AZtec Feature User Guide

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Part No. 51-1720-303

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Intended Audience

This user guide contains information for the user on how to use an Oxford Instruments AZtec EDS system with AZtecFeature software for particle analysis. It is suitable for both routine and advanced users and covers all aspects of using the AZtecFeature software for acquisition, reanalysis and processing of Feature data.

It is assumed that the user is familiar with the safe operation of a Scanning Electron Microscope (SEM) and related equipment and has the following:

- Basic SEM skills, for example, loading samples, focusing, changing magnification, producing images and moving the sample around within the microscope. If any of these are unfamiliar, please refer to the SEM manuals.
- Basic EDS sample preparation skills or access to samples that have been prepared in a suitable manner.
- A basic understanding of EDS (see also the EDS User Guide).

Contact

Oxford Instruments NanoAnalysis
Halifax Road
High Wycombe
HP12 3SE, UK

Tel: +44 (0) 1494 442255
Fax: +44 (0) 1494 461033

Email: nanoanalysis@oxinst.com
www.oxford-instruments.com

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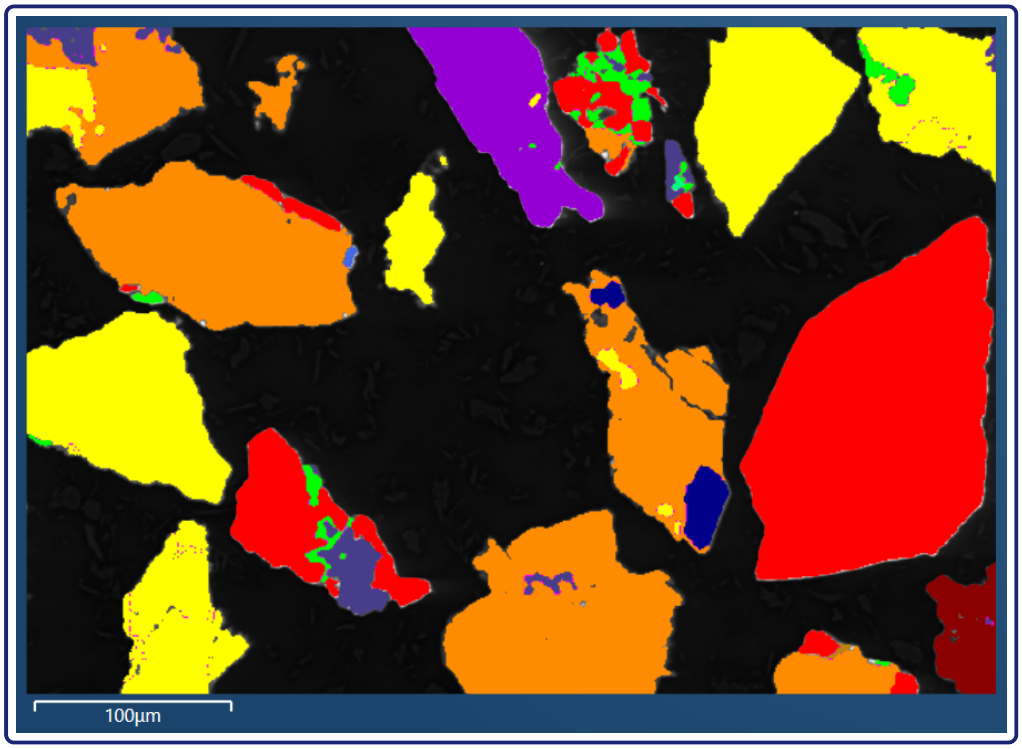
1. Introduction to AZtecFeature

AZtecFeature provides an automated approach for analyzing samples containing high numbers of features (i.e. particles) more efficiently and effectively than might otherwise be possible. It allows both morphological and chemical data for the features to be acquired and analyzed with the aim of determining the properties of the features and gaining a full understanding of the sample properties.

For example, for a zinc ore mineral sample that has been analyzed using AZtecFeature and the features classified (grouped) by chemistry, it is possible to visualize how the composition of the individual particles vary across the sample. In the image below, the features have been colored by class (groups of features with similar properties) making it possible to see how some particles (features) have a single composition whilst others have grains of different compositions within the particles (features). This is typical of such a sample.



AZtecFeature is a licensed application. The software can be accessed by selecting the “Feature” technique, from the EDS-SEM drop down menu:

1.1. Feature Applications

AZtecFeature's automated approach for feature analysis makes it suitable for a diverse range of applications. Some typical applications include:

- Technical cleanliness: used to identify and quantify contaminants in precision manufacturing processes in the electronics, semiconductor and automotive industries.
- Steel cleanliness: used to identify and quantify inclusions in steels.
- Engine-wear analysis: used to analyze wear particles found in lubricating fluids.
- Air filter analysis: used to monitor air quality and pollution by analyzing the particles in air filters.
- Abestos detection: used to identify and confirm asbestos fibres by measuring the size and shape of asbestos fibres.
- Geology and mineralogy: used to identify and measure phase compositions and textures.
- Forensic analysis: used to detect and analyze trace evidence material such as gunshot residue.

For the most common applications, Oxford Instruments offers application specific profiles for use with AZtecFeature, which are licensed and designed to meet the relevant industry standards. They include:

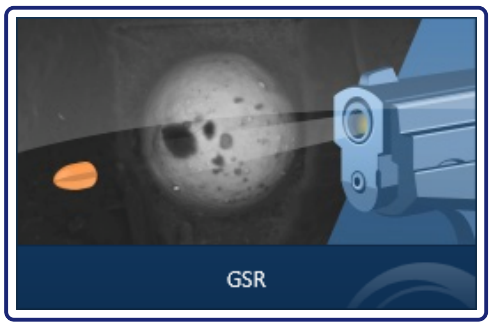
- The relevant settings for the application. These may include any of the settings present in AZtecFeature including:
  - The settings for the image and EDS spectrum acquisition.
  - The gray-level thresholds for detecting the features.
  - Whether to use second pass imaging and any filters.
  - Feature reconstruction.
- The relevant classification schemes.
- The step notes. These explain the procedure for setting up an acquisition for the specific application in a step by step manner.

These application specific profiles allow Feature acquisitions to:

- Be set up with the minimum amount of preparation in the minimum amount of time.
- Be run in the same way with the same settings every time (even with multiple users).
- Produce results that meet the relevant industry standards.

The application specific profiles currently available include:

- **AZtecGSR:**



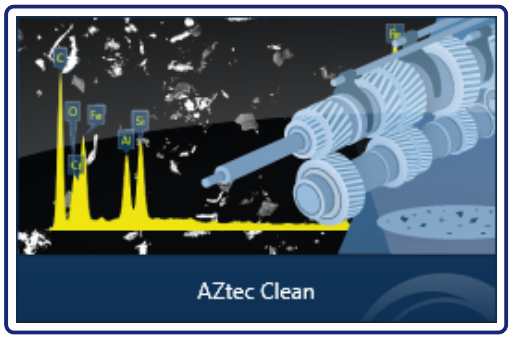
For the automated analysis of gunshot residue. It includes classifications for various ammunition types allowing for the automated confirmation of gunshot residue particles according to ASTM E1588 – 16 et.

- **AZtecSteel:**

For the automated analysis of inclusions in steel. It detects, measures and analyzes the non-metallic inclusions determining the steel cleanliness using the methods:

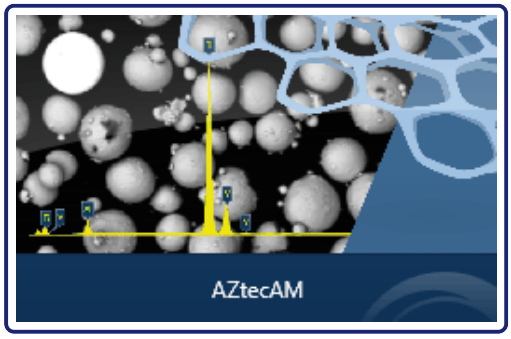
  - ASTM E2142 (E45), E2283 and E796-7
  - SIS 111116
  - DIN 50602
  - ISO 4967
  - EN 10247
  - JIS G0555
  - NFA 04-106
  - GBT 30834

- **AZtecClean:**



For the automated analysis of technical cleanliness samples and reporting of the data including component cleanliness codes to ISO 16232 and VDA 19.

- **AZtecAM:**



For the analysis of the metal powders used in additive manufacturing.

- **AZtecBattery:**

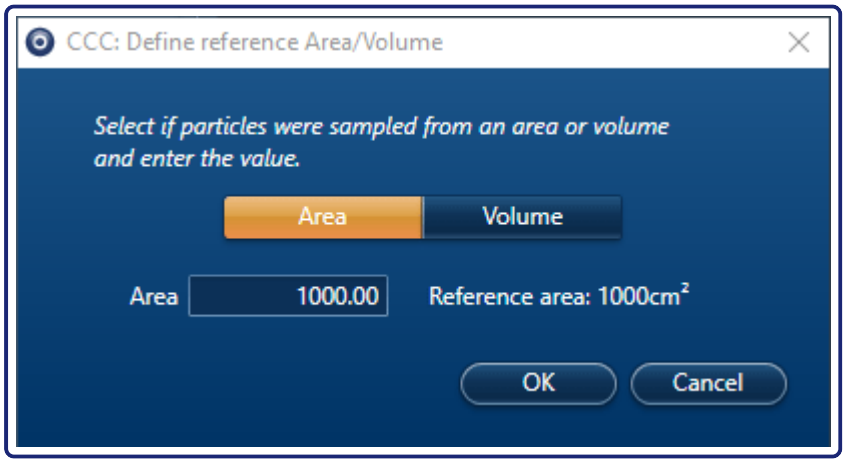
For the analysis of the contaminants found in the powder materials used in Li ion battery manufacturing.

1.1.1. Component Cleanliness Codes

To define the area or volume from which the component cleanliness codes (CCC) will be calculated:

1. Select the "CCC: Define component sampled area/volume" option.

   This will open the CCC: Define component sampled area/volume window:



2. Select whether to define the area or volume that the particles were sampled from.

   The currently selected option appears orange.

3. Enter the area or volume as appropriate.
4. Click Ok to complete the definition.

   The component cleanliness codes will now be included in the AZtecClean Component Cleanliness Code report available in the report templates.

2. AZtecFeature Workflow

There are two main types of Feature workflow that are commonly followed:

1. Non-routine or custom Feature analysis: custom settings are defined.
2. Routine Feature analysis: consistent results over multiple samples is important.

Non-Routine or Custom Feature Analysis

For non-routine or custom features analysis, generally every setting needs to be manually defined or optimized. It typically follows the procedure:

1. Locating the Acquisition Area: Determine a suitable acquisition area from which to set up and optimize the Feature acquisition.
2. Detecting Features: Acquire suitable images and set suitable thresholds for detecting the features.
3. Acquiring EDS Data: Set up and acquire EDS data and define filters to optimize the EDS data to be acquired.
4. Classifying Features: Set up the classifications to be used in analyzing the data.
5. Large Area Data Acquisition: Set up and run large area data acquisition including over multiple samples.
6. Feature Interrogation and Reacquisition: Reacquire features of interest and confirm which of the reacquired features should be kept in the dataset.
7. Reporting: Report the results of the feature analysis.

Routine Feature Analysis

For routine feature analysis, either a saved application or user profile containing optimized settings for the analysis is loaded and used. It generally follows the procedure:

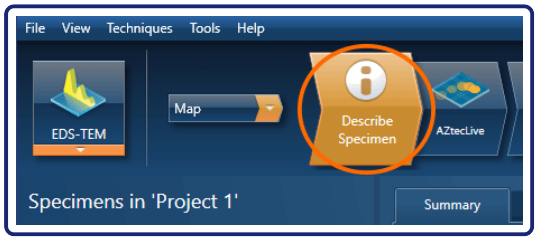
1. Loading an existing application specific profile.
2. Setting the Brightness and Contrast Levels: Ensuring the microscope image brightness and contrast is consistent for each run and that the same thresholds and settings can be used.
3. Large Area Data Acquisition: Loading an existing area layout or defining a new area and running large area data acquisition including over multiple samples.
4. Feature Interrogation and Reacquisition: Reacquire features of interest and confirm which of the reacquired features should be kept in the dataset.
5. Reporting: Report the results of the feature analysis.

2.1. Describing the Specimen

Before acquiring any data with AZtec, it is possible to enter information about the sample to be analyzed within the software. This information may take two forms:

1. General information about the sample that is just saved with the AZtec project. For example, the project summary.
2. Information about the sample that is used by the software.

This information is entered in the first navigator step "Describe Specimen":

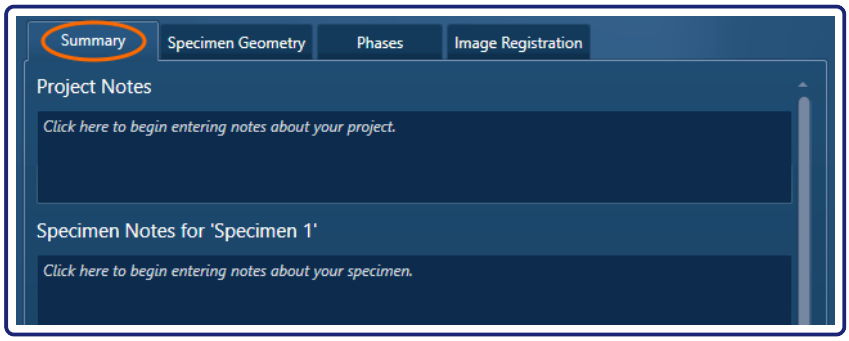


2.1.1. Project Summary

Within AZtec, it is possible to create notes about the sample and project that are saved with the project, allowing them to be referred to later.

To create notes:

1. Go to the Summary tab of the Describe Specimen step:



2. Click in the Project Notes, Specimen Notes or Site Notes section as appropriate.

   NOTE: *If the project already contains data, to add notes for different specimens or sites, select the specimen or site from the list on the left of the screen or from the data tree and then enter the information into the Specimen or Site field in the main workspace.*

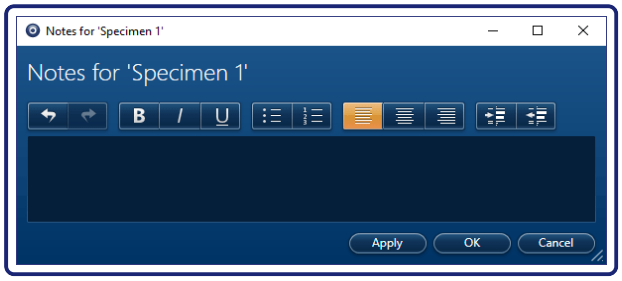
3. Enter the information required.

   Text can be formatted using the standard text formatting tools available in the formatting toolbar that appears above the field, when the field is active.

   Images and tables may be copied from other programs and pasted into the field.

To edit existing notes:

- Select the correct specimen or site and then click in the field under the Summary tab and edit the notes.
- Select the specimen or site to be edited from the list on the left of the screen of the Describe Specimen tab or from the Data Tree and select "Edit Notes". This will open the specimen or site Notes window where the information can be edited in the same way as for the Summary tab:



2.1.2. Specifying Specimen Coating

Coatings are generally used to provide a good electrical path to ground and help prevent non-conducting samples and oxides from charging under the electron beam. The most commonly used coating material for microanalysis applications is carbon because it has a minimal effect on the X-ray intensities. The coating should be made as thin as possible (typically 5 - 30 nm) in order to minimize its effect on the X-ray intensities.

This is because the coating has three main effects on the EDS analysis:

- Energy loss of the primary electron beam as it passes through the coating.
- Attenuation of the emerging X-rays.
- The contribution of characteristic peaks to the X-ray spectrum. For example, carbon coated samples will always display a carbon peak in the spectrum.

Within AZtec, during spectrum processing, any X-ray peaks arising from the specified coating element are automatically deconvolved. In addition to two other corrections (loss of X-ray intensity due to absorption of the emergent X-rays, and reduction of primary keV) are also performed. These corrections are particularly important for low keV spectra (~5 keV). The final quantitative results could have significant errors if no such corrections were applied. The corrections are applied in the following steps of calculations:

- Describe Specimen: Coating density and thickness are specified. The default density is that of the element at room temperature and pressure, but the value can be modified if required. If the thickness is set to zero, the coating element is deconvolved but no coating correction takes place. The coating correction is enabled by setting the thickness to a non-zero value.
- Standardization: The normalized area of the standard (I(std) / I(optimization)) is corrected for the coating. The value of the Standard Correction Factor is adjusted to take account of the selected coating, and the adjusted value is used in the Quant calculations.
- Full calculations: The quantitative results are corrected for the coating, accounting 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.

To specify a specimen coating within AZtec:

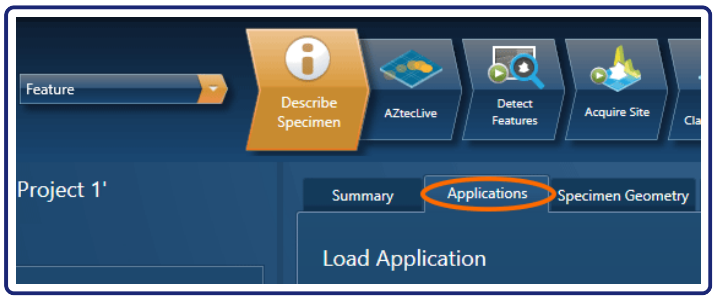
1. Check the "Specimen is coated" check box.
2. Select the coating element used.
3. Enter the thickness of the coating. Ideally it should be in the range of 5 - 30 nm.

4. The "Density (g/cm^3)" for the selected element at room temperature and pressure is automatically populated when the element is selected but may be edited if necessary.

Alternatively, if a specimen coating has been previously saved as part of a user profile, it may be loaded by clicking the "Load from Profile" button.

2.1.3. Application Specific Profiles

The application specific profiles available for use with AZtecFeature are located in the "Applications" tab of the Describe Specimen navigator step:

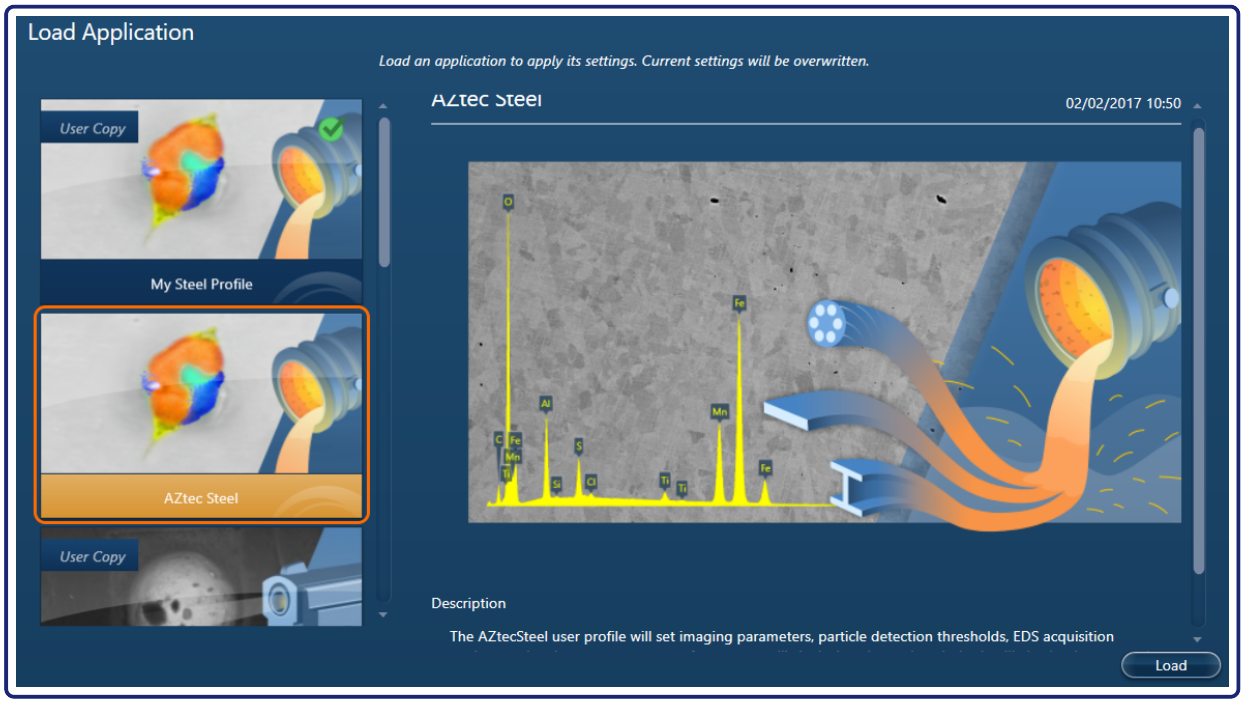


There are two types of application specific profile that may be present:

1. Oxford Instruments application specific profiles: Licensed read-only profiles designed to meet the relevant industry standards.
2. User application specific profiles: Application specific profiles that have been customized and saved as described in Saving an Application Specific Profile.

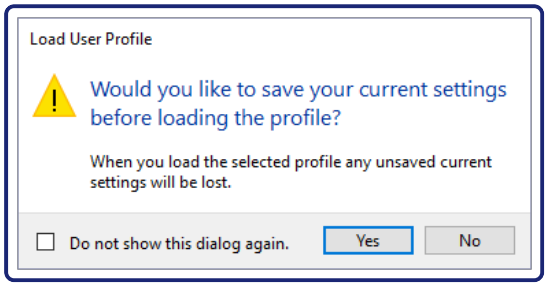
To load an application specific profile:

1. Select the Applications tab in the Describe Specimen step.
2. Select the application profile to be loaded from the list of profiles available:



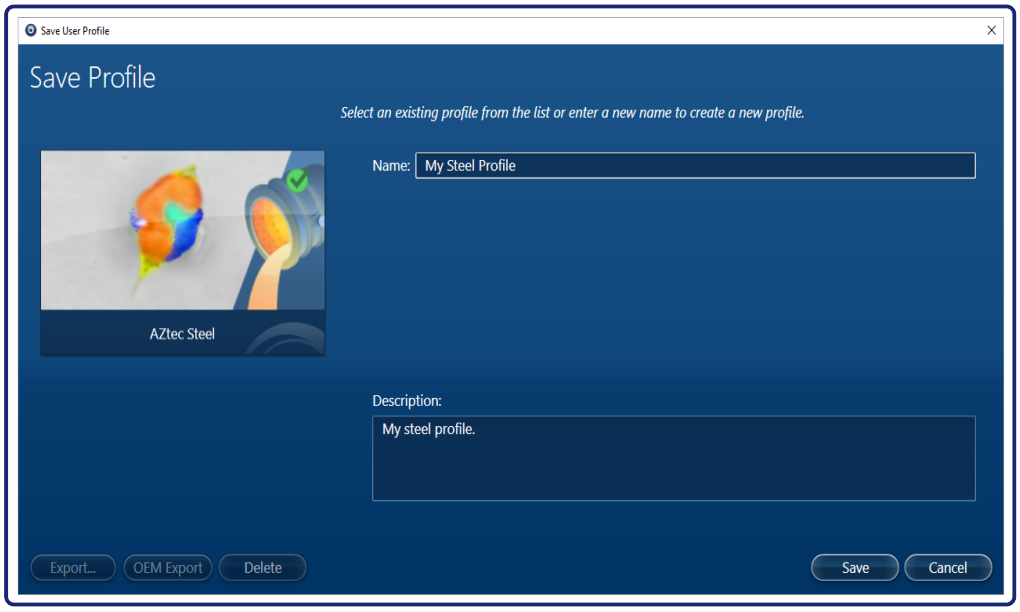
NOTE: *The currently selected application profile will have an orange background.*

3. Click “Load”.
   This will open the “Load User Profile” dialogue box.



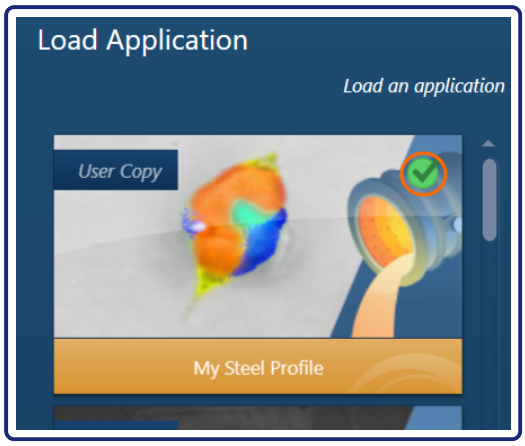
4. Click “No” to lose the current settings and immediately load the currently selected application profile.

   Click “Yes” to open the “Save User Profile” window where you may specify the profile name under which the current settings will be saved. The profile will be saved and added to the list of profiles available in the “Load Application” section of the “Applications” tab once you click the “Save” button.

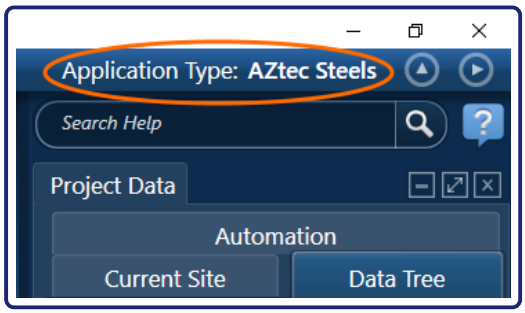


   When the save process has completed, AZtec will load the currently selected application profile.

   To signify that the application profile has been loaded, the application profile in the “Load Applications” section of the “Applications” tab on the “Describe Specimen” will be marked with a green tick.



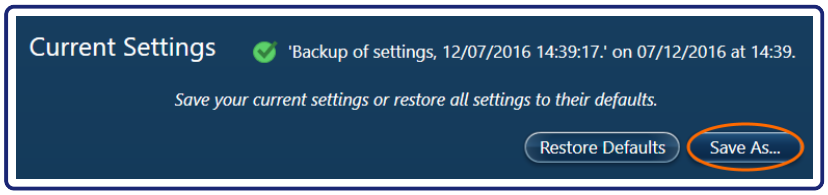
The “Application Type” displayed in the top right hand corner of AZtec will also update to display the type of application profile loaded.



