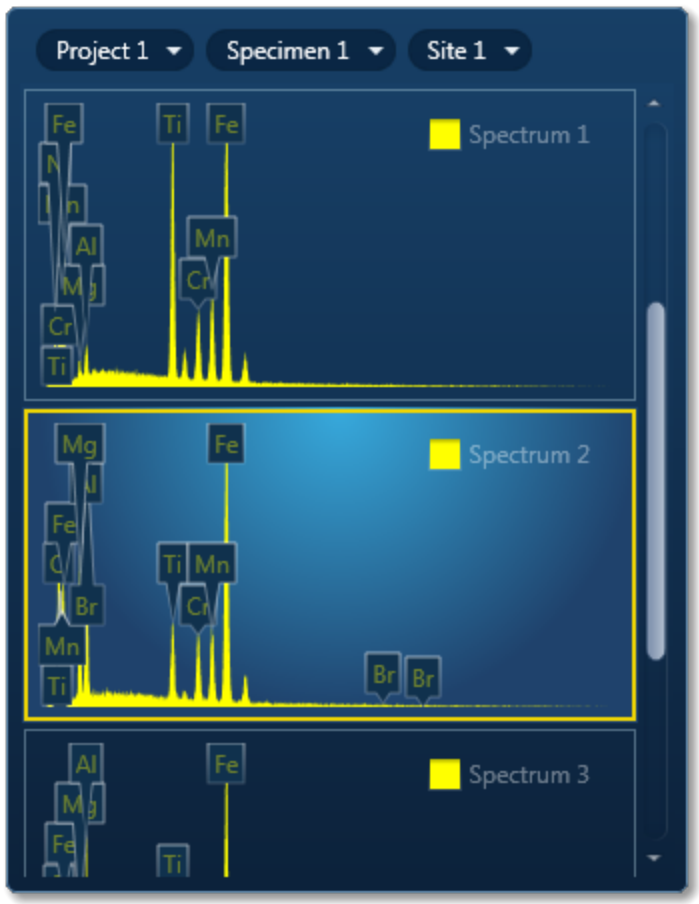
Real time Compare and instant MiniQuant options are available in the Acquire Spectra, Confirm Elements and Calculate Composition (Comparison of Results - Two Spectra template) steps. User can see results without having to move away from the acquisition mode. Using these options you can:

- See your results during analysis.
- Compare your current spectrum to a control spectrum during acquisition.
- View MiniQuant results in a table or a bar chart.

Click  in the top right corner of the Spectrum Viewer in Acquire Spectra, Confirm Elements or the Calculate Composition window to access the Compare & MiniQuant options:



In the above example, Spectrum 1 is the current spectrum and Spectrum 2 is the comparison spectrum. You can select the comparison spectrum from a Project currently available in the Data Tree. It can be from any Project, any Specimen and any Site of Interest currently available in the Data tree. To choose the comparison spectrum click on the down arrow (Spectrum 2 in the above example). Spectra available in the current Project, Specimen and Site of Interest are displayed as below:

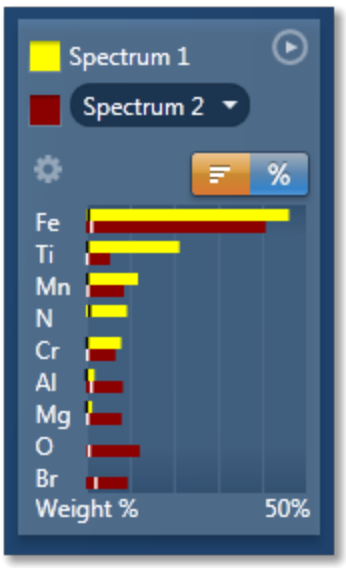


Click on the spectrum in the display to select it for comparison. The selected spectrum will be overlaid as a line spectrum over the current spectrum. The MiniQuant results are displayed in a table as shown in the example below:

The results are displayed as wt% (weight%).

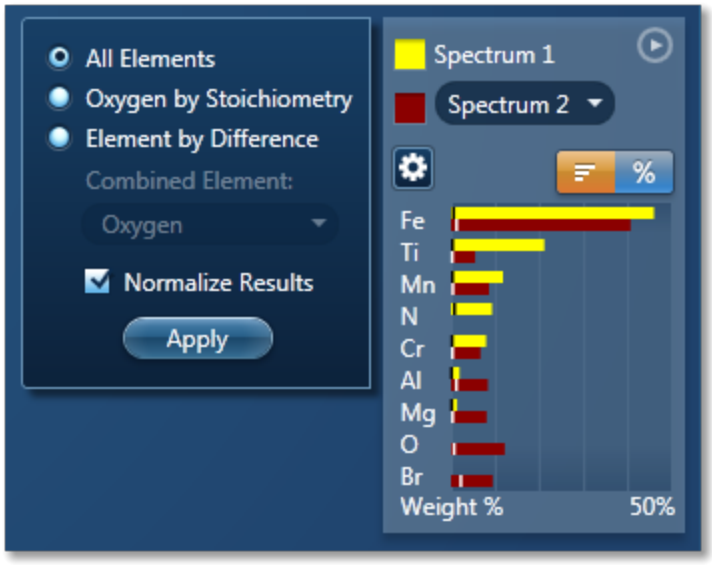
The statistical error is displayed as **σ** (weight% sigma) for the calculated wt%. It is the overall confidence figure for the analysis. You can use sigma to assess the results especially when an element is present at low concentration. For example, if an element concentration is 0.2 wt% and the **σ** is 0.12 wt%, the element might be detected at a statistically significant level if the acquisition time for the spectrum is extended. If the **σ** is 0.4 wt%, it is pointless to extend the acquisition time and it is safe to assume that the element if present, is at a level above the limit of detection for this technique.

Press  to display the results in a chart:



The sigma values are displayed as black or white vertical bands across the bars in the chart results as shown in the example above. In this case the full scale of the bar chart is 60%.

If you wish to change the MiniQuant Settings press  :



Make your selection by clicking on the radio button and then press the Apply button. The results will be updated immediately .

N o t e

The Quant Settings in the MiniQuant and Calculate Composition are the same. Updating one updates the other and vice versa.

Point & ID - Custom

Acquire And Confirm

In Acquire and Confirm step, four operations are combined into one window. Acquire and Confirm is the main step of the Point & ID Navigator in the Custom mode. It is aimed for users who do not require any guidance during their analyses. The workspace is divided into four quadrants. Each quadrant represents an application. For example, Scan Image is located in the top left quadrant, Acquire Spectra in the top right quadrant, Quant Results in the bottom left quadrant and Confirm Elements in the bottom right quadrant.

Press the relevant button in the toolbar,  to switch off/on an application from the view in any quadrant.

Press  to un-dock a quadrant view into a free floating window located in the top right corner of the view. Press  to switch it into a full screen view.

To re-dock the free floating window back into the main application window press  .

Each application has identical functionality as its counterpart in the Guided Navigator. To get help on each application follow the links below:

Scan Image on page 207

Acquire Spectra on page 105

Confirm Elements on page 129

Calculate Composition on page 141

Recommended Way Of Working In Point & ID - Custom Mode

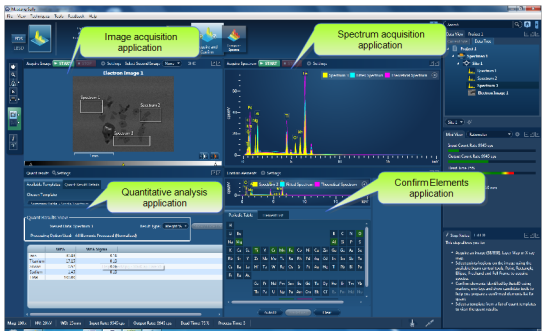
In the Custom mode, four smart components are available in one window. You can acquire, review, confirm and process data in one window. You do not need to move away from it during the analysis.

The four smart components are docked in the workspace as the default layout. Each component can be un-docked and have it as a free floating window. It can be resized and dragged to a second monitor to be viewed in full screen. There is a great deal of flexibility in the user interface to customize the layout to suit your requirements.

EXAMPLE

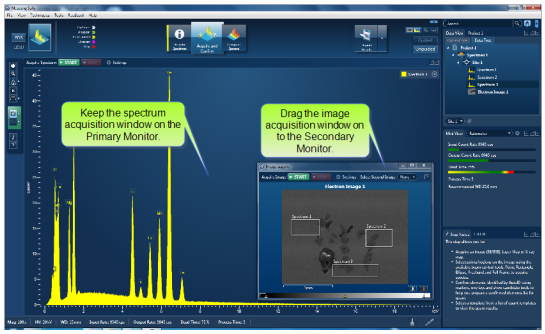
One way of working in the Custom mode is described with screen shots here.

The four components in the Acquire and Confirm window are docked in the four quadrants of the work space as shown in the screen shot below:



1. Press  in the top left quadrant to undock the Acquire Image window. The upper two quadrants are now filled with the Acquire Spectrum window.

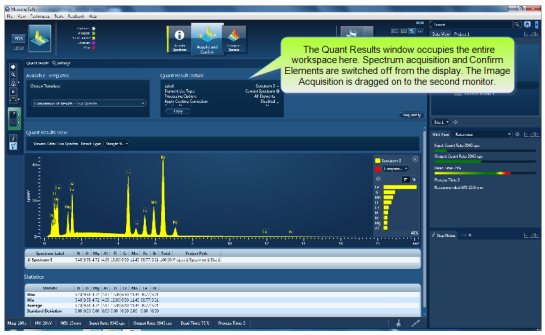
2. Click with the left mouse button in the title bar of the floating Acquire Image window and drag it to a second monitor.



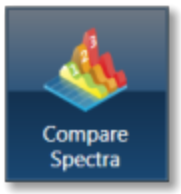
3. Toggle off the % button  in the toolbar near the top right of the main application to remove the Quant Results window from the display. The Confirm Elements window will slide in under the Acquire Spectrum window as shown in the screen shot below:

4. The Acquire Spectrum window can be removed from the display if you need to maximize the Confirm Elements display as shown below:

5. Once you have confirmed the elements, you may not require the Confirm Elements window. You can remove it from the display if you wish.
6. To be able to view the Quant Results, switch the Quant Results display on from the toolbar:



Compare Spectra



This step in both the Point & ID and Analyzer Navigators allows you to compare spectra acquired from different sites of interest and specimens from the currently opened projects .

You can compare spectra acquired using different settings for example energy ranges (0-10, 0-20 or 0-40 keV) and number of channels (1024, 2048 or 4096).

Spectra associated with the current Site can be added to the Compare table by holding down the control key and pressing Add Selected Spectra. Note that if you have acquired the spectra in Point & ID, the positions of all the spectra associated with the current Site of Interest are displayed on the image. You can add spectra from any Project, Specimen and Site of Interest from the Data tree into this table.

Select which spectra you wish to compare by selecting them individually from the Data Tree, Press 'Add Selected Spectra'. This will add all the spectra you wish to compare into the 'Compare' table:

If you want to remove any spectra from the table, highlight the spectrum and press 

You can choose which of the available spectra you wish all the others to be compared to by selecting your reference spectrum from the compare table and pressing Select Reference Spectrum.

Settings

You can change the color of individual spectra by selecting the color from the drop down list in the compare table.

To change the line thickness of individual spectra, select it from the Line Thickness drop down list in the Compare table.

To apply the chosen line thickness globally, select it from the Compare Spectra Settings from 

near the top of the Compare viewer.

Normalize

Normalize is a useful function for comparing spectra acquired using different input X-ray count rates such as spectra acquired with two different beam currents. Note that you can normalize spectra using a point or a region.

Normalize Spectra (Point)

• Select this option from the toolbar near the top left of the Compare Spectra screen.

• Double-click in the spectrum to set a normalization point along the X-axis.

• A window is drawn on either side of this point. The spectra in the Compare viewer are scaled to the average value of cps/eV (Y-axis) in the window.

Normalize Spectra (Region)

• Select this option from the toolbar near the top left of the Compare Spectra screen.

• Click and drag to set a normalization region along the X-axis.

• The spectra in the Compare viewer are scaled to the average value of cps/eV (Y-axis) in the normalization region selected in the previous step.

Smooth

The Smooth function is available from the context menus of the spectrum viewer. This is useful when comparing spectra where small differences may be obscured by statistical scatter.

The smooth function applies an energy-dependent filter to the spectrum. This has the effect of slightly broadening the peaks and also filtering out the rapid fluctuations due to statistics. Statistical fluctuations can sometimes appear like a real peak. When it is difficult to decide whether a peak is present or not, the smooth function substantially reduces the statistical fluctuation so that any real peak becomes more visible.

Map - Guided

Acquire Map Data

In this step, you can acquire X-ray maps from the full frame or selected regions of the specimen. The maps show the spatial distribution of all elements in the specimen. The results can be displayed as a Layered Image, where colors for each element are mixed together and overlaid on the electron image, or as individual maps. Spectra from selected regions can be reconstructed during or after data acquisition. Generating a Layered Image or X-ray maps can be a very useful way to find out what is going on in your specimen.

EXAMPLE

'I want to know where certain key elements are distributed over a defect. Once I have this information, I can determine what caused the defect and advise my production department.'

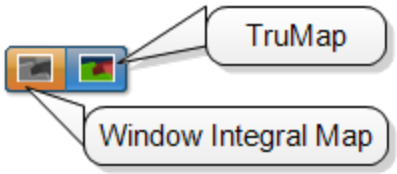
How to Acquire and Manipulate Maps

There are two different types of maps that you can acquire, Window Integral Maps or TruMaps.

Historically, Window Integral Maps have been the standard mode for X-ray maps. These are ideal when there are no overlapping peaks and you are not looking for trace elements in your specimen.

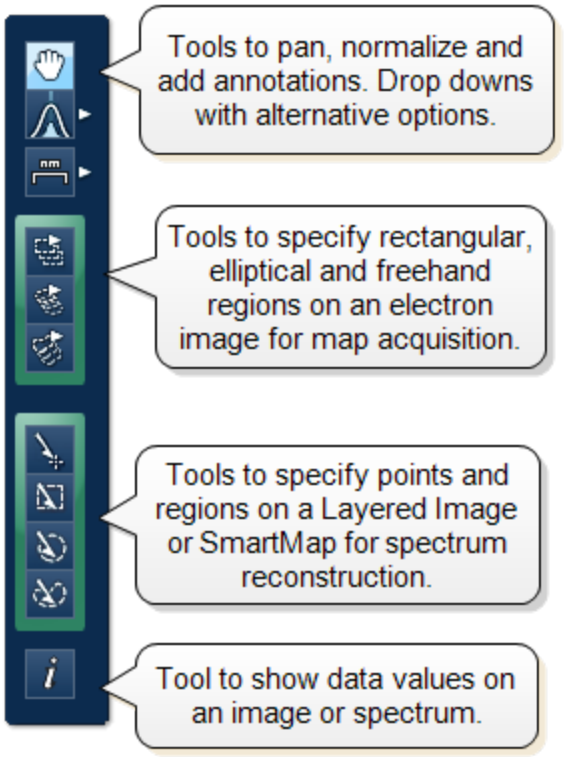
The second mode of mapping is with TruMaps which are ideal for specimen containing elements with overlapping peaks, and removes false variations due to X-ray background.

You can easily switch between the two modes of mapping during acquisition by pressing the appropriate button located at the bottom of the element map workspace:

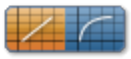


- Select the acquisition parameters from the Settings cog on the acquisition toolbar, and press 

to acquire map data from the full frame.
- To acquire maps from a region, select a map acquisition tool from Rectangle, Ellipse and Freehand tools available from the toolbar:

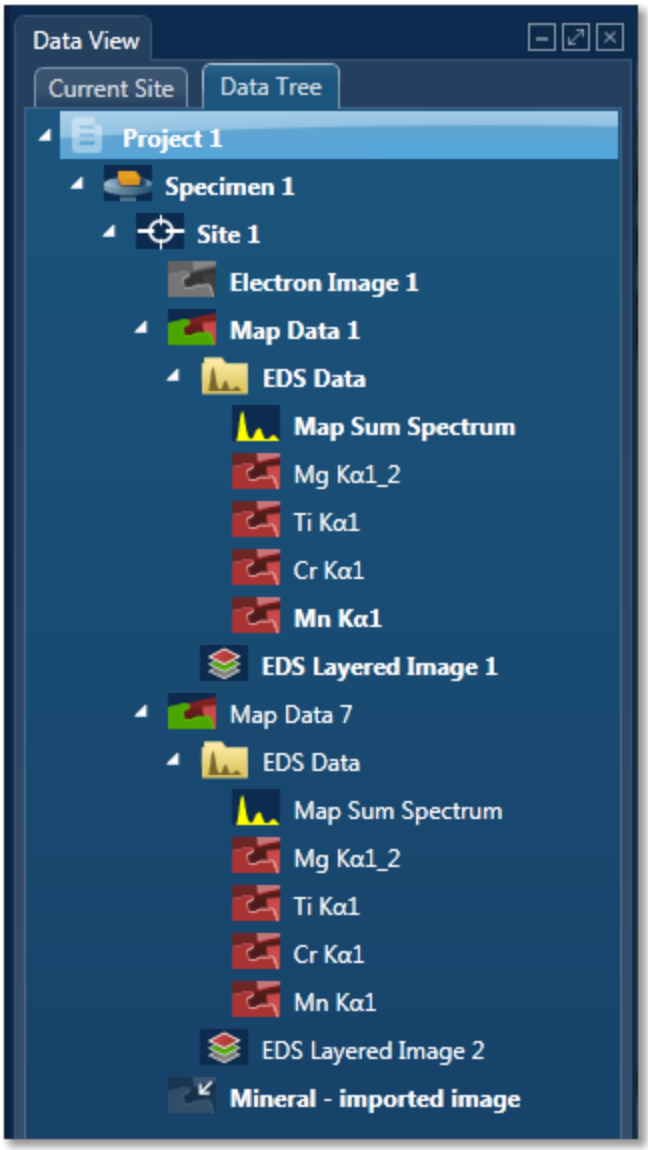


- Click on the image and drag with the left mouse to outline a region on the image. Maps will be acquired from the scanned region. During TruMap acquisition, a progressing green line is the map acquisition line followed by a yellow map processing line.
- A layered image, element maps and an electron image/s (SE/BSE) are displayed. You can choose how you wish to view your data from Standard, Interactive or Summary view available from the drop-down list.
- Adjust the slider bar to choose the number of maps per row.
- The layered image allows you to see the X-ray maps overlaid on the electron image.
- You can add or remove an X-ray map from the layered Image (combined Electron and X-ray map image) by toggling the Layered Image icon in the top left hand corner of each map.
- If you have lots of maps, it may be useful to minimize some of them pressing the minimize icon in the top right hand corner of each map.
- You may want to delete a map from the analysis completely. In which case press the delete icon in the top right hand corner of each map . This means this element will not be identified automatically (AutoID) and will be excluded from the current analysis. Note: If an element is present in a specimen, deleting or excluding it will affect the TruMap results.
- In the map display settings you can sort maps alphabetically, by atomic number or by maximum map intensity. You can also smooth maps by choosing the smoothing level from the Settings.

- Using the Auto Brightness and Gamma buttons  on the bottom right hand corner of the Map display window allows you to change the Brightness/Contrast and Gamma for all the maps. The Auto Brightness button optimizes the maps to give the best Layered Image and the Auto Gamma enables you to see all the map data including background noise.
- You can choose the color for your maps, adjust intensities and decide which maps to add to the Layered image . Alternatively, you can let the software do this automatically. Pressing the AutoLayer button  (which is located in the bottom right hand corner of the Map Display window) will automatically scale and color all the maps and select the best ones to provide an effective color image that delineates regions of different composition. Maps will be auto-brightness corrected and those that show similar structure will be assigned the same color. Maps that are very noisy will be shown in grey. The most significant map for each assigned color will be added to the Layered Image. See AutoLayer on page 173 for detailed information.

Data from Map Acquisition

The Data Tree gets populated with the new items as data is being acquired as shown in the screen shot below:



Electron image

It can be a secondary electron image (SE) or backscatter electron image (BSE). Appropriate detector hardware needs to be installed. You can also import an image into the Project.

Map Data

The EDS and EBSD Map data are contained in the Map Data folder. The EDS Data folder contains Map Sum Spectrum and X-ray Element Maps.

X-ray Element Maps

Two modes of mapping are available, Window Integral Maps and TruMaps. Press the appropriate button to select the mapping mode from  located at the bottom of the workspace.

Standard Window Integral maps (counts in the energy window) are acquired for the element list chosen for analysis. These are raw X-ray maps which are not corrected for background or peak overlaps.

Second mode of mapping is TruMap. You can process the map data as TruMaps which are corrected for background and peak overlaps.

EDS Layered Image

It is a composite image generated by overlaying selected X-ray maps on top of the electron image.

Viewing and Manipulating Maps

You can choose how you wish to view your data. Various tools are available to manipulate and view the X-ray maps. .

Map Size

You can choose the number of maps per row using the slider bar for displaying maps you wish to view in the Standard and Interactive display mode.

Display Modes

Maps can be viewed in three different display modes available from the drop-down list on the Display toolbar:

- Standard
- Interactive

In the Interactive mode, you can change the color of individual maps from the Hue drop-down list. The Layer Mode can also be chosen from Mix and Overlay modes available from the electron image.

- Summary

In the Summary view, you see details of the energy window and X-ray line used for each map in addition to other details such as Layer Name, Source (AutoID or User), Map Color and if it is selected for the Layered Image. See the screen shot below:

Link/Unlink

Press  to link images for manipulation of all layers using the Pan or Zoom control.

Press  to unlink images. You can manipulate individual layers using Pan or Zoom control.

Brightness and Contrast

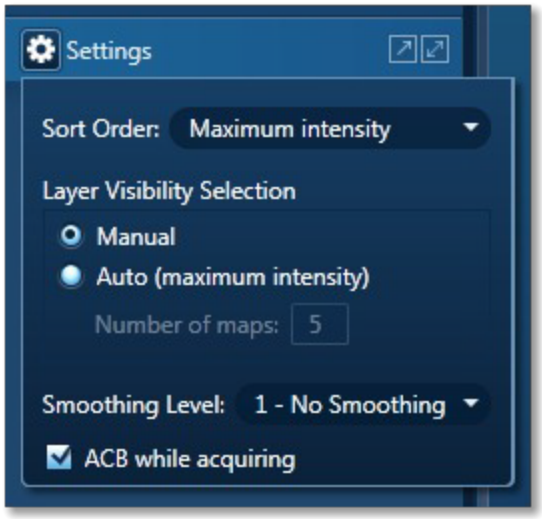
You can adjust the brightness and contrast of the currently selected image or map. Press  on the Display toolbar to open the Brightness and Contrast dialog.