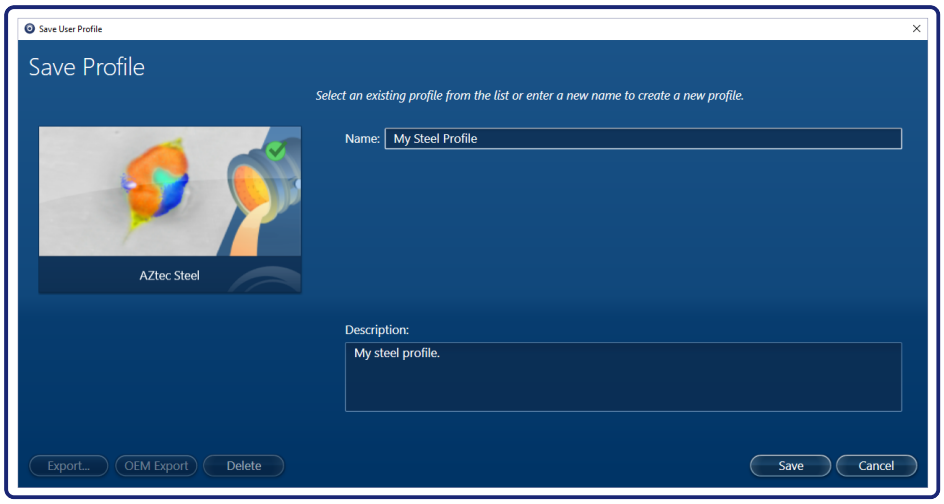
Saving an Application Specific Profile

The application specific profiles supplied with the system are read only. To customize one of these profiles:

1. Load the appropriate application specific profile from the Applications tab in the Describe Step.
2. Modify the settings as required.
3. Click “Save As” in the “Current Settings” section of the Applications tab.

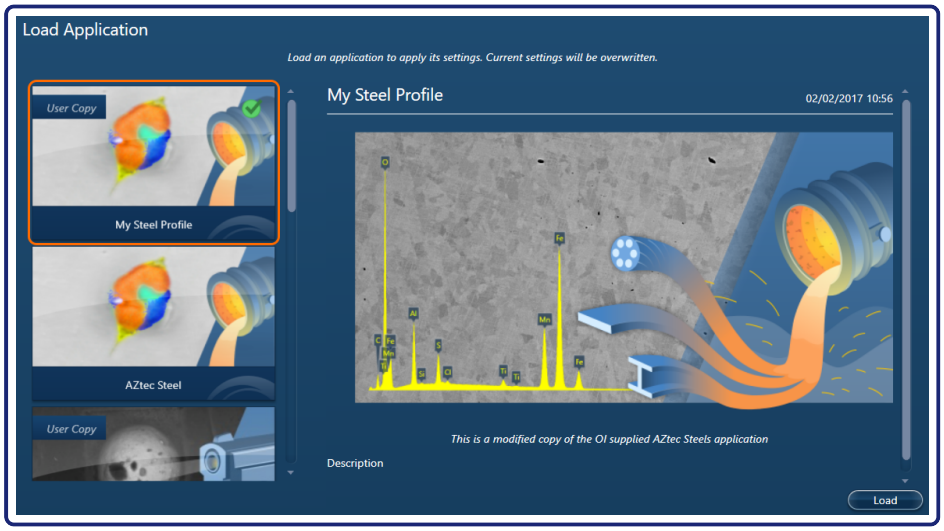


This will open the “Save User Profile” dialogue box.



4. Enter a suitable name for the profile to be saved as (i.e. My Steel Profile) and click “Save”.

   The application profile will now be saved and added to the list of profiles available in the “Load Application” section of the “Applications” tab. To signify that it has been created by a user it will be marked as a “User Copy”.

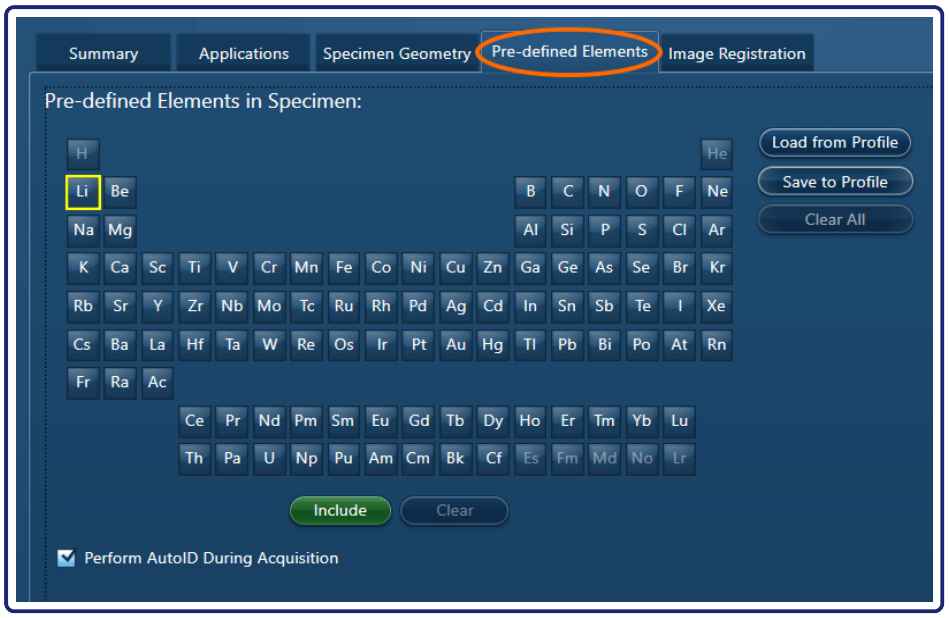


   This profile may now be loaded and used in the same way as any of the other application specific profiles.

2.1.4. Pre-Defining Elements

The Pre-defined Elements tab of the Describe Specimen navigator step can be used to:

- Define any elements that must be included in the analysis regardless of whether they have been automatically detected.
- Define whether AutoID should be performed during the EDS acquisition.
- Load a pre-defined set of elements that must be included from a user profile.
- Save the current set of pre-defined elements that must be included in the analysis to a user profile.



Any elements that are marked green in the periodic table of the Pre-defined Elements tab, are elements that must be included in the analysis. These elements will be identified in an EDS spectrum regardless of whether they are identified by AutoID. This can be beneficial for confirming whether the sample contains a specific list of elements and for viewing the contributions of each of the elements even if one of the elements is not present.

Elements may be included by:

- Double click on an element in the periodic table until it becomes green.
- Select an element so that it is highlighted in the periodic table (click once on it) and then click “Include”.
- Hold down the "Ctrl" key on the computer keyboard and select multiple elements in the periodic table so that they are highlighted. Press the "Include" button to set all of the selected elements to be included.
- Select to load a predefined list of included elements by clicking on the "Load from Profile" button. This will load the list from the currently loaded application specific profile.

To save the list of currently included elements to the current user profile, click the "Save to Profile" button to the right of the periodic table.

To stop elements from being included:

- Double click on the element in the periodic table until its background is no longer green.
- Select the element so that it is highlighted in the periodic table (click once on it) and then click "Clear".
- Press the "Clear All" button to remove the include setting for all of the currently included elements.
- Hold down the "Ctrl" key on the computer keyboard and select multiple included elements in the periodic table so that they are highlighted. Press the "Clear" button to remove the include setting for all of these elements.

The "Perform AutoID During Acquisition" option is enabled by default. It may be disabled by unchecking the check box situated directly below the periodic table. When AutoID is enabled during EDS acquisition, AZtec automatically:

- Identifies and analyzes the peaks in the spectrum.
- Deduces the elements responsible for producing the peaks.
- Labels the peaks in the spectrum accordingly.

2.2. Locating the Acquisition Area

When setting up a Feature acquisition and optimizing the settings, it is important to ensure that the area of the sample being analyzed is representative of the sample. It should also ideally contain at least one of each of the types of features that are to be classified. This is to ensure that suitable settings including the gray-level thresholds, filters and EDS settings are selected for every feature type to be analyzed.

A useful tool for locating such an area of the sample, is AZtecLive which can be used to simultaneously acquire EDS data along with electron images, even when the stage is moving. This allows the constituent elements, their relative abundance and distribution and the sample morphology to all be visualized and characterized in real-time. Appropriate areas of the sample can then be quickly and easily selected for more in-depth analysis.

2.2.1. Using AZtecLive

To use AZtecLive:

1. Select any elements that must be included or excluded whether or not they are present from either:
   - The Elements pane.
   - The Pre-defined Elements tab in the Describe Specimen navigator step.

   NOTE: *If elements are included or excluded from the Elements pane in the AZtecLive navigator step, they will override any elements that have been set in the Describe Specimen navigator step.*
2. Select whether to improve the quality of the EDS maps when the stage is stationary.
3. Select suitable settings for acquiring the image and EDS data using the Acquire Live settings window.
4. Click Scan, to start scanning the current field of view on the microscope.

   AZtecLive starts acquiring the electron image and simultaneously EDS data from the area scanned by the electron beam. The image and EDS data are continuously updated.

   If AutoID is selected in the Pre-defined Elements tab of the Describe Specimen step, the elements in the Live Sum spectrum will be identified and displayed on the spectrum.

   If any elements have been set to must be included, the element maps for these elements will be displayed.
5. To detect the elements present in the current field and visualize the element maps for these elements, click "AutoID" in the Elements pane.

   The appropriate element maps will now be displayed.

   NOTE: *Once AutoID has been performed, the list of element maps displayed is fixed. To update the list, click AutoID in the Elements pane. Any additional elements detected will be added to the element map display. No element maps will be removed even if the element is no longer present. To remove an element, deselect it or set it to Exclude in the Elements pane. To clear the entire list of element maps, click "Clear All" in the Elements pane.*
6. Move around the specimen by:
   - Using the microscope controls.
   - Double clicking on a point on the electron image or EDS maps. The stage will move to be centered on the point.

- Selecting a field of interest in the Live Trace Mini View and then selecting "Move To" to move to that field.

7. To check for the presence of additional elements, click "AutoID" in the Elements pane.
8. To view the spectrum for a single spot, for example to visualize the elements present in a particular feature, click "SPOT" to put the beam into spot mode. The position of the beam is marked on the electron image and EDS maps using a yellow cross. Click elsewhere on the electron image or on one of the EDS maps to move the beam to that location.

   To return to scanning the entire field of view, click "SCAN".
9. To save the current data, click "Save Site Data" in the acquisition toolbar. A Live Trace item will be added to the data tree.

   If this is the first Live Trace to be saved or if the stage position, magnification, or accelerating voltage has changed since the last save, a new site is created for the data.

   In scan mode, the electron image, displayed element maps and sum spectrum are saved to the current site.

   In spot mode, the current point spectrum is saved to the current site. In addition, if not already present in the current site, the electron image, element maps and sum spectrum will be saved.

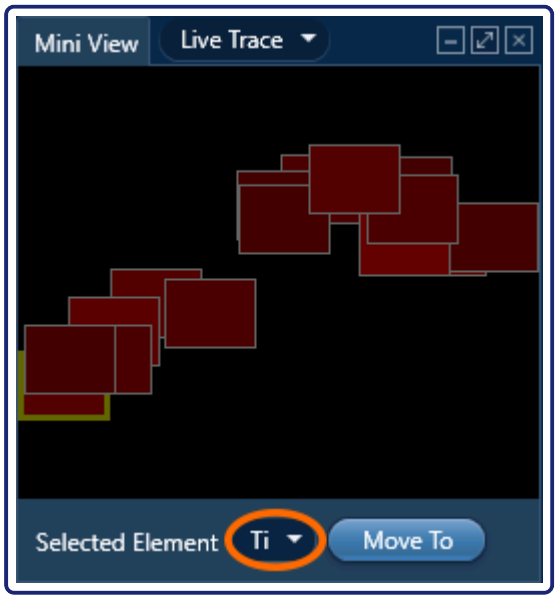
2.2.2. Returning to a Specific Field

While in the AZtecLive navigator step, the Live Trace Mini View tracks and records the microscope stage positions for each of the field of view's visited. The Live Trace Mini View may then be used to:

- Visualize the fields that contain a specific element.
- Select a field of interest.
- Return to the selected field of interest.

To use the Live Trace to return to a specific field:

1. In the Live Trace Mini View use the Select Element drop down menu to select the element of interest:



   All fields that contain the element will now be shaded red. The brighter the shade of red the greater the weight % of that element present in the field.

NOTE: *The shades of red are normalized to the field with the highest concentration.*

2. Select the field of interest within the Live Trace Mini View by clicking on it. Once selected the field will have a yellow border.
3. Click the "Move To" button at the bottom of the Live Trace Mini View window.

   The microscope stage will now move to the stage coordinates saved for that field of view.

2.2.3. Locking a Registered Image to Live Trace

By default, if an image is registered as part of the current AZtec session and project, it will automatically be loaded as a background to the Live Trace mini view. Once the project or session is closed, the image will be lost. Additionally, if a new image is registered to the project, then the most recent registered image will be added as the Live Trace background.

With the Live Trace mini view, it is possible to lock an image to the Live Trace so that it is used permanently across multiple projects and AZtec sessions, until it is unlocked.

To lock a registered image to Live Trace:

1. Register the image to be locked as a Live Trace background using .
2. Right click in the main part of the Live Trace window to access the Live Trace context menu.
3. Select the "Remember Registered Image" option.

   The currently registered image will now be displayed as the background image in Live Trace, until it is unlocked.

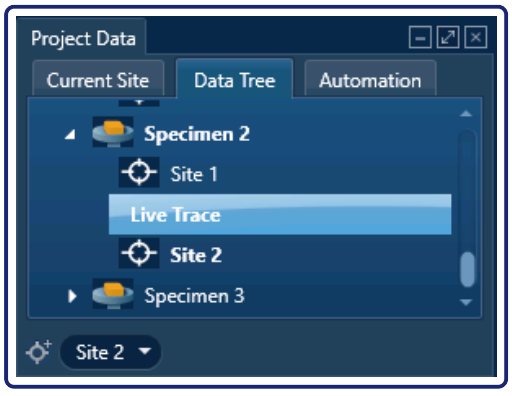
To unlock a registered image from Live Trace:

1. Right click in the main part of the Live Trace window to access the Live Trace context menu.
2. Select the "Clear Registered Image" option.

   The registered image will now be unlocked from Live Trace. When a new image is registered it will now be displayed as a background in the Live Trace.

2.2.4. Deleting a Live Trace

A Live Trace is automatically saved for each specimen within an AZtec project. For example:



In some situations it may be desirable to delete the Live Trace, for example if the trace has become overcrowded or you wish to repeat your investigation of the specimen. In these situations the Live Trace can be deleted by:

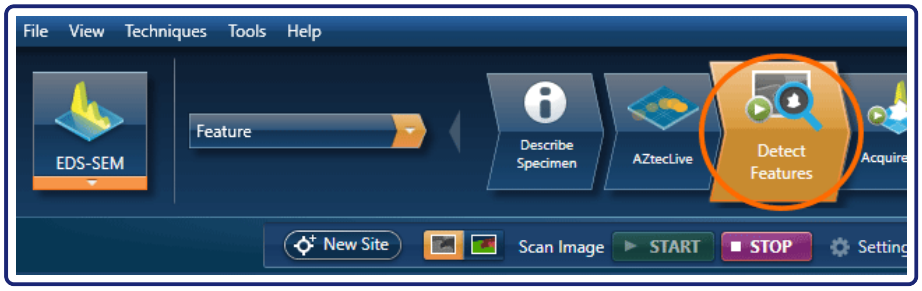
1. If an AZtecLive acquisition is running, click "Stop" to stop the acquisition.
2. In the Data Tree tab of the Project Data view, locate the Live Trace item for the current specimen.
3. Right click the Live Trace to access the context menu and select delete.

   The Live Trace will now be deleted from the data tree.

2.3. Detecting Features

The first step in feature analysis is to detect the features that are going to be analyzed.

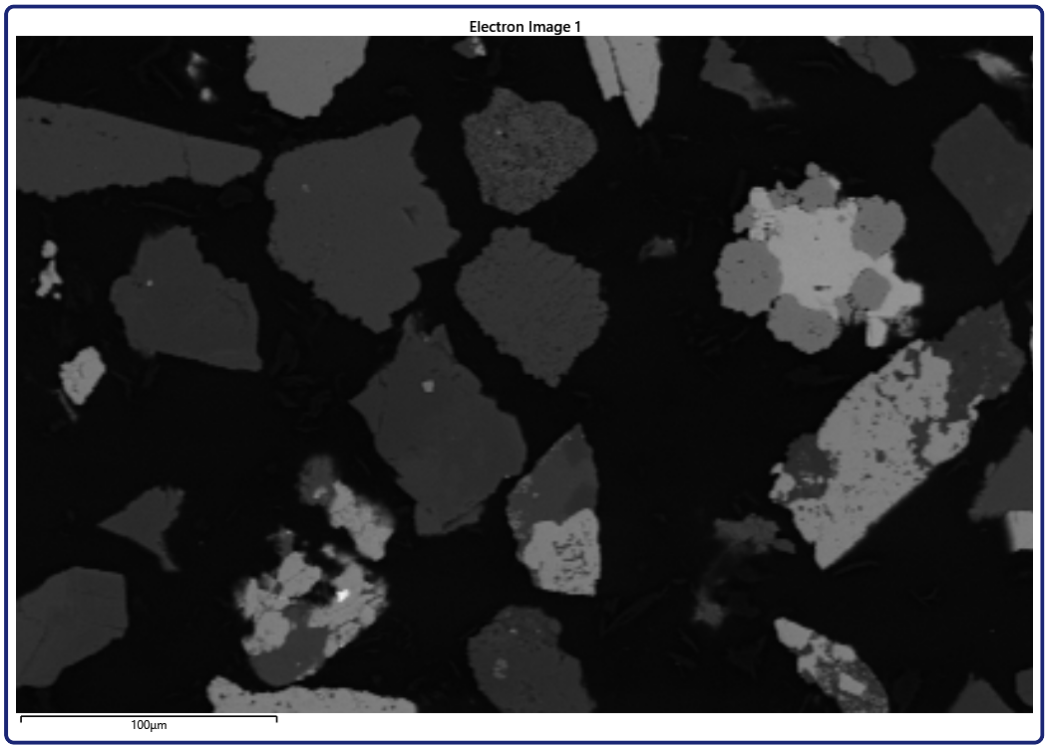
This is performed using the Detect Features navigator step:



There are two parts to Detecting Features:

1. Acquiring an electron image of the sample with sufficient quality to detect the features accurately.
2. Detecting the features of interest on the electron image.

For Feature analysis, any electron image that shows up all of the features that are to be detected may be used. However, BSE images are ideal because areas or features with different chemical compositions show up in the images as having different contrast to each other. For example:

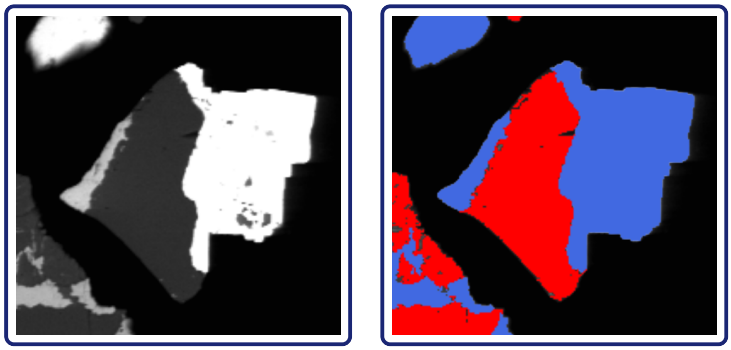


For information on how to acquire and optimize an electron image, see the Acquiring an Electron Image section.

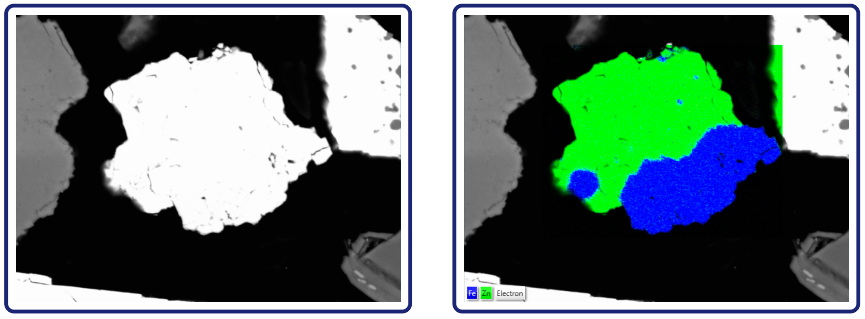
Once an electron image that shows up all of the features to be detected has been acquired, the gray-level thresholds to be used for detecting the features may be specified. A gray-level threshold is a range of gray-level values. Any pixel within the electron image that is found to have a value that falls within the range of the gray-level threshold is assigned to be a feature within that gray-level threshold.

It is possible to specify either:

- One threshold, where all of the features that have a gray level that is different to the background are included in threshold and will be analyzed further.
- Multiple thresholds, where features with areas or grains with different gray levels are split into multiple features. For example, the feature in the electron image below (left) can be treated as multiple separate features, each with their own morphology and composition, by defining multiple gray-level thresholds (right):



Some features may be made up of several grains or components that have a similar density and hence appear to have a very similar contrast level in the electron image, but have a different chemical composition, which means that each grain should be treated as a separate feature. For example, many types of cement contain features with both silicate and carbonate grains or sulphide and sulphate grains. These grains have a similar density and hence contrast to each other, which means that even when the electron image acquisition settings are optimized, it is not possible to distinguish the different grains from each other. The images below are an example of this. In the BSE image (left), the central feature appears as a single feature with the same contrast which is suggestive of the same composition throughout. However, the EDS map (right) shows how this feature actually has two separate grains with different chemical compositions:



For this particular situation, AZtecFeature offers Threshold Phase Detection. This is a licensed application, where phase maps are collected for all features within the selected threshold and any features that are identified as having multiple phases are automatically split into multiple separate features. The Feature analysis can then continue as normal.

It is also possible to have situations where a sample contains many dense fibers or particles, which mean that although the features of interest may be visible by eye, they are of very similar contrast gray-levels to the background and cannot be separated from the background using the standard threshold method. An example of a sample that might exhibit this type of problem is a solid sample such as a rock sample.

For this particular situation, AZtecFeature offers Full Field Phase Detection. This is a licensed application where instead of using gray-level thresholds to distinguish the features, an electron image and then a full EDS map are acquired and the features including the background are identified using phase detection. Once the features have been identified, the Feature analysis can then be set up and performed as normal.

2.3.1. Acquiring an Electron Image

To acquire an electron image:

1. Select the "Detect Features" navigator step:

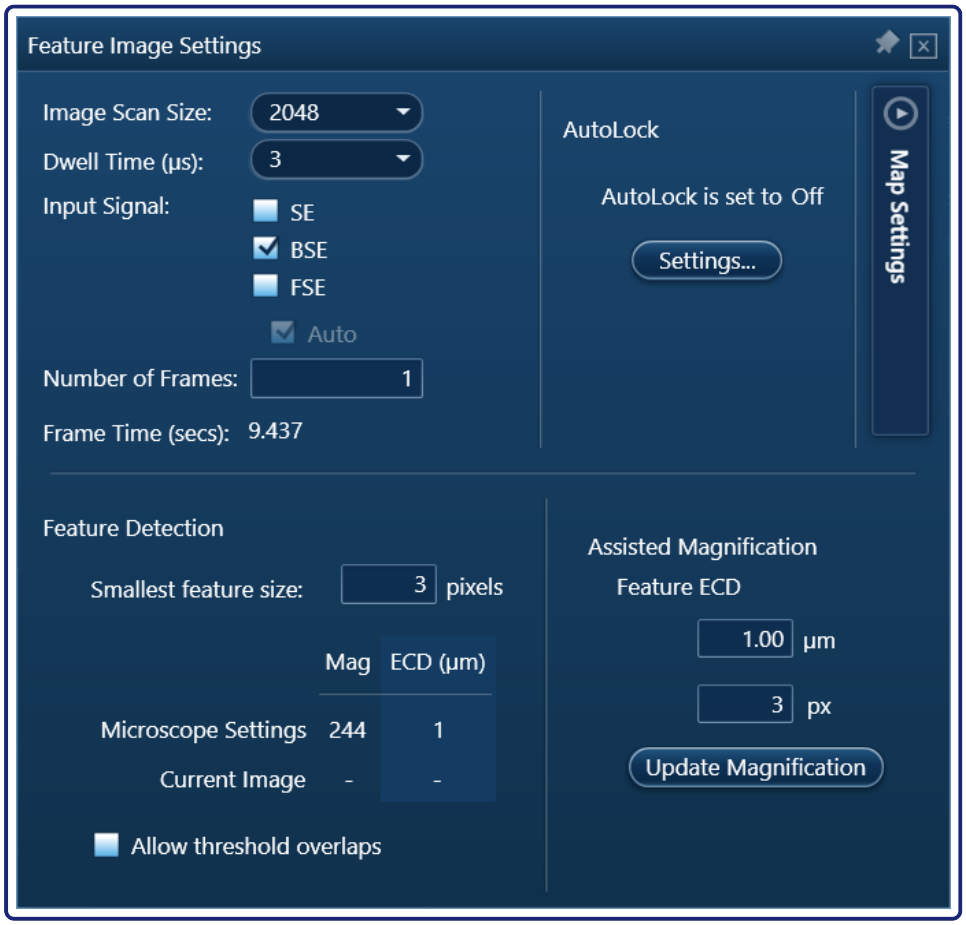
2. Ensure that the "Acquire an Electron Image" icon is selected in the acquisition toolbar:

3. Click the "Start" button in the acquisition toolbar.

   The electron image will be acquired using the current settings.

To acquire an electron image with different settings click the settings icon in the acquisition toolbar:

This will open the "Feature Image Settings" window:



This settings window may be used to specify:

- The general image settings including the input signal type, the image resolution and the dwell time.
- Whether to use the "AutoLock" drift correction.
- Some feature detection settings.
- Whether to use "Assisted Magnification" to specify the minimum number of pixels that are required to resolve a specific feature size and to calculate a suitable magnification to do that.

For more information on selecting suitable settings, refer to the Optimizing the Image Settings section.

If the electron image quality remains poor quality, for example, it remains noisy, its quality may be improved using gray level filters as described in the Optimizing the Image Using Filters section.