Auto Brightness and Auto Gamma

Using the Auto brightness and Gamma buttons  on the bottom right hand corner of the Map display window allows you to change the Brightness/Contrast and Gamma for all the maps. The Auto Brightness button optimizes the maps to give the best Layered Image and the Auto Gamma enables you to see all the map data including background noise.

Element Maps View - Settings

You can manipulate and view the data by using various parameters available in the Settings:



Sort Order

There are three different ways of sorting maps:

Alphabetically

By atomic number

By maximum intensity in map - sorts on the value of the brightest pixel in cps.

Layer Visibility Selection

You can choose how the visibility of layers selected in the layered image. There are two options: Manual and Automatic. In the Manual mode, you must select which X-ray maps to be included in the layered image.

In the Automatic mode, first N maps (Number of Map that you entered) are selected by the maximum intensity.

Smoothing Level

The maps may contain a lot of statistical noise if there is not sufficient data. The noise can mask the distribution of elements in the maps. You can filter out some of this noise by applying Smoothing Level. This operation applies a lowpass filter to an image to smooth the data.

Smoothing Level, 3X3

The lowpass filter uses the following 3x3 kernel:

1/9 1/9 1/9

1/9 1/9 1/9

1/9 1/9 1/9

Smoothing Level, 5x5

The lowpass filter uses the following 5x5 kernel:

1/25 1/25 1/25 1/25 1/25

1/25 1/25 1/25 1/25 1/25

1/25 1/25 1/25 1/25 1/25

1/25 1/25 1/25 1/25 1/25

1/25 1/25 1/25 1/25 1/25

ACB While Acquiring

Check this option if you wish to apply automatic brightness or automatic gamma to maps during acquisition depending on your pre-selection of Auto Brightness or Auto Gamma.

See also:

Acquire Map Data - Settings below

Context Menu - Map Viewer on page 174

Acquire Map Data - Settings

The settings cog is located near the top of the Acquire Map Data screen. Clicking on it with the mouse displays the available settings:

Resolution

You can set the resolution of your maps by choosing the number of pixels in the X dimension over which the beam scans. The number of pixels in the Y dimension will depend on the aspect ratio of your microscope image.

If you are collecting X-ray data from the entire image using the number of pixels used will be the number set in the map resolution option.

If you define an area using the rectangle, Ellipse or Freehand tool X-ray data will be collected from only this defined area with a proportional number of pixels.

Acquisition Time

There are two options available for maps acquisition time:

Until Stopped

If you choose this option the system will carry on acquiring data until you stop it.

Fixed Duration

You can choose number of frames you wish to acquire by entering the number in the Frame Count dialog.

Number of Channels

Select the number of channels from the drop down list of 1024 and 2048 with which you display the spectrum. The number of eV/channel will depend on both the energy range and the number of channels you select.

Energy Range (keV)	Number of Channels	eV/channel
0-10	2048	5
0-10	1024	10
0-20	2048	10
0-20	1024	20
0-40	2048	20
0-40	1024	40

In the Auto mode, the **AZtec** system checks for the energy range selected and sets the appropriate number of channels.

Energy Range (keV)

Select a spectrum energy range from the available options of Auto, 0-10, 0-20 or 0-40 keV from the Energy Range drop down list.

The appropriate energy range should be selected in conjunction with the current microscope accelerating voltage. If the accelerating voltage is above 10 kV, in order to view lines which may

be excited above 10 keV, the 20 keV range should be chosen. Below 10 kV, it may be more appropriate to choose the 10 keV range since no lines above 10 keV will be excited.

In the Auto mode, the **AZtec** system checks for the accelerating voltage set on the microscope and selects a suitable energy range in the software.

Process Time

Select the Process Time from the drop-down list of Process Times, Default and 1 to 6. The Process time is the length of time spent reducing noise from the X-ray signal coming from the ED detector during processing. By selecting different Process times it is possible to reduce differing amounts of noise. The longer the Process time, the lower the noise. If noise is minimized, the resolution of the peak displayed in the spectrum is improved, in other words, the peak is narrower and it becomes easier to separate or resolve, from another peak that may be close by in energy.

If Default is selected, the Process Time is automatically set to a suitable value.

There is a trade off between the Process time that is used, and the speed at which data can be acquired into the X-ray spectrum. Process time 1 is the shortest, and as such, gives the highest X-ray acquisition rates, but at some cost to resolution. Process time 6 is the longest, and gives the highest resolution, but at some cost to maximum acquisition rate. The longer the Process time, the slower data can be acquired, i.e. the higher the system Deadtime will be for a given input count rate. (The input rate is not affected by the pulse processor).

Pixel Dwell Time (µs)

The default value for dwell time per pixel is 100 µs.

Frame Live Time (s)

The value of frame live time depends on the map resolution and pixel dwell time.

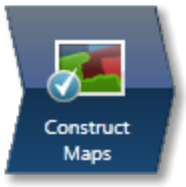
Brightness, Contrast And Gamma Controls

You can adjust the brightness and contrast of the currently selected image or map. Press  on the Display toolbar to open the Brightness and Contrast dialog.

Auto Brightness and Auto Gamma

Using the Auto brightness and Gamma buttons  on the bottom right hand corner of the Map display window allows you to change the Brightness/Contrast and Gamma for all the maps. The Auto Brightness button optimizes the maps to give the best Layered Image and the Auto Gamma enables you to see all the map data including background noise.

Construct Maps



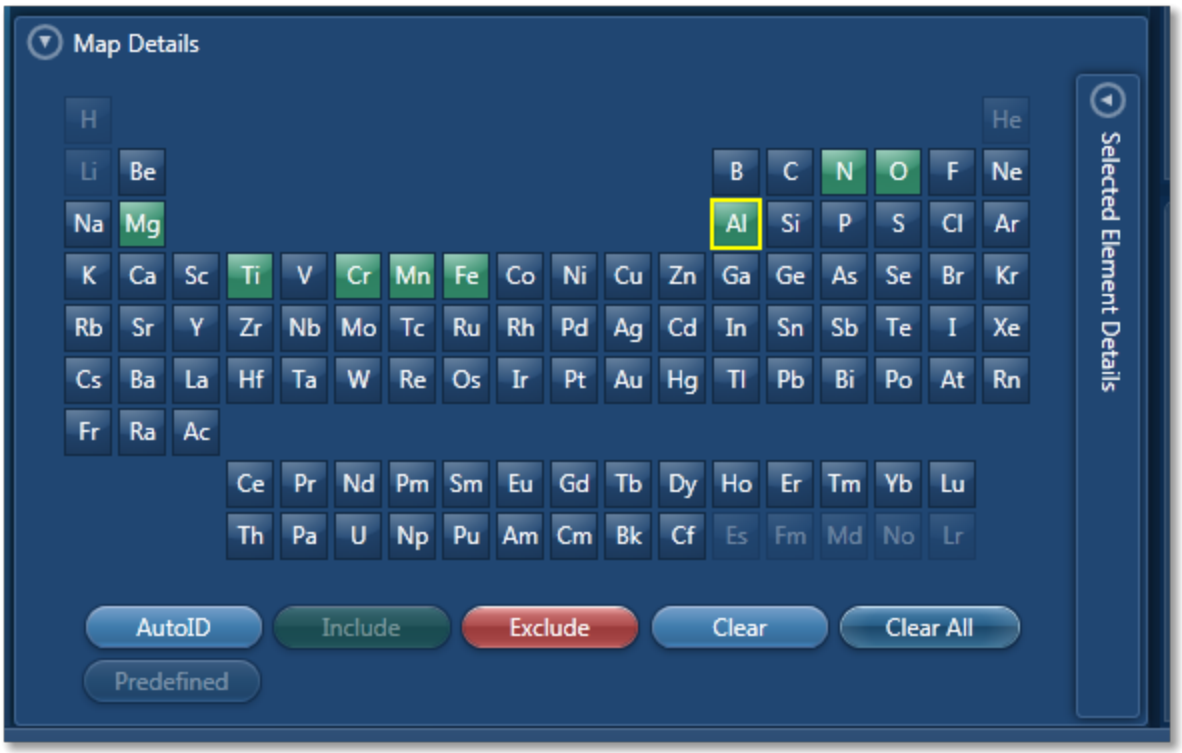
In this step, you can select which elements to map and which ones to exclude.

You can change the default X-ray line used for Window Integral Maps for any given element. It is also possible to define energy windows whose widths you can specify yourself rather than using the auto width calculation.

Tools are provided to interrogate the map data to confirm the elemental composition of user specified areas of interest. You can navigate to the Confirm Elements step from within the Construct Maps step.

Map Details

Map Details dialog allows you to choose elements you wish to include or exclude for mapping. You may have pre-defined the known elements in your specimen in the Describe Specimen step. You can map these elements by pressing the Pre-defined button in the Map Details dialog. There may be unexpected peaks in the spectrum. You can use AutoID for selecting elements for mapping.You can access Map Details option from  located at the bottom of the workspace:



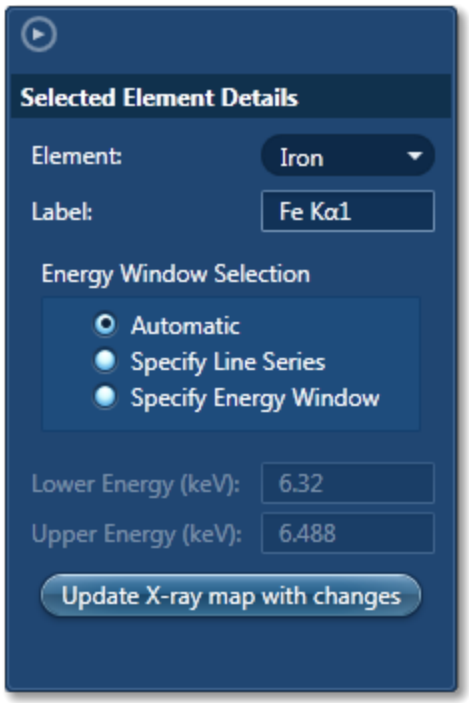
To include an element for mapping either double-click on its symbol on the periodic table or click the Include button. All the elements selected for mapping are green color coded on the periodic table. To exclude an element from being identified by AutoID and excluded from being mapped,

click on its symbol on the periodic table to select it and then press the Exclude button. This element will be removed from the analysis. All excluded elements will be red color coded on the periodic table. Note: An excluded element if present in the specimen may affect the TruMap results.

To remove an element map from the display, select it by clicking on it and then press the Clear button. It will be removed from the display. Press the Clear All button to remove all maps from the display. Remember the maps will be displayed again when you press AutoID or include elements manually.

Manual selection of energy windows and X-ray lines:

- Press  on the Map Details dialog to open the Selected Elements Details:



The default setting is Automatic X-ray lines and energy window width selection.

- To manually define the width of the energy window, select the Specify Energy Window option. Enter the values for Lower Energy (keV) and Upper Energy (keV) and press 

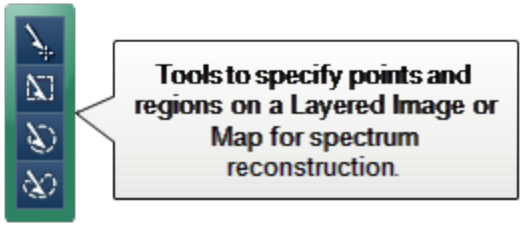
. The map will be acquired using the defined window width.
- To manually select the X-ray line for mapping an element, select the Specify Line Series option. Select the line from the Line Series drop-down list and press 

. The map will be acquired using the specified X-ray line.

Reconstruct spectra from Layered Image or Maps using Point, Rectangle, Ellipse and Freehand tools

The spectrum reconstruction tools are available in the toolbar on the left of the workspace:

- Select the spectrum reconstruction tool from the four available options:



- Click on the Map and drag with the left mouse to select a region. A reconstructed spectrum is displayed in the spectrum viewer and it is also added to the data tree.
- MiniQuant results of the reconstructed spectrum are displayed. You can compare the sum spectrum and the reconstructed spectra.
- To confirm the elemental composition of a phase you can navigate to the Confirm Elements step in the Point & ID package from the link below the Layered Image Viewer. For details refer to Online Help.

See Also:

AutoLayer below

Context Menu - Map Viewer on next page

AutoLayer

By identifying and combining the elements that vary in a sample, AutoLayer helps you visualize both phase and element distribution using a single image.

You can choose a color hue for each of the X-ray maps and adjust brightness and contrast on each map individually, or use the "AutoBrightness" or "AutoGamma" buttons to apply an automatic setting to all maps. Colored maps can be mixed together or "layered" on top of an electron image to generate the "Layered Image" view and there is a control on each map window to select whether to include the map in the Layered Image combination. The idea of mixing is to make regions of different material content appear in different colors. An overlay can be used to relate this material content to the topographic detail that is usually visible in the secondary electron image. If the electron image is a backscattered electron (BSE) image, the intensity may be controlled more by material content than by topography. You may therefore prefer to assign a color to a BSE image and an option is provided on the electron image to either assign a color and "mix" it (as if it was an X-ray map) or use a grey scale and "overlay" the mixture of colored X-ray maps. If you choose different colors for similar maps and mix them together, the resulting mixture color will not bear any relationship to the original colors so it will be difficult to make sense of the layered image. If you are analyzing specimens where you know what elements are likely to appear, then manual color mixing is straightforward. However, for more complex situations or when you are dealing with an unknown specimen you should find the AutoLayer function helpful.

If you have a series of X-ray maps displayed, the "AutoLayer" button will run an algorithm to analyze the spatial content in the maps to decide and select the best maps to use for the layered image. It will also adjust contrast and brightness and assign a suitable color hue to the maps to give a useful layered image. If maps have a lot of statistical noise, they are unlikely to be selected, otherwise the layered image would show a lot of random colored dots. When a set of

maps show similar spatial content, they will be assigned the same hue, but only the best map will be chosen for the mix. Sometimes a noisy map will be assigned a color but it will not influence the mix. If a map has not been assigned a color, it either has too much noise, or enough different maps have already been found to provide a good mix. In the case where there are many different materials in the field of view, it is worth checking those maps that have not been allocated a color to see if they show any features that are not obvious in the layered image.

Context Menu - Map Viewer

A number of useful shortcut menus available as right mouse click in the map viewer are shown in the table below:

Context Menu Item	
Reset Image Scale	
View	Color Bar
	Scale Bar
Export	Save As (Original Resolution)...
	Save As...
	Copy
	Print
	Email...
	Settings...
Details...	

Map - Custom

Acquire And Construct

Scan Image, Acquire Map Data and Construct Maps are laid out as separate steps in the Guided mode of the Map application. There are four components that make up these three steps: an Image window, an X-ray map window, a Spectrum reconstruction window and a Confirm elements window.These four components are combined in the Custom mode to give you a single workspace called Acquire and Construct. It offers the convenience of working in one window without having to move away from it.

The user interface components are docked in the workspace in the four quadrants. Each component can be undocked in a free floating window. It can be dragged on to another monitor, resized or displayed in the full screen view.

There is a toolbar  located near the top right corner of the workspace with icons which allow you to toggle on/off each component.

The user interface elements are described below:

Electron Image/Layered Image

The Scan Image component is docked in the top left quadrant. It allows you to acquire an electron image and a Layered image. You can choose to display either the electron image or the Layered Image.

Press  to acquire or display the electron image. Press  to acquire map data or display the Layered Image.

Element Maps

The Element Maps component is docked in the top right quadrant of the Acquire and Construct workspace. You can acquire element maps here and view them in three different ways, Standard, Interactive or Summary view. To get details of all the functions follow the Acquire Map Data link below.

Spectrum Viewer

The bottom left quadrant displays the current spectrum. It can be a Sum Spectrum or a Reconstructed Spectrum. At the top right corner of the Spectrum Viewer, there is a link to the Confirm Elements step of the Point & ID Navigator. It is a useful option for identifying and confirming small peaks in the spectrum. Select Map to get back into the Acquire and Confirm workspace from the Confirm Element screen.

Selected Element Details

The Map Details is located in the bottom right quadrant of the workspace. From the Selected Element Details, you can select which elements you wish to map. You can define the energy windows for window integral maps and select the X-ray lines you wish to use for mapping instead of using the automatically selected energy window and lines. When you select a map from the element map display, the energy window and X-ray lines markers for this element are displayed in

the spectrum viewer. To read details of defining energy windows and choosing X-ray lines, follow the link to Construct Maps topic below.

See also:

Acquire Map Data on page 162

Construct Maps on page 171

Acquire Map Data - Settings on page 168

Context Menu - Map Viewer on page 174

Linescan - Guided

In the Guided mode the Linescan navigator has four steps:

Describe Specimen, Scan Image, Acquire Line Data and Construct Linescans. First two steps are described in the earlier section.

Acquire Line Data

In this step you can acquire element linescans along a line defined on the electron image or map. The data can be processed as Window integral or TruLine.

To acquire linescans:

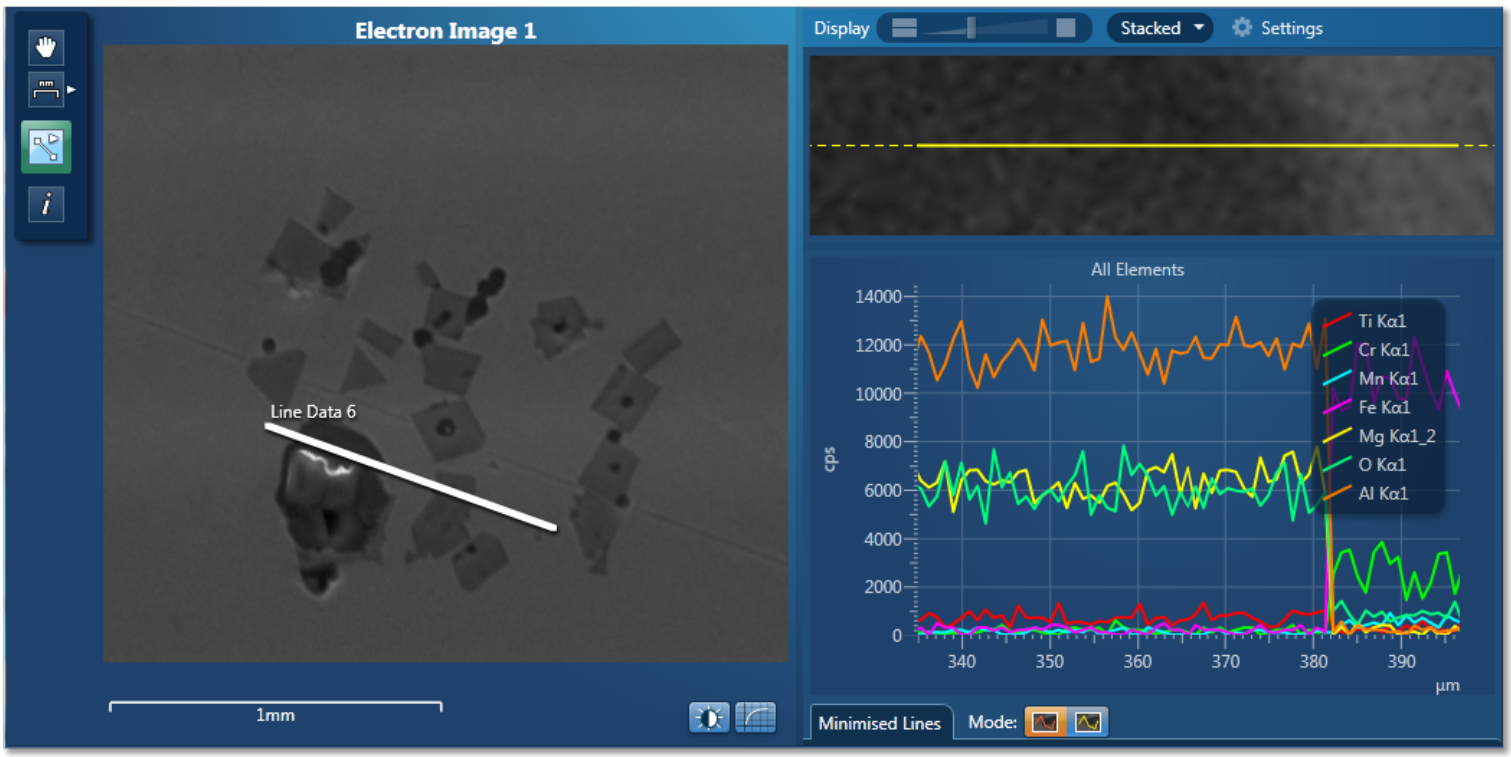
Select  the Acquire Line tool from the toolbar on the left.

Click on the image to set the start point and then drag the mouse to define the line. Release the mouse to set the end point. A line with start and end points is defined on the image.

Press  to start acquisition. A relevant section of the image is zoomed and rotated above the Linescan viewer. This action aligns the defined line horizontally to match the x-axis of the Linescan viewer.

Element linescans start to populate the Linescan viewer from left to right as the data is being acquired. The elements for which linescans are being acquired are chosen in the Describe Specimen step selecting either the Auto ID option or Pre-defined Elements or both.

The Acquire Line Data screen is shown below:



The progress of line data acquisition is displayed in Current Site tab in the Data View:

You can stop the acquisition by pressing  .

The Linescan data can be processed as Window Integral or TruLine from the controls located at the bottom of the Linescan viewer. The TruLine data processing will use the TruLine settings from the EDS Element settings tab in the User Profile screen. You can access the User Profile from the Tools menu. See User Profile on page 17.

You can specifically define:

- Whether the threshold is on or off by checking/un-checking 'Apply TruLine Threshold'
- Choose Sigma Threshold between 0.0 and 3.0

For Linescan Settings see Acquire Line Data - Settings on page 185.

Linescan display and manipulation

Three different views are available from the controls in the top right corner of the Acquire Line Data screen:

1. Display Electron Image Full Screen
2. Display Linescans and Electron Image
3. Display Linescans Full Screen

Two options are available to view the Linescans:

- Stacked - multiple linescans overlaid are displayed in a single view.
- Vertical Tiles - individual element linescans are displayed in a separate view. You can change the height of each view using the Display slider bar.

You can pan and zoom linescans using the mouse controls. Both the viewers, image and line view respond synchronously to the mouse interactions.