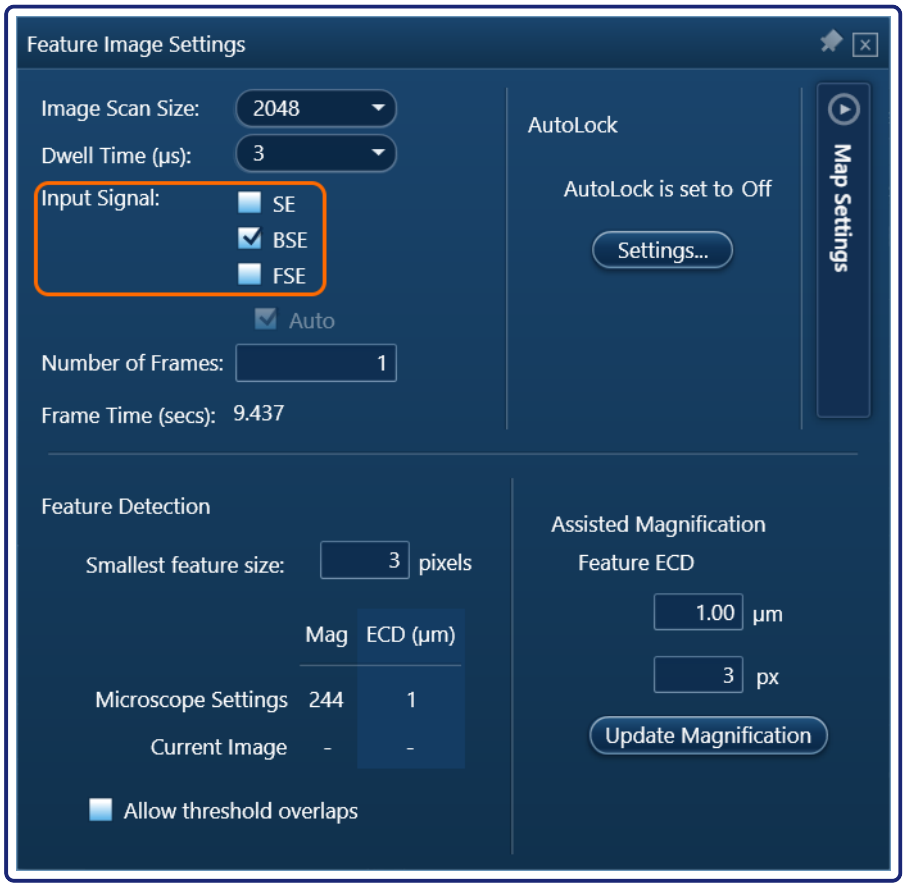
Optimizing the Image Settings

When selecting the magnification and acquisition conditions for acquiring an electron image to be used within a Feature analysis, there are a number of factors and compromises that should be considered:

- **Input signal:**

  Typically the most useful type of image for Feature analysis are backscatter electron images. This is because this image type shows up different phase densities as different contrast levels allowing the features to be easily distinguished.

  Depending on the configuration of the system, select the image input type from either the microscope or the Image Settings menu, which is accessed from the toolbar at the top of the "Detect Features" step as appropriate.



- **Brightness and Contrast:**

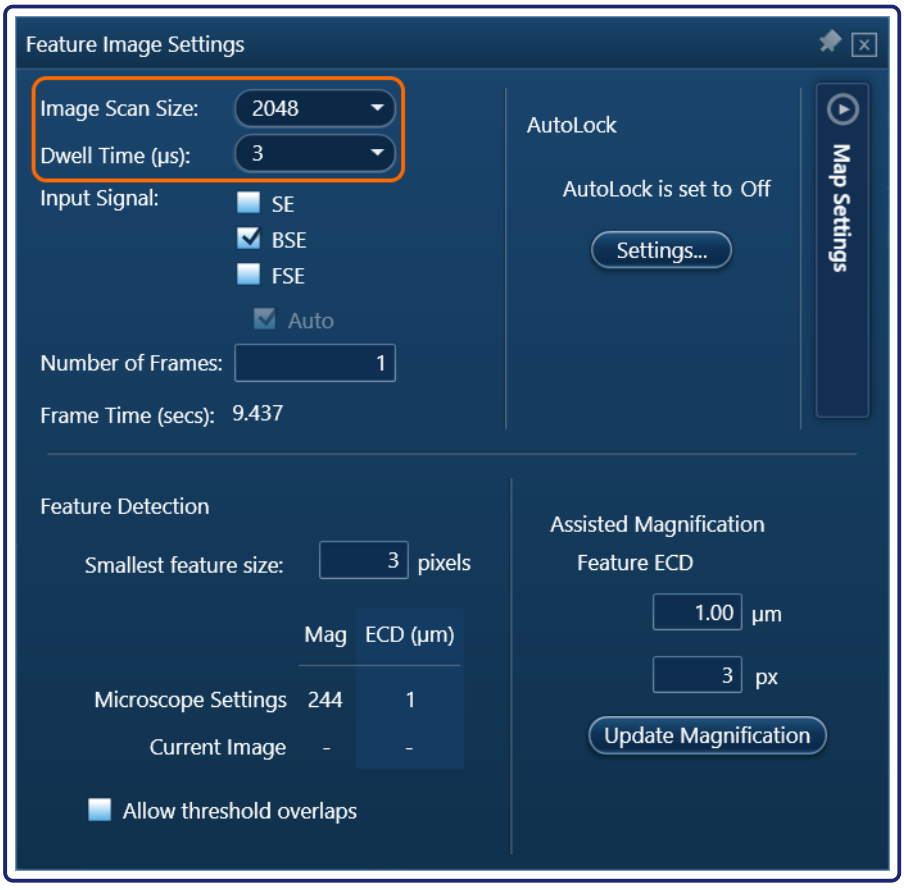
  In order for the features to be clearly observed in the image and for gray-level thresholds to be used to allow the software to effectively pick out the features, it is important that the microscope has a good brightness and contrast range. The microscope should be set up so that the brightest features appear white and the darkest features appear black.

  In addition, in order to ensure repeatability between runs by setting the imaging conditions to be the same each time or throughout a single long run, it may be beneficial to perform an in-run image calibration. To use the in-run image calibration capability, an image calibration must be performed prior to the run and then the software checks the brightness of a reference area periodically during the run. If a variation is found, the software will make adjustments to the gray level thresholds used to detect the features to compensate. For more information on using this capability, see the Microscope Setup section of the help.

- **Image acquisition settings:**

  For accurate feature analysis it is important that the electron images are of “good enough” quality for the software to be able to accurately identify all of the features that are to be analyzed and for their morphology to be measured. However, especially if performing Feature analysis over a large area with a high number of fields, it may be necessary to make a trade off between image quality and speed.

  The Feature Image Settings menu, which is accessed from the toolbar at the top of the "Detect Features" step may be used to select the resolution and dwell time to be used for acquiring the image.

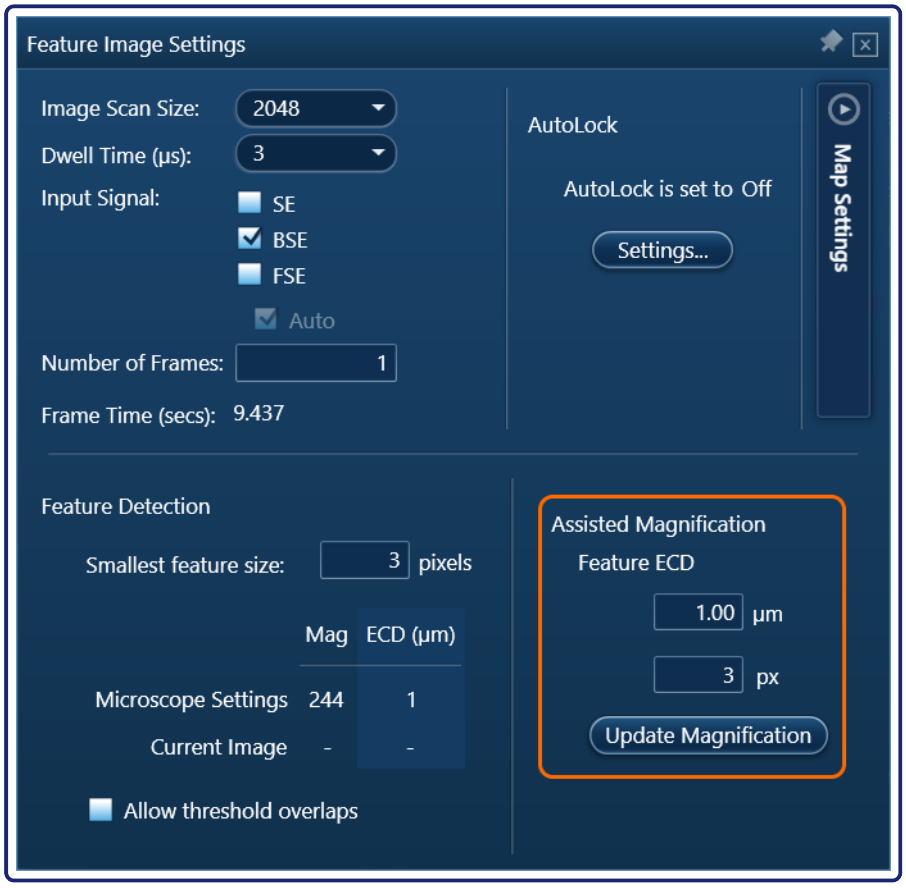


  Generally for Feature it is recommended to use:

  - A high resolution: allows the lowest magnification possible to resolve the features to be used.
  - A fast dwell time: allows the acquisition time to be kept to a minimum.

- **Microscope magnification:**

  For large area acquisitions, to optimize the acquisition time, it is important to use the minimum number of fields and hence magnification to cover the area. However, it is also important to ensure that the smallest features are still resolved correctly. To assist with this optimization, AZtec offers "Assisted Magnification", where the physical size of a feature (e.g. 1.00 µm) and the number of pixels that there must be within a feature of this size (e.g. 3 px) can be specified as shown below. When the "Update Magnification" button is clicked, AZtec calculates the appropriate magnification to meet these parameters and updates the microscope so that it uses this value:



Optimizing the Image Using Filters

If the electron image is poor quality, for example it is noisy, AZtec may not be able to identify all of the features of interest correctly. It is possible for the noise in the image to be reduced using gray level filters, which will work on the entire image.

The gray level filters currently available in AZtec include:

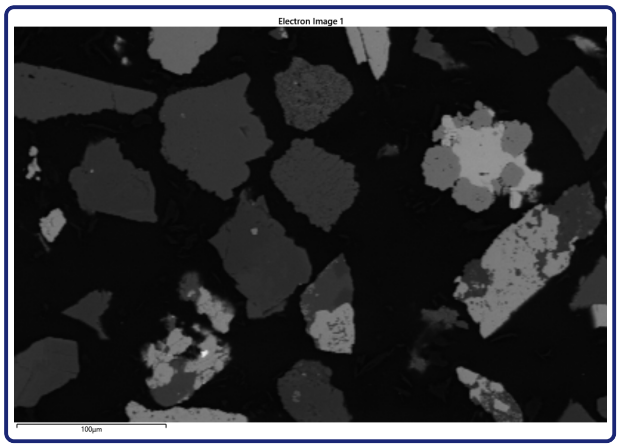
- **Smooth Filter:** This filter converts a noisy image with discontinuous features into a less noisy image with clear solid features by averaging the brightness levels of a pixel with that of its neighbors.

  NOTE: *This filter may cause the edges of the features to be reduced or distorted and result in a blurred effect. To preserve the edges of features, the Median Filter is likely to be preferable.*

- **Gaussian Smooth Filter:** This filter is similar to the smooth filter, but with a stronger smoothing effect.

  NOTE: *This filter reduces noise but can also reduce detail. It will produce a stronger smoothing effect than the Smooth Filter, but will also generally preserve the feature edges better.*

- **Median Filter:** This filter removes any unusually bright or dark pixels from the image so that the final image appears smoothed. For example:



Original Image

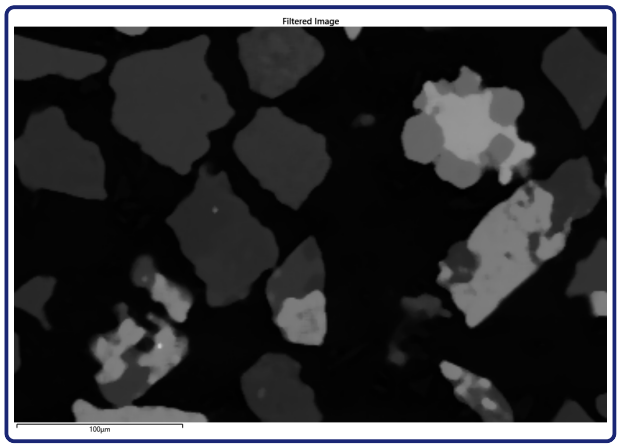
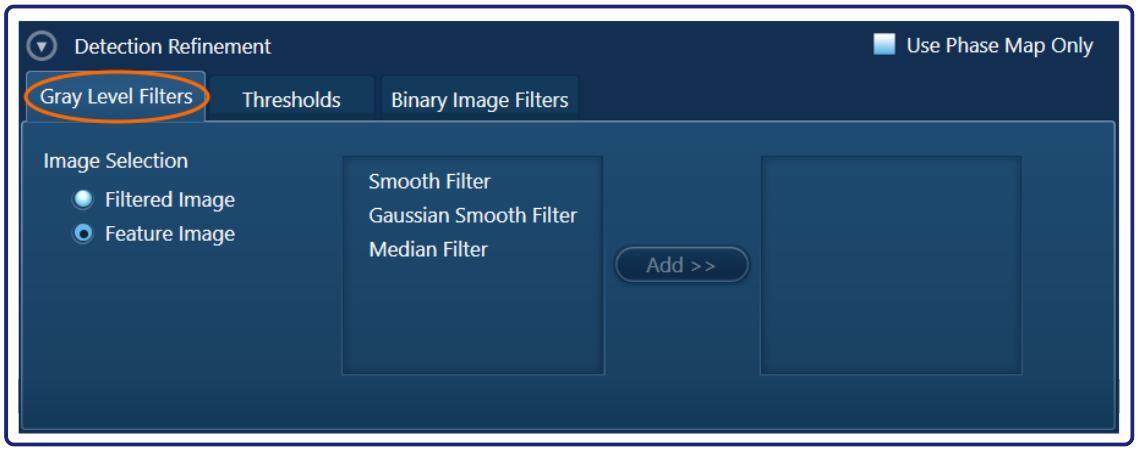


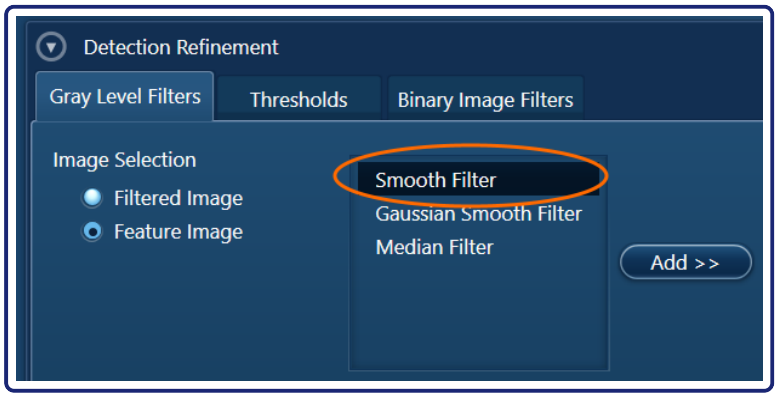
Image after a median filter, strength 2 has been applied.

To apply an image filter to a noisy image:

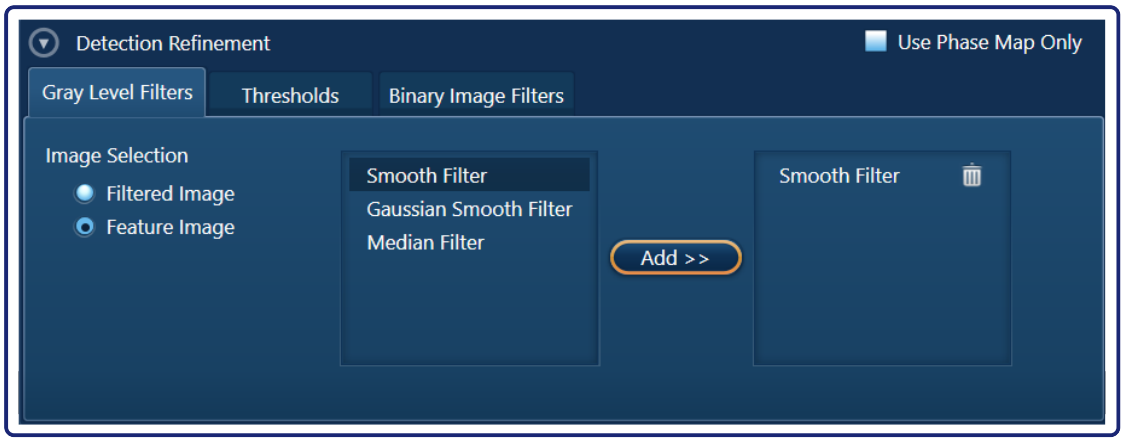
1. From the "Detection Refinement" panel in the "Detect Features" step, select the "Gray Level Filters" tab.



2. Select whether to view the as acquired "Feature Image" or the "Filtered Image" if a filter has already been applied.
3. Select the filter to be applied. i.e. to select the smooth filter:

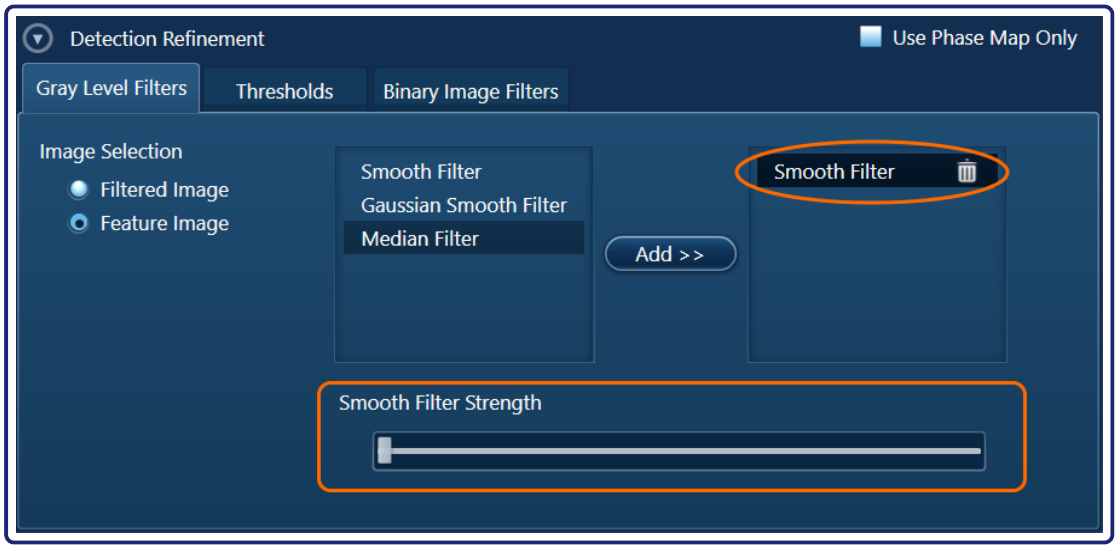


4. Click "Add" to apply the filter to the image:



The filter will be applied to the image and added to the column on the right to show that it has been applied to the image.

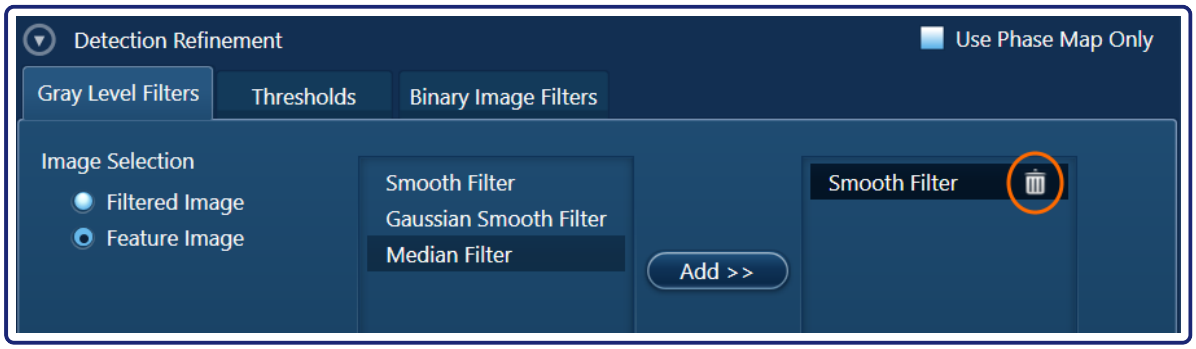
5. To adjust the strength of an applied filter, select the filter from the column on the right. A slider bar will appear at the bottom of the "Gray Level Filters" tab:



The effect of the adjustment can be observed in the filtered image.

6. Repeat steps 2 - 5 to add further filters.

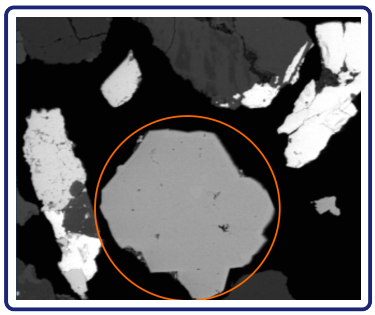
To remove a filter from the image click the trash can icon to the right of the filter in the column on the right:



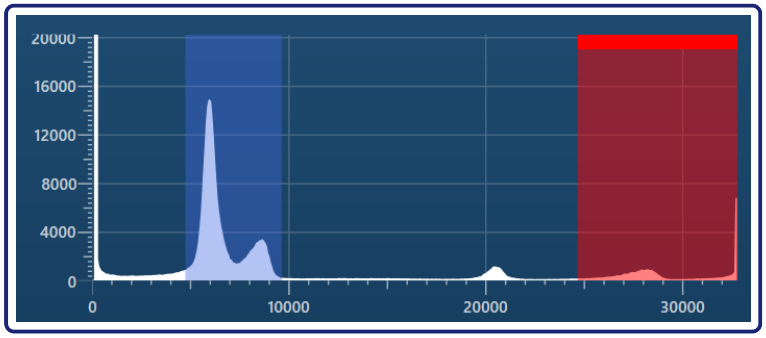
2.3.2. Detecting the Features

In order to automatically identify the features in the electron image, gray-level thresholds are used to specify the range of image gray-levels that correspond to the features. During the acquisition, the gray-level for every pixel in the electron image is analyzed. Any pixels that have a value within one of the defined thresholds are assigned to be a feature within the threshold they match, while any features with a gray level that falls outside of any of the defined gray-level thresholds are ignored. As such, it is very important that the upper and lower bounds of the gray-level thresholds are set carefully. If they are not, it is possible that either some features of interest will not be detected or that background noise will be detected as small features.

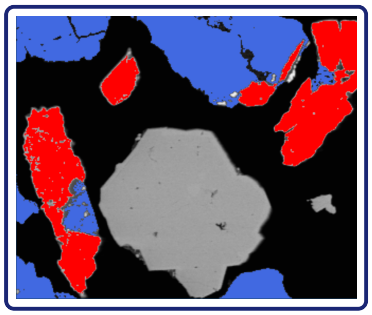
Depending on the application, it may be desirable to use either a single threshold to detect all features or multiple thresholds to distinguish and group features of different types. An example of where this might be useful is when only very specific features are to be analyzed. For example, for the electron image below, only the darkest and brightest features in the image are to be analyzed and not mid gray-level features such as the one circled in orange:



In this case, two separate gray-level thresholds may be created; one for the darkest features and one for the brightest features. The mid gray-level features are not included in either threshold. This is demonstrated in the threshold graph below, where one threshold is marked in blue and the other in red. The gray-levels between the two thresholds are not assigned to any threshold:



The result of applying these two gray-level thresholds on the electron image is shown below. The features are colored according to the threshold that they belong to:



Defining Gray-Level Thresholds

Gray-level thresholds may be defined in one of two ways:

- Directly from the Detect Features step as part of the project. These thresholds can also be saved as part of a user or application profile and used with future projects.
- Loaded as part of a user or application profile.

NOTE: *If a new project is being created and doesn't use either a user or application specific profile, then the last used gray-level thresholds will be displayed by default.*

If a user or application profile that contains gray-level thresholds is loaded, AZtec will start detecting the features as soon as the electron image is acquired.

If no profile is loaded, AZtecFeature will start detecting the features in the electron image that fall within that threshold as soon as a gray-level threshold is defined.

In both cases, as soon as a change is made to a gray-level threshold or to one of the other settings that affects the feature detection (e.g. an image filter), AZtec will redetect the features using the new settings.

The following sections describe the different methods available for defining gray-level thresholds within the Detect Features step. They include:

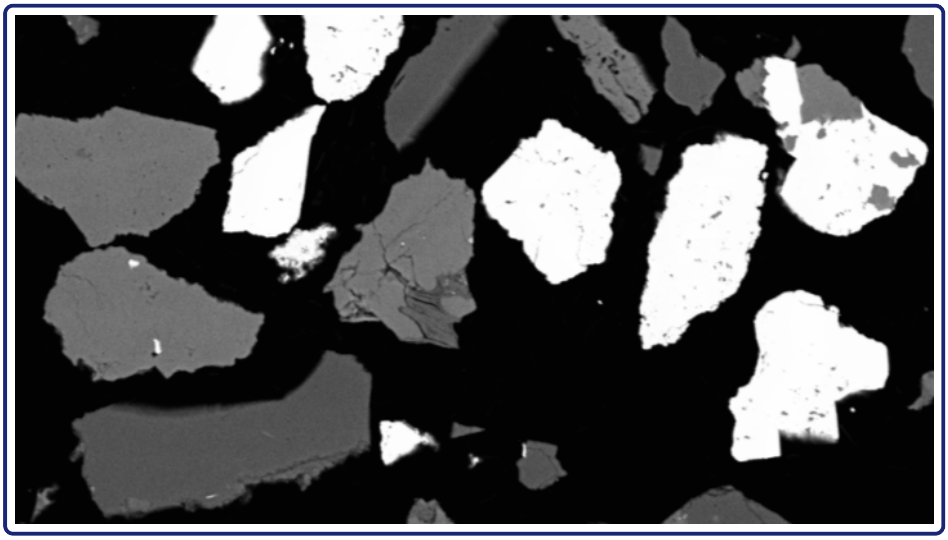
- Assisted threshold creation.
- Manual threshold creation.

Assisted Threshold Creation

AZtec's assisted threshold creation tool is designed to make defining gray-level thresholds quick and intuitive.

To use the assisted thresholding method to define gray-level thresholds:

1. Acquire a high quality electron image:

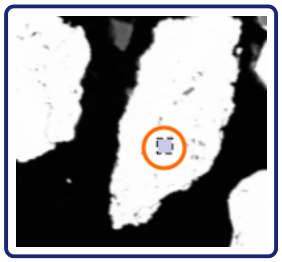


2. Select the wand tool from the toolbar on the left of the screen:

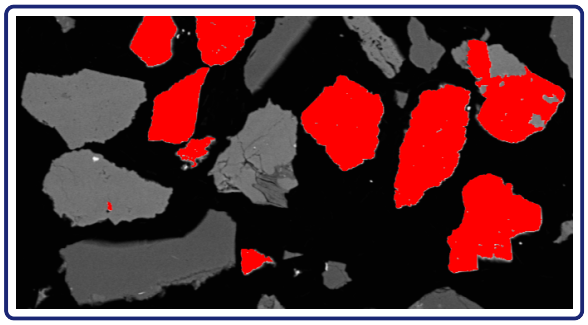
To change the size of the area to be used to create the threshold range, hover the mouse over the arrow to the right of the wand tool. The different grid options available will be displayed:

Click on one of the options to select it.

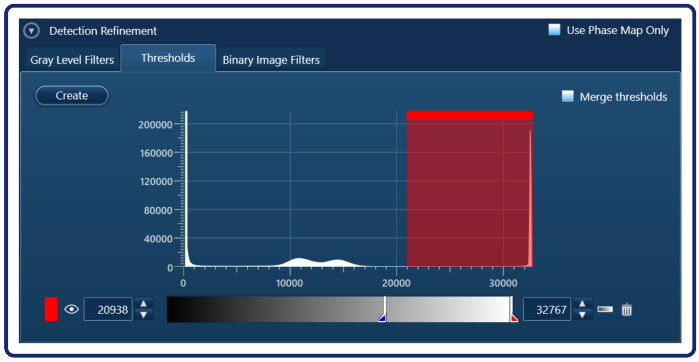
3. Click on the part of a feature, whose gray-levels are to be added to the threshold. The area selected will be marked by a shaded square of the relevant size (i.e. 15 x 15 Grid):



If the "Color by Threshold" option is selected for the image, the electron image will update to display all features within the created threshold in the threshold color:



A new threshold will be added to the list of thresholds displayed at the bottom of the "Threshold" tab of the "Detection Refinement" pane. The gray-level histogram will be updated to have the threshold region highlighted in the threshold color:

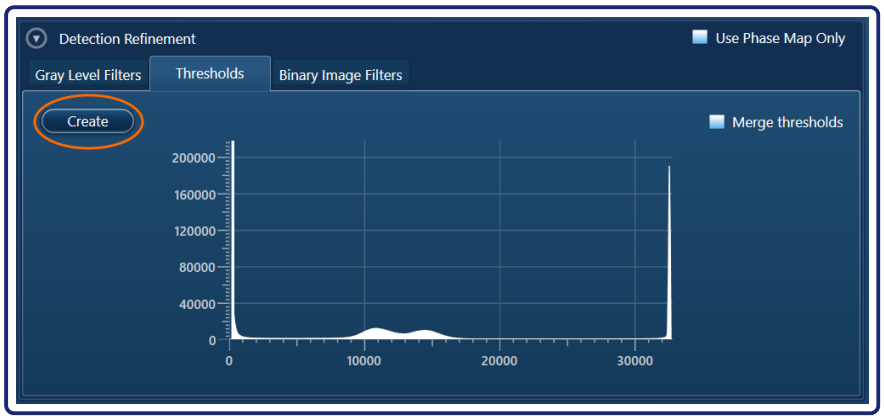


4. The gray-level range can be edited from the histogram or from the list of thresholds displayed at the bottom of the tab (see the Optimizing the Threshold Definitions section for more details).
5. To add further thresholds, if the wand tool is still selected, repeat steps 4-6, otherwise repeat steps 2-6. Each new threshold will be assigned its own unique color.

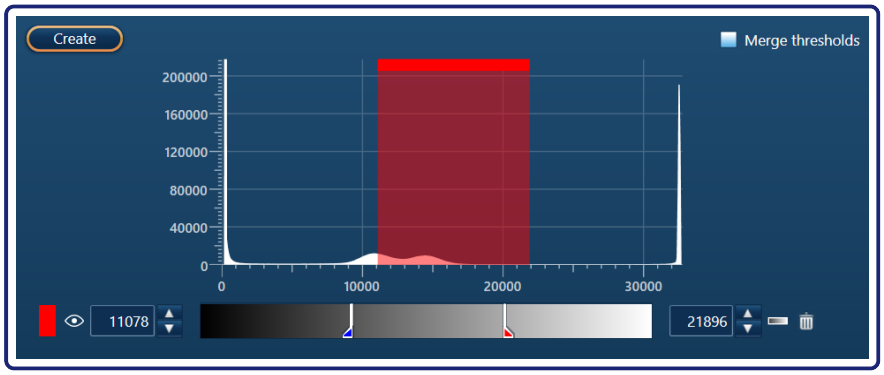
Creating Thresholds Manually

To create a threshold manually:

1. In the "Thresholds" tab in the "Detection Refinement" pane, click the "Create" button:



This will create a new threshold which will appear as a highlighted region on the gray-levels histogram and as a new entry in the threshold list below the histogram:



2. Edit the threshold to cover the relevant gray-level threshold range by either editing the:
   - Highlighted region on the histogram.
   - Entry in the threshold list.

   For information on how to edit the thresholds, see the Optimizing the Threshold Definitions section.

NOTE: *A new threshold may also be defined by pressing the "Shift" key down on the computer keyboard and clicking and dragging the mouse over the region of the histogram for which the threshold is to be created.*

Optimizing the Gray-Level Threshold Definitions

Once defined, gray-level thresholds may be edited or optimized by:

- Editing the threshold definitions from the histogram.
- Editing the threshold definitions from the list of thresholds.
- Merging two thresholds into a single threshold.
- Allowing overlapping thresholds.

The steps are applicable for both gray-level thresholds created within a project or loaded from a user or application profile.

Editing a Threshold from the Histogram

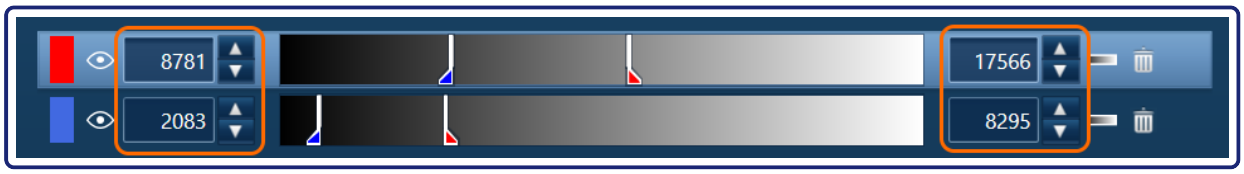
A threshold can be edited from the histogram by either:

1. Hovering the mouse over the highlighted region on the histogram until a cursor with four arrow heads pointing in different directions appears. Press the left mouse button down on the histogram and drag the mouse to move the highlighted region about.
2. Hovering the mouse over one edge of the highlighted region on the histogram until a cursor with two arrow heads pointing to the left and right appears. Press the left mouse button down and drag the mouse to the left or right to move that edge to the left or right (i.e. increase or decrease that limit).

Editing a Threshold from the List of Thresholds

There are two ways that a threshold can be edited from the list of thresholds displayed in the "Thresholds" tab of the "Detection Refinement" pane:

1. By editing the maximum and minimum gray-level threshold values displayed at either end of the gray-level bars:



   To adjust the thresholds either:

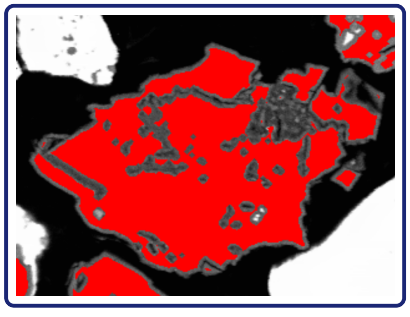
   - Edit the values displayed in the fields.
   - Use the up and down arrows to the right of the fields.

2. By hovering the mouse over one of the markers on the gray-level bars until a cursor with two arrow heads pointing to the left and right appears. Pressing the left mouse button down and drag the marker to the left or right to increase or decrease that limit.

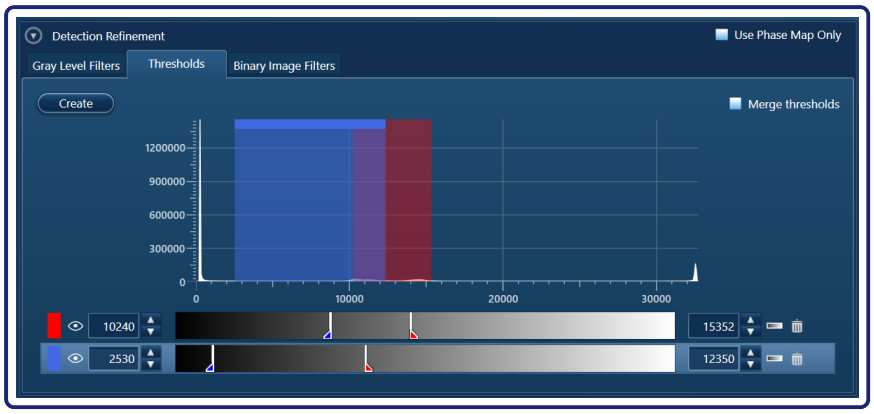
NOTE: *Unless overlapping thresholds has been allowed, if there are multiple thresholds present, a threshold may only be adjusted until it touches the next.*

Merging Thresholds

When the assisted thresholding tool is used, it is possible to find that the majority of a feature is included within the threshold, but that there is a region with slightly different gray-levels that is not included. For example:



In this case, if the assisted thresholding tool were used to select part of the unselected region of the feature, a new threshold would be created and would overlap with the existing threshold. i.e:

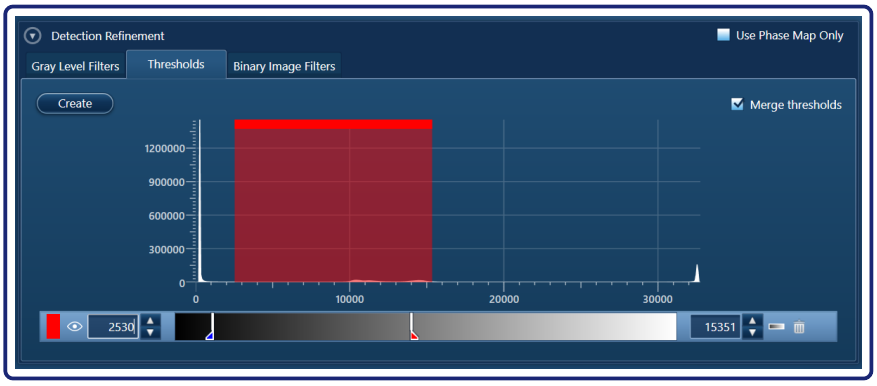


If the overlapping thresholds option is off, this wouldn't be allowed.

If the overlapping thresholds option is on, the feature would be detected as two separate features, with large regions in each feature that overlap each other. This is not ideal for accurate feature detection.

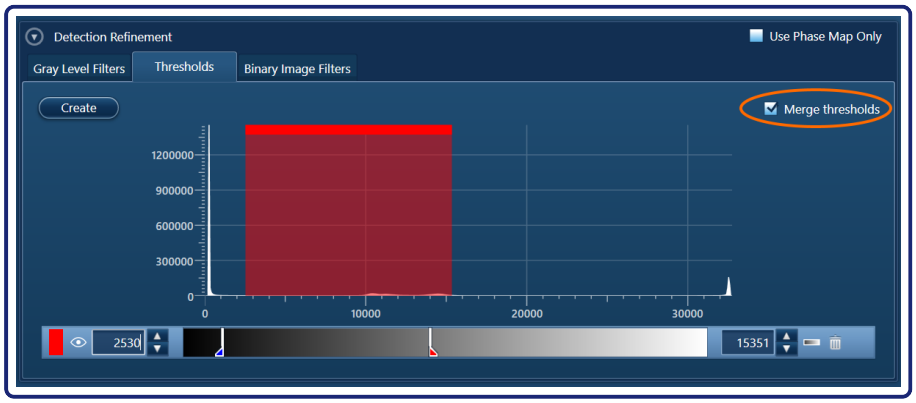
If the "Merge thresholds" tool is used in conjunction with the assisted thresholding wand tool, a new threshold will be created that will immediately merge the two thresholds together (as long as the new threshold touches or overlaps with an existing threshold). This results in one threshold that covers a greater range being created and the feature being detected as a single feature that lies within a single threshold.

For the example above, the feature and threshold histogram would now appear as:



To use the Merging Thresholds tool:

1. Create the first threshold.
2. Check the "Merge thresholds" button in the "Thresholds" tab of the "Detection Refinement" pane:



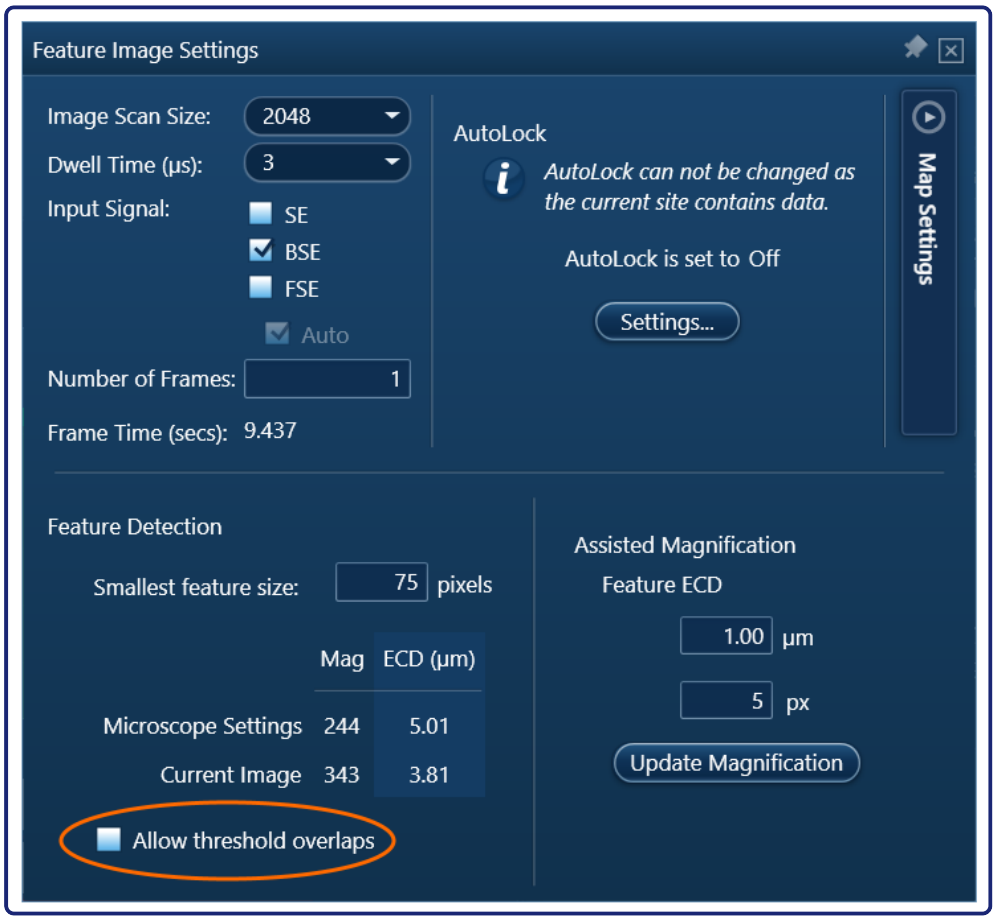
3. Create the second threshold. If the two touch or overlap, the software will instantly merge the two thresholds into one single new threshold.

Overlapping Thresholds

The "allow threshold overlap" option allows two thresholds to be defined with gray-level values that overlap each other. For these thresholds, features with gray-level values that fall inside both thresholds will be assigned to both thresholds and as such will be counted twice. This option can be useful for applications where certain features belong to multiple groups and it is desirable to analyze and count the features as part of both of these groups.

To allow multiple thresholds to overlap each other:

1. Open the Feature Image Settings from the acquisition toolbar.
2. Check the "Allow threshold overlaps" option:



NOTE: *This option can lead to double counting of features as they are associated with more than one gray-level threshold.*

Optimizing how the Features are Detected

Once the gray level thresholds have been specified and optimized, it may be necessary to also optimize how the features are detected to ensure that there are no inaccuracies in the morphology measurements of the features. There are two ways in which the feature detection can be optimized:

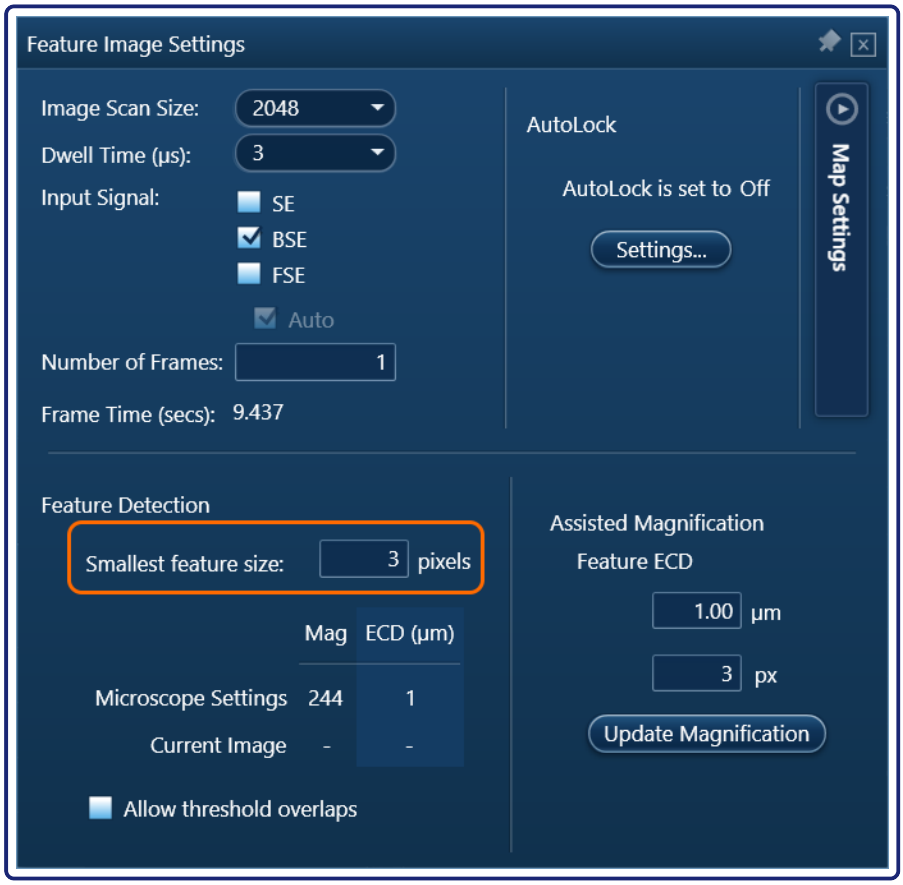
1. Setting the minimum size for a feature.
2. Using binary image filters.

Specifying the Minimum Size for a Feature

If the electron images contain small areas of noise, it is possible that the noise can be detected as features. This can lead to large numbers of features that do not exist being identified. To prevent this noise being identified as features, it is possible to specify the minimum feature size in pixels by:

1. Open the "Feature Image Settings" menu using the "Settings" icon on the acquisition toolbar of the "Detect Features" step:

2. In the "Feature Detection" section edit the number of pixels in the smallest feature size:



3. In the acquisition toolbar, click the "Detect Features" button to redetect the features with this setting.

   The feature detection will now use this value when detecting features to set the smallest feature size (in pixels) that will be allowed.

> ***NOTE:*** *This setting is independent of the assisted magnification settings.*

Using Binary Image Filters

Binary image filters are a powerful way of being able to change how features are detected.

For example, variation in the gray-levels at the edges of the features may mean that they are not detected correctly. This can lead to inaccuracies in the morphology measurements. Binary image filters may be used to correct this issue.

The binary image filters currently available include:

- **Dilation Filter:** Adds a layer of pixels around all features, thus increasing the effective area.
  This filter is useful in situations where the gray-level thresholds do not detect the edges of the features accurately, and increasing the threshold range will result in noise being detected as features.

  NOTE: *This filter may cause features that are close to each other to become joined up into a single feature.*

- **Erosion Filter:** Removes a layer of pixels from around all features, decreasing their effective area.

  NOTE: *If used repeatedly or with a high strength, this filter can diminish features and even cause them to be completely removed.*

- **Close Filter:** Fills any holes inside features and eliminates small details by smoothing the boundary from the outside.

  NOTE: *This filter is the equivalent of applying the dilation filter followed by the erosion filter.*

- **Open Filter:** Discards small features while keeping the largest features that have a shape similar to the original features.

  NOTE: *This filter is the equivalent of applying the erosion filter followed by the dilation filter.*

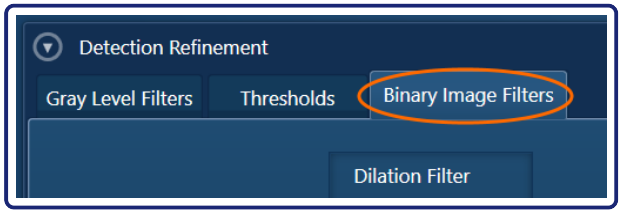
- **Separate Features:** Erodes the edge of a feature and then dilates it without recombining adjacent features. The original shape is retained.

  NOTE: *This filter is particularly useful for features with similar shape and size, that slightly touch each other.*

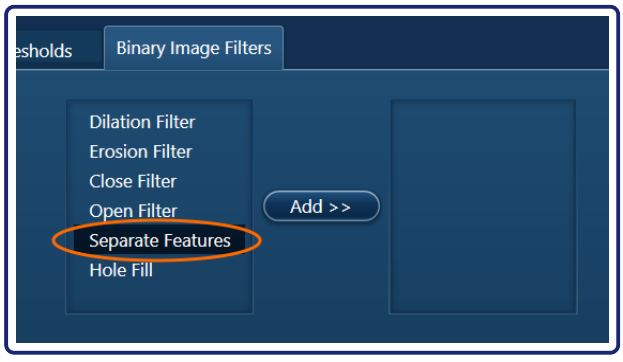
- **Hole Fill:** Fills any part of a the electron image that is completely enclosed by pixels that belong to a feature.

To apply a binary image filter:

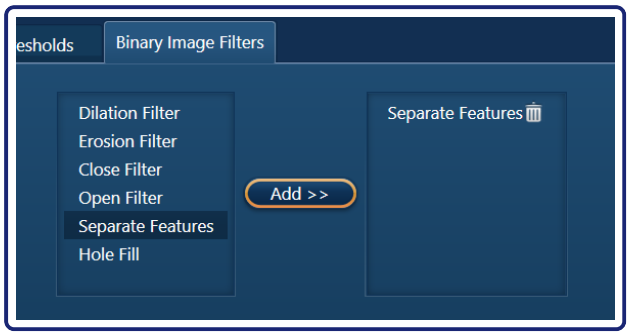
1. In the "Detection Refinement" pane of the "Detect Features" step, select the "Binary Image Filters" tab:



2. Select the filter to be applied. i.e. to select the "Separate Features" filter:

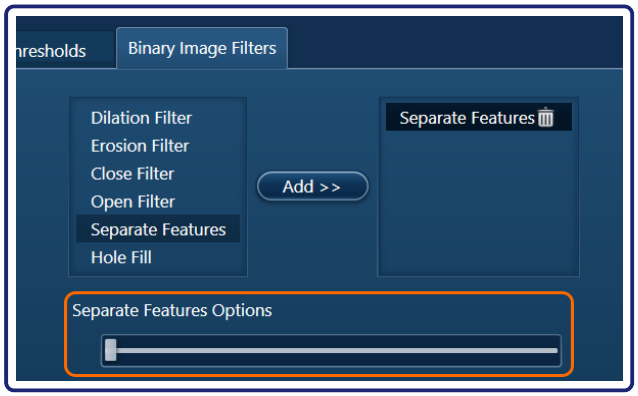


3. Click "Add" to apply the filter to the image:



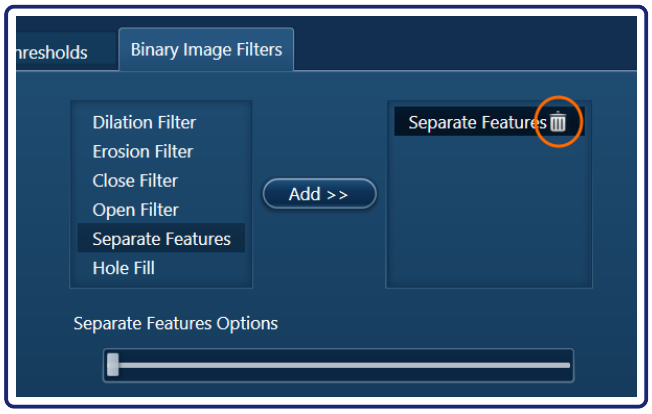
The filter will be applied to the image and added to the column on the right to show that it has been applied to the image.

4. To adjust the strength of an applied filter, select the filter from the column on the right. A slider bar will appear at the bottom of the "Binary Image Filters" tab:



The effect of the adjustment can be observed in the image.

5. Repeat steps 2 - 4 to add further filters.
6. To remove a filter from the image click the trash can icon to the right of the filter in the column on the right:

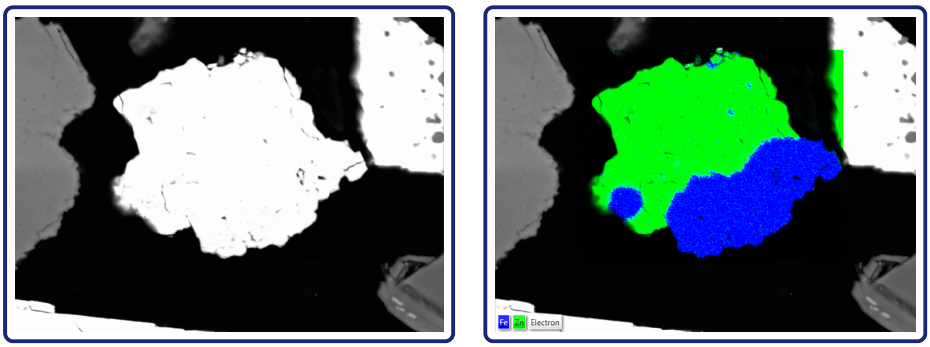


Separating Phases with Similar Gray-Levels into Individual Features

Some samples may contain features that are made up of several grains or components that have a similar density and hence appear to have a very similar contrast in the electron image. However, they actually have a different chemical composition to each other which means that ideally each grain should be treated as a separate feature. For example, many types of cement contain features with both silicate and carbonate

grains or sulphide and sulphate grains. These grains have a similar density and hence contrast to each other, which means that even when the electron image acquisition settings are optimized, it is not possible to distinguish the different grains from each other.