- Left mouse button down similar to the spectrum viewer:
  - Move left / right – pan left/ right (if view is expanded)
  - Move up / down – change the scale height (min is y value clamped to 0)
- Mouse wheel
  - Zooms x range in/out around current x value (defined by mouse location). The image will expand/shrink to match the data displayed. If the data is not visible in the viewer because of pan/zoom state, the line on the rotated image will change to a dotted yellow line to indicate there is more data.
- Linescan viewer specifics:
  - Dragging directly on the axis will pan the range
  - Mouse wheel on the axis will expand / reduce the range

The thickness of the line in the plots can be set globally from the Linescans Viewer tab in the Preferences screen. The thickness values in pixels are as tabulated below:

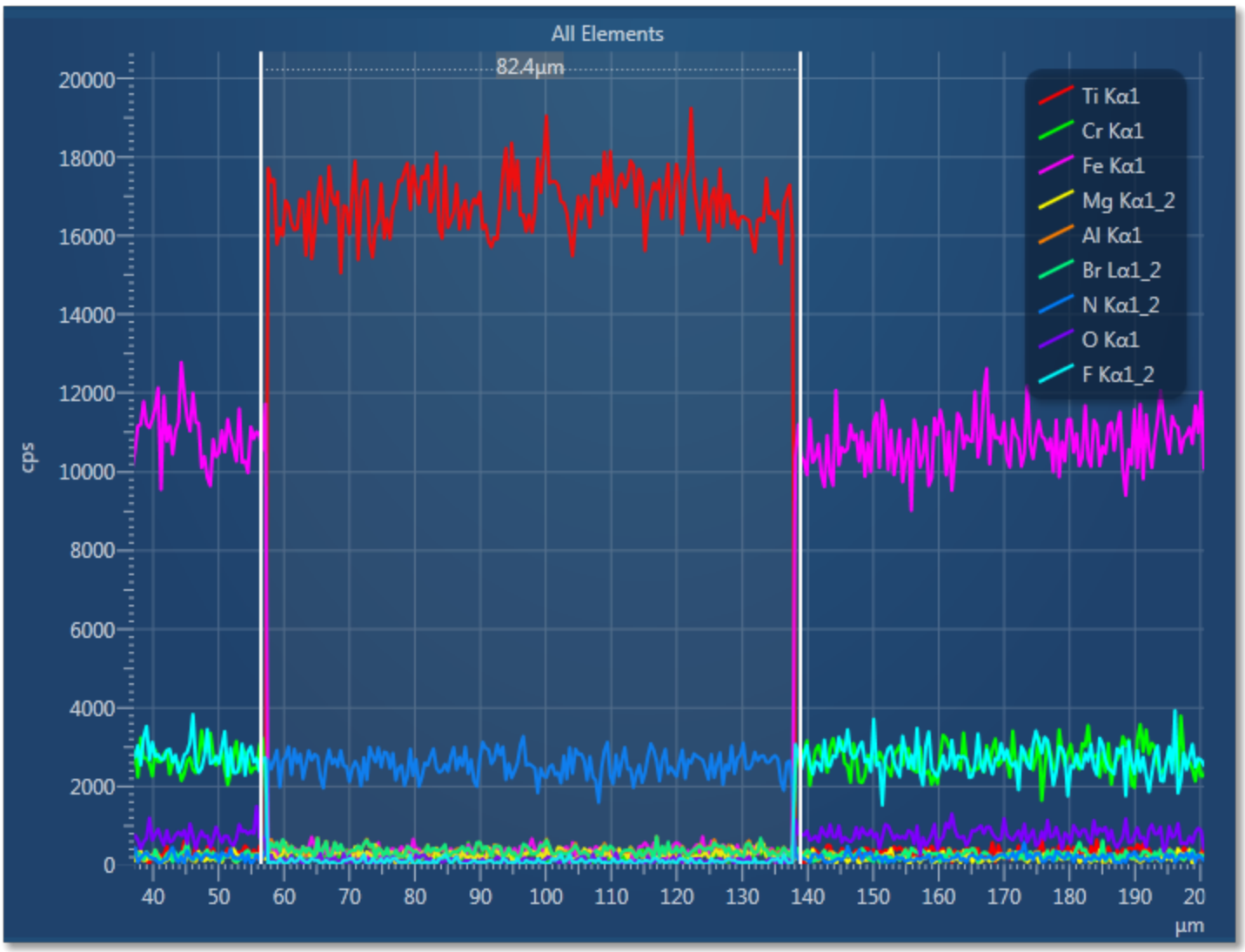
	Thickness in Pixels
Thin	0.5
Normal	1.0
Thick	2.0

	Thickness in Pixels
Thicker	4.0

In addition you can change the color and thickness of individual profiles from the Linescan viewer settings.

Caliper Measurement

The distance between two points on a Linescan viewer can be measured using the Caliper tool. After selecting the tool from the toolbar on the left, move the mouse over a Linescan viewer (stacked or tiled). A cursor will appear in the viewer the mouse is over. This cursor will track the mouse movement. Double click to set the first measurement point. Once set, further movement of the mouse will cause a region to be painted on the viewer showing the distance between the two points, with units. This will update as the second cursor is moved. Double clicking in the same viewer will fix the position of the second cursor and stop any further updates.



NOTE

Unlike calipers on an image, the linescan calipers are not saved with the data. When you switch to a different tool the caliper information will disappear (and will not reappear when you switch back).

A new region can be drawn by double clicking in the viewer at the new (start) point. You can then define the extent of the measurement by placing the second marker, as described above.

To get rid of the region on the viewer, you should switch to another tool on the toolbar.

In the Vertical Tiles view, you can use the Caliper tool on individual linescans to display the distance between two points.

You can view counts for elements by clicking  within the bounds of the viewed data in the Linescan viewer. It places a vertical cursor at that location and displays the counts for each element in that location. The Info tool is available from the toolbar on the left.

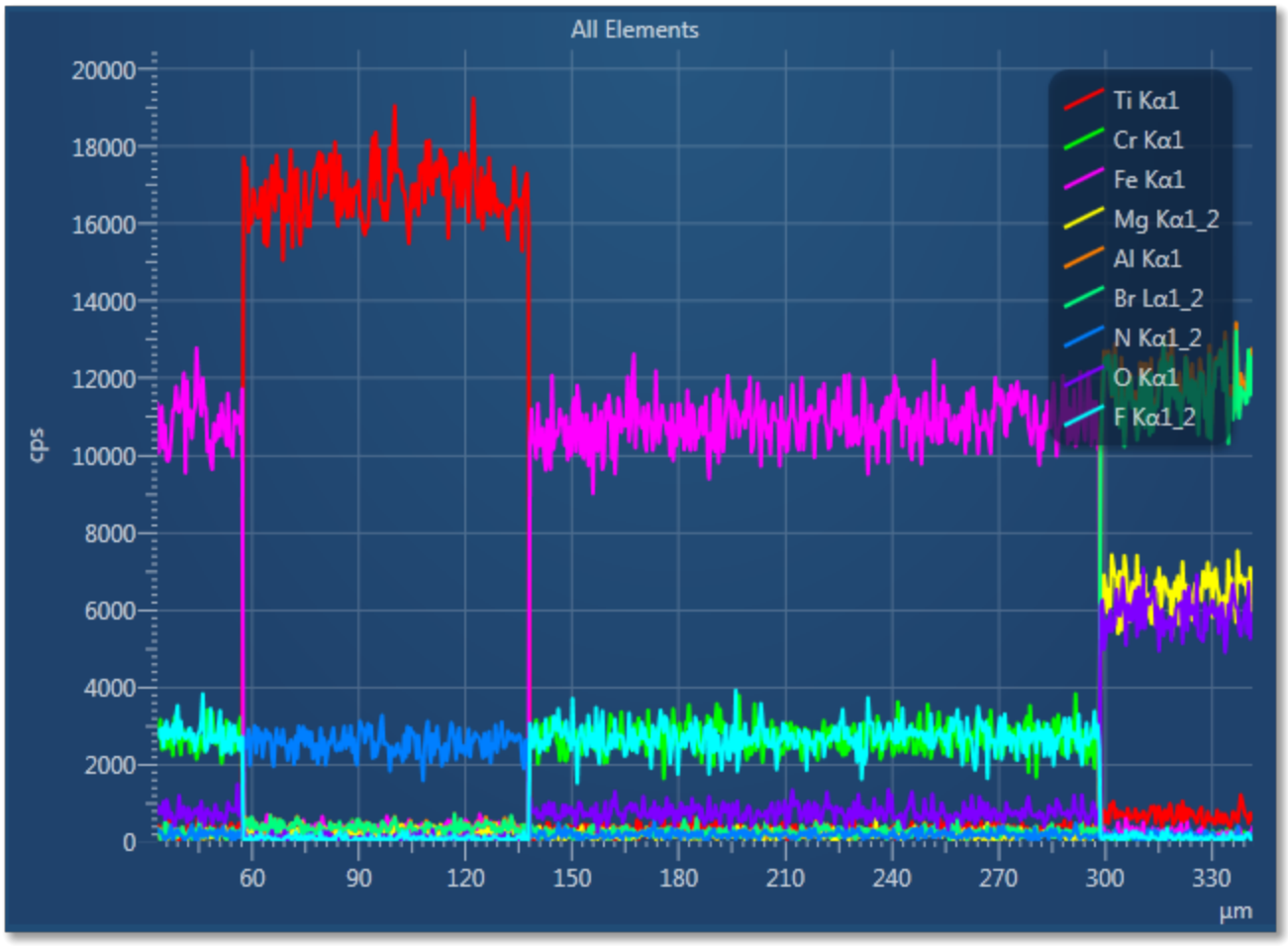
Normalize Y-Axis

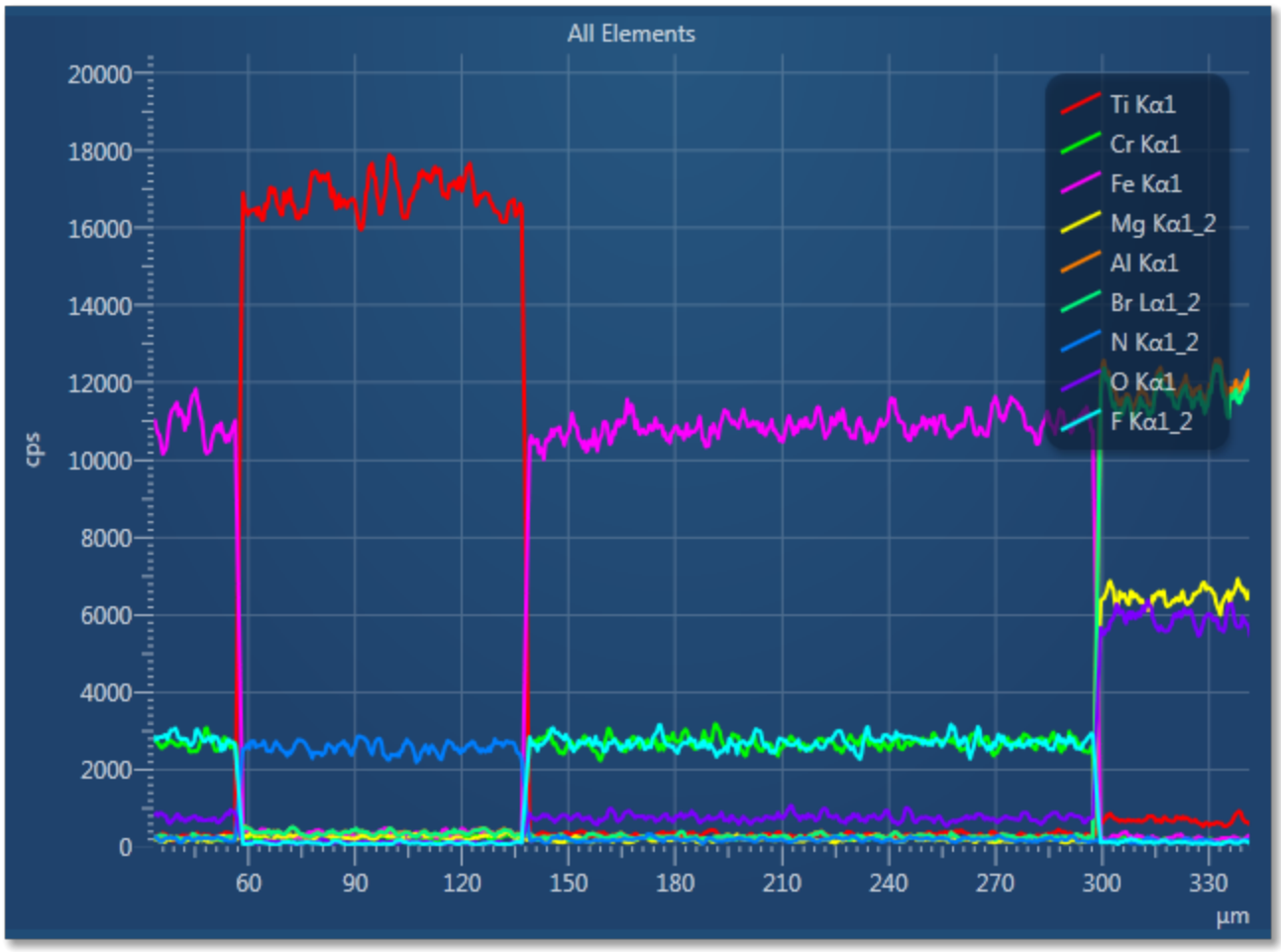
This option is available on the context menu of the Linescan viewer. It allows you to compare linescans with very different maximum count rates. The maxima of linescans are scaled to the full height of the viewer. It allows you to view the details of the minima of linescans with low count rate.

Note that there is no Y-axis on the normalized linescans because the absolute scale is meaningless.

Smoothing Factor

The Smoothing Factor option is available from the Linescan viewer settings. It allows you to smooth the linescans after normalization for visual clarity as demonstrated in the screen shots below:


All Elements
cps
20000
18000
16000
14000
12000
10000
8000
6000
4000
2000
0
60
90
120
150
180
210
240
270
300
330
µm
Ti Kα1
Cr Kα1
Fe Kα1
Mg Kα1_2
Al Kα1
Br Lα1_2
N Kα1_2
O Kα1
F Kα1_2



The Smoothing Factor uses moving averages to remove fluctuations of data.

There are three options available are:

- 1: No smoothing applied
- 3: Data averaged over three points
- 5: Data averaged over five points

Acquisition Settings

The acquisition settings are available from 

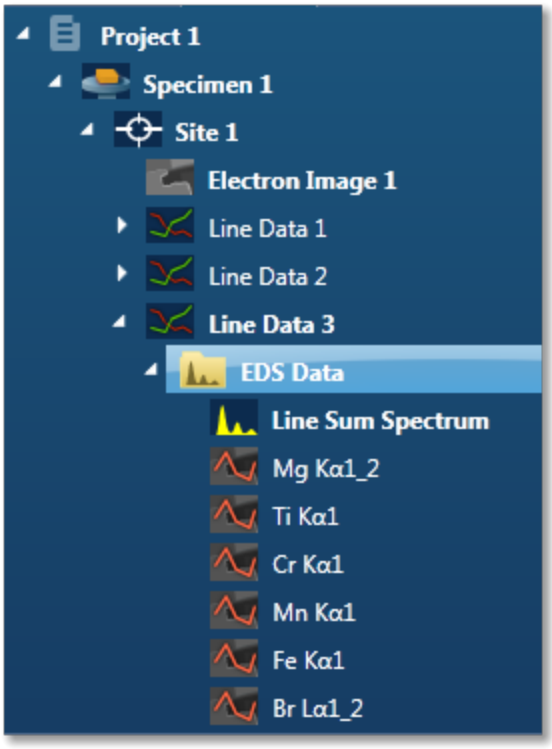
in the step title bar. You can set the following parameters before you start acquisition of linescans:

- Acquisition Time
  - Until Stopped
  - Fixed Duration
    - Number of Passes
- **Number of Channels**
- **Energy Range (keV)**
- **Process Time**

- **Pixel Dwell Time (ms)**
- **Number of Points**

Linescan Data

The data tree contains a Line item under the Site; this is the container for the line data. By default, this is labeled as 'Line Data #' where # is an auto-increasing number under the current site(Site 1) as shown below:



The Line item is the container for EDS Data. All linescans and the sum spectrum are contained within the EDS Data.

The name of the element linescan is composed of the element symbol followed by the lines series used for TruLine/Window Integral data analysis.

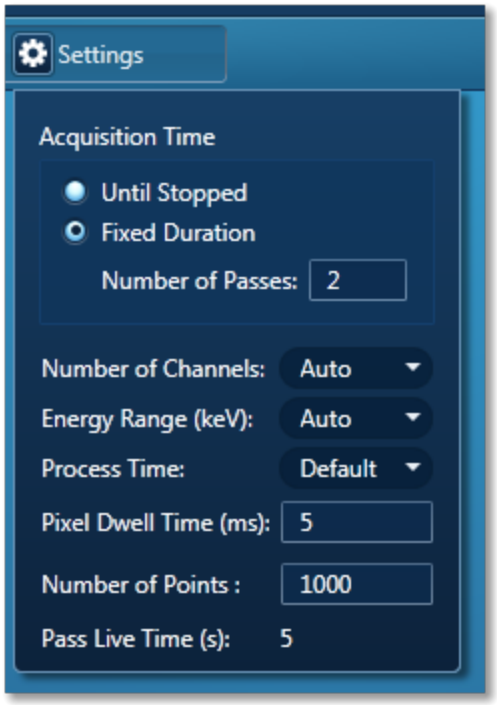
The sum spectrum is called Line Sum Spectrum. The region the spectrum comes from is visible on the electron image. This is the same region as where the linescan data is acquired from.

Data Export

Right click on the linescan viewer to access the Export menu. It has five different ways of exporting the linescans: Save As, Copy, Print and Email. The exported image includes the relevant information from the Caliper or Show data values tool.

Acquire Line Data - Settings

A settings cog in the Acquire Line Data window provides access to the settings for acquiring linescans:



You can specify the Acquisition Time, Energy Range (keV), Number of Channels, Process Time, Pixel Dwell Time (ms), Number of Points in the line and Live Time (s) per Pass.

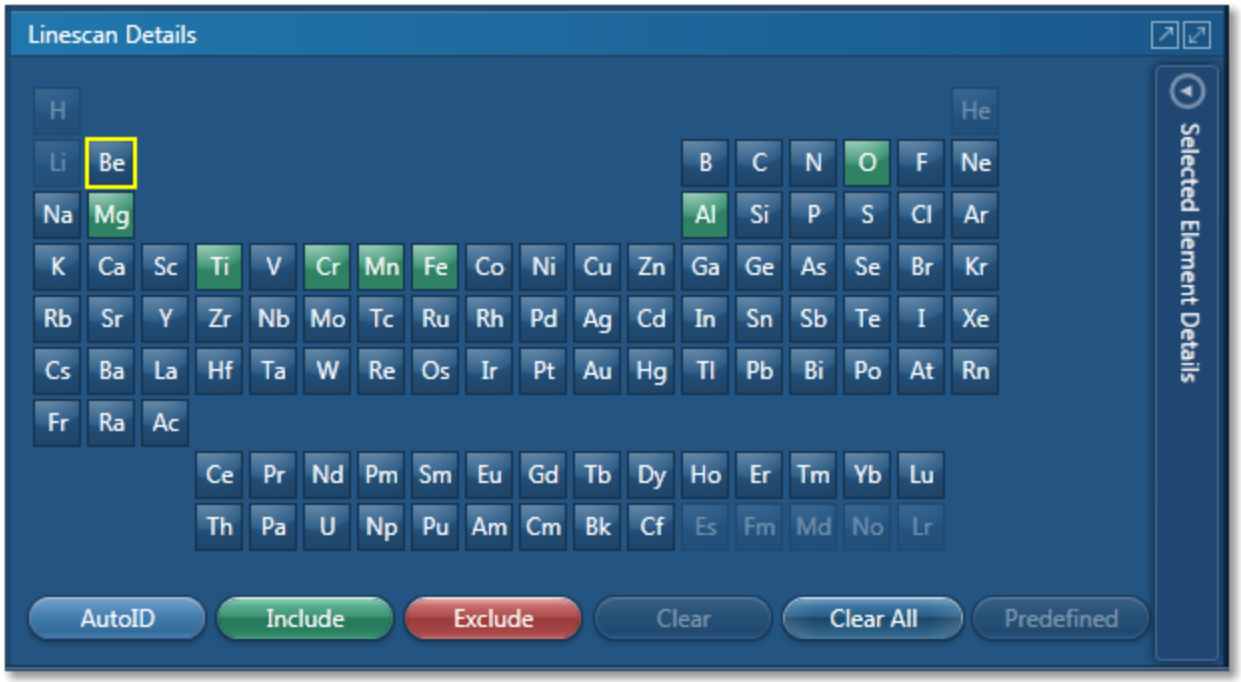
In the Auto mode, the system checks for the accelerating voltage selected on the microscope and sets the appropriate spectrum Energy Range. Based on the Energy Range selected, an appropriate value for the Number of Channels is set automatically.

Use the Default Process Time if you wish to acquire good quality data at the optimum speed.

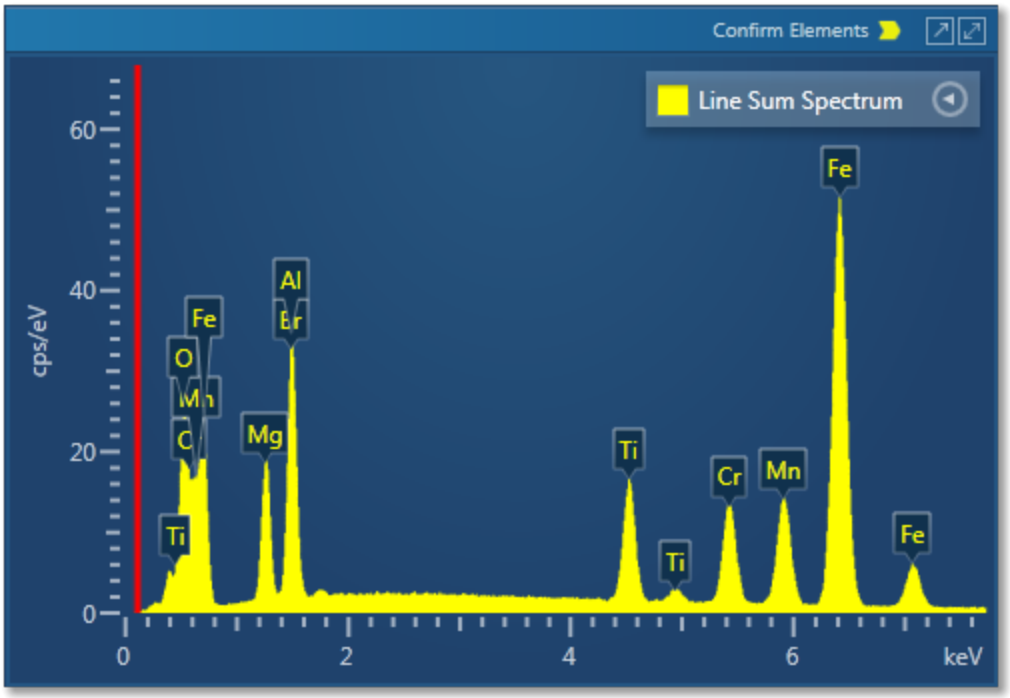
Construct Linescans

In this step you can define energy windows and configure X-ray line series to update the display of element linescans in the viewer.