The images below are an example of this. In the BSE image (left), the central feature appears as a single feature with the same contrast which is suggestive of the same composition throughout. However, the EDS map (right) shows how this feature actually has two separate grains with different chemical compositions:

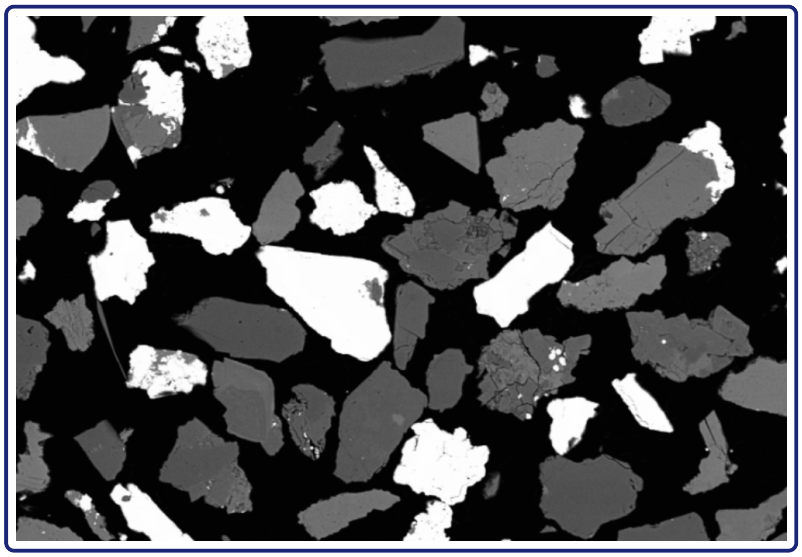


To allow these types of features to be detected correctly, AZtecFeature offers "Threshold Phase Detection". This is a licensed option that collects phase maps for all features within the selected "problem" threshold. Then, any features that are identified as having multiple phases are automatically split into multiple separate features. The Feature analysis can then continue as normal.

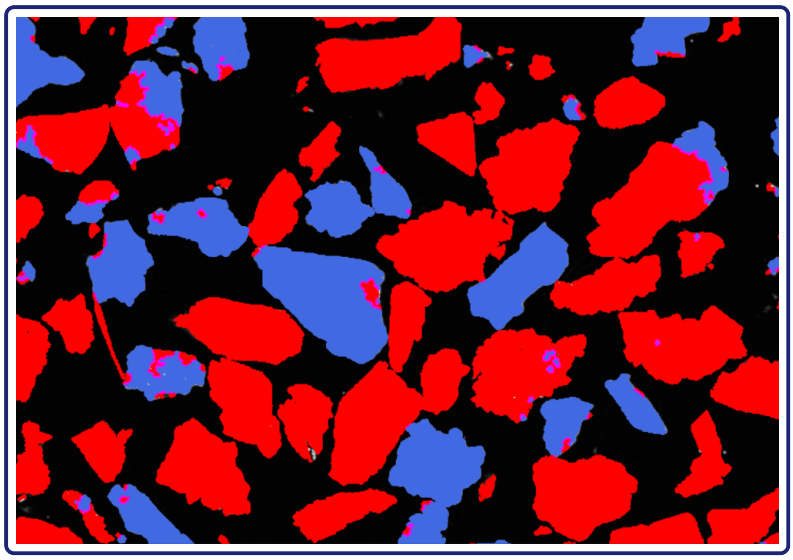
To use Threshold Phase Detection:

1. From the "Detect Features" step, acquire an electron image and define thresholds to detect all of the features as normal. Ideally all features with multiple phases should be put into a single threshold so that they are separate from the other features. This is because phase detection is time consuming and it is not desirable to perform it on features that do not require it.

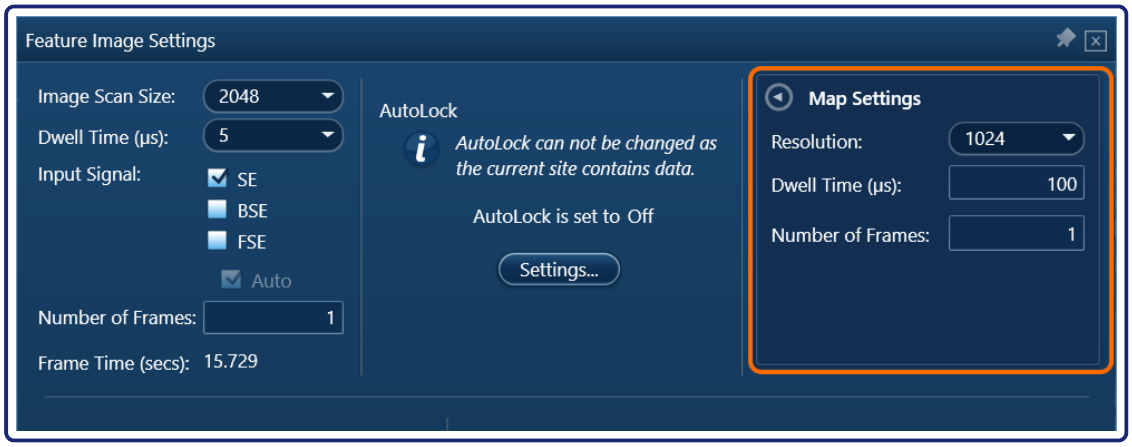
   i.e. For the electron image below, the brightest features are the features with multiple phases that need to be identified with threshold phase detection:

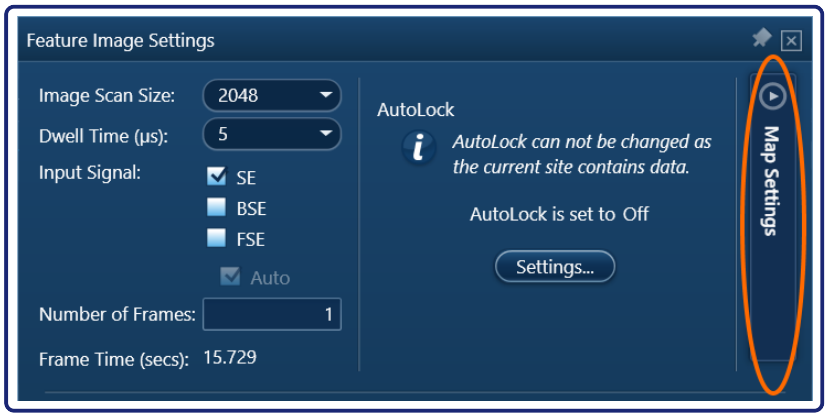
   These features can be detected in a separate threshold (blue) to all other features (red) as shown by the "Color by Threshold" map in the image below:



2. In the "Feature Image Settings", accessed from the "Settings" icon on the acquisition toolbar of the Detect Features step, use the "Map Settings" field to specify the EDS settings to be used for the threshold phase detection:



If this field is not visible it can be accessed by clicking on the "Map Settings" button at the right of the "Feature Image Settings" window.



In order for all of the phases in the sample to be detected correctly with AutoPhase, it is important that the data contains plenty of counts. If not, it may fail to detect some of the phases or get sufficient detail. As speed is also a factor (it takes much longer to acquire an EDS map than an electron image) a good

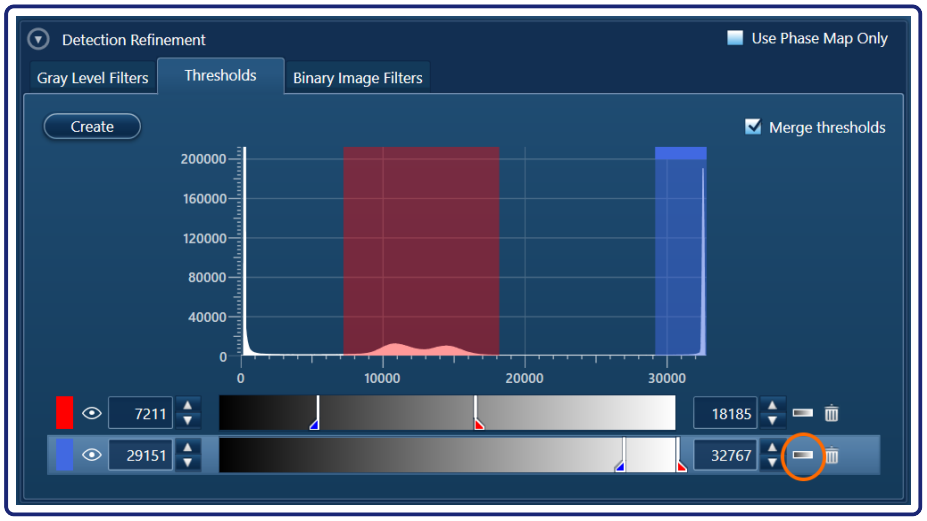
starting point is to try using a relatively low resolution (e.g. 512) and a longer dwell time (e.g. more than 200 µs).

At the bottom of the "Map Settings" field, an estimate of the full frame time for the map will be displayed. This value assumes that EDS data is being collected for every pixel in the field, so is a worst case estimation of the time it would take to do threshold phase detection on the entire field. However, it may still be useful in helping to make the best compromise between data and time.

3. From the list of defined thresholds at the bottom of the "Thresholds" tab in the "Detection Refinement" pane, identify the threshold that contains all of the features that are made of multiple phases.

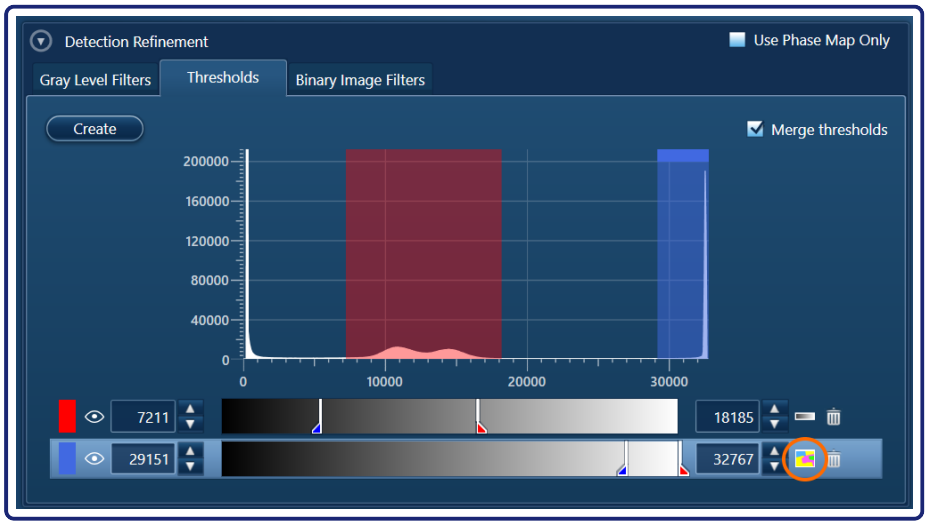
> ***NOTE:*** *It is possible to perform threshold phase detection on more than one threshold.*

4. Select to do a phase map for this threshold by clicking on the gray scale icon to the right of the threshold:

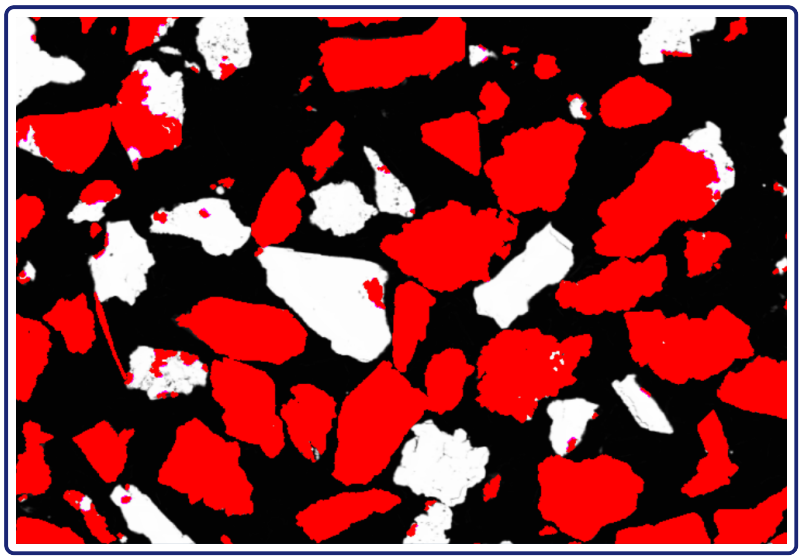


The phase map will immediately start being acquired.

The icon will update to show that there is now a phase map for that threshold:

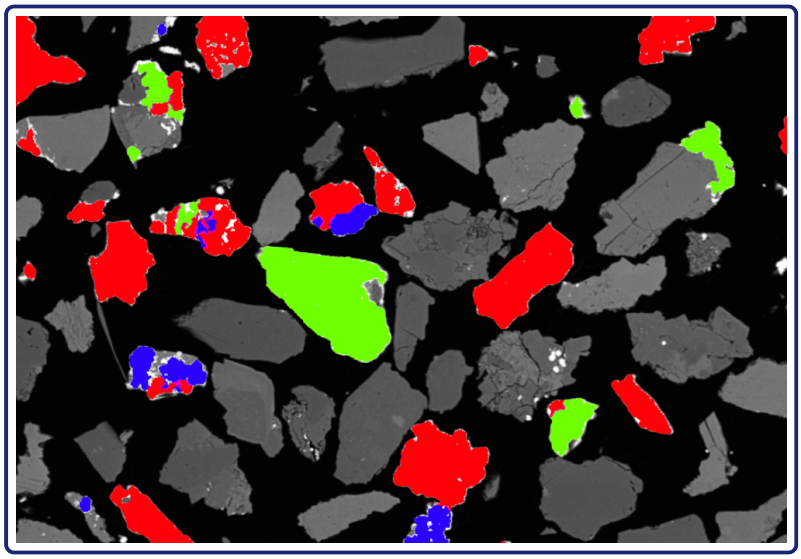


The "Color by Threshold" map will be updated so that the threshold that the phase detection is being carried out for is no longer displayed. This is because this threshold will no longer be used as it is replaced by a phase map:



As the threshold phase detection completes:

1. A "Color by Phase" map will be generated showing the phase map for the features that were in the threshold that was selected for "threshold phase detection":



2. The "Color by Feature" map shows how the features are made up:

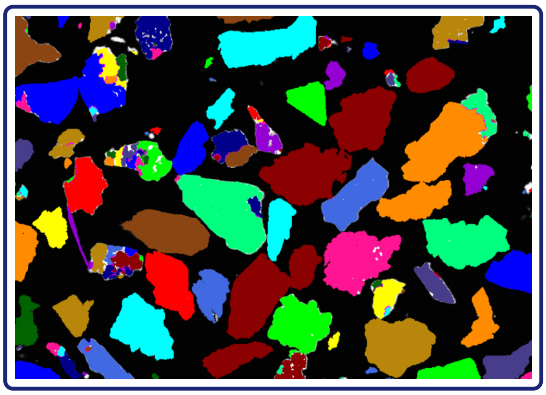


Image showing how after threshold phase detection, a number of features are made

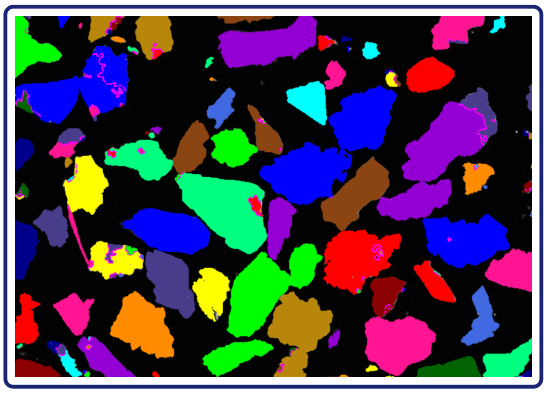
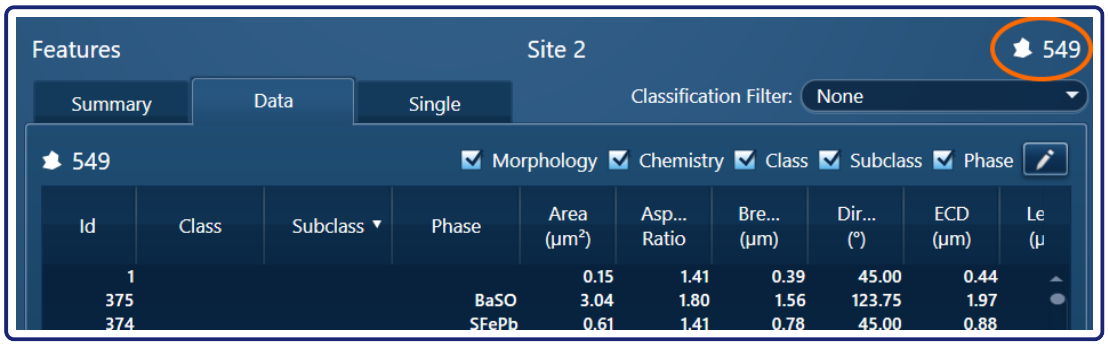


Image showing the result of feature detection before threshold phase detection has been applied.

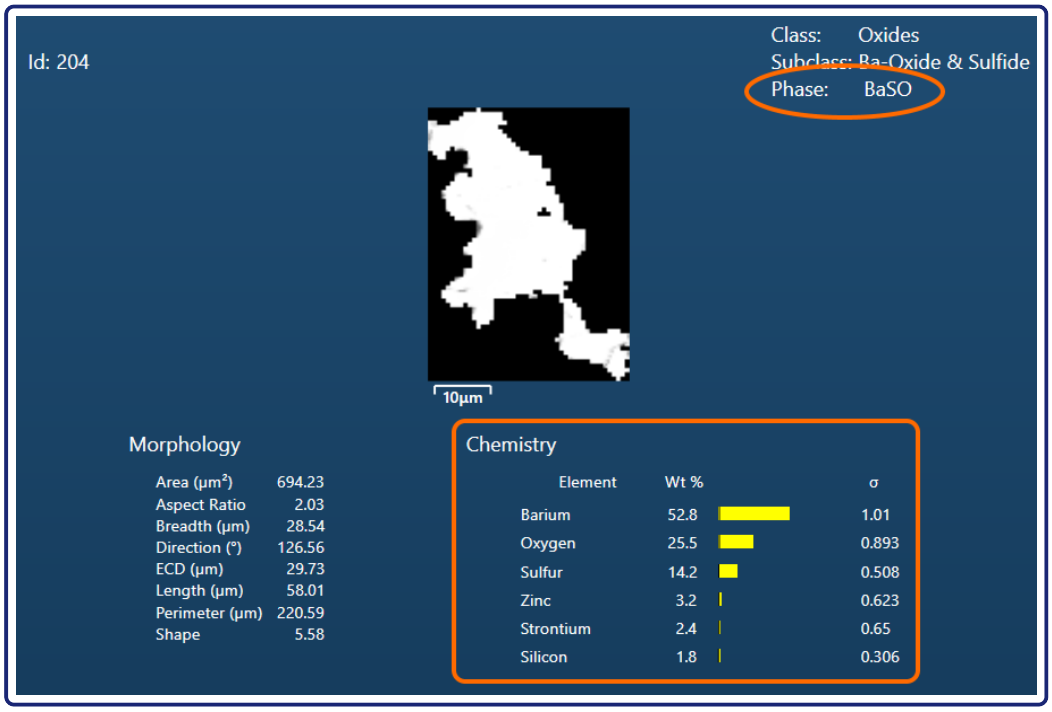
up of multiple grains with different phases. Most features are detected as single large features.

3. The morphology of every feature in the map is measured.
4. In the Feature Data Reviewer pane:
   - The number of features detected will be updated. A feature that is found to contain multiple grains with different phases is deleted and replaced by with one feature for each individual grain.



NOTE: *The new features will have a different feature Id to the original feature.*

   - For features that were analyzed with phase map, the name of the phase that the feature was detected as and the chemistry information acquired will be displayed:



The rest of the Feature acquisition can now proceed as normal. However,

- If the survey scan option is selected, the survey scan will run but will only be based of the image. i.e. it will take the number of features detected before the threshold phase detection is performed.
- If data is acquired over a large area, all of the data will be acquired as normal, however the EDS map data for the features detected using threshold phase detection will not be analyzed until the end of the run. This is because AutoPhase requires a complete list of elements for the entire large area map before it can run.

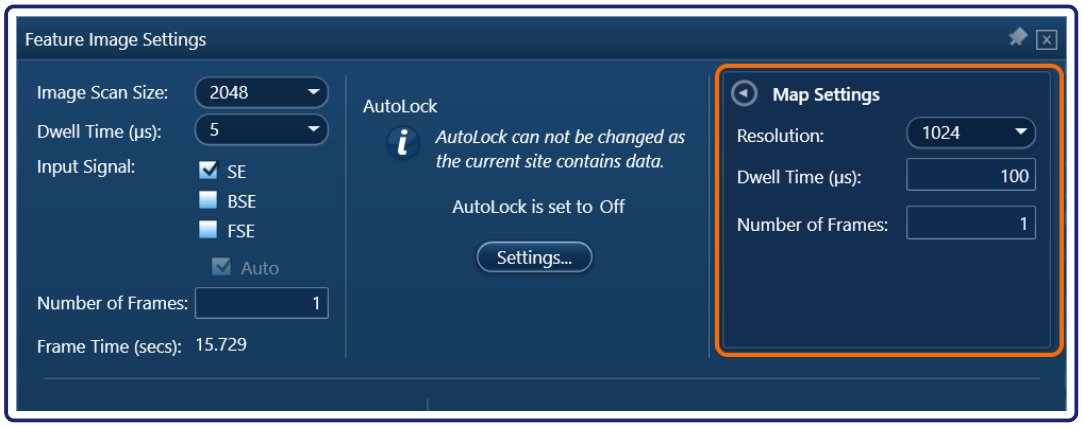
Separating Features from Backgrounds with Similar Gray-Levels

In some solid samples such as solid rock sections, it is possible to have many dense fibers or particles, which have very similar contrast gray-levels to the background. Although the features of interest in these samples may be visible by eye, they cannot be separated from the background using the standard thresholding method.

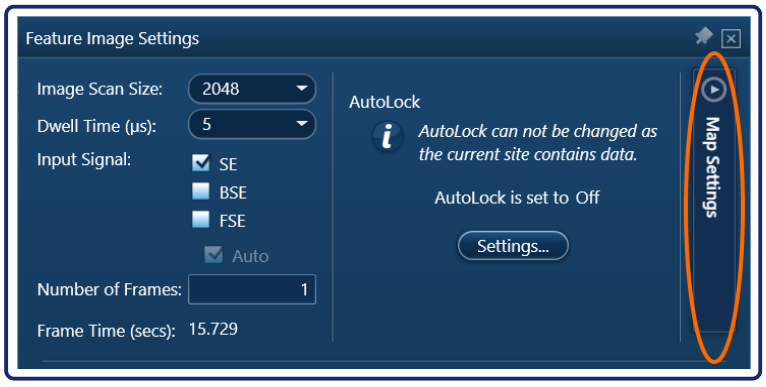
For this particular situation, AZtecFeature offers "Full Field Phase Detection", a licensed application where instead of using gray-level thresholds to distinguish the features, an electron image and then a full EDS map are acquired and the features including the background are identified using phase detection. Once the features have been identified, the Feature analysis can then be set up and performed as normal.

To use Full Field Phase Detection:

1. Use the "Feature Image Settings" which is accessed from the acquisition toolbar in the "Detect Features" step to specify the settings that will be used to acquire the electron image as per a normal Feature acquisition.
2. In the "Feature Image Settings" use the "Map Settings" field to specify the EDS settings that are to be used as part of the full field phase detection:



If this field is not visible it can be accessed by clicking on the "Map Settings" button at the right of the "Feature Image Settings" window.

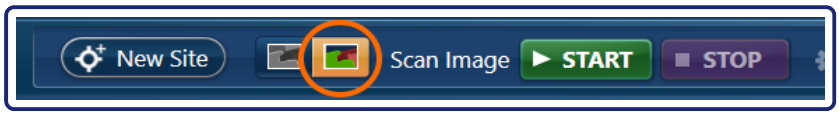


In order for all of the phases to be detected correctly with AutoPhase, it is important that the data contains plenty of counts. As speed is also a factor (it takes much longer to acquire an EDS map than an electron image), a good starting point is to use a relatively low resolution (e.g. 512) and a longer dwell time (e.g. more than 200 µs).

NOTE: *At the bottom of the "Map Settings" field, an estimate of the full frame time for the map will be displayed. This value may be useful in helping make the best compromise between data and time.*

3. Click the "Acquire EDS Data" button in the acquisition toolbar on the "Detect Features" step.

   This specifies that both an electron image and an EDS map should be acquired and a full field phase detection be performed:



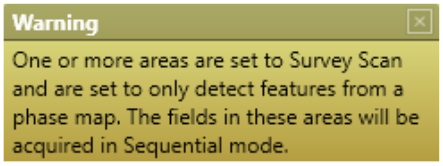
4. Click the "Start" button to start the acquisition of the electron image and EDS map.
5. Once the EDS acquisition has completed, AutoPhase will be run and feature detection will be performed on the entire map field, including the background. The morphology of every feature will also be measured.

   The detected features can be viewed as an image by selecting the "Color by Feature" option for the image pane. The number of detected features and their details including their phase and chemistry information can be viewed from the Feature Data Viewer.

6. Remove unwanted features including the background from the rest of the feature analysis, using classifications. For information on how to do this see the classification section of the help.
7. Proceed with the feature analysis as normal.

   When the data is acquired, it is acquired as normal, however the EDS map data is not analyzed until the end of the run. This is because AutoPhase requires a complete list of elements for the entire acquisition before it can run.

NOTE: *If the survey scan option is selected, the survey scan will not run. Instead the fields will be acquired sequentially. A yellow warning message notifying this will be displayed:*



Refining the Accuracy of the Feature Location

When selecting the settings for acquiring the electron image, it is generally necessary to make a trade off between noise and accuracy, and speed. Even with modern backscatter electron detectors, there is generally some lag between the electron beam hitting a feature and the brightness associated with that feature being seen by the detector. This means that if the electron beam is scanned quickly, the feature can appear several pixels later in the image than it actually is. As microscopes generally scan from left to right, this means that the features will generally appear in the image as being slightly to the right of where they actually are. For large features, this may not be such a problem, but for small features, this could mean that when the electron beam goes to the expected location of a feature, it actually misses it and the EDS data collected is incorrect.

One solution to this problem is to scan the electron beam very slowly, because as the speed of the acquisition is reduced, the lag on the detector becomes less significant. However, this would lead to a very slow acquisition of the electron images, which is undesirable especially if acquiring data over very large areas with high numbers of fields.

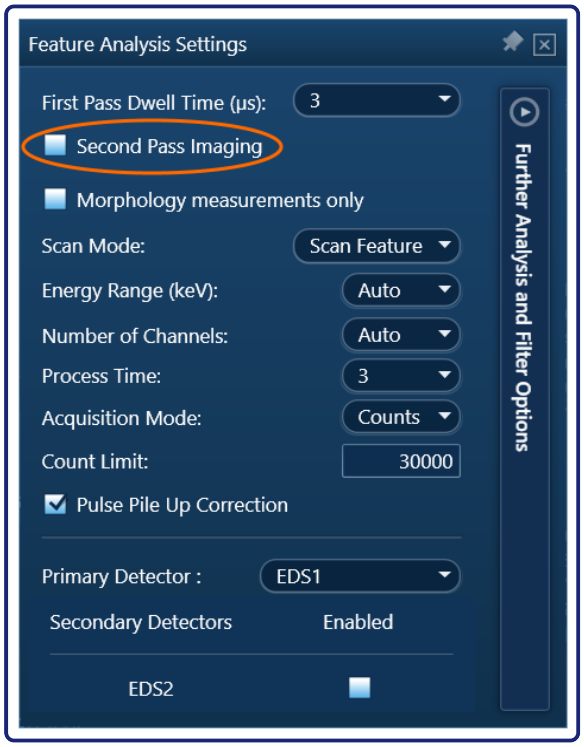
Instead, a better solution is to use a two pass imaging approach. In this approach, for the first pass, the whole field of view is scanned at a high speed (low dwell time) so that the software can detect the approximate location of each feature. Then on the second pass, only the areas that were found to contain features in the first pass image are scanned. This time they are scanned much slower (using a high dwell

time) allowing for the location and size of the features to be detected more accurately. This method means that while a number of pixels are scanned at a slow scan rate, the total time to acquire both electron images is much less than a single image acquired at a low scan rate.