You can use AutoID for initial display and then add or remove elements as you wish using the periodic table and the controls available in the Linescan Details dialog:

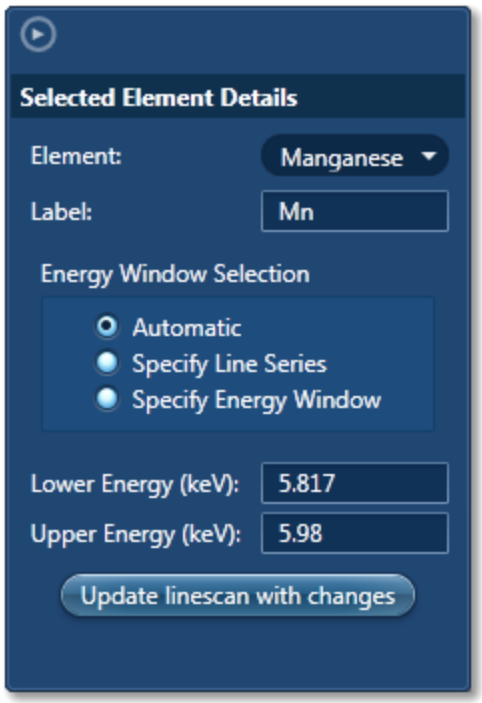


In addition, you can view the Line Sum Spectrum and navigate to the Confirm Elements step from within the Construct Linescan step to manually confirm elements:

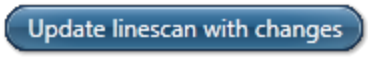


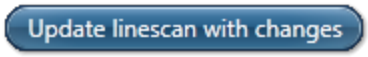
Manual selection of energy windows and X-ray lines:

Press  to open the Selected Elements Details dialog:



The default settings are automatic X-ray line series and energy window width selection.

To manually define the width of the energy window, check the 'Specify Energy Window' option. Enter the values for Lower Energy (keV) and Upper Energy (keV) and press 

To manually select the X-ray line for an element linescan, check the 'Specify Line Series' option. Select the line from the Line Series drop-down list and press 

Linescans Display

There are three different display options available from the controls,  near the top right corner of the Construct Linescans screen:

- Display image full screen
- Display linescans and image
- Display linescans full screen

Linescan - Custom

In the Custom Mode, the Linescan navigator has two steps:

The Describe Specimen step is explained in the earlier section.

Acquire And Construct - Linescans

The three components, Scan Image, Acquire Line Data and Construct Linescans are laid out as separate steps in the Guided mode of the Linescan application. These three components are combined in the Custom mode to give you a single workspace called Acquire and Construct. It provides the convenience of working in one screen without having to move away from it.

The user interface components are docked in the four quadrants in the workspace. Each component can be undocked as a free floating window. It can be dragged on to another monitor, resized or displayed in the full screen view.

There is a toolbar  located near the top right corner of the workspace with icons which allow you to toggle on/off each component.

The user interface elements are described below:

Acquire Electron Image and Line Data

In the top left quadrant, you can acquire an electron image first and then define a line to acquire the line data.

Press  to select the image acquisition mode. Then press  to start electron image acquisition.

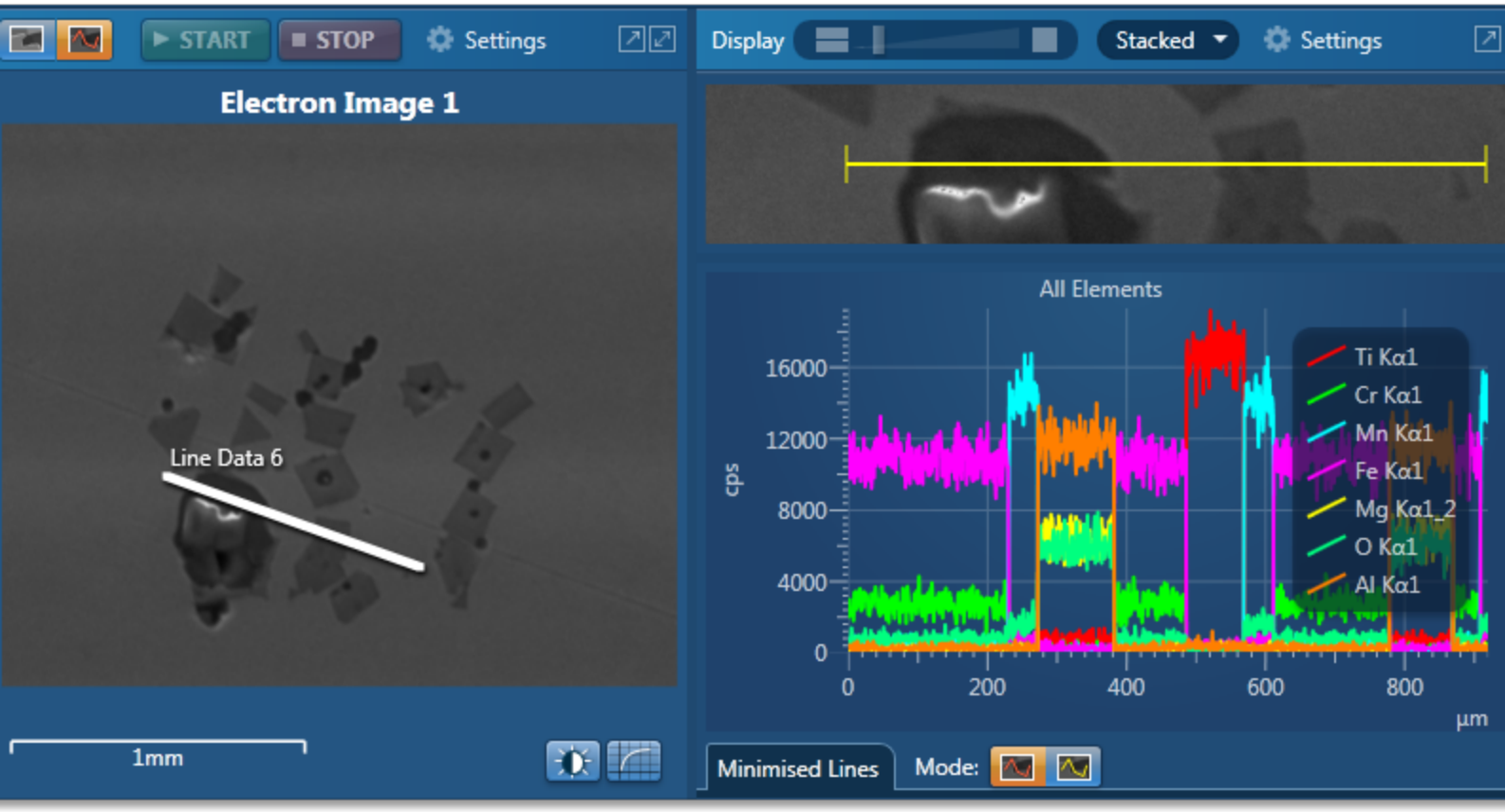
On completion of image acquisition, press  to switch to the line data acquisition mode.

Press  to select the line tool in the toolbar on the left.

Click on the image to set the start point and then drag the mouse to define the line. Release the mouse to set the end point. A line with start and end points is defined on the image.

Press  to start the line data acquisition. A relevant section of the image is zoomed and rotated above the Linescan viewer. This action aligns the defined line horizontally to match the x-axis of the Linescan viewer.

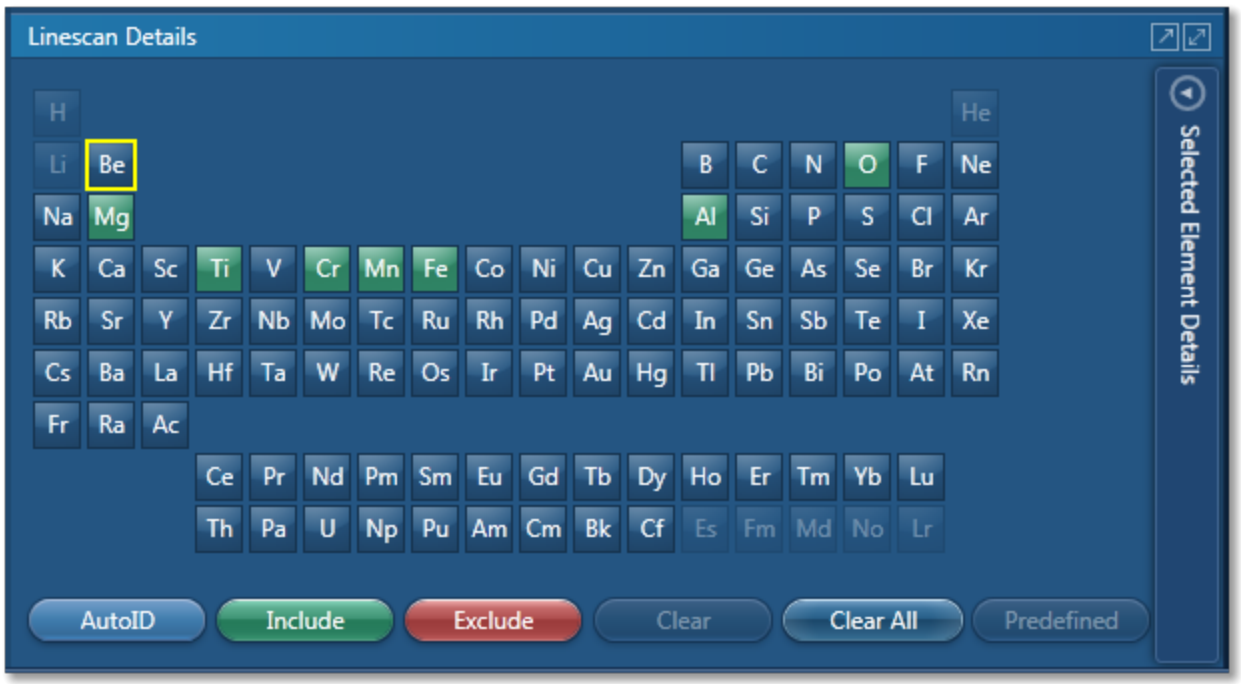
Element linescans start to populate in the Linescan viewer from left to right in the top right quadrant as the data is being acquired as shown in the screen shot below:



Selected Element Details

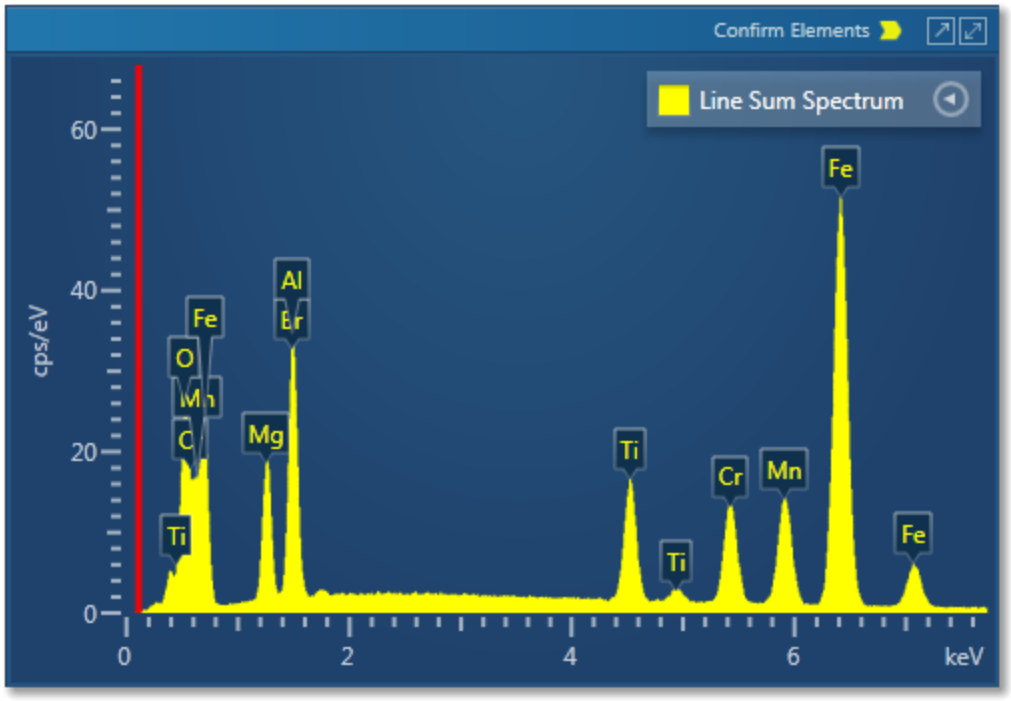
In the bottom right quadrant, you can define energy windows and configure X-ray line series from Selected Element Details.

AutoID can be used for initial display. You can add or remove elements as you wish using the periodic table:



Spectrum Viewer

The spectrum is available in the bottom left quadrant. You can view the Line Sum Spectrum and navigate to the Confirm Elements step from within this component to manually confirm elements:



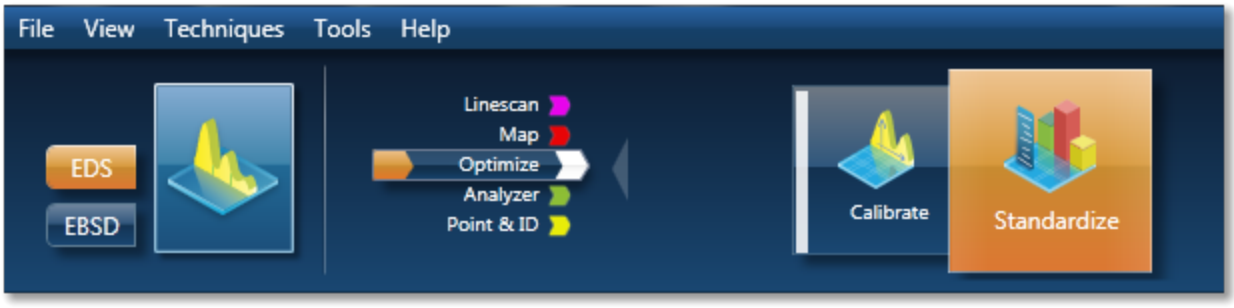
Optimize

There are two components in the Optimize navigator, Calibrate and Standardize.

Calibrate is described in the earlier section under Setup for EDS. The Standardize component will be described in detail here.

Standardize

The Standardize application allows you to setup your own standards for quantitative analysis. It is accessed from the Optimize navigator:



Use the links below for further details about:

Why Standardize? below

Getting Started with Standardization on page 197

Managing Standardizations on page 199

Why Standardize?

In **AZtecEnergy** Quantitative analysis can be performed without the need to measure standard materials since your system is supplied with a complete set of default standardizations. However, in specific cases, using your own standards will lead to an improvement in your quantitative results. The purpose of Standardize is therefore to enable you to set up your own standards for quantitative analysis. When you use your system for the first time and click on the Standardize step, your own standards database will be created. At this stage your database will contain only the Factory standardizations. Once you have standardized entries, your standards database will be modified accordingly.

Quantitative analysis of elements in any Specimen, requires an accurate measure of the intensity of peaks, before the concentration of elements in a Specimen can be calculated. In determining peak areas in spectra, two problems arise:

- **A typical spectrum contains characteristic peaks, which are superimposed on a slowly varying background, which is 'noisy' because of statistical variations. This background contribution needs to be carefully subtracted from the spectrum.**
- **The energy resolution imposes a limit on the separation of peaks. Identification of peaks is generally not a problem, but overlapping peaks**

require deconvolution, before being able to extract the true peak intensities relevant to the elements present in the Specimen.

Once these intensities have been determined, a comparison is then made with standards of known composition, followed by application of matrix corrections, before the concentration of each element can be determined.

What does standardization do?

In order to make a direct comparison between intensity and concentration, a standard Specimen is referred to in which the relationship between Istd and Cstd is accurately known where Istd is the intensity from the standard and Cstd is the concentration of the standard. Once this is known, this ratio can be used to determine the concentration of that element in an unknown Specimen (Cspe) since the intensity of the element in the Specimen (Ispe) can be measured. Let Cxspe be the concentration of element X in the unknown Specimen and Ixspe be the intensity of the relevant peak from element X in the unknown Specimen. All intensities are assumed to have been corrected for background.

The concentration of element X in the unknown Specimen can be approximated as:

Cxspe={Cxstd(Ixspe/Ixstd)}

and is often referred to as the Apparent concentration or the uncorrected concentration. Once these 'Apparent concentrations' have been determined, the element weight percents are then calculated by applying a matrix correction to the measured intensity ratios. These corrections attempt to account and correct for the effects of X-rays traversing the Specimen matrix such as absorption of X-rays in the material.

The ratio in value between the Apparent concentration and the true concentration is a measure of the matrix corrections which need to be included in the calculation. However, the need for the correction is minimized if the composition of the standard Specimen is as similar as possible to the composition of the unknown Specimen. This simply means that the effect on the X-ray intensity of X-rays traversing the Specimen and standard is similar. Since these matrix corrections can be calculated with only a certain degree of accuracy, the choice of standard material is very important if the quantification is to be as accurate as possible.

Why Standardize?

The need to standardize depends very much on the level of accuracy you require from your analysis on any one material. As a rule of thumb:

- **If you require accuracy such that the relative errors are less than 2%, you should standardize.**
- **If you are quantifying elements whose X-ray lines are in the low energy region of the spectrum (which may be the case if you are using an accelerating voltage of less than 15kV, or the element you are quantifying has an atomic number less than 11), standardization will improve your quantitative results.**
- **If the matrix corrections are high such as would be in the case of quantifying Al in a Pd matrix, (e.g. light in heavy, heavy in light), where your intensity correction Ic is either >1.25 or < 0.8, you should standardize. The intensity correction is given in the quantitative results.**

Not necessary to standardize if

- **You only want to know which phase it is.**
- **Your standards are of a poor quality (rough, dirty).**

Getting Started With Standardization

In **AZtecEnergy** Quantitative analysis can be performed without the need to measure standard materials since your system is supplied with a complete set of Factory standardizations. However, in specific cases, using your own standards will lead to an improvement in your quantitative results. The purpose of Standardize is therefore to enable you to set up your own standards for quantitative analysis.

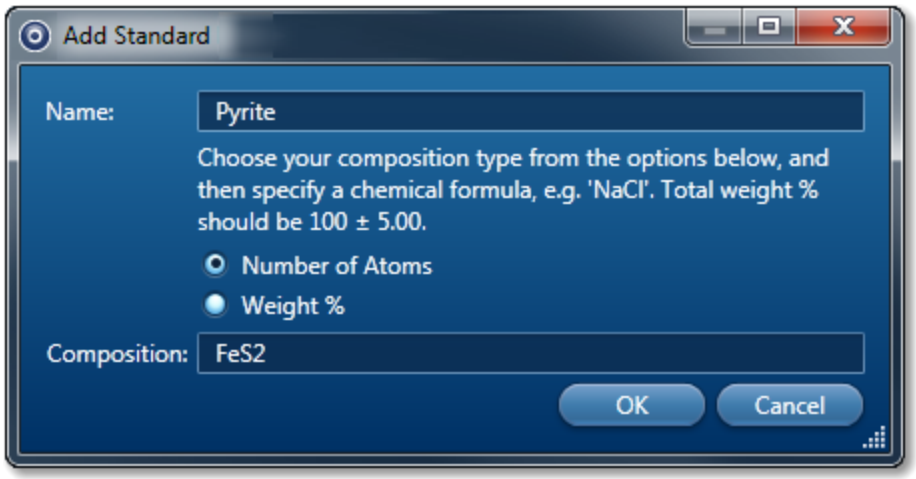
When you use your system for the first time and click on the Standardize step, your own standards database will be created. At this stage your database will contain only the Factory standardizations. Once you have standardized entries, your standards database will be modified accordingly.

Standardize allows you to add your own standards blocks and enter compositions of all standards on each block. You can standardize on any of the elements available in the standards.

Adding composition of standards

You can build your standards database by adding blocks of standards and the compositions of individual standards on each block. Note that if you wish to use pure element standards you do not need to add standards.

- Press Standardize on the Optimize navigator. The Standardize screen is displayed.
- Press Add to add a block in the Standards Compositions area.
- Enter the name for the block and press OK. Your block will appear in the Block list box.
- Press Add to add a standard. The following dialog is displayed:



- Enter name for the standard.
- Enter composition of the standard by choosing either Number of Atoms or Weight%. When you know the chemical formula select the option, Number of Atoms. The formula is validated as you enter it. If you enter it in a wrong format for example feS2 or FES2, it will not be accepted. For Weight% option, you need to enter the element symbol followed by weight e.g., for FeS2, it will be Fe 46.55 S 53.45. It will be symbol weight symbol weight until you have added all elements. The total weight% has to be between 95% and 105%. If it falls outside this range you will be warned about it.

Standards

Standards are materials which are used to relate the intensity of a peak in a spectrum to the concentration of that element in the specimen. They are materials in which the concentrations of all the elements are accurately known. Standards may be pure elements or compounds. High quality reference standards are essential to perform accurate quantitative microanalysis in the SEM. Not only must their chemical composition be well characterized, but they must also be microscopically homogeneous, stable under the electron beam and prepared with a flat, polished surface.