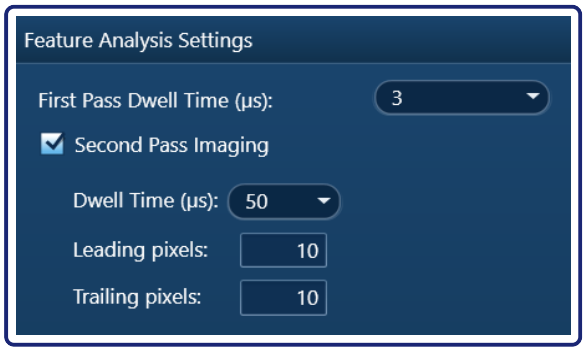
To use the two pass imaging approach:

1. Set up the acquisition of the first pass image in the "Detect Features" step, as though it were a normal image acquisition. Ensure that a short dwell time (i.e. less than 10µs) is used.
2. Move to the "Acquire Site" step to set up the second pass image.
3. Open the "Feature Analysis Settings" window by clicking on the "Settings" icon in the acquisition toolbar:

4. Check the "Second Pass Imaging" option:



5. Enter the acquisition settings for the second pass image:



- Dwell Time (µs): This must be set to a value higher than that used for the first pass image. Typically 20 - 100 µs is used.

- Leading pixels: Enter the number of pixels before the pixel where the feature was observed in the first pass image that the software should start scanning from.
- Trailing pixels: Enter the number of pixels after the pixel where the feature was observed in the first pass image that the software should stop scanning at.

> ***NOTE:*** *The default number of leading or trailing pixels is 10 pixels. The number used can be customized depending on the system and the amount of lag experienced.*

6. To verify the settings for the second pass image click the "Acquire" button in the "Acquire Site" step. This will cause the second pass image as well as any EDS acquisition to be undertaken for a single field.

2.3.3. Visualizing the Results of the Feature Detection

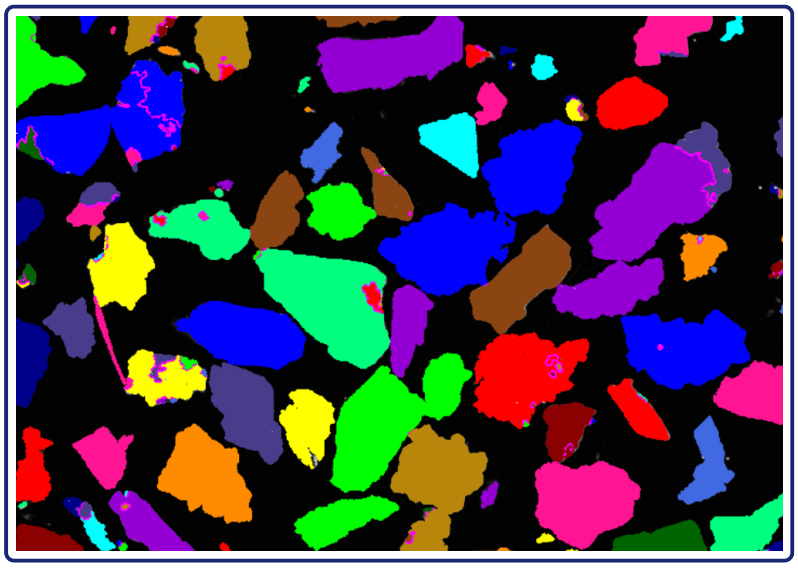
As AZtec completes the feature detection, it automatically:

- Gives every feature its own unique identification number.
- Measures the morphology of every feature.
- Applies the classification scheme (if one has been defined).

If the feature detection is re-run, for example because one of the settings that affects the feature detection has been changed, the entire feature list is deleted and regenerated as part of the feature detection.

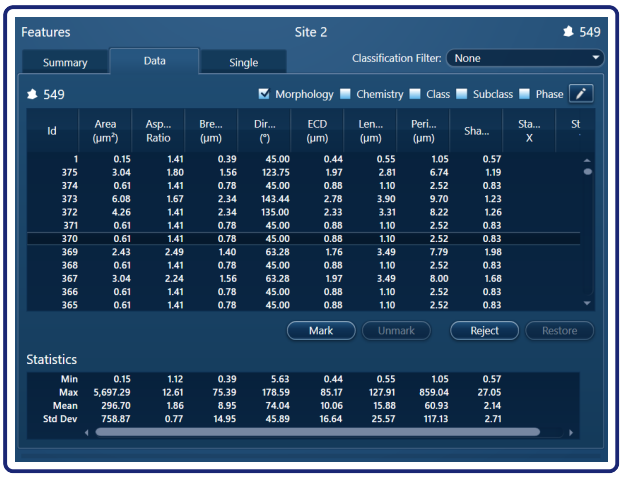
The results of the feature detection can then be visualized:

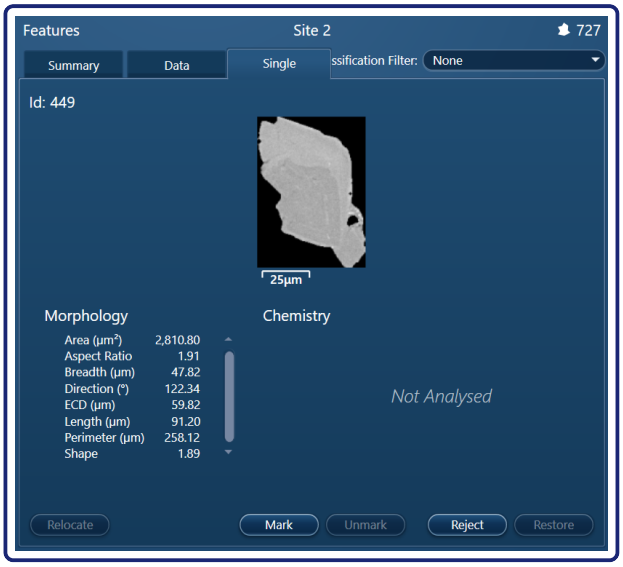
- In the image pane of the "Detect Features" step as a "Color by Feature" map, where each feature is displayed in a unique color:



  This map display is useful for visualizing how the features have been detected and ensuring that they have been detected correctly. For example, it is possible to see if two touching features have been identified as two individual features or as a single large feature.

- In the Feature Data Viewer pane, available on most steps including the "Detect Features" step, where the data can be viewed as a summary graph or table (if the "Morphology" option is selected) for all features, or in detail for a single feature. For example:



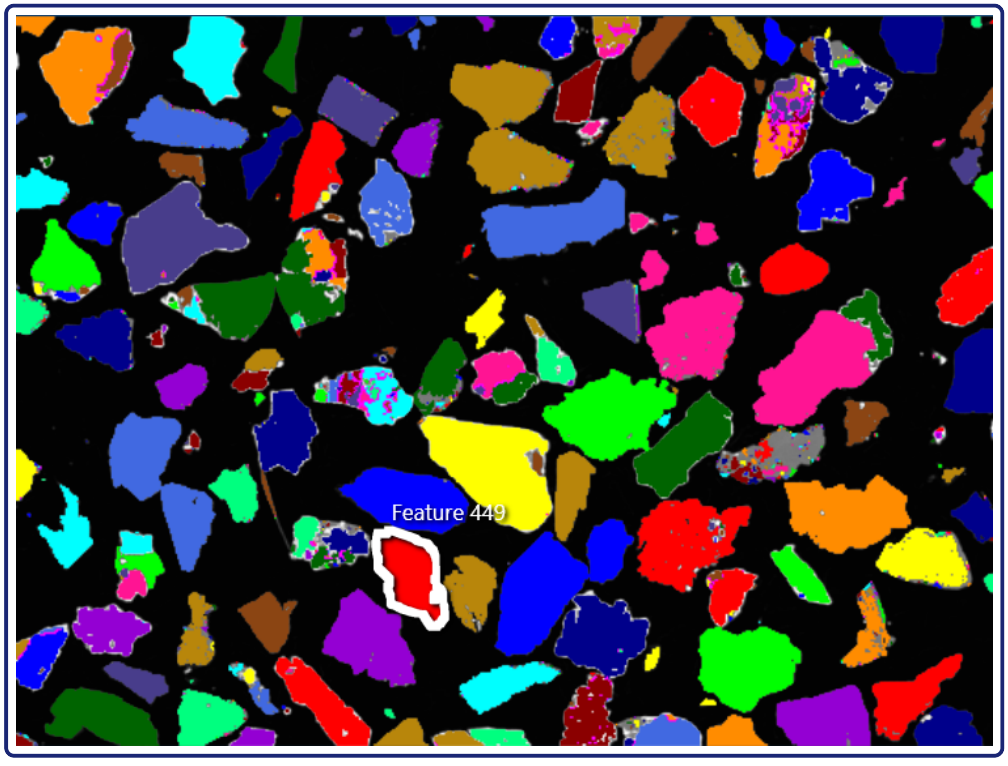


For more information about using the Feature Data Viewer, see the Reviewing Feature Data section of the help.

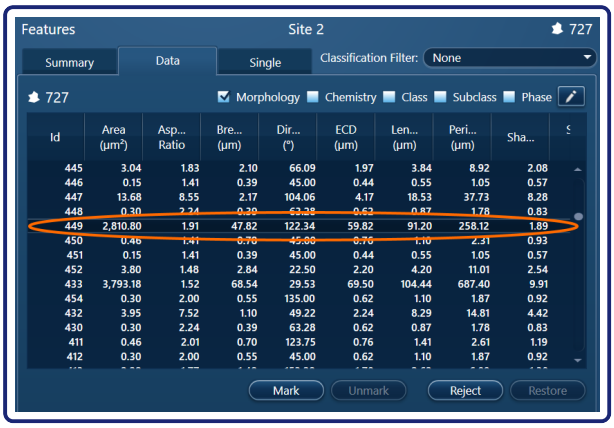
To assist with interrogating the data, in the toolbar on the left of the screen is the select feature tool:

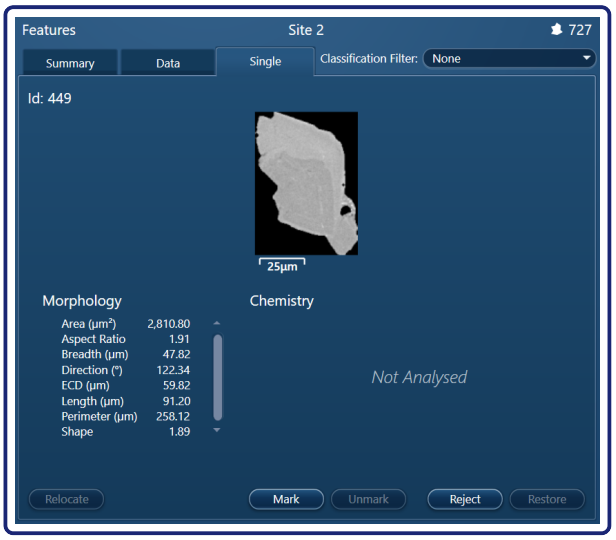
When this tool is selected:

- Click on a feature in the image pane so that it is highlighted. For example:



- The same feature will be highlighted in the Data and Single tabs of the Feature Data Viewer pane:



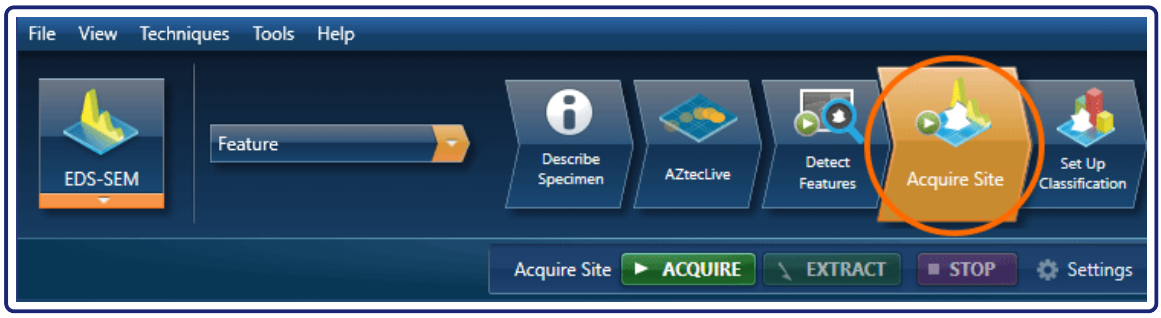


- A feature may also be selected using the Data tab of the Feature Data Viewer pane, and will be highlighted in the image pane and in the Single tab of the Feature Data Viewer.

2.4. Acquiring EDS Data

Once the features have been detected correctly, consider the EDS data to be acquired and analyzed. The Acquire Site navigator step may then be used to:

- Define the EDS acquisition conditions.
- Test the EDS acquisition conditions by acquiring EDS data for every feature in a single site.
- View the results of the EDS acquisition within the Feature Data Viewer.
- Confirm that the quantitative analysis is suitable.



There are two main areas of consideration when setting up how to acquire the EDS data:

1. **The EDS acquisition settings:**

   Consider the quality of data that needs to be acquired to give the required result as well as how long it would take to acquire that data.

   For Feature analysis it is generally desirable to achieve a high throughput while detecting the presence of certain elements or the absence of others. As such, a lower process time and number of counts than those that would be used for full quantitative analysis may be suitable because they generally result in a lower acquisition time while still producing the desired result.

2. **How to optimize the acquisition:**

   Consider the data to be acquired and the features that the data needs to be acquired for. Can filters be used to optimize the acquisition by:

   - Filtering out features that are not of interest so that time is not spent acquiring EDS data for them.
   - Identifying specific features which require greater amounts of EDS data to be acquired in order for them to be resolved accurately.

When viewing the results of the EDS data analysis, the main areas of consideration are:

1. **The EDS data quality:**

   Consider the quality of data and whether it shows the desired results. Use the "Show Spectrum for Acquiring Features" option to view the spectrum and the Feature Data viewer to view a summary of the EDS data.

2. **The quantitative analysis settings:**

   Consider how the quantitative analysis is done. Of particular importance is whether thresholding is enabled as it affects:

   - The data displayed in the Feature Data Viewer.
   - The value that the sigma thresholding level is set to (even if the "Enable thresholding" option is off).

   This is because it affects the "must be detected" classification setting.

2.4.1. EDS Data Acquisition

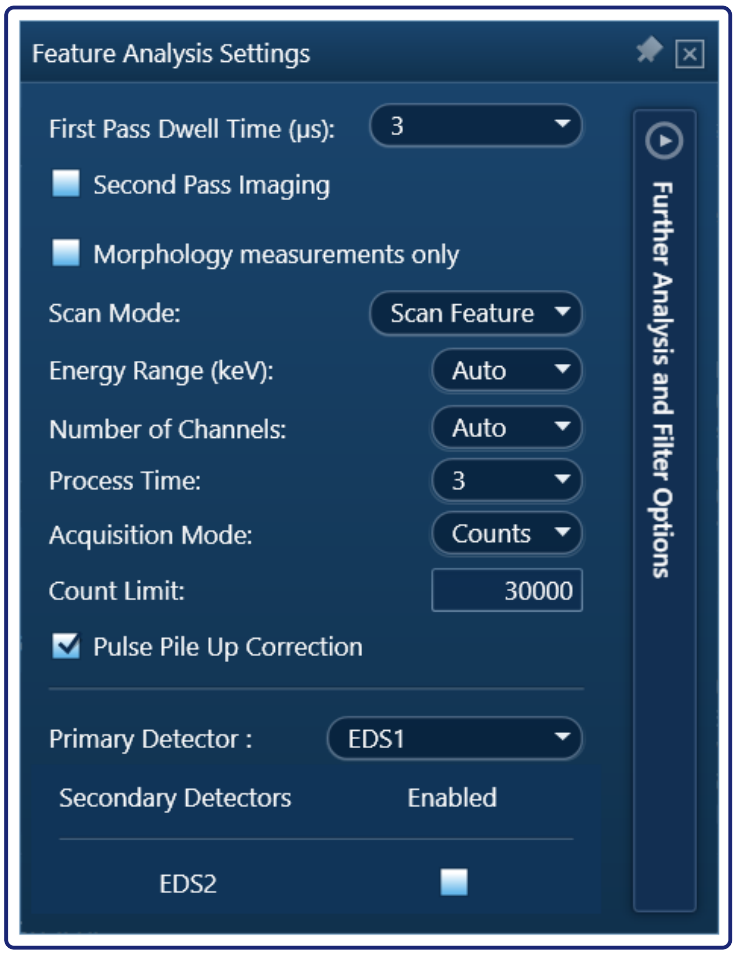
The aim of acquiring EDS data for a single site of interest in the "Acquire Site" step of AZtecFeature is to:

- Verify that the EDS settings are suitable to identify the elements of interest present in the features.
- Verify that the EDS settings are suitable for the acquisition to be extended to a large area acquisition.
- Verify that the quantitative analysis settings are suitable.
- Set up and test classifications, which are used to put the features into groups of interest for further analysis.

To set up to acquire EDS data:

1. Select the EDS acquisition settings from the Feature Analysis Settings window.

   To access the Feature Analysis Settings window, click on the "Settings" icon on the acquisition toolbar in the "Acquire Site" step:



   For more information on selecting suitable EDS Settings, see the EDS Acquisition Settings section.

2. Specify any morphological or EDS filters and further EDS analysis to be performed from the "Further

Analysis and Filter Options" section of the "Feature Analysis Settings" window:

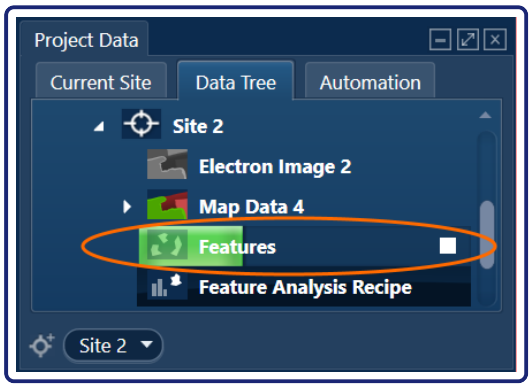
For more information on using filters to identify features for further analysis, see the Optimizing the Acquisition Time Using Filters section.

3. Click the "ACQUIRE" button on the acquisition toolbar to start the EDS acquisition.

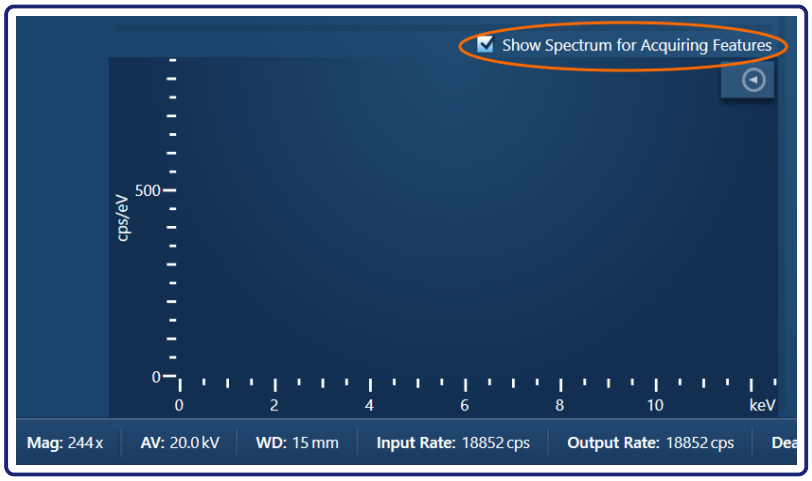
   The EDS acquisition will take place for the currently selected site.

As the data is acquiring:

- The progress of the acquisition can be monitored from the Data Tree:



- The spectra can be viewed as they are being acquired by checking the "Show Spectrum for Acquiring Features" option at the top of the spectrum viewer.



> ***NOTE:*** *For very fast acquisitions, every third or fourth spectrum is displayed.*

- The quant result can be viewed in the Data Viewer as soon as it has been calculated.

> ***NOTE:*** *For threshold and full field phase detection, the quant result is not calculated until the acquisition has completed.*

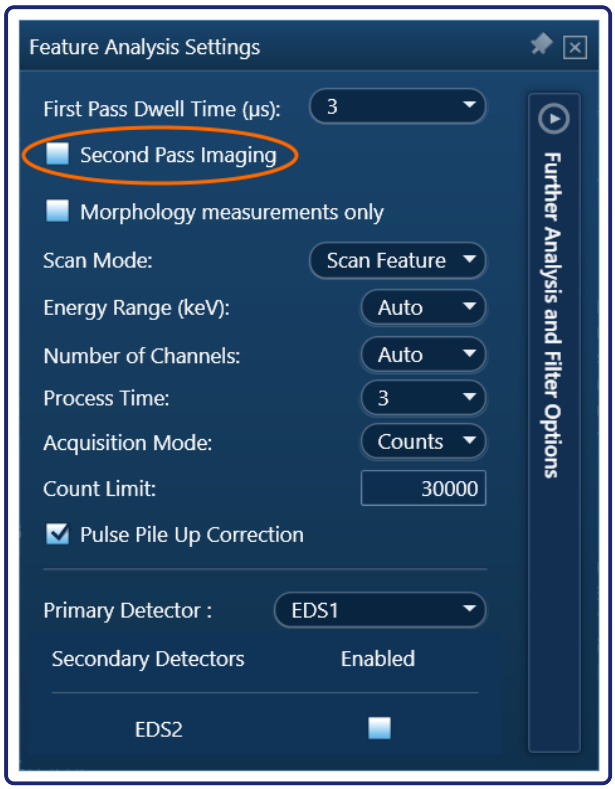
EDS Acquisition Settings

The settings for the EDS acquisition can be specified by clicking on the "Settings" icon on the acquisition toolbar in the "Acquire Site" step.

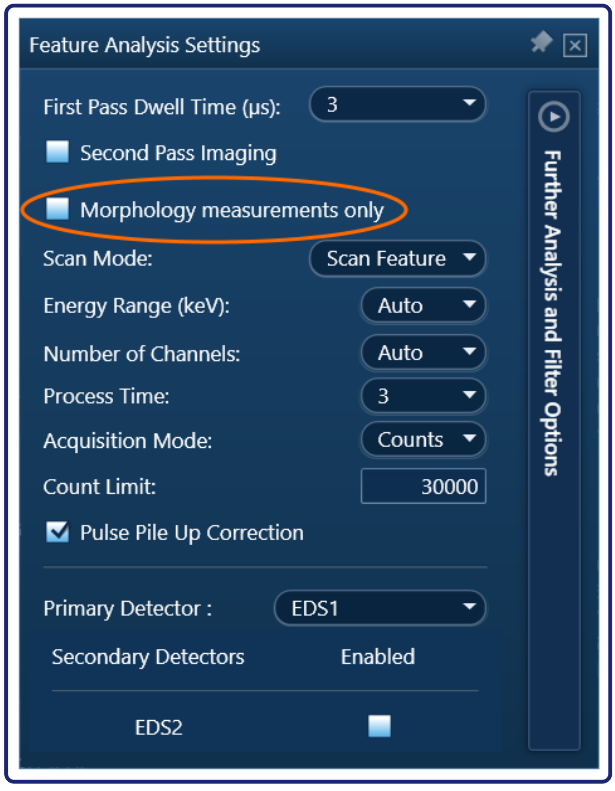
This will open the "Feature Analysis Settings" window:

1. Select whether to refine the accuracy of the feature location using the "Second Pass Imaging" option.

   For more information on this option, see Refining the Accuracy of the Feature Location.



2. Select whether to acquire only morphology data by checking the "Morphology measurements only" option, or to acquire both morphology and EDS data by unchecking the "Morphology measurements only" option.



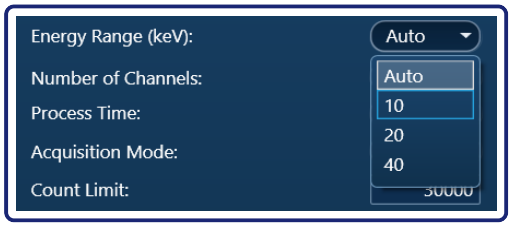
   The "Morphology measurements only" option is useful if only the feature size is being characterized. It is very fast to complete because it only requires electron image to be acquired.

If EDS data is to be acquired the following settings should be specified:

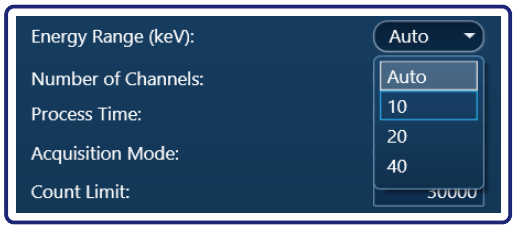
1. **Scan Mode:** Use the drop down menu to select between:
   - Scan Feature: The EDS data is acquired as the electron beam is rastered over the entire feature. The resulting EDS data gives the average composition for the feature.
   - Spot: The EDS data is acquired for the longest chord. This method is good for small spherical features with uniform composition.

NOTE: *The longest chord can be thought of as being calculated by drawing a grid over the feature and finding the longest line. The center of that line is the point from which the spectrum is acquired.*

2. **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 most suitable energy range depends on the microscope accelerating voltage and the elements to be detected. It is important to ensure that all energy lines that are likely to be excited will be detected and displayed.

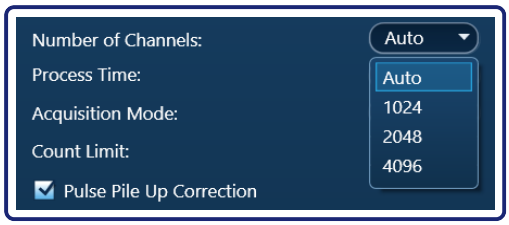
The default value is "Auto", where AZtec checks the accelerating voltage set on the microscope and selects a suitable energy range.

If the microscope is set to 10 kV, the 0-10 kV energy range is most suitable. Plotting higher energies will not reveal any additional data as no energy lines above 10 kV will be excited.

If the microscope is set to 15 kV, the 0-20 kV energy range is likely to be more suitable as it will allow the energy lines between 10 and 15 kV to be revealed.