How to standardize

- Ensure that the spectrum to be used for standardization is displayed in the spectrum viewer. This may be a spectrum you have just acquired in either the Analyzer or in Point & ID or you may wish to standardize using a stored spectrum.
- Select the standards block you wish to use from the Block drop-down list in the Standards Composition section.
- Select the standard that you wish to use from the Standard drop-down list.
- If you wish to set up a Deconvolution element, select it and add it to the Deconvolution text box.
- Select either Pure Element or Element from Standard (Compound standard) as appropriate from the Perform Standardization section. X-ray line markers will be displayed for the selected element (K lines are in red, L lines in green, M lines in purple and N lines in cyan.)
- Select the line you wish to standardize on from the X-ray Line Series drop-down list.
- Having selected the element and the line for standardization, press 

to perform the standardization. The current and new values of standardization will be displayed.
- Press 

to update the standardization. The existing values will be overwritten by the new values. You will be asked if you wish to use the new standardization for Quantitative analysis.

Note

The Accept button will be grayed out if the Standardizations file is selected for quant. You need to deselect it in the Quant Settings dialog (available from the Calculate Composition screen) if you wish to standardize on any entry in this file.

- In Calculate Composition step, when you press Requantify, the new standardization will be used and displayed in Quant Results Details if you select the Full Results template.
- If you have not accepted the new values for standardization, no changes will be made to the existing standardization.

Managing Standardizations

Your **AZtecEnergy** system is supplied with a Factory Standardizations database. When you use your system for the first time and click on the Standardize step, your own standards database will be created. At this stage your database will contain only the Factory Standardizations. Once you have standardized entries, your standards database will be modified accordingly. To manage your Standardizations the following functions are provided:

Creating a new standardization file

To create a new standardization file:

- Press the Manage button in the Standardize screen and then select the Create File tab.
- Select an existing file from the Factory Files or User Files. This file will be used to populate the entries in the new file.
- Enter the name for the new file and press the Create button. A new file will be created. You can overwrite the existing entries in the new file with your own standardizations.
- To use this new standardization file, select it in the Quant Settings in the Calculate Compositions step for quantitative analysis.

N o t e

The Factory Standardization file is available to all users of the system. However, files created by individual users are user specific.

Deleting a user standardization file

Remember that you can not delete the Factory Standardization file. User created files can be deleted.

To delete a User Standardization file:

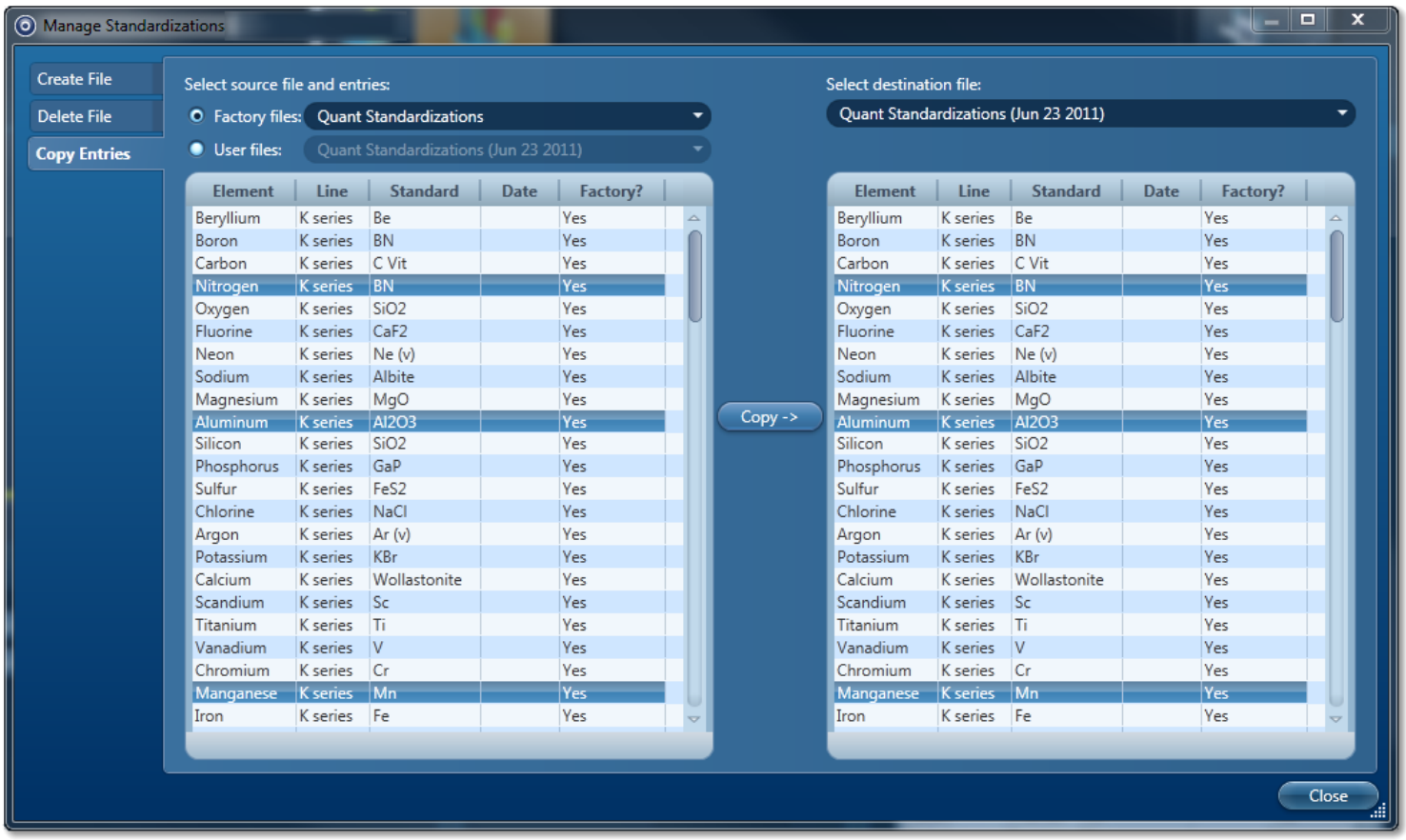
- Select the Delete File option from the Manage Standardization dialog.
- Select the standardization file to delete from the drop-down list.
- Press the Delete button. The selected file will be deleted. Note that this file will not be deleted if it has been selected for quant. You will be warned about it when you press the Delete button.

Restoring standardization entries

The Copy Entries option allows you to restore standardizations from the Factory File to a User File or from one User File to another User File:

- Press the Manage button in the Standardize screen and then select the Copy Entries tab.
- Select User or Factory Standardization File as the Source File.
- Select your standardization file which contains the modified entries as the Destination file.
- Select the entry in the Factory Standardization file that you wish to restore by clicking on it.

- Then Press the Copy button to restore this entry across to your file. The modified entry in your file will be overwritten with the Factory entry. For copying multiple entries hold down the Ctrl key while selecting individual entries:



- Press the Copy button to copy the selected entries.

Sharing standardization files

You can share standardization files with other users of the **AZtecEnergy** system by using the Export and Import options available in the User Profile dialog from the EDS Quant Setting tab:

- Select User Profile from the Tools menu.
- Select EDS Quant Settings in the User Profile dialog.
- Select the Standardization file from the Quant Standardizations.
- Press the Save As button. The Save User Profile dialog is displayed.
- Enter the name for the User Profile or select an existing User Profile from the list in the Save User Profile dialog.
- Press the Export button. The Standardization file with .ois extension and User Profile file with .config extension are exported.
- You can share these files with other users using the Import option in the User Profile dialog.

AZtecHKL

EBSD - Map

The Map navigator has six steps which are described below:

Describe Specimen

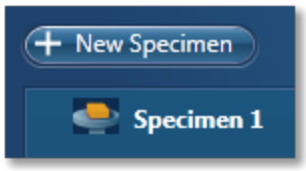
In this step there are three tabs, Summary, Specimen Geometry and Phases.

Summary

In the Summary view you can write notes on the Project and the Specimen within the Project. (For convenience you can also copy images/diagrams and text from other documents/emails and paste into these windows). Notes are saved with the Project and you may edit notes in any step of the Navigator.

This helps to capture the important information during your experiments. Right click with the mouse on the Project or Specimen entries in the Data Tree and then select Edit Notes to write/modify the relevant notes.

You can add new Specimens to the current Project by pressing the New Specimen button:



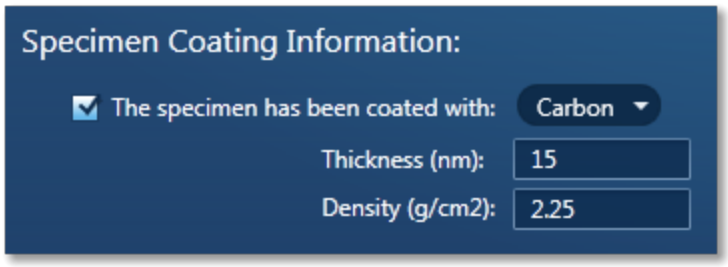
Note that you may write notes about each Specimen and save them.

EBSD

The Phases for Acquisition are listed in this view together with the number of reflectors, color and the option to include/exclude them during analysis.

EDS

You may add coating information for each specimen. This information is then sub sequentially used during the calculation of the quantitative results.



To specify a coating element, check the coating option and select an element from the Periodic table.

You should then enter both the Thickness and Coating density in order for a full coating correction to be applied during the calculation of the quantitative results. Note that the default element is Carbon with the following default values for thickness and density respectively: 10 nm and 2.25 g/cm3.

The default density is that of the element at room temperature and pressure where appropriate. The thickness and density may then be modified if required.

The peaks associated with the element which you have selected will automatically be deconvolved from the spectrum prior to quantification but excluded from the calculation of composition.

Please see the topics on Specimen Geometry and Phases via the links below:

See Also

Specimen Geometry below

Phases on the facing page

Data Tree on page 71

Mini View on page 78

Step Notes on page 79

Specimen Geometry

Specimen Tilt

This area of the application allows you to define the way that the Specimen is tilted in the chamber with respect to the horizontal plane.

Diffracted electrons only escape from a depth in the order of a few tens of nanometers deep from the sample surface. At low tilt angles the total interaction volume close to the surface is very small compared to the interaction volume deep within the material. Consequently, at zero or low tilt, the proportion of diffracted electrons in the overall electron yield may be so low as to be undetectable. Tilting the sample improves the diffracted component to background yield ratio by increasing the volume of near surface material excited. Thus EBSD is generally carried out at approximately 70 degrees tilt.

Pretilted Specimen Holder

If you are using a Pretilted Specimen holder for your experiment, check the corresponding box and enter the corresponding Tilt Angle. Note that this option is only enabled in the application if it has been checked in the Configuration Tool under ‘Enable Software Features in Application’. If you are not using a pretilted holder this angle will be zero. Remember to switch off the Pretilt option when you are not using a pretilted holder since it will affect EDS and EBSD data.

Stage Tilt

The Stage tilt value is automatically read from the microscope via the Microscope Control. However, if this value is not automatically read, you may enter the value in the Microscope Control window.

Total Specimen Tilt

This value is the sum of the Stage tilt and the angle of the Pretilted holder. This is the tilt angle which is being used by the software for analysis, so check that the specimen tilt is correct before doing any experiments. This can also be shown in the Status Bar and is shown by default.

Specimen Orientation

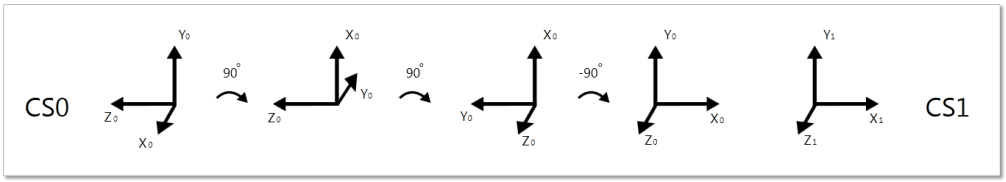
In the Specimen Orientation tab it is possible to define a data rotation which is saved with the Project.

The data shown in the application is always the original, unrotated data so the selection in the Specimen Orientation tab does not affect the way the data is displayed however it works as a placeholder for saving information about the Specimen Orientation. If a rotation transformation is saved with the data then the .cpr file after export to CHANNEL5 format will also contain information about this rotation, so that data viewed in the CS0 coordinate system (Sample Primary Coordinate system) will be shown with the saved rotation. Once the data is exported it can also be rotated from CHANNEL5's Virtual Chamber tool and this tool can also be used to alter any rotation saved from AZtec.

The six buttons shown are associated with the six standard orientations and are a quick way of specifying the Specimen Orientation. The lower seventh button allows the user to manually type in a rotation in the numeric fields to the right.

When EBSD data is rotated it is between two coordinate systems; CS1 (Data Acquisition Coordinate system) and CS0 (Sample Primary Coordinate system). If the sample coordinate system and acquisition coordinate system are coincident, then the default rotation will be 0, 0, 0.

The data rotation is defined as the rotation from CS0 to CS1. For example the rotation 90, 90, -90 means that the CS0 coordinate system is related to CS1 in following way:



The first angle is the rotation around the coordinate systems z axis, the second angle is the rotation around the rotated x axis and the third angle is the rotation around the rotated z axis required in order to make the two coordinate systems coincide.

Note that the scanning system always has the x axis horizontal, the y axis vertical and the z axis pointing out of the image so the orientation of the CS1 is always the same.

Phases

In order to index an EBSP, the software needs to know what phase(s) is present in the specimen. This step provides the functions necessary to locate a phase in a database and add phases to the list of phases to include during acquisition.

Phases in Database

You can select a database by using the drop down menu in the Database menu. The database list shows the database files present in the CHANNEL5 directory and will also include user defined databases if present.

When you have selected a database all phases in the database will be listed. Highlight the desired phase in the phase list to view information about the unit cell of the selected phase, the phase details and the list of calculated reflectors to the right hand side of the work area. The

calculated expected intensities of the Kikuchi bands or reflectors are shown in the Reflectors tab. Note that these intensities are given for families of reflectors.

You can also scroll to a phase in the database by entering the start of its phase name into the space provided. It will then highlight the best matching phase in the list.

Once you have found the phase that you are looking for, press the 'Add Phase for Acquisition' button. This will now load the phase into list of 'Phases for Acquisition' and it will be used for indexing EBSPs. You may repeat the process and include more phases if you wish.

3-D Phase View

The 3-D Phase view may be shown with or without the unit cell within the spherical simulation of the Kikuchi bands. Use the context menu to select different view modes of the 3-D simulation.

The Kikuchi Map gives a spherical simulation of the Kikuchi bands for the unit cell orientation visible. This can be freely rotated using the mouse. You may also adjust the appearance and the number of Kikuchi bands using the options on the 3-D Phase View context menu by selecting a different kV and Simulator Reflectors.

The unit cell visualization gives a 3-D simulation of the unit cell of the selected phase, with the a, b and c axes marked respectively in red, green and blue. Using the mouse you can freely rotate this simulation.

Phases for Acquisition

In the list of 'Phases for Acquisition' it is possible to include/exclude individual phases. When the phase is not included, that phase will not be used by the software for indexing EBSPs.

The number of reflectors per phase used during indexing can be adjusted by selecting the appropriate number from the drop down list. This number tells the software how many theoretical Kikuchi bands to utilise during the indexing process.

Lower numbers generally result in faster indexing, but may also give a lower hit rate (% of EBSPs indexed) and more wrong or misleading solutions.

If you wish to add a phase from a cry or hkl file to the "Phases for Acquisition" list, press the 'Add from File' button.

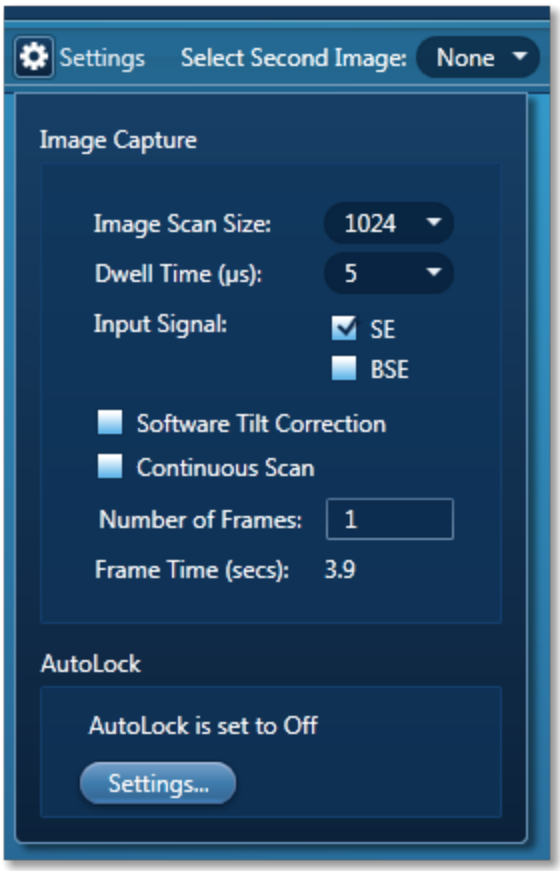
Once you have acquired the EBSD data into a Specimen, you can not remove phases, you can only add them. However you can disable them (this is to ensure data coherent in a Specimen for future applications).

Scan Image

In the Scan Image step you can acquire an electron image into a 'Site'. A 'Site' is generally seen as a folder that contains images and analyses related to a particular area on a Specimen.

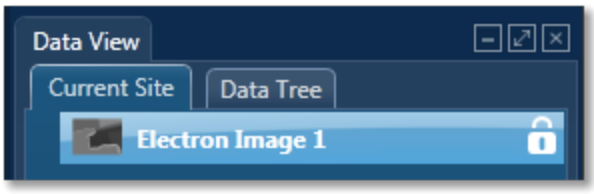
Press 

to start the image acquisition according to the current acquisition parameters. If you wish to change the acquisition parameters press the Settings cog on the Acquisition Toolbar. The Image Settings dialog is displayed:



You can select Image Scan Size, Dwell Time (µs), Input Signal (note that the label on the Input Signal will reflect whatever has been set during the system guided install for example SE, BSE or FSD), either Continuous Scan or Number of Frames and Frame Time (secs).

You are not restricted in the number of images you can have in a Site. Just ensure that the images you wish to keep are padlocked in the data tree to stop them being overwritten as shown in the screen shot below:



Toggle between saving or replacing the current image with successive image acquisition.

Press 

to stop image acquisition. Acquisition will stop at the end of the current frame. Click again to stop immediately. Note that when you navigate from the step acquisition will stop at the end of the frame.

Acquisition Toolbar

The acquisition toolbar is located near the top of the Scan Image screen under the Navigator. It has buttons for starting and stopping the image acquisition, the Settings cog for selecting the image acquisition parameters and a button to link/unlink images for manipulation:

Extensive tools are provided in the Scan Image screen to manipulate and enhance electron images.

There is a toolbar near the top left side of the screen. It has tools to pan and annotate the image. There are five different tools to add annotations as shown in the screen shot below. You can easily edit and delete annotations.

Selecting the Show Data Values tool from the toolbar and clicking anywhere on the image will display the Intensity value at that point.

T i p !

You can zoom in and out of the image using the mouse wheel.

Manual and Automatic Brightness, Contrast & Color Control Tools

Manual and Automatic brightness, contrast & color adjustment tools are located near the bottom right of the screen.

Context Menus

The Image viewer is provided with the Context menus for copying, exporting and printing images.

To find details about the Toolbars, Settings, Context Menus and Brightness & Contrast Adjustment tools follow the links below.

AutoLock

If your Specimen is drifting, then you can activate AutoLock from the Image Settings to ensure that any analysis you do corresponds to the true location on your image.

For EDS, if you do not want to collect an image and just want to acquire spectra, then you can skip this step and go straight to the Acquire Spectra step.

See Also:

Scan Image Toolbar on page 95

Scan Image - Settings below

Context Menus - Image on page 115

Brightness, Contrast and Gamma Controls on page 170

AutoLock on page 96

Scan Image - Settings

The selectable parameters that control image acquisition (Image Scan Size, Dwell Time and Number of Frames) should be chosen according to your specific requirements. Both the time taken and the data storage size of the image are dependent on these parameters.

For a quick look at the specimen select the lowest image scan size and the fastest speed. This will enable you to decide whether you require either a higher pixel density, in order to observe finer detail such as small features, or a longer dwell time in order to improve the image quality by reducing the noise.

The available acquisition parameters are:

- Image Scan Size
- Dwell Time (µs)
- Mains Synchronize
- Input Signal
- Software Tilt Correction
- Continuous Scan
- Number of Frames
- Frame Time (secs)
- AutoLock

Image Scan Size

In general, the resolution of an image or Image Scan Size is defined as the number of picture points or pixels along the x and y axes e.g., 256 x 256, 512 x 512 or 1024 X 1024. The quality of the image improves as the resolution at which an image is acquired is increased. However, a microscope monitor/CRT is usually a rectangular display (rather than square), so the resolution is

displayed as a rectangle i.e., 256 x 200 in order to take into account the aspect ratio. The y dimension is set at installation, when imaging is calibrated. It will vary with each system.

Select the Image Scan Size for image acquisition from the following drop down options available:

64

128

256

512

1024

2048

4096

8192

Dwell Time (µs)

Images can be acquired using different speeds. The beam dwells on each pixel for a specified length of time while the signal is collected and then it moves to the next pixel. So the speed at which an image is acquired depends on the dwell time.

Speed	Dwell time
Fastest	1 µs
Fast	5 µs
Normal	10 µs
Medium	35 µs
Slow	65 µs
Slowest	400 µs

Mains Synchronize

Selecting Mains Synchronize on the Image Setup window, synchronizes the start of each scanned line to the mains supply. This will help to reduce mains borne interference in the image. Note that the acquisition time will be marginally longer than when mains synchronize is not selected.

Note that Mains Synchronize will only be visible if the appropriate hardware is installed.

Input Signal

For EDS, secondary electron imaging is generally most appropriate if you are imaging a sample which has topography whereas backscattered imaging is a very useful means of identifying areas of different composition on flat samples. Secondary electron imaging is the most common form of imaging and for a first look at your sample, choose this mode.

If you are analyzing a flat, polished sample and you can see weak contrast, switch to back-scattered imaging which will tend to enhance this contrast by showing up areas of different phases.

For EBSD, Forward Scattered Imaging is often used. A high proportion of the electrons scattered during EBSD carry imaging information. Because of the high angle of tilt dictated by the collection geometry required for EBSD, many electrons are scattered forward and down towards the bottom of the phosphor screen. These electrons carry similar information to the conventional backscattered electron signal. Using Forward Scattered Electron (FSE) imaging diffraction contrast is enhanced and the resultant signal makes the presence of individual grains easy to identify. The forward scattered electron signal produced is therefore ideal for EBSD investigations. However, the user may use any electron signal as required for the reference image.

Continuous Scan

If the Continuous Scan option is checked, you will see the image start to scan down the window and it will continue to refresh after each frame. If there are any instabilities in your specimen (e.g., charging or drifting problems) then these will be apparent as the image may shift slightly after each scan.

In order to stop the continuous scan, press the Stop button.

• Click once and the scan will stop when the current frame is complete.

• Click twice and it will stop immediately.

Note that when navigating to a different step, the scan will stop at the end of a frame.

Number of Frames

Enter the number of times you wish the beam to scan the site of interest for image acquisition.

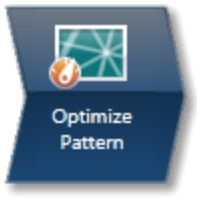
Frame Time (secs)

The frame time is displayed in seconds. The value of frame time depends on the resolution, speed and mains synchronize if available.

See Also:

AutoLock on page 96

Optimize Pattern



This step contains the necessary functions to allow optimal EBSP acquisition and processing.

Monitoring the EBSP

The electron image shown in the top left quadrant is the image collected in the Scan Image step. As you enter the Optimize Pattern Step the position beam tool is highlighted on the toolbar. Positioning the beam around the image allows you to check the quality of the EBSPs from different points on the specimen. The EBSP is shown in the top right quadrant (unprocessed EBSP). When the tool is selected the beam can be controlled by the mouse as well as by the keyboard (Shift will give a coarse shift and Ctrl will give a fine shift with the arrow keys). Alternatively, press Center to position the beam at the center of the image. Press the Off button to release the beam.

Adjusting the Camera Settings

Select the binning and gain for the camera, suitable for the analysis, and then set the exposure time to get suitable illumination. Alternatively press Auto to automatically adjust the exposure time to achieve a signal strength between 85 and 95 (see below).

The Nordlys detector (whether NordlysNano or NordlysMax) allows you to adjust the quality of the diffraction pattern to suit the particular type of analysis.

Binning

By clustering groups of pixels (binning), it is possible to collect lower resolution EBSP's at higher speeds. Depending on the detector used, various binning options are available. The table below illustrates the general trend for binning levels and when to use them:

Binning	Suggested Use
None	High resolution EBSPs for posters and publications.
2x2	Regular EBSD analyses where accuracy is more important than extreme speed – e.g. phase identification.
4x4	Regular EBSD analyses where speed is an important issue (e.g. routine grain size & texture analyses) .

Binning	Suggested Use
8x8	High speed analyses where a slight loss in accuracy is not important (e.g large area texture analyses).

Camera Gain

Adjust the gain level to suit your experiment. High gain will increase the sensitivity of the camera but may introduce more noise as it is the total signal (signal + noise) that is amplified. The noise level indicator (see below) is provided in the application to allow you to look at the effect of adjusting the gain on the quality of unprocessed EBSP and hence which setting works best for your specimens.

Exposure Time

Once you have selected the level of binning, enter a camera exposure time (also known as the integration time). Even with low signal strength values, the software copes very well with such EBSPs.

If the exposure time is set too low, there will be insufficient signal in the image and it will appear too dark. If the exposure time is set too high, part of the image may be over-saturated forming a white area.

The exposure time (for a given binning level) will depend on the probe current you have used to collect your electron image. With some microstructures, it will be necessary to work with low probe currents to achieve the spatial resolution necessary to resolve the desired features. In this case you will need to adjust the exposure time and binning accordingly.

Histogram of the Unprocessed EBSP

This histogram allows you to look at the distribution of pixel intensity in the unprocessed EBSP. You may use the mouse wheel to adjust the size of the histogram.

- **Signal Strength**

The signal strength is a value which lies between 0 - 100. It corresponds to the position of where the end tail of the histogram lies on the x axis of the histogram. We recommend that you use a value between 85 and 95. If the signal strength is too low or too high, it will appear in the red region. If the signal strength is an acceptable value, it will appear in the green region.

Anything above 95 is strongly not advised as it could mean over exposure.

- **Noise Level**

This is a useful tool to monitor the noise level as you change parameters such as gain, binning and exposure time. The value is the percentage of noise in the image where 100 corresponds to no signal but all noise whereas 0 corresponds to all signal.

- **Time per Frame**

The time per frame is the time taken for the camera to read out one EBSP. Depending on the camera settings this time can differ slightly from the requested integration time.

Image Processing Settings

Initially, any small clusters of pixels arising due to defects or scratches on the phosphor will be masked out and disregarded in further processing of the EBSPs such as background correction. Background correction methods as well as frame averaging are then available to use to improve the quality of the EBSPs. The processed EBSP is displayed below the unprocessed EBSP to show this improvement. Once the selection is made, these settings will be used whenever an EBSP is acquired. It should also be noted that automatic stretching of the processed image takes place in order to make full use of the dynamic range in the image.

Background method

An EBSP consists of a series of relatively weak Kikuchi bands on a strong, non-linear background. Removing this background produces a much clearer EBSP. When a background correction method is applied, the EBSP pattern is divided by a model of the background, and the ratio that is obtained is then multiplied by a pixel whose value is mid range. Note that division is used because the strength of the pattern signal correlates with the variation in the background.

There are two methods commonly used when applying a background correction 'Static' and 'Dynamic'.

- A static background is a model of the background generated by averaging a large number of pattern images based on the signal from many different orientations.
- A dynamic background is a model of the background extracted from and used on the same pattern image. It can be derived by fitting a suitable mathematical model of the background to the image, or by filtering out the high frequency pattern, taking the low frequency residual as the background.

Static background

In order to use a Static background, press the Collect button and select the number of frames. A higher number of frames will give cleaner EBSPs but will take longer to collect. Note that the default value is 64 frames. You are then able to use the Static background correction by checking this option.

The simplest way to define a background is to rapidly scan an area of the specimen that contains many grains and while acquiring an average EBSP. Backgrounds for single crystals may be produced by heavily defocusing the electron beam on the specimen.

Advantages:

- A static background can compensate for sensitivity variations even scratches in the phosphor.
- The background does not have to be calculated for each EBSP acquired.

Disadvantages:

- The background is likely to change position and magnitude when the
  - Position of the detector changes.
  - Position of the Specimen changes in the chamber.
  - Mean atomic number (Z) changes significantly in a multi-phased material.
  - Position of the electron beam changes on the specimen surface at low magnification.
  - Accelerating voltage is changed.

- Stage tilt angle is changed.
    - Note that any changes to gain, binning or exposure time mean that a new static background should be collected.

Auto Background

Check the Auto Background routine option to background correct the acquired EBSP's on the fly.

The Auto Background process is very efficient at preserving the original shape and features of the data such as the Kikuchi bands whilst removing the unwanted background.

Advantages:

- Seamless process requiring no user intervention.
- Independent of acquisition conditions.

Disadvantages:

- The dynamic correction is, per EBSP, slower than the static one because the background has to be calculated for each pattern.
- It cannot compensate for local irregularities in the sensitivity of the phosphor.

Frame Averaging

Enter the number of frames you wish to acquire. These frames are then averaged to reduce the noise level in your EBSP. A higher number of frames will give cleaner EBSPs but will take longer to collect. The time per frame displayed under the histogram includes the frame averaging.

Please note that there is a slight difference between the frame averaging that is applied to the live monitoring of EBSPs and the frame averaging that is applied when snapping an EBSP or doing mapping. The frame averaging method for monitoring uses a rolling average buffer so that the view can be refreshed at the rate of the camera. Other EBSP acquisitions will collect precisely the number of frames from the camera, as specified in the “Frame Averaging” setting for each beam position, and average those frames together to form a single processed EBSP.

See Also:

Optimize Pattern - Toolbar below

Context Menus - Image on page 115

Brightness, Contrast and Gamma Controls on page 170

Optimize Pattern - Toolbar

Tool	Description
	You can move the image using the Pan tool. Use the wheel mouse to zoom in and out.

Tool	Description
	Five tools are available to add annotations: Caliper, Angle, Text, Rectangle and Ellipse. Select the tool by clicking on it and then click on the image to add annotation. For example to add text select the Text annotation tool, click on the image where you wish to enter the text and then start typing the text. To delete annotation double click on it to select it and then press the Delete key on the keyboard or use the context menu to select and to delete.
	When the tool is selected, positioning the beam around the image allows you to check the quality of the EBSPs from different points on the specimen. The EBSP is shown in the top right quadrant (unprocessed EBSP). The beam can be controlled by the mouse as well as by the keyboard (Shift will give a coarse shift and Ctrl will give a fine shift). The On/Off/Center functions are linked with this tool. If On is pressed, the tool will automatically be selected.
	With this tool you can view the Intensity and beam position for any pixel in the image. Simply select the Show Data Values tool from the toolbar and then hover on image. The values will be displayed as you move from pixel to pixel.

Optimize Solver

This step contains the necessary functions to allow you to acquire, index and refine EBSPs.

Positioning the Beam

As you enter this step, the ‘Acquire an EBSP from a point' tool is selected by default. When this tool is selected the beam can be positioned on the image and its position can be controlled by the mouse as well as by the keyboard (Shift will give a coarse shift and Ctrl will give a fine shift). Note that you can also center the beam by pressing the Center button.

Once the beam is positioned, release the mouse and you are ready to snap a pattern. As described below, if Auto is checked, a pattern will automatically be snapped but if it is not, you should then press the ‘Snap’ button.

If you wish to release the beam back to SEM control, press Off.

In addition to acquiring a live EBSP by positioning the beam, you may wish to optimize the solver settings based on EBSPs from previously acquired EBSD Maps. It is often very useful to check the solver settings before setting up an area for reanalysis. In the same manner as described above, select the 'Extract EBSP from EBSD Map' tool on the toolbar. This tool will allow you to place the cursor on the map and extract the EBSP from the specified position. When the cursor is placed the EBSP is automatically extracted. If the Auto function is enabled then the band detection and indexing will automatically take place.

Band detection and Indexing of the Processed EBSP

Auto

By enabling Auto, the system will automatically snap a live EBSP, detect the bands and try to index with the selected settings. It will also automatically update whenever a change is made to beam position, the EBSP, the detected bands or the analysis settings and phases.

If you do not select Auto, you must press Snap, Detect and Index in order to go through the steps of snapping a pattern, detecting the bands and indexing the pattern.

Load EBSP

This function allows you to load an EBSP from file together with its calibration and acquisition conditions. You will need to fill in the acquisition conditions when loading the EBSP in order for AZtec to be able to analyze the EBSP.

Depending on the calibration information available with the EBSP, the calibration conditions will either be those based on the AZtec system calibration or a previously acquired calibration file. In the latter case you will need to add additional information into the required fields.

Settings

Under Settings, adjust the Hough resolution, number of bands and band detection method to ensure you aid the identification of the acquired EBSP. You should also ensure that you have included the phases you wish to use and their corresponding number of reflectors.

Band Detection Area

Selecting the 'Edit Band Detection Area' tool on the Optimize Solver toolbar will allow adjustment of the band detection area. When the tool is active the Area of Interest will be displayed on the EBSP and by use of the mouse, the area can be moved or resized.

Edit EBSD Bands

The application will automatically detect a number of Kikuchi bands, depending on the number of bands you have set it to detect. However, you have the ability to edit any existing band, delete bands or manually add bands. In order to interact with the detected bands select the 'Edit EBSD Bands' tool on the Optimize Solver toolbar. This will allow you to delete bands, draw new bands or modify existing bands.

Context menu

Right click on the EBSP to access various options in the context menu such as blinking the solution and removing the display of detected bands. It is also possible to switch on/off the display of the Pattern Center, marked with a green cross. Further options are available under Preferences from the main menu.

Status bar beneath the EBSP

Cycle Times

Two cycle times are shown below the EBSP. The Analysis time is the time it takes for the software to perform the analysis of the acquired EBSP and the Detector time is the time it takes for one EBSP to be acquired by the detector and transferred to the PC.

The Analysis time will depend on the selected analysis parameters, and the Detector time will depend on the selected detector settings. In order to acquire data at high speed it is important to keep both the Analysis time and the Detector time low. If the analysis time is highest then the system will acquire at a lower speed than indicated by the detector time.

Number of Bands

This is the number of bands detected on the EBSP.

Band Contrast

Band contrast is an EBSP quality number. The higher the number, the better the EBSP quality.

Band Slope

Band slope is an EBSP quality number. The higher the number, the better the EBSP quality.

Hough Viewer

The Hough space display, accessed by pressing X, shows the EBSP after transformation into Hough space. The Hough transformation converts Kikuchi bands into peaks which are used to find the edges or centers of bands during automatic band detection. Depending on the number of

bands you have entered under Settings, these maxima will be marked with numbers to show which ones correspond to the detected bands. The highest number corresponds to the strongest peak. You may toggle between the two icons on the Hough Space display window to switch between showing all bands or currently selected band.

Move the mouse over Hough Space and the corresponding location on your EBSP, will be displayed. Hover over the maxima to see how it relates to the band in the EBSP.

Solutions

This area shows the results of the EBSP indexing process. A simulation of the selected solution will be overlaid on the EBSP allowing a visual comparison between the simulation and the original EBSP. Note that the order of the solutions can be changed if you select 'Use Band Widths in Sorting' under Settings in the Processed EBSP area if you are using the edges of the bands during band detection (See later).

The following parameters are displayed for each solution:

MAD

MAD or Mean Angular Deviation is the goodness of fit of the solution. The smaller the number, the better the match between the detected Kikuchi bands and the simulation. A number less than 1° is acceptable for most systems.

If Advanced Fit has been switched on, then the Advanced Fit index ("AFI") will also be displayed instead of the MAD. This, like the MAD value, is also a goodness of fit parameter. However, it is independent of the band detection process, and larger AFI values indicate better solutions. The AFI value is also affected by the quality of EBSP.

Orientation

These are the three Euler angles that describe the orientation of the crystal lattice as determined by the indexing procedure.

Refinement

The refinement routine tries to compensate for any instability in the readout of WD or ID. You may choose to refine your calibration based on a selected solution. You should ensure that this solution is correct as this refinement will potentially produce an offset in Working Distance (WD) and Insertion Distance (ID) that will subsequently be applied when indexing any subsequent patterns.

Phases for Acquisition

You should ensure that you have included phases you wish to solve with within the Phases for Acquisition area. If you wish to add or delete any phases, this can be done in the Describe Specimen Step. However, you can include or exclude individual phases from the list within the Optimize Solver step or change the number of reflectors and color can be set per Phase in this step.

In addition, details about any highlighted phase can be viewed in the Phase area by selecting the 3D Phase View, Phase Details and Reflectors tabs.

See Also:

Optimize Solver - Settings on next page

Context Menus - Image on page 115

Brightness, Contrast and Gamma Controls on page 170

Optimize Solver - Settings

Detect

Select the settings to 'Detect Band edges' when the edges of the Kikuchi bands are sharp and clearly visible. The band edges are detected based on an initial detection of the peak position in the Hough space and then a fine tuning (using the edges) of the bands on the EBSP is performed. For blurred or narrow bands, Band centers may be better.

Number of Bands

This is the number of bands used for indexing. Increasing the number of bands will give slower but more reliable indexing. The default value is 7. The relation between the number of bands and the number of reflectors are critical in order to get the best performance of the system and it is therefore important to optimize these two parameters.

Hough Resolution

The Hough Resolution is the radius of the AOI in pixels. The following table is a good guideline as to which Hough resolution to use. However, it is worth testing different Hough Resolutions to see what value provides the optimum results for your specimens.

Resolution = 40-45	Ideal for fast data collection, where small angular errors (<2°
Resolution = 60	A good compromise between speed and angular resolution.
Resolution = 75-80	Ideal for more accurate, but slower indexing.

Use Band Widths in Sorting

In many specimens, two phases with the same crystal structure co-exist but where the only difference is a small difference in band width.

When checked, this option enables phases of the same crystal structure to be discriminated from their respective EBSD patterns using band widths provided their lattice parameters differ by >10%.

A number of indexed solutions for your analysis are shown in the area below your snapped EBSP. Note that the solution order can be changed if you select ‘Use Band Widths in Sorting’ if you are using the edges of the bands during band detection.

Use Advanced Fit

Switching on the Advanced Fit mode will improve the angular accuracy of the indexing procedure, but will significantly slow down the indexing process. Once checked, enter the Advanced Fit Level you wish to work with (1 = low, 4 = high). Advanced fit goes back to the full EBSP and optimizes the solution fit.

Note that for standard use, Advanced Fit should not be switched on.

Band Detection Area X

This is the X coordinate of the Band Detection Area Center. The Band Detection Area can be moved by selecting the 'Band Detection Area' tool on the Optimize Solver toolbar and dragging the Area displayed with the mouse. Alternatively you may enter a value here. As the Band Detection Area is moved, this value will automatically update.

Band Detection Area Y

This is the Y coordinate of the Band Detection Area Center. The Band Detection Area can be moved by selecting the' Band Detection Area' tool on the Optimize Solver toolbar and dragging the Area displayed with the mouse. As the Band Detection Area is moved, this value will automatically update.

Band Detection Area Radius

The Band Detection Area can be resized by selecting the Band Detection Area tool on the Optimize Solver toolbar and dragging the perimeter displayed with the mouse will change this value.

Apply Refinement

Check this if you wish to apply a previous refinement to the solver.

Acquire Map Data

A Map is a regularly spaced grid of automatically acquired and solved EBSPs. In this step you can setup acquisition of EBSD or combined EBSD & EDS data from either the full area or a selected area.

How to Acquire Maps

The default way of selecting an area to map is by using the Map Area Calculator tool which is selected by default as you enter this step. This tool allows you to link the acquisition time, step size and area of a rectangular map region.

Alternatively, to acquire map data from a region, select the required map acquisition tool from the standard region Rectangle, Ellipse and Freehand tools available from the toolbar. If you wish to do a full area map, select any of the region tools and press start. If you wish to select a reduced area map, select one of the standard region tools, click on the image and drag with the left mouse to outline a region on the image. Maps will then be automatically acquired from the scanned region on releasing the mouse.

The Map Area Calculator

The Map Area Calculator tool works in conjunction with the settings that appear above the image when the Map Area Calculator tool is selected from the toolbar.

There are three ways to use the calculator:

- It is possible to lock the Step size. After defining the acquisition area the calculator will automatically show the acquisition time duration and vice versa.
- It is also possible to lock the acquisition time, then either while defining the acquisition area the Step size will be adjusted or by defining the Step size, the acquisition area will be adjusted to keep the acquisition time constant.
- Alternatively, the acquisition area can be locked, then either by defining the acquisition time the calculator will adjust the Step size or by defining the Step size, the acquisition time will be adjusted to keep the acquisition area constant.

When using the Link Aspect Area button, the width to height ratio of the map area is linked and changes in one direction will automatically result in a change of the other direction.

Note that whatever settings you have locked, you may move the acquisition area using the mouse and these settings will be retained. Pressing the ‘Center’ button will automatically reposition the area to be mapped in the centre of the field of view.

If you define the parameters for the map and then press the ‘Maximize’ button, the software will automatically fill the field of view with as many points as possible with the defined step size.

Select the acquisition parameters from the Settings cog on the acquisition toolbar and press Start to acquire map.

When EDS is switched on, the settings for Number of Channels, Energy Range and Process Time will be available as for EDS mapping. Note that the resolution and dwell time of the element

maps will be determined by the EBSD map setup. The results can be displayed as a layered map, or as individual maps, depending on the view you select. Individual maps and layered maps are automatically stored within the current project file.

The box on the SEM image shows the location and size of the area to be mapped. Note that the area can be positioned and rescaled using the mouse but you should ensure that the area fits completely within the field of view. The area from where the data will be acquired is shown on top of the electron image.

Defining a map region using the standard region acquisition tools

To acquire map data from a region, select the required map acquisition tool from the Rectangle, Ellipse and Freehand tools available from the toolbar. Note that by default, map data will be acquired from the full area. Click on the image and drag with the left mouse to outline a region on the image. Maps will be automatically acquired from the scanned region on releasing the mouse.

	**Rectangular** Click on this icon to select the Rectangular Tool. Click and drag the mouse on the image to outline a rectangular area. When you release the mouse button, an area will be outlined and map data will be acquired from it. This is a useful tool for examining regular shaped features and areas on an image.

	**Ellipse** Click on this icon if you wish to define an elliptical area on the image. Click and drag the mouse on the image to outline an area. When you release the mouse button, an area will be outlined and map data will be acquired from it. This tool allows you the flexibility of outlining an oval or ellipsoid feature on an image. Note: The ellipse is formed as the greatest ellipse within the square area that the mouse is drawing.
	**Freehand** Click on this icon if you wish to acquire a spectrum from an irregular shaped feature on the image. Click and drag the mouse around the feature on the image. Once you have defined the feature release the mouse button. Map data will be acquired from it.

Map data will be acquired according to the resolution currently set under Settings. If you wish to use a different step size to the one determined by the resolution, type in the required step size.

Map Display

If you have selected the mode to view the maps in addition to your acquisition area, the layered image, maps (both EBSD and EDS, if selected) and electron image/s can be displayed. In this

mode, you can choose how you wish to view your data from Standard, Interactive or Summary view available from the drop-down list above where the maps are displayed.

Map data will be acquired according to the resolution currently set under Settings. If you wish to use a different step size to the one determined by the imaging resolution, type in the required step size.

Map Size

You can choose the number of maps per row using the slider bar for displaying maps you wish to view in the Standard and Interactive display mode.

Display Modes

Maps can be viewed in three different display modes available from the drop-down list on the Display toolbar:

- Standard
- Interactive
- Summary

Link/Unlink

Press  to link images for manipulation of all layers using the Pan or Zoom control.

Press  to unlink images. You can manipulate individual layers using Pan or Zoom control.

Brightness and Contrast

You can adjust the brightness and contrast of the currently selected image or map. Press  on the Display toolbar to open the Brightness and Contrast dialog.

Auto Brightness and Auto Gamma

Using the Auto brightness and Gamma buttons  on the bottom right hand corner of the Map display window allows you to change the Brightness/Contrast and Gamma for all the maps.

Layered Images

- The layered image allows you to see the X-ray or EBSD maps overlaid on the electron image. For EBSD, the default layered image is the electron image together with the Phase Color Map if you have more than one phase, however you can edit this configuration as detailed below. If there is only one phase, the IPF Z is shown.
- The EDS layered image consists of an electron image and X-ray maps whose selection is defined according to the current settings.
- You can add or remove a layer from the layered Image by toggling the Layered Image icon  in the top left hand corner of each map.