3. **Number of Channels:**

Select the number of channels that are used to display the spectrum data from the available options of Auto, 1024, 2048 or 4096 (4K) in the "Number of Channels" drop down menu.

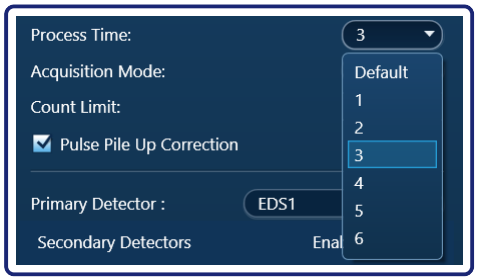


The default value is "Auto", where AZtec automatically sets the appropriate number of channels.

The most suitable number of channels depends on the energy range being used and the resolution (eV/channel) with which the spectrum is to be displayed.

4. **Process Time:**

Select a suitable process time from the available options of Default, 1, 2, 3, 4, 5, and 6 from the "Process Time" drop down menu.



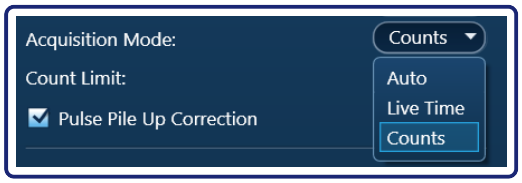
The process time adjusts the pulse processor settings, including the length of time spent processing the X-ray signal coming from the EDS detector and averaging noise from the data. Reducing the amount of noise will improve the resolution of the spectrum and may help resolve elements that have similar energies. However, it increases the amount of time it takes to acquire the data.

The default value is "Default", which uses the process time "4". Process time “1” is the shortest and hence gives the highest X-ray acquisition rates, but at some cost to the resolution. Process time “6” is the longest and gives the highest resolution with the narrowest peaks, but at some cost to the maximum acquisition rate.

For AZtecFeature, it is generally recommended to select a lower process time for higher throughput (i.e. 3). It is generally acceptable to do this because the experiment is looking for the presence of certain elements, or the absence of others, not a quantified composition.

5. **Acquisition Mode:**

Select an acquisition mode from the available options of Auto, Live Time and Counts from the "Acquisition Mode" drop down menu.



- **Auto:** In this mode data is acquired until there are sufficient counts (500,000 counts) in the spectrum in order for the software to be able to quantify the spectrum.
- **Live Time:** Data is acquired for a fixed time, which is entered in seconds.

> ***NOTE:*** *The live time does not correspond to the total time for the acquisition to complete. Instead it is the time for which the system is processing counts into the spectrum. This means that the total acquisition time is longer than the live time, because it compensates for the output rate of the detector*

being less than the input rate by the degree of deadtime. For efficient data acquisition you want to ensure that the deadtime is between 20% and 50%. If it is greater than 50% you should consider reducing the process time or if this is not suitable reducing the beam current on the microscope.

- **Counts:** Specify the total number of counts to be in the spectrum. When the acquisition reaches this number of counts it is stopped.

6. **Pulse pile up correction:**

   Select whether to apply pulse pile up correction.

   Pulse pile up occurs when an X-ray arrives at the EDS detector and triggers the measuring system whilst it is still processing a previous X-ray. This results in the energy of the two X-rays being added together and a peak being formed in the spectrum at an energy which does not correspond to any of the elements in the sample. The largest pulse pile up peaks tend to occur at twice the energy of the main peaks.

7. **Primary Detector:**

   If the system has multiple detectors, select which detector is to act as the primary detector.

   Select whether to also acquire data from the additional detectors, by checking the relevant detector boxes under secondary detectors.

Optimizing the Acquisition Time Using Filters

Filters are a useful way of reducing and optimizing the Feature acquisition time by allowing:

- The morphology information from the electron images to be used to identify the features to be analyzed with EDS.

  I.e. Only acquire EDS data for features that fall into a certain size range.

- The EDS acquisition time to be extended using 2nd and 3rd pass EDS filters for features that require additional EDS data to improve the results.

  I.e. Elements with complex overlapping peaks.

The morphological and EDS filters can be specified from the "Acquire Spectra" step by clicking on "Further Analysis and Filter Options" in the "Feature Analysis Settings".

This will maximize the "Further Analysis and Filter Options" tab , where the acquisition is shown as a flowchart:

Select whether to:

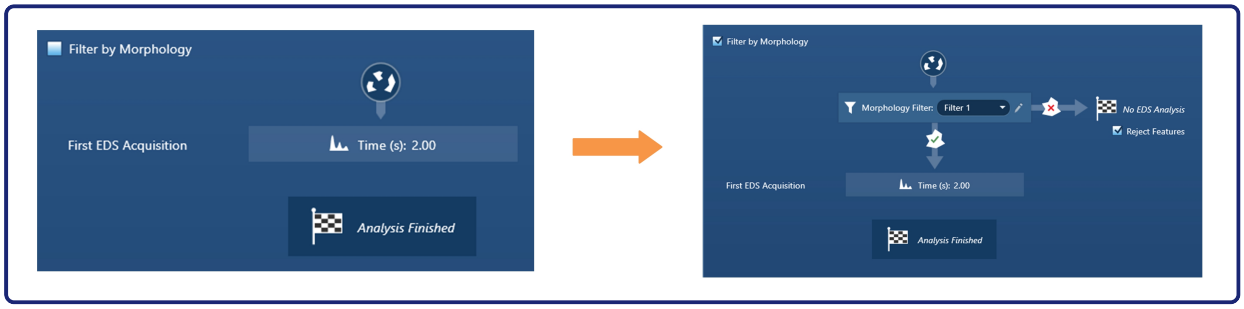
- Carry out an initial morphology filter on the detected features before the first pass EDS acquisition.
- Filter the features further based on EDS or morphology criteria and acquire second and third pass EDS data.
- Reject features with values outside of the ranges defined by the filters from the analysis. (Rejected features will not be included in the main data table, but can be viewed by selecting the appropriate

rejected filter from the classification filter drop down menu in the Review step.
Note, you can also reject features automatically using a classification scheme. This method is better for post processing data. See the "Classification Scheme" section.

> ***NOTE:*** *The flowchart will update depending on the options selected.*

To add filters and additional EDS acquisitions to the Feature experiment:

1. Select the relevant filter option (i.e. "Filter by Morphology" or "Acquire Second Pass EDS"). This will add a filter followed by an EDS step to the flowchart. For example:



2. Select an existing filter using the drop down menu, or create a new or edit an existing filter by clicking the pen icon.

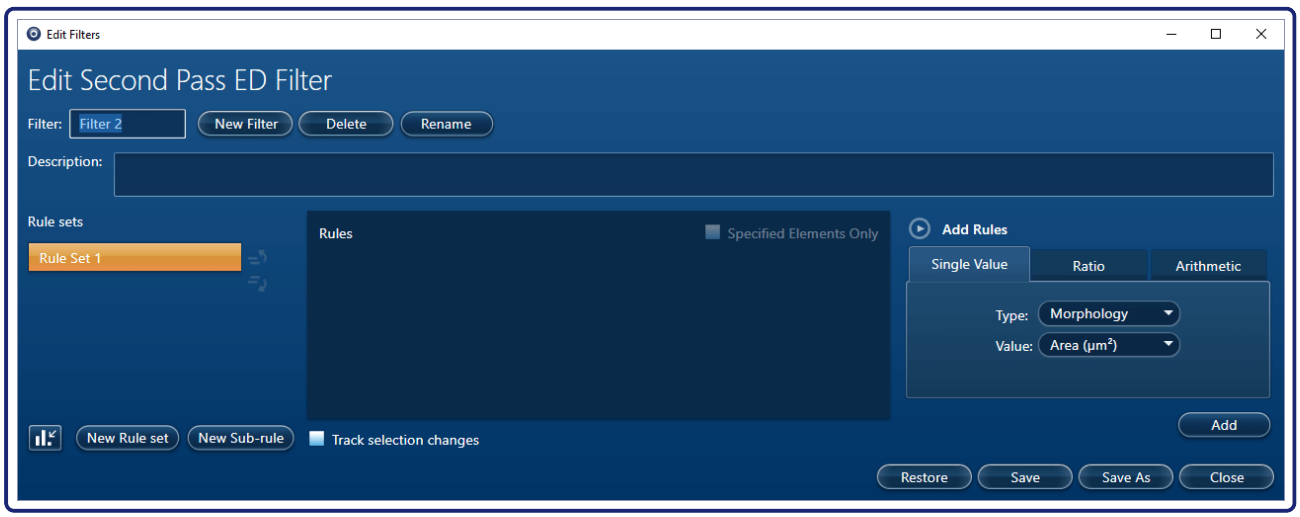
> ***NOTE:*** *For the morphology filter, only morphology rules can be defined.*

3. Select whether or not to reject features that do not match the filter. In addition to being excluded from any further acquisition or analysis, these features are not included in the data table.
4. Specify the EDS acquisition time. Use the "Feature Analysis Settings" menu to specify whether the EDS acquisition mode is in "counts" or "live time". This mode will be used for all EDS acquisitions.

> ***NOTE:*** *For the first EDS acquisition define the time or the number of counts in the settings menu. For the second and third EDS acquisitions define the time or number of counts in the flowchart itself.*

Creating and Editing Filters

The "Edit Filters" window is used to create new filters or edit existing filters to be used by the feature experiment. It is accessed by clicking on the pen icon for the relevant filter in the "Further Analysis and Filter Options" flow chart which is accessed from the "Feature Analysis Settings" on the Run step.



To create a new filter:

1. Click the "New Filter" button and enter a name for the filter in the "Filter" drop down menu box.
2. If required, enter a description for the filter in the "Description" section.
3. Define the rule sets and sub-rules to be used as described in the Rule Sets and Sub-Rule Sets and Creating Filter Rule Sets from Classes sections.
4. For each rule set and sub-rule that has been defined add the rules it is to use as described in the Creating Rules section.
5. Save the filter by clicking the "Save" or "Save As" buttons.
6. Click "Close" to close the window and return to the main AZtec software.

To edit a filter:

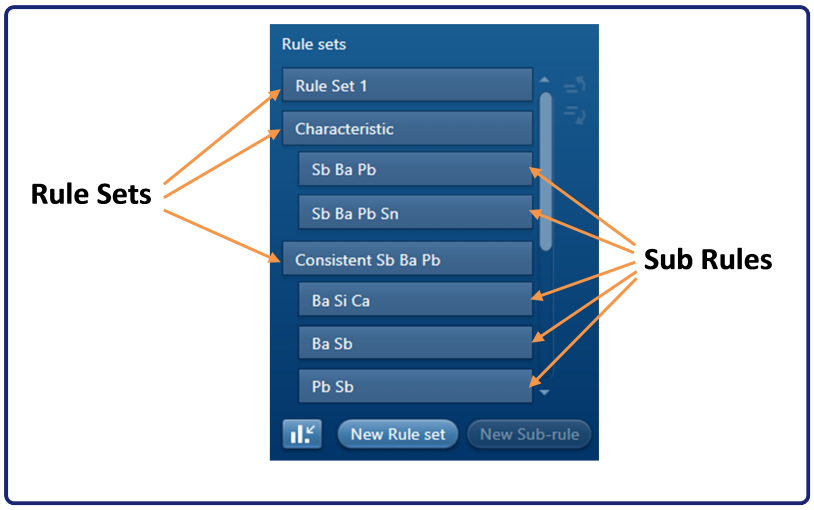
1. Select the filter from the "Filter" drop down menu.
2. Edit the rule sets and sub-rules as described in the Rule Sets and Sub-Rule Sets and Creating Filter Rule Sets from Classes sections.
3. For each rule set and sub-rule that has been defined, the rules may be edited as described in the Editing Rules section.
4. Save the filter by clicking the "Save" button.
5. Click "Close" to close the window and return to the main AZtec software.

Rule Sets and Sub-Rule Sets

When a new filter is created, a rule set "Rule Set 1" will be created and listed under "Rule Sets" on the left of the window. The name of the rule set can be changed to a more meaningful one by double clicking on the rule set name until it becomes editable:

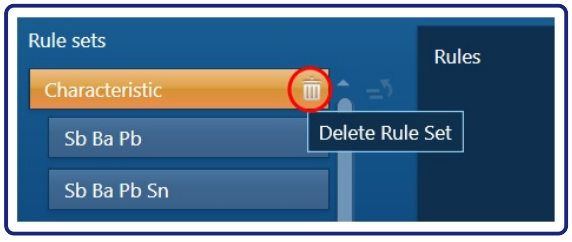
Type a new name and press enter on the computer keyboard to submit the change.

Further rule sets can be added to a filter by clicking on the "New Rule set" button. They can be added to sub-rule sets by clicking on the "New Sub-rule" button. As many rule sets and sub-rules can be defined as required. For example:



The order in which the rule sets and sub-rule sets will be applied can be changed by selecting an item and then moving it up or down in the list using the arrows highlighted in the image below:

A rule set or sub-rule set can be deleted by clicking the trash can icon which appears when the mouse is hovered over the item as shown below:



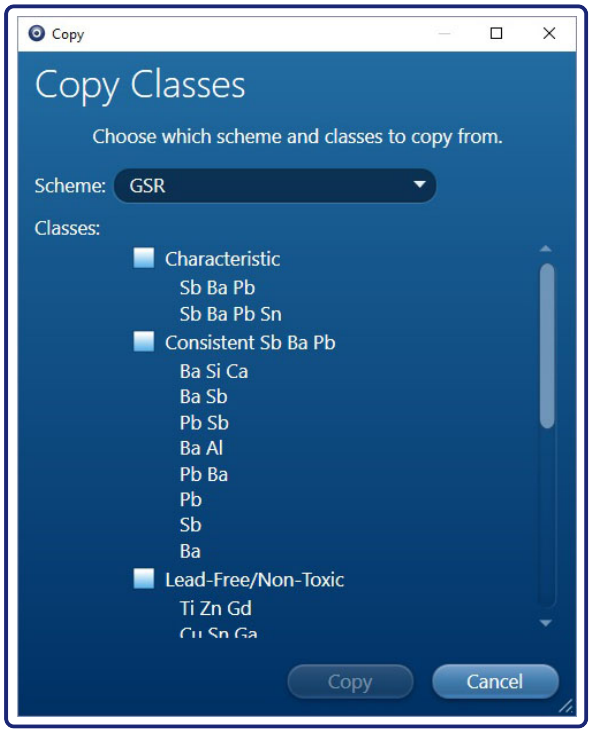
The rules defined for the rule sets and sub-rule sets will have the following behavior:

- For a single rule set the feature must meet all of the rules for that rule set to pass to the next stage of the acquisition. If it does not, it will not be included in any further acquisition or analysis.
- If multiple rule sets exist for a filter, then the feature must pass at least one of the rule sets in order to pass to the next stage of the acquisition. If it does not meet the criteria defined by any of the rule sets then it will be excluded from any further acquisition or analysis.
- If multiple sub-rule sets are defined for a single rule set, then the feature must meet the criteria for the rule set (if any have been defined) and then also meet the criteria for one of the sub-rule sets, in order to pass to the next stage of the acquisition. If it does not meet the criteria defined by either the rule set or any of the sub-rule sets then it will not be included in any further acquisition or analysis.

Creating Filter Rule Sets from Classes

If the project contains a set of classifications that are similar to the filters to be defined, then rather than having to define all of the filters manually, it is possible to create a filter rule set directly from the classes. To do this click the “Create filter rule sets from classes” button in the bottom left hand corner of the edit filters window:

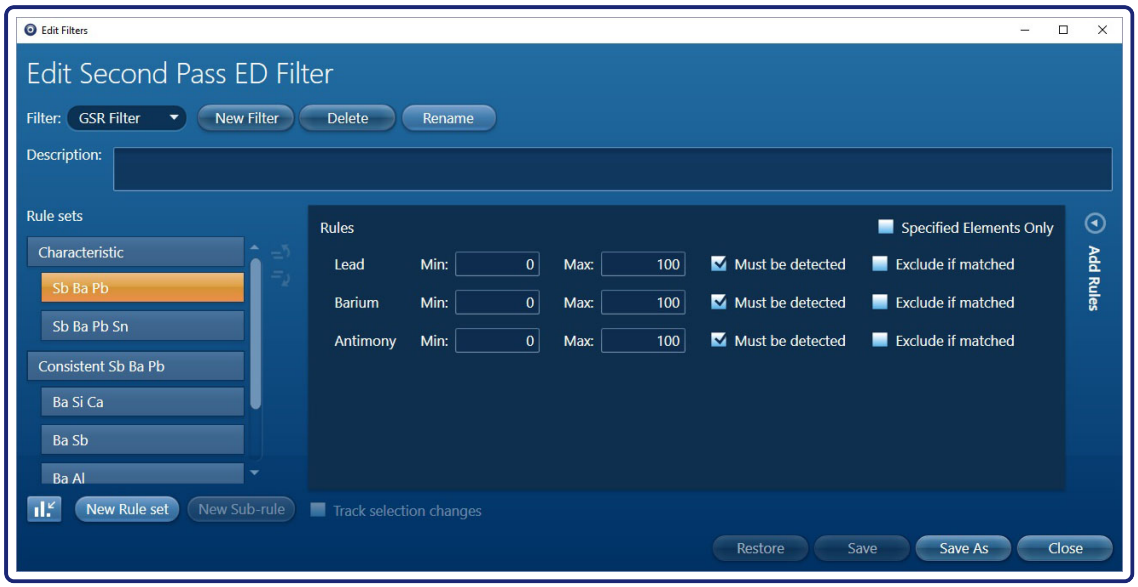
This will open the "Copy Classes" window:



In this window:

1. Select the scheme from which the classes are to be copied into the filter.
2. Check the tick boxes for the classes that are to be copied into the filter.
3. Click the “Copy” button to copy the classes into the filter and close the “Copy Classes” window.

The "Edit Filters" window will now show all of the classes and sub-classes that have been copied in to the filter as a series of rule sets and sub-rules. For example:



These filters can be edited in the same way as filters that have been created manually.

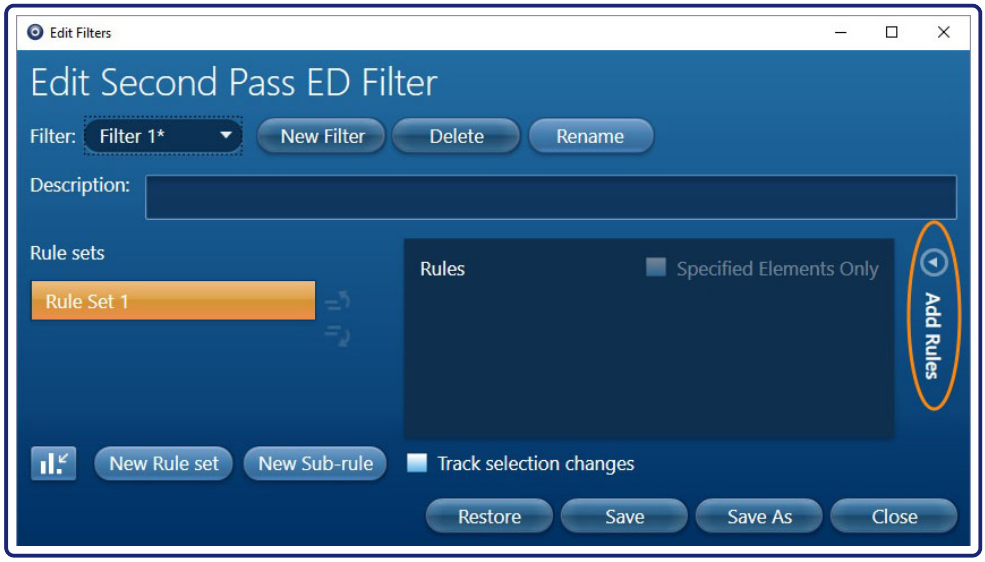
NOTE: *Once the classes have been copied into a filter, the filter and the classification scheme become independent of each other. Making a change to the filter will not affect the classification scheme and vice versa.*

Creating Rules

For a given rule set or sub-rule set, any number of rules can be defined.

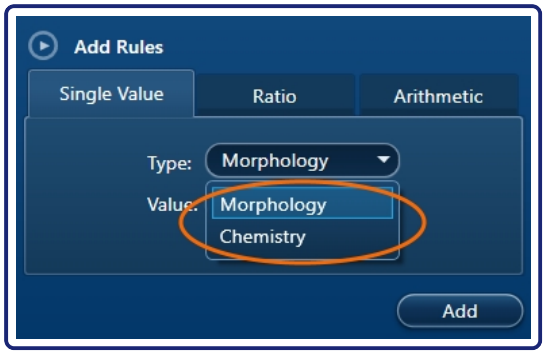
To create a new rule:

1. Expand the “Add Rules” tab at the right of the “Edit Filters” window to see the “Add Rules” section of the window:



2. Select whether to create a rule based on a single value or a ratio by clicking on the appropriate tab.

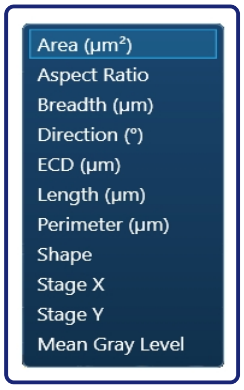
3. Choose between creating a morphology or a chemistry rule using the "Type" drop down menu:



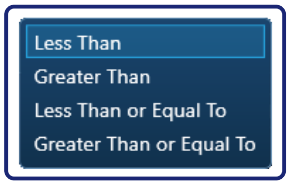
4. Select the measurement value for the rule.

   If "Chemistry" is selected as the type, this list will be a list of elements or the total number of counts.

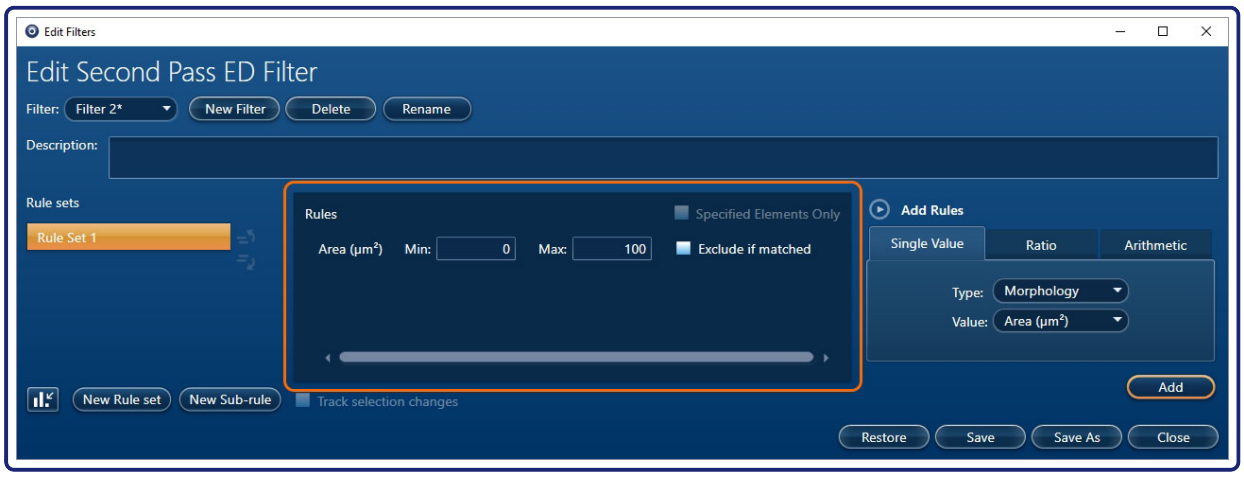
   If "Morphology" is selected as the type, the values available will include:



   If "Arithmetic" is been selected as the type, the type will be Wt% Expression and the values available will include:



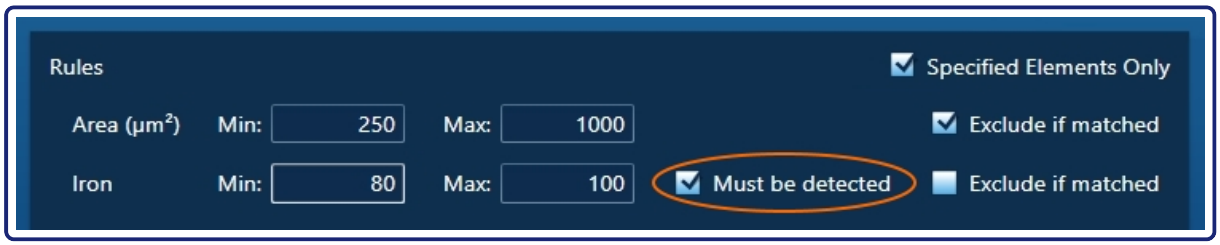
5. Click "Add" to add the rule to the rule set or sub-rule. The rule will now be added to the "Rules" section in the center of the "Edit Filters" window.



6. For each single value or ratio criteria that has been added, enter the minimum and maximum values for the search range for that criteria.

   For an arithmetic criteria, enter the rule as a simple formula made up of element symbols and wt% values. For example, the arithmetic formula in the image below states that the weight percentage for the elements Ca and O must be greater than 50 wt%:

7. For each chemistry rule based on a single value, select whether or not to check the "Must be detected" option, to the right of the rule definition.



   If this option is active, then the result must be within the range defined by the rule and also be statistically significant in the quant result to pass. If this option is off, then the result only needs to be within the range defined by the rule to pass. The default is for this option to be selected.

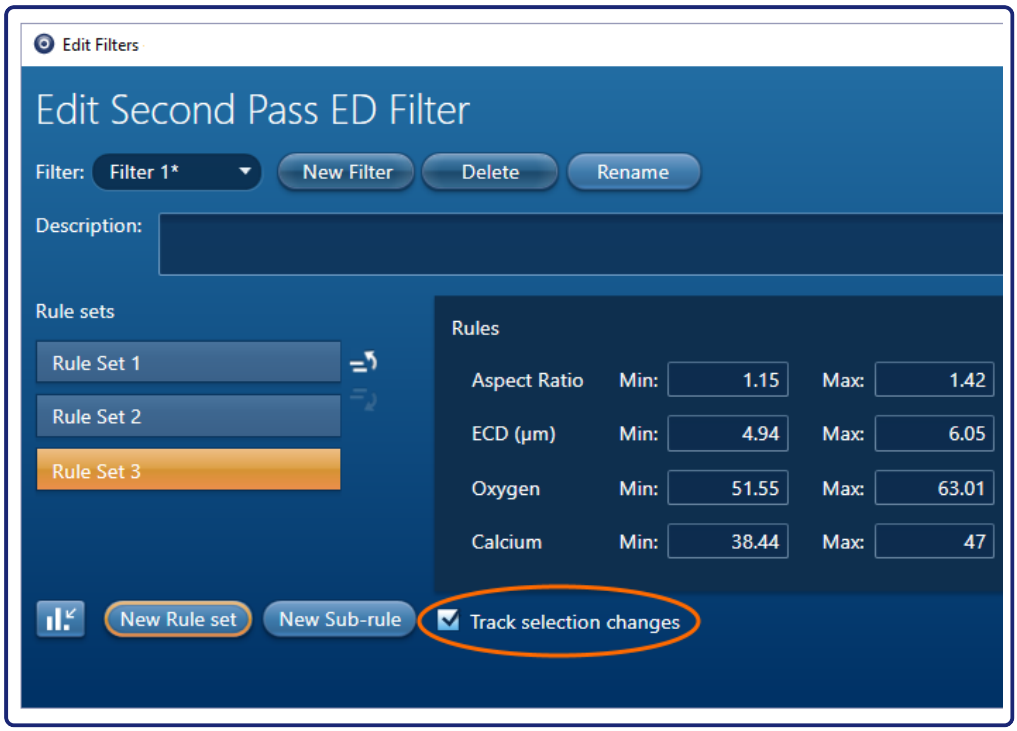
   NOTE: *This relates to the sigma value for quant thresholding which can be set up in quant setup.*

8. For all rules, choose whether or not to use the "Exclude if matched" option. If this option is active, any feature that meets the criteria in the rule is excluded from the class.