- If you have lots of maps, it may be useful to minimize some of them pressing the minimize icon in the top right hand corner of each map.
- You may want to delete a map from the analysis completely. In which case press the delete icon in the top right hand corner of each map. In the case of EDS, if an X-ray map is removed, it means this element will not be identified automatically (by AutoID) and will be excluded from the current analysis. Note: If an element is present in a specimen, deleting or excluding it will affect the TruMap results.
- You can choose the color for your maps, adjust intensities and decide which maps to add to the Layered image. Alternatively, you can let the software do this automatically for EDS. Pressing the AutoLayer button (which is located in the bottom right hand corner of the Map Display window) will automatically scale and color all the maps and in the case of EDS maps select the best ones to provide an effective color image that delineates regions of different composition. Maps will be auto-brightness corrected and those that show similar structure will be assigned the same color. Maps that are very noisy will be shown in grey. The most significant map for each assigned color will be added to the Layered Image.

Data from Map Acquisition

Once data acquisition starts, the Data Tree gets populated with new items as shown in the screen shot below:

Electron image

This can be a secondary electron image (SE) or backscatter electron image (BSE) but for EBSD analysis it will generally be a forescatterd electron image (FSD) depending on the detector hardware installed.

Map Data

EDS and EBSD Map data are contained in their respective Map Data folders. As Data acquires, EBSD Maps will acquire into the EBSD Data folder. If you have selected the option to acquire EDS data in addition to your EBSD data, EDS Maps will acquire into an EDS Data folder.

The EBSD Data folder contains the following EBSD images:

- Band Contrast
- Phase Color
- Euler Color
- IPF X Color
- IPF Y Color
- IPF Z Color

The EDS Data folder contains:

- Map Sum Spectrum
- X-ray Element Maps

X-ray Element Maps

Two modes of mapping are available, Window Integral Maps and TruMaps. Press the appropriate button to select the mapping mode from  located at the bottom of the workspace.

Standard Window Integral maps (counts in the energy window) are acquired for the element list chosen for analysis. These are raw X-ray maps which are not corrected for background or peak overlaps.

The second mode of mapping is TruMap. You can process the map data as TruMaps which are corrected for background and peak overlaps.

Layered Images

Layered images are composite images generated by overlaying selected maps.

If you have chosen to acquire EDS data in addition to EBSD data, two layered images will automatically be created:

- EDS Layered Image (#)
- EBSD Layered Image (#)

For EBSD, the default layered image is the electron image together with the Phase Color Map if you have more than one phase, however you can may edit this configuration. For EDS, the layered image consists of an electron image and X-ray maps whose selection is defined according to the current settings.

Post Acquisition Image

A new scan of the electron image with the current settings after the map is finished can be acquired by selecting this option under Map acquisition settings. This can be used for checking drift of the specimen.

T i p s

Hover the mouse over the Map Data entry on the Current Site to see the acquisition progress and information such as speed and hit rate.

You may wish to delete a map from the analysis completely, in which right click to access the context menu on the Data tree or Current site.

Reanalyze Map regions

If you have acquired an EBSD Map with stored EBSPs it is possible to reanalyze a map region with new settings. Setup the required phase and solver settings (in previous steps) and then use one of the reduced area reanalysis tools from the toolbar to specify the area which you want to reanalyze as shown in the table below:

Icon	Description
	Click on this icon to select the tool. Click and drag the mouse on the image to outline a rectangular area. When you release the mouse button, an area will be outlined and map data will be reanalyzed from it. This is a useful tool for examining regular shaped features and areas on an image.
	Click on this icon if you wish to reanalyze data from an irregular shaped feature on the image. Click and drag the mouse around the feature on the image. Once you have defined the feature release the mouse button.

Icon	Description
	Click on this icon if you wish to define an elliptical area on the image. Click and drag the mouse on the image to outline an area. When you release the mouse button, an area will be outlined and map data will be reanalyzed from it. This tool allows you the flexibility of outlining an oval or ellipsoid feature on an image. Note: The ellipse is formed as the greatest ellipse within the square area that the mouse is drawing.

Reanalyzed map data will be automatically stored in the data tree as shown below:

See Also:

Context Menu - Map Viewer on page 174

Acquire Map Data - Settings below

Display Modes and Map View Settings on page 231

Acquire Map Data - Settings

Resolution

The resolution of a map is defined as the number of picture points or pixels along the x and y axes e.g., 256 x 256, 512 x 512 or 1024 X 1024. The quality of the image improves as the resolution at which an image is acquired is increased. A microscope monitor/CRT is usually a rectangular

display (rather than square), so the resolution is displayed as a rectangle i.e., 256 x 200 in order to take into account the aspect ratio. The y dimension is set at installation, when imaging is calibrated and it will vary from system to system.

Select a resolution for Map acquisition from the following options available

64 x 64

128 x 128

256 x 256

512 x 512

1024 x 1024

2048 x 2048

4096 x 4096

Step Size (nm)

This is the size of the spacing between beam acquisition points. As you change the resolution, this will be updated. If you wish to use a different step size to the one determined by the resolution, type in the required step size.

Include EDS

Check this option if you wish to acquire EDS data with your EBSD Data.

Number of Channels

Select number of channels from the drop down list of Auto, 1024, 2048 or 4096 (4K) with which you wish to display the spectrum. The number of eV/channel will depend on both the energy range and the number of channels you select:

Energy Range (keV)	Number of Channels	eV/channel
0-10	4096	2.5
0-10	2048	5
0-10	1024	10
0-20	4096	5
0-20	2048	10
0-20	1024	20
0-40	4096	10
0-40	2048	20
0-40	1024	40

In the Auto mode, the software checks for the energy range selected and sets the appropriate number of channels.

Energy Range (keV)

Select a spectrum energy range from the available options of Auto, 0-10, 0-20 or 0-40 keV from the Energy Range drop down list.

An appropriate energy range should be selected in conjunction with the current microscope accelerating voltage. If the accelerating voltage is above 10 kV, in order to view lines which may be excited above 10 keV, the 20 keV range should be chosen. Below 10 kV, it may be more appropriate to choose the 10 keV range since no lines above 10 keV will be excited.

In the Auto mode, the software checks for the accelerating voltage set on the microscope and selects a suitable energy range in the software.

Process Time

Select the Process Time from the drop-down list of Process Times: Default and 1 to 6. The Process time is the length of time spent reducing noise from the X-ray signal coming from the EDS detector during processing. By selecting different Process times it is possible to reduce differing amounts of noise. The longer the Process time, the lower the noise.

If noise is minimized, the resolution of the peak displayed in the spectrum is improved, the peaks are narrower and it becomes easier to resolve the peak from another peak that may be close by in energy.

If Default is selected, the Process Time is automatically set to a suitable value.

Post Acquisition Image

If this option is selected, a new scan of the electron image with the current settings after the map is finished can be acquired by selecting this option under settings. This can be used for checking any drift of the specimen.

Display Modes And Map View Settings

The settings are described below:

Display Modes

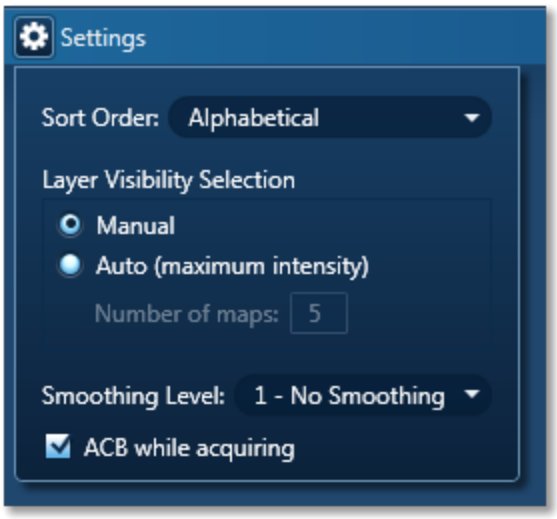
Maps can be viewed in three different display modes available from the drop-down list on the Display toolbar:

- Standard
- Interactive
- Summary

In the Summary view, you see details of the energy window and X-ray line used for each EDS map if you have selected to acquire EDS maps with your EBSD data. Other details such as Layer Name, Map Color (where appropriate) and if it has been selected for the Layered Image are given.

Map View Settings

You can manipulate and view the data by using various parameters available in the Settings:



Sort Order (EDS)

There are three different ways of sorting maps:

- Alphabetically
- By atomic number
- By maximum intensity in map - sorts on the value of the brightest pixel in cps.

Layer Visibility Selection (EDS)

You can choose how the visibility of layers is selected in the layered image. There are two options: Manual and Automatic. In the Manual mode, you must select which X-ray maps to be included in the layered image.

In the Automatic mode, first N maps (Number of Map that you entered) are selected by the maximum intensity.

Smoothing Level

The maps may contain a lot of statistical noise if there is not sufficient data. The noise can mask the distribution of elements in the maps. You can filter out some of this noise by applying Smoothing Level. This operation applies a lowpass filter to an image to smooth the data.

Smoothing Level, 3X3

The lowpass filter uses the following 3x3 kernel:

1/9 1/9 1/9

1/9 1/9 1/9

1/9 1/9 1/9

Smoothing Level, 5x5

The lowpass filter uses the following 5x5 kernel:

1/25 1/25 1/25 1/25 1/25

1/25 1/25 1/25 1/25 1/25

1/25 1/25 1/25 1/25 1/25

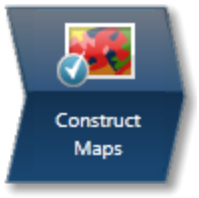
1/25 1/25 1/25 1/25 1/25

1/25 1/25 1/25 1/25 1/25

ACB while acquiring

Check this option if you wish to apply automatic brightness or automatic gamma to maps during acquisition depending on your pre-selection of Auto Brightness or Auto Gamma.

Construct Maps



In this step, you have the option to work more closely with your acquired Maps and construct new EBSD and Layered Images. If you have acquired an EBSD Map with stored EBSPs it is also possible to reanalyze a map region with new settings such as new solver settings or even solving by including different phases.

Map Display

In a similar way to the 'Acquire Map Data' step, a layered image, maps (both EBSD and EDS, if selected) and electron image/s are displayed. You can choose how you wish to view your data from Standard, Interactive or Summary view available from the drop-down list above where the maps are displayed. You can add or remove maps from the layered Image by toggling the layered Image icon in the top left hand corner of each map.

If you have more than one map, it may be useful to minimize some of them pressing the minimize icon in the top right hand corner of each map.

Map Size

You can choose the number of maps per row using the slider bar for displaying maps you wish to view in the Standard and Interactive display mode.

Display Modes

Maps can be viewed in three different display modes available from the drop-down list on the Display toolbar:

- Standard
- Interactive
- Summary

Link/Unlink

Press  to link images for manipulation of all layers using the Pan or Zoom control.

Press  to unlink images. You can manipulate individual layers using Pan or Zoom control.

Brightness and Contrast

You can adjust the brightness and contrast of the currently selected image or map. Press  on the Display toolbar to open the Brightness and Contrast dialog.

Auto Brightness and Auto Gamma

Using the Auto brightness and Gamma buttons  on the bottom right hand corner of the Map display window allows you to change the Brightness/Contrast and Gamma for all the maps.

Constructing and Deleting EBSD Images

In order to construct new EBSD Images, expand the 'Construct EBSD Images' panel and press the required Image. A new EBSD image will appear under the EBSD Data node in the Data tree. If you click on any image on the Data tree, it will appear in the image viewer area of the application.

You may wish to delete a map from the analysis completely. In order to do this, right click to access the context menu on the Data tree or Current site.

Reanalyzing a Map region

If you have acquired an EBSD Map with stored EBSPs it is also possible to reanalyze a map region with new settings such as new solver settings or even solving by including different phases. Setup the required phase and solver settings (in previous steps) and then use one of the reanalysis area tools from the toolbar to specify the area which you want to reanalyze.

Icon	Description
	Click on this icon to select the tool. Click and drag the mouse on the image to outline a rectangular area. When you release the mouse button, an area will be outlined and map data will be reanalyzed from it. This is a useful tool for examining regular shaped features and areas on an image.
	Click on this icon if you wish to reanalyze data from an irregular shaped feature on the image. Click and drag the mouse around the feature on the image. Once you have defined the feature release the mouse button.

Icon	Description
	Click on this icon if you wish to define an ellipsoid area on the image. Click and drag the mouse on the image to outline an area. When you release the mouse button, an area will be outlined and map data will be reanalyzed from it. This tool allows you the flexibility of outlining an oval or ellipsoid feature on an image. Note: The ellipse is formed as the greatest ellipse within the square area that the mouse is drawing.

Orientation information

The 'Orientation Information' tool will allow you to click on a point on the map (or image) and the solution and unit cell orientation will be shown in the Orientation Information area. If data was acquired with stored EBSPs the solution can be displayed together with the EBSP which helps you to interrogate the acquired data.

Phase ID

The Phase ID navigator has six steps. Describe Specimen, Scan Image and Optimize Pattern are described in the Map section. Three steps which are unique to Phase ID are described in detail below:

Acquire Data

The use of the EBSD to identify unknown phases in a material is called Phase Identification (Phase ID). For many years, EBSD has been used to discriminate between several phases in a specimen using Phase discrimination either by analyzing single patterns from various phases or by automated mapping of such phases.

Phase ID takes this approach a step further by utilizing chemical analysis in conjunction with a crystallographic phase database in order to produce a list of candidate phases. These phases are then used to index the EBSP from the 'unknown' phase.

The steps in a phase ID analysis are typically:

- Locate a grain or particle of the unknown phase. Forward Scattered imaging will help to locate areas of different phases.
- Acquire both EDS and EBSD data simultaneously
- Determine the composition of the phase using EDS analysis.
- Search a crystallographic phase database for all phases using composition ranges of the elements present.
- Index the EBSP using the list of candidate phases.
- Determine the identification of the unknown phase.

Data Acquisition

In this step, you can monitor both EBSD and EDS data coming from specific locations or collect and store data from specific points on your specimen.

Acquire Data toolbar

	Depending on the focus of the mouse, you can move the electron image, Spectrum or Pattern using the Pan tool. Use the wheel mouse to zoom in and out.

	To add text on your electron image, select the Text annotation tool, click on the object where you wish to enter the text and then start typing the text. To delete annotation double click on it to select it and then press the Delete key on the keyboard. To delete all annotations on the object, choose Select All from the Annotations context menu on the image viewer and then press the Delete key on the keyboard.
	Click on this icon to select the Point Tool from the toolbar and then click on the image to start monitoring as you hold down the mouse.
	**From the Spectrum** With this tool you can view the Energy (keV) and counts in any channel of the spectrum. Simply select the Show Data Values tool from the toolbar and then hover on spectrum. The values will be displayed as you move from channel to channel. **From the Electron Image** Clicking anywhere on the image will display the Intensity value at that pixel position.

Monitoring the signals

Click on the acquisition tool  and press the mouse down on the electron image to see the monitoring signals for both EDS and EBSD. Move the mouse over the image to monitor both the EDS and EBSD signals. Once the mouse is released, acquisition will take place according to the acquisition settings for EDS and EBSD.

Spectrum Monitor provides a dynamic way to see what X-rays are being detected at any given moment. It is useful for a quick survey of the specimen to find an area of interest for analysis. Spectrum Monitor uses the current spectrum acquisition settings with the additional setting of the refresh rate for monitoring the spectrum. This refresh time is referred to as the Buffer Size. The default is 20 but can be changed under the Settings for Spectrum Monitor in the Miniview. Increasing the Buffer Size corresponds to a longer refresh rate.

Data collection

Click on the acquisition tool  and click on a location on the electron image. Acquisition will immediately start under conditions currently set for both EDS and EBSD. EBSD acquisition will

use the settings currently set in Optimize Pattern. EDS acquisition will use the parameters currently set under EDS Settings. Please select the link below for details on EDS Acquisition settings.

A Point Data node will immediately appear both in the Data Tree and Current Site views. The associated collected data (EDS Spectrum and EBSP) will be grouped together under this node with a corresponding label. Note that this label can be renamed by selecting the rename option from the context menu on the Data tree and Current Site Data Views.

Depending on the acquisition settings, EDS and EBSD could be acquiring for different lengths, however acquisition will continue until both spectrum and pattern acquisition are complete. The progress of acquisition is displayed on the Current Site tab on the Point Data node.

You may queue up several points to acquire data from by clicking with the acquisition tool on the electron image. Acquisition will continue until all the data has been acquired or the stop button is pressed. Note that the corresponding points are marked on the electron image.

See Also:

Acquire Data - EDS Settings

Context Menus - Image on page 115

Context Menus - Spectrum Viewer

Compare Spectra & MiniQuant Results on page 150

Current Site on page 24

Data Tree on page 71

Search Phase

This step is divided into three main parts:

- Confirming the presence of elements in your spectrum.
- Setting up the search criteria
- Conducting the Phase Search

Spectrum selection

The spectrum displayed in the Spectrum viewer corresponds to the one stored displayed under the currently highlighted Point Data node. Highlight a different Point Data node to display another Spectrum. Alternatively, select the required spectrum from the drop down list box positioned above the spectrum viewer, this will allow selection of not only spectra acquired from the Acquire Data step but also sum spectra or spectra acquired elsewhere in the application.

Confirming the elements in your Spectrum

Part of this step is designed to help you confirm the elements that have been identified by AutoID in your spectrum. The options available are those found in the Confirm element step in the EDS part of the product. These elements are then used to create an element list for qualitative and quantitative analysis. Note that extensive tools including Element Series Markers, Overlays, Element Profiles and Show Candidate Elements are available to help you to manually confirm your elements.

If you wish to manually confirm the automatic peak identification:

- Press the question mark icon to select the Show Candidate Elements tool from the tool bar on the left hand side of the interface.
- Double click on a peak in the spectrum viewer.
- The candidate elements are displayed in a stacked spectra view on the right hand side of the window (you can double click on any of these elements to add or remove it from the confirm elements list).
- You can control what overlays you see in the Spectrum viewer via the 'Confirm Elements Settings'. These overlays can be very useful in helping you to interrogate complex spectra.
- Press Include/Exclude once you are satisfied with the identification of each element to build your list of confirmed elements.

Setting up the Search Criteria

The section under ‘Composition Used For Search’ displays the Quant results for the currently displayed Spectrum in Wt% and At% calculated according to the currently selected Quant Settings. Note that the calculation of the composition takes into consideration the overall tilt of the specimen as entered in the Describe Specimen Step. This chemical information forms the basis of the

search in the databases. However there are some extra settings provided which allow you to optimize the success of your search.

It is worth noting the following points:

- The EDS system may not be set up for obtaining optimized quantified data under EBSD Conditions as the Specimen is highly tilted. You should therefore allow large error margins on the chemical data.
- Light elements may not be detected. Therefore, if you suspect carbides, borides, hydrides to be present in your sample, you should add these manually to the periodic table.
- You should also be aware of the limitations of your databases. For example, database entries may include minor elements (e.g. rare earth elements), hydrous phases (with OH2) or end members of solid solution series. Even in steels, databases will often include the Fe end member, rather than including Cr, Mn, Al etc.
- You should be aware of the difference in spatial resolution of the EBSD and EDS Techniques. Particles < 200nm across may give good EBSPs, but the EDS signal will come mainly from the surrounding matrix.

The following options apply to all elements listed in the table.

Uncertainty

The Uncertainty controls how large the error margins on the quantified EDS data should be. The default for this parameter is 100%. The default value is set high to ensure that phases are not missed during a search due to inaccuracies in the chemical information in the structural databases or errors related to quant on highly tilted samples.

Threshold

The Threshold controls the minimum (allowed) percentage of any element to be automatically included. Note that 10% is the default value for this. If the percentage found of the particular element is less than the threshold, the element is optionally included during the search.

Search Condition

These options apply to the individual entries in the table.

Include

This means include this element and its search range in the Phase Search if the minimum concentration of the element is greater than the threshold value set.

Optional

This means optionally include this element and its search range in the Phase Search if the minimum concentration of this element is less than the threshold value set.

Exclude

This means exclude the element and its search range in the Phase Search.

Wild Cards

A number of wild cards can also be used in the search which means that you are including 0, 1, 2...unknown elements during the search.

You should also note that adding wildcards can significantly slow down the search process of the database.

As an example a search using Ti and one wildcard will find Ti as well as all combinations of Ti and one other element such as TiC and TiN.

Conducting the Phase Search

A list of available databases is shown. Check the databases you wish to search through and press Search. The results of the Phase Search are shown in the 'Phase Search Results' table.

The name of the phase, the database from which it was found, the Space Group and the Composition are all reported in this table. If you wish to limit the search to fewer databases, uncheck the database and press Search again. After performing search, the list of found phases are now stored associated with the highlighted spectrum. This will be used in the next step.

Databases

User created databases can also be used for the phase search process; however it requires that the databases are first copied into the C:\CHANNEL5 directory.

See Also:

Confirm Elements - Settings on page 130

Confirm Elements - Tools on page 131

Element Lists on page 146

Peak Labels on page 116

Compare Spectra & MiniQuant Results on page 150

Quant Settings on page 143

Identify Phase

The purpose of this step is to use the phases in the 'Phase Search Results' area to index the EBSP shown in the image viewer and display the solution(s). The phase that gives the best solution to the EBSP can then be manually added to the list of phases for acquisition. This phase is then available to use, for example, during mapping.

Phase Search Results

This list of phases comes from the spectrum and is generated from the previous step. You can now prepare it for indexing. The list of phases together with the number of reflectors and phase color is shown in this table. You may wish to review the details of a particular phase. To do this, highlight the phase from the list and select the tab you wish to use from the Phase viewer below.

Phase Color

The colors for the phases are picked automatically with the same color being used for the phase as used in the 3D Phase View and the simulation used on the EBSP. You can manually change the color if you wish, but the software will attempt to pick a unique color for each phase.

Maximum reflectors

Rather than having to set the number of reflectors for each phase, you can set a maximum. This means that the closest value to this maximum while still being lower will be automatically found for the number of reflectors for each phase . You can then manually change it afterwards. Note that changing the maximum value will automatically trigger another update of the reflector values for each phase.

Exclude phases from list

In situations where there are a number of phases found it may be useful to exclude some of the phases from the list. Uncheck the phases you wish to exclude when indexing the EBSP.

In order to make a potentially long list of phases more readable, you may wish to display only the included phases. This can be controlled from the 'Show excluded' check box.

Choice of EBSP

The EBSP displayed in the image viewer corresponds to the current EBSP - the one displayed under the highlighted Point Data node. Highlight a different Point Data node in order to display another EBSP. Alternatively, select the required EBSP from the drop down list box positioned above the image viewer. This EBSP might have been acquired at a different time or from a reconstructed point. Use the drop down list box to pick an EBSP that is acquired at a different time/point than the highlighted spectrum.

Indexing the EBSP

There is no limit to the number of phases that can be used for indexing. However, the greater the number, then the slower the Phase ID process becomes. For example, if you have over 100 phases, then it would be advisable to try and restrict your search criteria before indexing the EBSP.

You may check the Auto box which means that band detection and indexing will automatically take place if you change any settings or adjust any of the parameters in the Phase Search Results list. Alternatively, you can manually detect and index the EBSP by pressing the respective buttons. Since indexing is generally slower than normal because of the high number of phases, it is advisable not to use Auto.

Suggested Settings

Adjust the Maximum number of reflectors to a suitable value before indexing. This value is dependent on the quality of the EBSP from the unknown phase, but typically you may want to use more reflectors (e.g. 75-100) than for normal EBSD analysis. Note that increasing the maximum number of reflectors will also slow down the indexing process.

To optimize band detection, it is recommended that you use a high Hough resolution, for example 70, and a greater number of bands, for example 7-9, than for standard EBSD analysis. If the EBSP has well defined, sharp Kikuchi bands, use the Band Edge detection. Alternatively, use Center detection. Careful manual band detection is often the preferred method for accurate Phase ID.

It is advisable in the first instance to switch off the Advanced Fit mode.

The software will now try to index the EBSP using all of the possible phases you have included in the Phase Search lists. This may take a few seconds if you have many potential phases. Note that solving does not involve the 'Phases for Acquisition' list in Describe Specimen.

When the indexing process is complete, any solutions will be displayed below the EBSP in the Analysis area. If there is more than one solution, scroll through the different solutions and visually check the accuracy of the indexing by viewing the simulations. The MAD value displayed in the solution list will provide a good estimate of how well the simulation matches the EBSP. Whilst higher MAD values indicate a better match, it might not be correct if the wrong phase or settings have been used in the process so always check that the solution matches the EBSP. Select the solution from either the phase list or solution list.

Multiple Solutions

In an ideal situation, there will be one solution which is clearly correct. However, there may be several different phases which appear to give a good match. In such cases one or more of the following steps may help to identify the correct solution:

- Check the simulation using more reflectors, by adjusting the number of reflectors in the Phase Search results view.
- Adjust the database search by adjusting the compositional ranges for individual elements if necessary (previous step).
- Optimize the band detection by manually adding more bands if necessary.
- Switch on Advanced Fit. Note that if you had many solutions (>10) then this may take a long time.

Adding Phase for Acquisition

The phase from the solution that you consider the ‘correct’ solution can then be added to the usual list of phases for acquisition (in Describe Specimen) by pressing the ‘Add Phase for Acquisition’ button. You may wish to experiment solving with this full list of phases and a link to the Optimize Solver step is provided.

See Also:

Optimize Solver on page 217

Hardware Control

In this section various software tools that control the hardware are described.

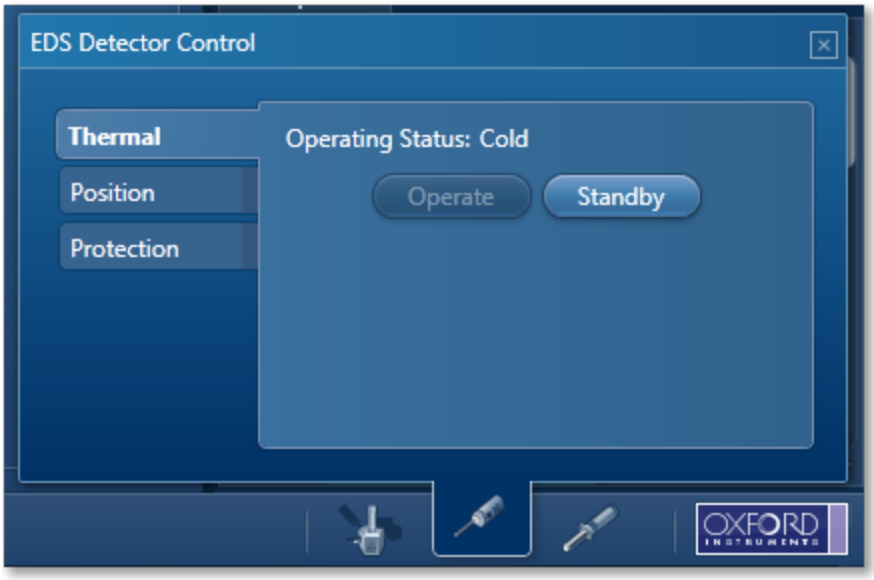
Detector Control

There is a separate control for EDS and EBSD detector hardware which provides information about the hardware status. Each control is accessible from the Detector Control icon in the right-hand side of the Status bar. The Detector Control is displayed as a pop out dialog.

The EDS Detector Control software is described under three current EDS detectors:

- **X-Max Detector**

In the case of X-Max detectors there are three tabs, Thermal, Position and Protection:



Thermal

The Thermal tab displays the current operating status of the detector. The possible states are shown in the table below:

State	Description
Standby	Cooling is powered down. Allows power save and detector longevity (Steady orange LED)
Warm	Detector is not ready for data acquisition (Steady orange LED)
Cool	Detector is ready for data acquisition (Steady blue LED)
Warming	Detector is warming after selecting the Standby mode
Cooling	Detector is not ready for data acquisition (Flashing blue LED)
Fault	A fault has developed (Red LED)

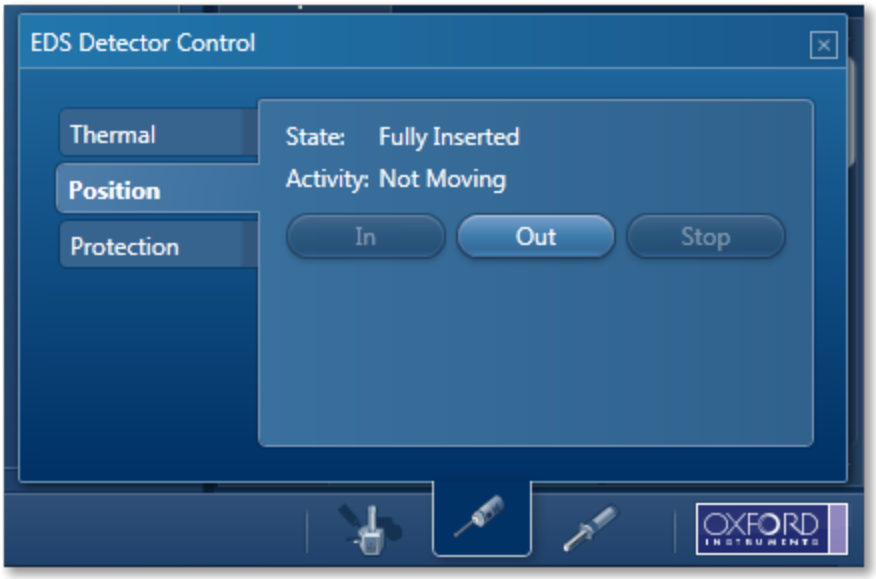
There are two buttons in the Thermal Control tab, **Operate** and **Standby**. Pressing the Operate button initiates the cooling process. When the detector is not in use, pressing the Standby button puts it in the Standby state.

N o t e

If the detector is not cold or it is in the process of cooling, the spectrum acquisition will be disabled.

Position

The Position tab displays the current slide state of the detector:



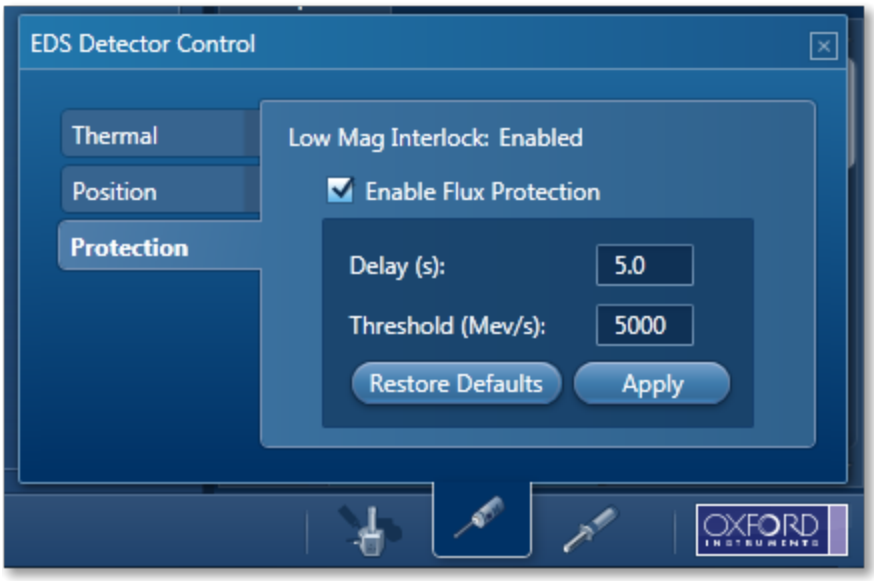
There are three buttons on the Position tab, **In**, **Out** and **Stop**. Pressing the **In** button will start moving the detector into the chamber. The **Out** button will start retracting the detector from the chamber and **Stop** will stop the detector at the current position. The possible detector states are shown in the table below:

State	Description
Fully Inserted	The detector is fully inserted into the microscope chamber and ready for acquisition
Fully Retracted	The detector is fully retracted from the microscope chamber
Indeterminate Position	The detector is at some position in between the end stops
Fault	A fault has developed

The possible activities that may be displayed are Stopped, Moving in, Moving out and Auto-retracting.

Protection

Depending on the software licenses that you have, two options are available to protect your detector from damage by X-rays:



Low Mag Protection

This option is enabled on the X-Max detector provided the system has the relevant license (Low Mag Protection, 06) installed. The Low Mag Interlock status is displayed on the Protection tab as shown in the screen shot above. Putting the microscope into the low magnification initiates auto-retraction of the detector to protect it from the X-rays.

Note that the microscope needs to have hardware interlock for Low Mag Protection to work.

When the user switches out of low magnification mode, the detector will need to be moved back into the chamber by pressing the **In** button.

Flux Protection

The Flux Protection is only available if appropriate license (Detector Flux Protection, 05) is installed. A checkbox for enabling/disabling this option is available on the Protection tab on the TEM system. You can enter the values for Delay in seconds and Threshold in Mev per second (Mega electron volts per second). When the X-ray flux exceeds the threshold value for longer than the specified delay time, the detector will auto-retract.

The user will need to move the detector back into the chamber by pressing the **In** button. If the overload condition persists, the detector will auto-retract again.

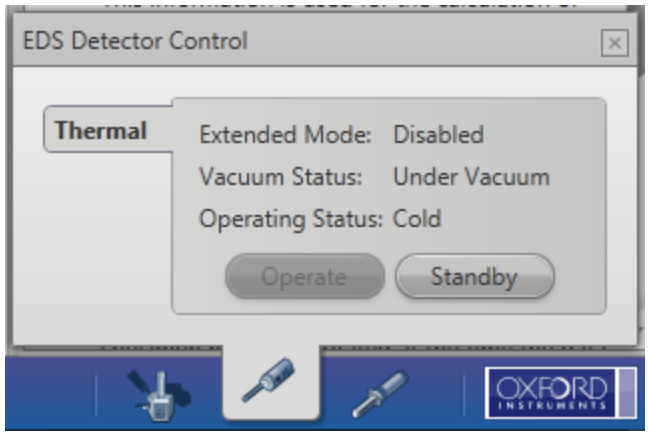
You can restore the default values for Threshold and Delay by pressing the Restore Defaults button if you have overwritten them.

- **X-act Detector**

The Detector Control has Thermal tab:

Thermal

There are two buttons on the Thermal control tab, **Operate** and **Standby.** Pressing the Operate button initiates the cooling process and pressing the Standby button puts the detector in the standby mode.



The Thermal control tab displays the current operating status of the detector:

State	Description
Standby	Cooling is powered down. Allows power save and detector longevity (Steady orange LED)
Warm	Detector is not ready for data acquisition (Steady orange LED)
Cool	Detector is ready for data acquisition (Steady blue LED)
Warming	Detector is warming after selecting the Standby mode
Cooling	Detector is not ready for data acquisition (Flashing blue LED)
Fault	A fault has developed (Red LED)

The Thermal control tab displays the current state of the vacuum in the chamber:

- Under Vacuum - the chamber is under vacuum
- Vented - The chamber has been vented
- Fault - A fault has developed

The Thermal control tab also displays the extended mode state.

N o t e

The start button for spectrum acquisition is disabled if the detector is not cold or it is cooling down.

- **LN2 Detector**

The Detector Control has a number of tabs depending on the type of detector. The tabs are described below:

Thermal

The Thermal tab displays the LN2 status:

State	Description
Ok	The liquid nitrogen level is ok
Low	The liquid nitrogen level is low
In Air	The liquid nitrogen sensor is exposed to the air
Sensor missing	The liquid nitrogen sensor is not plugged into the x-stream

If the LN2 level is low, there will be an audible alarm. You can silence the alarm for one hour by pressing the Mute button.

Position

If the detector has a motorized slide, the Detector Control will show the Position tab.

This tab shows the current slide state of the Si(Li) detector as shown in the table below:

State	Description
Fully Inserted	The detector is fully inserted into the microscope chamber and ready for acquisition
Fully Retracted	The detector is fully retracted from the microscope chamber
Indeterminate Position	The detector is at some position in between the end stops
Fault	A fault has developed

The Position tab displays the activity, Not Moving, Moving In and Moving Out.

There are three buttons on the Position tab of the Si(Li) Detector Control, In, Out and Stop. These controls are used to move the detector in and out of the chamber, and stop it at the current position.

Shutter

If the detector has a pneumatic shutter, there will be a tab for the shutter control.

The Shutter tab has two buttons, **Open** and **Close** to allow the shutter to be opened and closed.

The status of the shutter is either Open or Closed.

EBSD Detector Control

The EBSD detector control is used for controlling the EBSD detector positioning as well as to feed back information related to the positioning/movement mechanism. This control can be accessed from the status bar as shown below:

States

State	Description
Fully Inserted	The detector is moved as far into the chamber as the mechanical end stop allows. This position is set by the service engineer and cannot be changed by the customer.
Fully Retracted	The detector has moved as far out of the chamber as it can.
Intermediate Position	The detector is at an inserted position which is not the fully inserted position or the reference position.
Reference Position	The detector is at the position which has been saved as a reference position by use of the handset.
Auto Retracted	The Touch Sensor has been triggered and the detector has moved all the way out to the home position.

Activity State

State	Description
Not Moving	The detector is not currently moving.
Moving In	The detector is currently moving into the chamber.
Moving Out	The detector is currently moving out of the chamber.

State	Description
Homing	When calibrating the hardware the detector will go through a homing routine which ensures that it finds the correct 0 position for the counter mechanism.
Auto Retracting	The Touch Sensor has been triggered and the detector has automatically started moving out of the chamber.

Position: the insertion distance from fully retracted position is shown in mm (can also be shown in the status bar). This is important because it always shows the position of the detector and constantly updates when the detector is moving.

Touch Sensor

State	Description
Not Touching	The front part of the detector has Touch Sensors and none of these sensors are currently triggered.
Touching	One of the Touch Sensors on the front of the detector is triggered.

Interlock State

On some systems it is possible to setup an interlock between the SEM and the EBSD electronics. The option is not available for all SEMs and the functionality also varies between systems. On some instruments a configured interlock will not limit the detector movement while on others it will not allow the detector to be inserted into the chamber when the interlock is active which means that it cannot move in and if it is already inserted then the detector will be retracted.

State	Description
Allow Movement	This is the default state which is shown when there is no interlocking taking place either because there is no interlock configured or because the interlock allows the detector to be moved.

State	Description
Prevent Movement	This state will only appear if the interlock is configured and the SEM is in a state in which the interlock will not allow the detector to be inserted.

The six buttons shown in the position tab is for actively controlling the movement of the detector.

Pressing the In button will start moving the detector into the chamber until either the movement is stopped by the operator or the detector reaches its fully inserted position.

Pressing the Out button will start moving the detector out of the chamber until either the movement is stopped by the operator or the detector reaches its fully retracted position.

Pressing the Stop button will at any time stop the detector movement immediately.

The **Move To** button is for moving the detector to a specific position. In order to use this first enter the requested insertion distance and then press the **Move To** button.

The **Step In** and **Step Out** buttons move the detector a fixed distance either in or out. The distance is first entered in the field to the right and then by pressing the **Step In** or **Step Out** button the detector will either move in or out by the requested distance.

Microscope Control

The Microscope Control application is provided for controlling and reading the microscope parameters. When you press  located on the right hand side of the Status Bar, the Microscope Control is displayed as a pop up window.

The current value of each parameter is displayed in the appropriate entry box in the Microscope Control as shown in the screen shot below. In this example the Column tab is selected:

The exact way in which each of its functions operates depends on the facilities available on the microscope on which the EDS system is installed. Where possible, parameters can be changed either from the electron microscope controls or the Microscope Control and both systems will be updated accordingly. In some cases it may be possible that the parameters from the microscope are read automatically but can not be changed in the Microscope Control.

If Microscope conditions can not be read automatically, you will have to manually enter the values (see below). It is important that the correct values are entered such as WD (working distance) and magnification as these will be used during quantitative analysis and image calibration.

Column parameters as working distance, magnification and high voltage are also important for the EBSD systems performance, so if these are not read automatically then they must be entered manually.

How to change parameters in Microscope control

Enter a new value into the entry box adjacent to the parameter and press the Set button. The column parameters are Magnification, Working Distance (mm) and High Voltage (kV) which are described below:

Magnification

Magnification is used when calculating the length of the scale marker bar which can be superimposed on an image or the length of a linescan. You can change this in the Microscope Control window.

Working Distance (mm)

Working distance is the distance between the point of focus of the electron beam and the final lens, i.e., when this is changed, the current through the lens is changed. You should ensure that the working distance set on the microscope, in millimeters, is the desired value for performing X-ray microanalysis. The recommended value for your instrument is displayed at the bottom of the Microscope Control window.

Note that if you change the working distance on the microscope, your image may then be out of focus, in which case you will need to adjust the Z of the stage to bring it into focus.

High Voltage (kV) or Accelerating voltage

It is particularly important to have the accelerating voltage set to the correct value, since it is used by the quantitative calculation when calculating intensity corrections. You can change this in the Microscope Control.

Stage

You can access the stage parameters from the Stage tab in the Microscope Control window:

Stage tilt

To display or change the stage tilt value, select the Stage tab on the Microscope Control window.

If your stage tilt is motorized, the current value can be displayed and changed. More commonly, the stage tilt is not motorized but, if you are working with tilted samples, it is necessary to enter the current tilt value. If you are working with tilted specimens and you are going to use the spectrum for quantitative analysis, it is important to enter the correct value since it is used by the quantitative analysis program to calculate the specimen geometry.

EBSD orientation data relies on knowing the sample tilt, so if the stage tilt can not be read automatically then it must be entered manually in order for the orientation data to be correct.

See also:

Microscope Parameters on the facing page

Microscope Parameters

- Microscope Control reads and controls the microscope parameters. Ensure that the values in the Microscope Control window correspond to the current microscope parameters.
- You can change the values displayed by changing the appropriate controls on the microscope. This will automatically update the displayed values in the Microscope Control window.
- If microscope parameters can not be read automatically, you will need to manually enter the values of kV and magnification directly into the spaces provided in the Microscope Control. Access the Microscope Control by pressing located on the right hand side of the Status Bar. All images subsequently collected will be acquired with these parameters. Note that if you change the magnification on the microscope and forget to enter this new value into the Magnification box in the Microscope Control window the scale marker will be incorrectly calculated.

Accelerating voltage (kV)

What is it?

The voltage applied to the electron gun that causes electrons to accelerate down the electron optic column. The higher the accelerating voltage, the greater the energy and the shorter the wavelength of the electrons striking the specimen.

Why is it important?

- The energy of electrons striking the specimen dictates what X-ray lines can be excited and their relative intensities.
- For quantitative calculations, the software needs to have an accurate value for kV.
- At higher kV, the higher energy incident electrons penetrate deeper and scatter more widely into the specimen so the excitation volume for X-rays is larger.

What value should I use?

Choosing 20kV is a good starting point particularly if the specimen is unknown. At this kV at least one series of X-rays from every element will be excited.

- Choose a lower kV if you are concerned about:
  - Accuracy of quantification of light elements since the lower penetration at low kV will reduce the absorption correction.
  - Analysis of a small particle, inclusion or a film less than 10 µm in depth since a smaller excitation volume will enhance the contribution from these features.
- Reducing the kV may reduce the options for easy element identification. A higher kV will excite the higher energy lines. The Br K line will be excited by 20kV but at 10kV, only the Br L line will be excited which overlaps with the Al K line.

Magnification

What is it?

The magnification of an image is formally defined as the ratio of the length of one line of the electron beam on the monitor to the width of the area scanned on the specimen. However, since

monitors vary in size and the image may be printed, magnification on its own is not enough to work out the size of a feature.

Why is it important?

Magnification is used by the software when calculating the length of the scale marker bar to display beneath all electron and X-ray images. The marker bar will scale with the size of the image and is a more reliable indication of feature size.

Which Magnification should I use?

Electron Imaging

In order to see greater detail in your electron image; increase the magnification of the microscope. This effectively means that the electron beam rasters over a smaller area of the specimen. Depending on your microscope, magnifications of up to 300,000 can be attained. However, above these magnifications, no greater detail is observed because of the size of the scanning probe. Any greater magnification is often referred to as 'empty magnification'.

Element Mapping

If you are acquiring X-ray data from a point, choose a magnification so that you see sufficient detail to allow you to position the beam.

Choosing a magnification greater than 1000 times will usually ensure that you are analyzing in the center of the field visible to the X-ray detector and will allow you to scan over this area to obtain a map.

Note that the beam diameter is usually much smaller than the excitation volume so that even if you position the beam on a small feature in an electron image, the X-ray data that you obtain may originate from the surrounding material.

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