9. For all of the rules within the current rule set or sub-rule set, select "Specified Elements Only", to specify that the feature must contain only the elements listed within the rules and nothing else.

10. Choose whether to allow "Track Selection Changes".

    If this option is active, the value ranges and rules will be updated, based on the features selected in the data table in the main AZtec software. As different features are selected, the value ranges and element rules will be updated to correspond with those features.



Editing Rules

If the filter is being edited from the morphology filter step of the "Further Analysis and Filter Options" flow chart, then there will only be the ability to create or edit morphology rules.

If the filter is being edited from one of the EDS filter steps that appear just before the second or third pass EDS acquisition, then there will be the ability to create or edit both morphology or chemistry rules.

For both morphology and chemistry rules, the rules may be based on:

- A single measurement value. This is the simplest and most common rule type. Select a single measurement type as the measurement criteria.
  eg) The weight % of Fe must be between 55% and 100%.
- The ratio of two measurement values. Specify the ratio between two measurements as the measurement criteria. This method can be useful when looking for a compound.

  NOTE: *Additional elements can also be present in the feature*

  eg) The Si:O ratio search range for the weight % of SiO2 must be between 0.8 and 1.

A rule can be edited by selecting it within the Edit Filters window and then changing any of its settings.

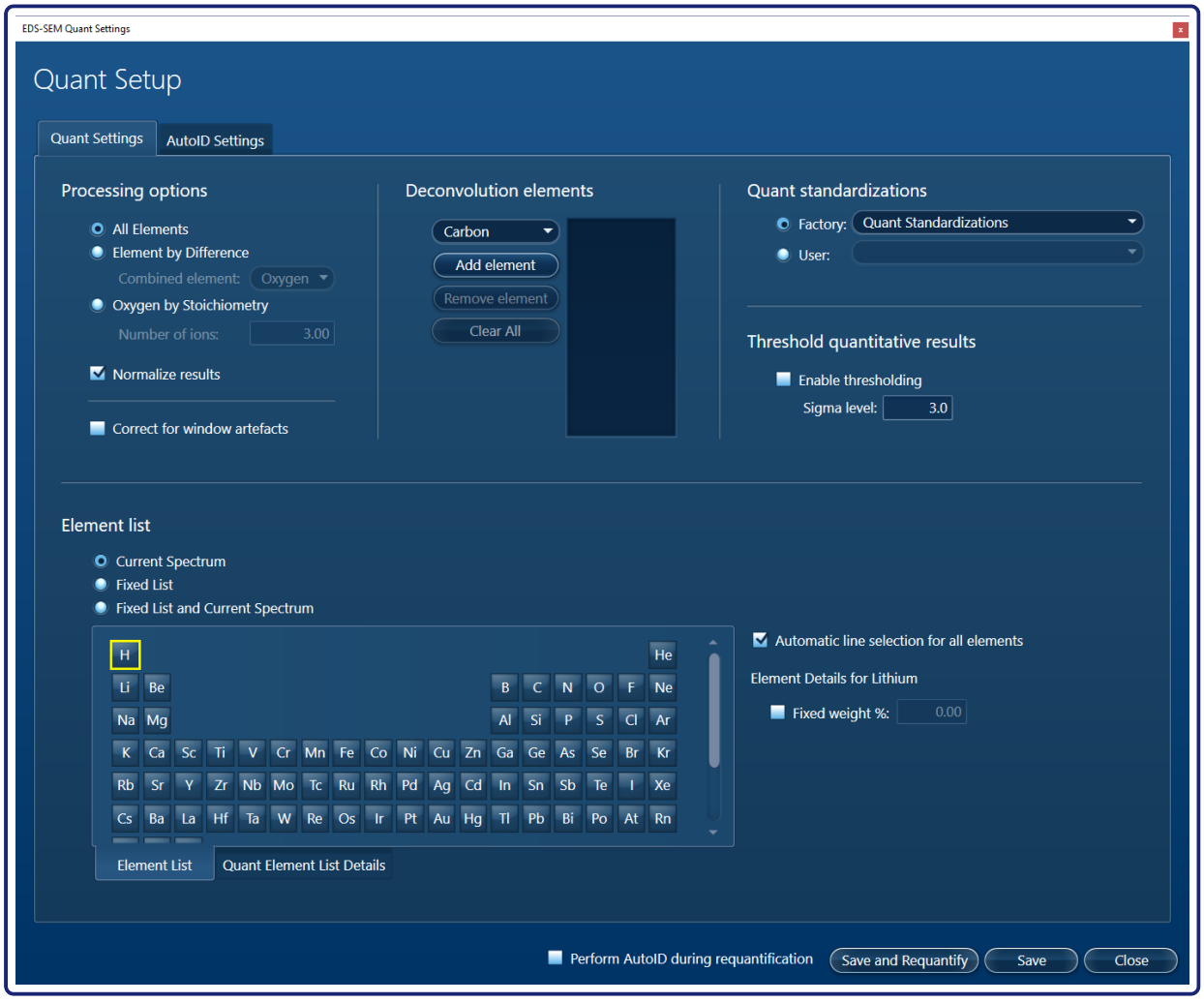
A rule can be deleted by hovering over the rule to see the delete icon and then clicking the delete icon:

2.4.2. EDS Quantitative Analysis

In AZtecFeature, the quantitative analysis of every feature is performed immediately after the EDS data acquisition for that feature. It is performed using the current quantitative analysis settings regardless of where they were set (i.e. the quant settings can be specified from the User Profile, the Point & Id navigator or the Feature navigator).

To check or specify the settings to be used for the current Feature quantitative analysis open the "EDS-SEM Quant Settings" window by clicking on the "Quant Setup" icon on the acquisition toolbar of the "Acquire Site" step:

This will open the EDS Quantitative Analysis Settings window:



The majority of settings here are the same as for standard quantitative analysis. The main settings that are of particular importance for Feature are:

- **Normalize results:** Feature does not take into consideration any beam measurements that have been made. It is therefore recommended to always normalize the results.
- **Enable thresholding:** If this option is selected, the sigma thresholding level will be taken into consideration when calculating the quant results for every feature. The result of this setting will be

reflected in the data displayed in the Feature Data Viewer. It is recommended that the sigma value should be left as the default value "3.0".

- **Sigma level:** Even if the "Enable thresholding" option is not selected, this sigma value is always taken into consideration for the "must be detected" classification criteria. It is recommended that the sigma value should be left as the default value "3.0".
- **Perform AutoID during requantification:** If this option is selected, for every feature in the current site, or if the site is part of an area for the current area, the current element list is deleted and then AutoID and quantitative analysis are performed as part of the requantification procedure. If this option is not selected, a fixed element list should be defined as otherwise no elements would be included in the spectrum after the current element list has been deleted.

If any of the settings are changed after the initial acquisition and analysis, click the "Save and Requantify" button to rerun the quantification with the current settings. The quantification procedure will be run for every feature in the current site, or if the site is part of an area for every feature in the area. This is because to compare features, every feature must be acquired and analyzed with the same settings.

2.4.3. Viewing EDS Data

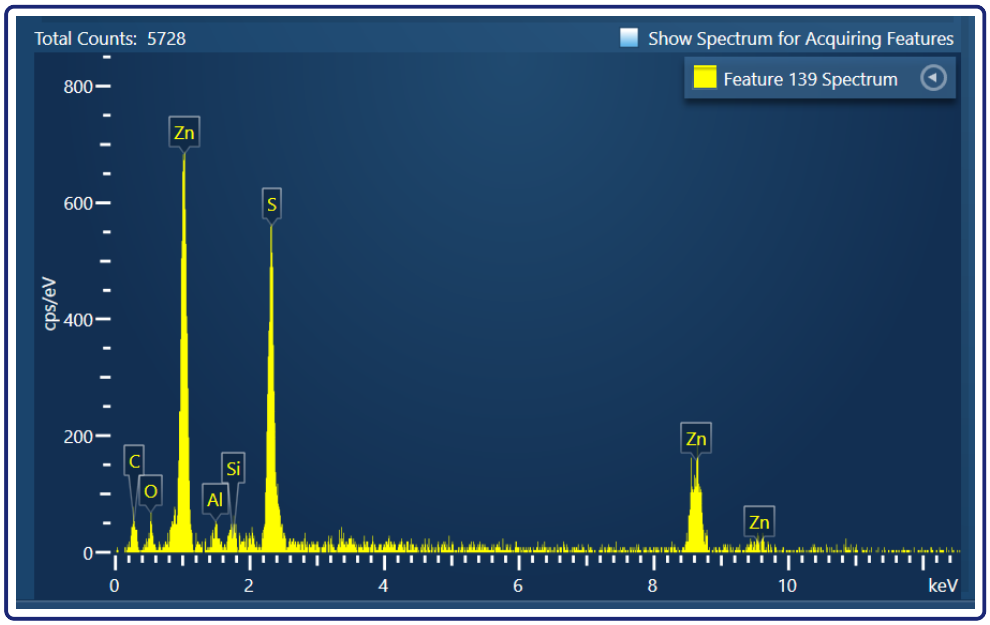
Once the EDS data has been acquired, the "Acquire Site" step can be used to view the data and confirm that:

- The EDS acquisition settings are suitable to resolve the elements present in the features.
- The EDS acquisition settings are suitable to be used for a large area run of the sample.
- The quant settings are suitable.
- The classification criteria are correct if a classification scheme has already been created or loaded.

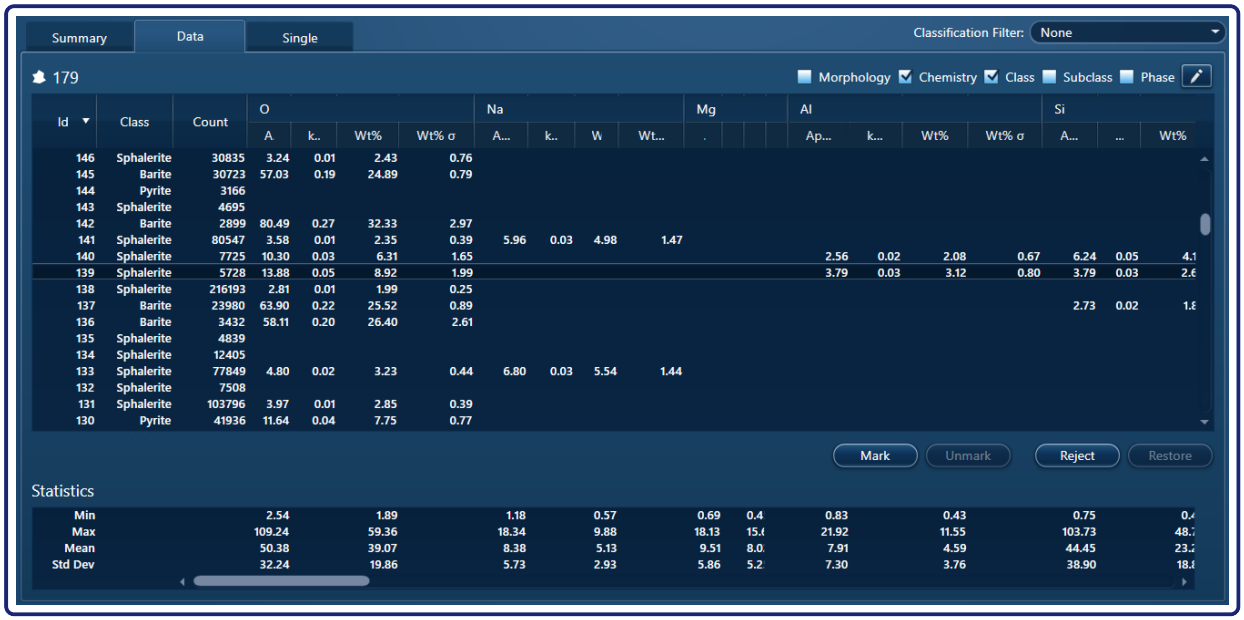
If any of the settings are found to be unsuitable, they may be adjusted and the EDS data reacquired for the current site, before proceeding to a large area acquisition.

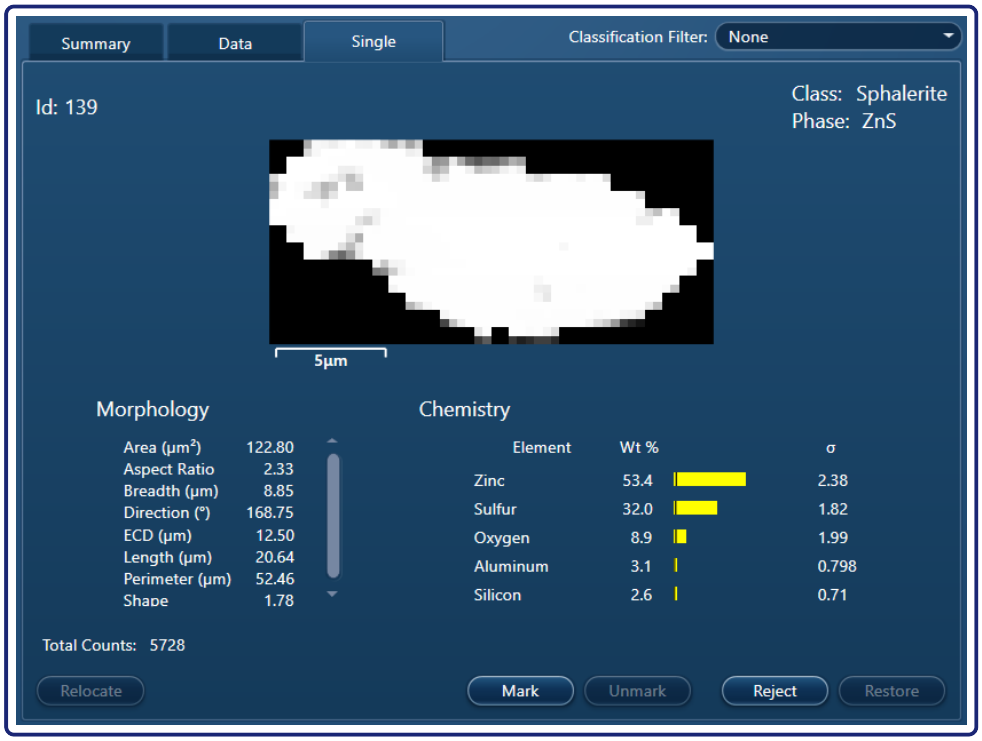
To assist with determining the suitability of the EDS acquisition and quantitative analysis settings, there are a number of ways in which the EDS data can be viewed:

- For a single feature in the spectrum viewer:



- In the Feature Data Viewer pane (available on most steps including the "Acquire Site" step) the data can be viewed as a summary graph or table (if the "Chemistry" option is selected) for all features, or in detail for a single feature. For example:





To assist with interrogating the data, in the toolbar on the left of the screen is the select feature tool:

When this tool is selected, click on a feature in the image pane to see the corresponding feature highlighted in the Feature Data Viewer pane and Spectrum Viewer Pane and vice versa.

2.5. Classifying Features

Once the features have been detected and the EDS data for them acquired, AZtec can automatically categorize the features into a number of groups, or classes, using a classification scheme. This can be useful for:

- Filtering out features that are not of interest.
- Identifying particular types or groups of features of interest.
- Narrowing down the results to focus only on the features of interest.

Once a classification scheme has been applied to a dataset it is possible to:

- Get statistics for the different classes (groups).
- See where particular classes containing certain types of features occur on the electron image.
- Reject features that fall into particular classes.
- Visualize the results in charts and graphs.

Classification schemes can be created as part of a project or loaded as part of a user profile such as the AZtecSteel application profile. If a classification scheme is loaded as part of a user profile, then it is loaded before any data is acquired. If it is created as part of a project, then it may be created:

- Before any EDS data has been acquired: Requires knowledge of the sample including the expected result and how the features are to be classified.
- After the EDS data has been acquired for a single site: The morphology and EDS data for the site can be used to help determine the classification criteria to be used.
- After the EDS data has been acquired for a large area: The data for the area can be used to help determine the classification criteria to be used.

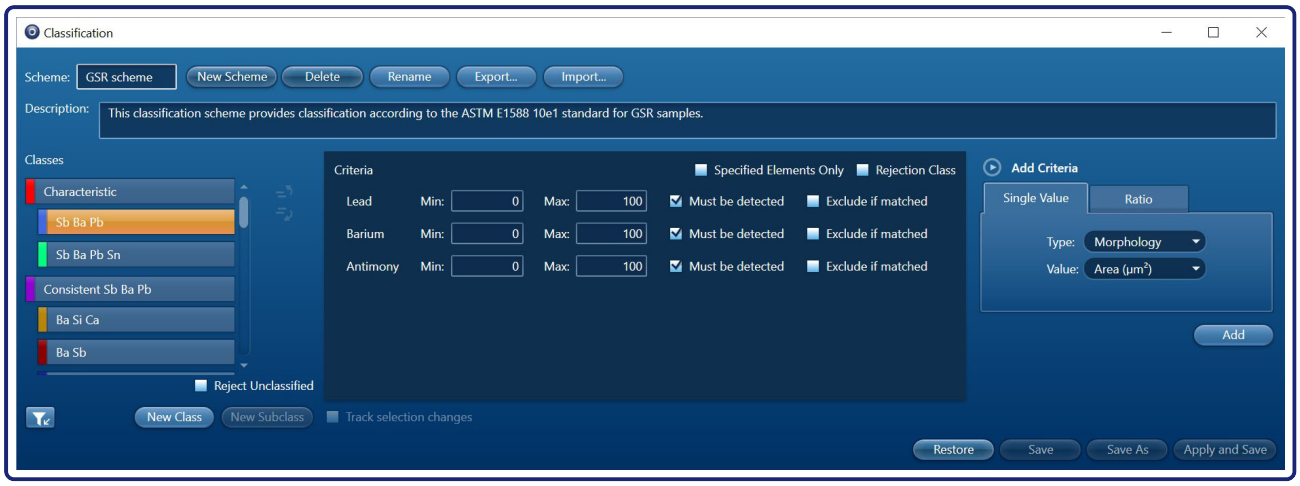
Classification schemes are automatically applied to the data as the EDS data acquisition takes place as part of quantifying and analyzing the results. They are applied per site, or if the site is part of an area, per area. They can be edited or a different classification scheme applied to the data after the acquisition has completed.

When a project containing a classification scheme is saved, the classification scheme is also saved so that it can be later loaded with the data allowing it to be reviewed and edited.

When setting up and optimizing a feature acquisition on a single field so that the acquisition can later be applied to a large area, the classification scheme is defined or optimized from the "Set Up Classification" step of the Feature navigator. However, it is also possible to setup or edit classification schemes based on a large area dataset from the "Review" step. The same classification tools and options are available in both steps.

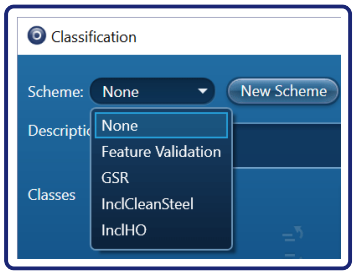
To specify, view and edit classification schemes from the Set Up Classification and the Review steps click on the maximize "Classification" icon or the undock icon in the bottom left hand corner of the software.

This will maximize the classification tab or open it in a new window:



2.5.1. Accessing Saved Classification Schemes

Any classification schemes that exist on the system, or are associated with a loaded project, can be accessed from the "Scheme" drop down menu in the Classification window:



There are three types of schemes available:

- Factory schemes: These are loaded as part of an application specific profile (i.e. AZtecSteel).
- Schemes that were created on the current PC: These are loaded as editable files.
- Schemes that were created on another PC (and do not exist on the current PC): These schemes are listed with the scheme name plus the area or site from which they were loaded. They are loaded as read only files.

Classification schemes can be copied and shared with other AZtec PC's using the "Import" and "Export" buttons. The classification scheme is exported in .oif file format. Once imported, it can be opened as an editable file.

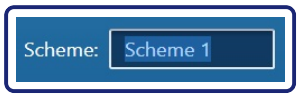
To edit a read only classification scheme, create an editable copy of it by clicking the "Save As" button in the classification window.

2.5.2. Creating a New Classification Scheme

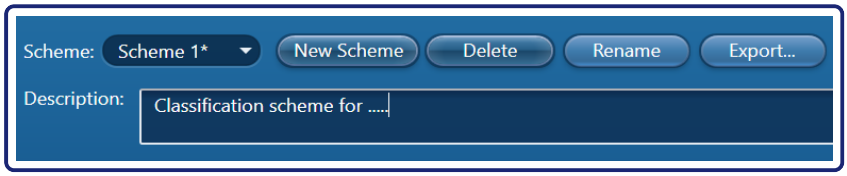
To create a new classification scheme, in the classification window:

1. Click the "New Scheme" button

2. Enter a name for the classification scheme in the "Scheme" drop down menu box.

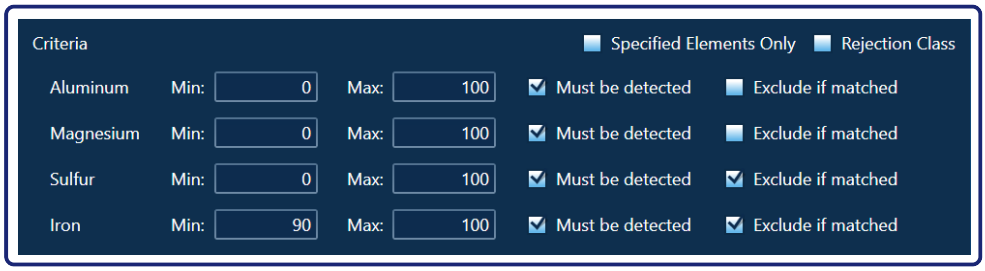


3. Enter a description for the classification scheme in the "Description" section.



4. Define the classes and sub-classes to be used (see the Working with Classes section) or create classes from previously defined filters (see the Creating a Classification Scheme from a Filter section).

5. For each class and sub-class that has been defined add or edit the criteria that it will use as described in the Creating Criteria section.



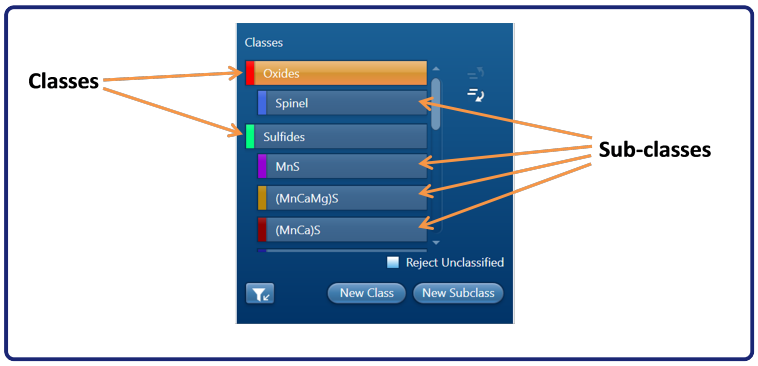
6. Apply and save the classification scheme by clicking the "Apply and Save" button, or to only save the classification scheme without applying it to any data, click the "Save" button.

Working with Classes

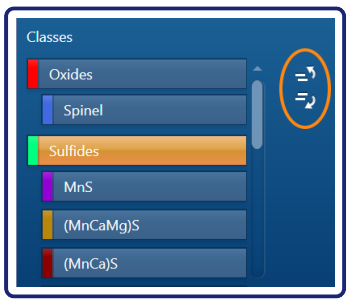
When a new classification scheme is created, a new class, "Class 1" will be created and listed under Classes on the left of the window. To change the name of the class to a more meaningful one, double click on the class name so that it becomes editable:

Type a new name and press enter on the computer keyboard to submit the change.

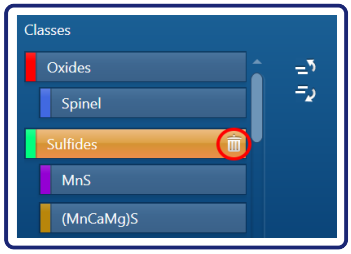
Further classes can be added to a classification scheme by clicking on the "New Class" button. Sub-classes can be added by clicking on the "New Subclass" button. As many classes and sub-classes as required can be defined. For example:



To change the order in which the classes will be applied, select the class to be moved from the list and then click either the up or down arrow to the right of the list to move the class:



To delete a class or sub-class, hover over the class or sub-class until the trash can icon appears. Click on the trash can icon to delete the item:



The criteria defined for the classes and sub-classes will have the following behavior:

- For a single class, the feature must meet all of the criteria to be included in that class.
- For multiple classes, the feature will be classified as whichever class it meets the criteria for first. This means that the order in which classes appear in the classification scheme is important.
- If multiple sub-classes are defined for a single class, the feature must meet the criteria for the class (if any have been set) and then also meet the criteria for one of the sub-classes.
- If there are multiple sub-classes and the feature meets the criteria for more than one sub-class, it assigns the feature to the subclass which makes the strongest assertions for the feature based on the number of criteria and the quant result.

When making edits to the criteria for the classes and sub-classes:

- Preview the effects of the edits in the image and data currently displayed.
- If not happy with the preview, return to the saved class by clicking the "Restore" button.

- If happy with the preview, apply the classification scheme to the entire area and save it by clicking the "Apply and Save" button.

Creating Criteria

For a given class or sub-class set, any number of criteria can be defined. The criteria may be based on morphology or chemistry information. For both types of criteria, the criteria may be based on:

- A single measurement value. Select a single measurement type as the measurement criteria. eg) The weight % of Fe must be between 55% and 100%.
- The ratio of two measurement values. Specify the ratio between two measurements as the measurement criteria. This method can be useful when looking at compounds. eg) The Si:O ratio search range for the weight % of SiO_2 must be between 0.8 and 1.

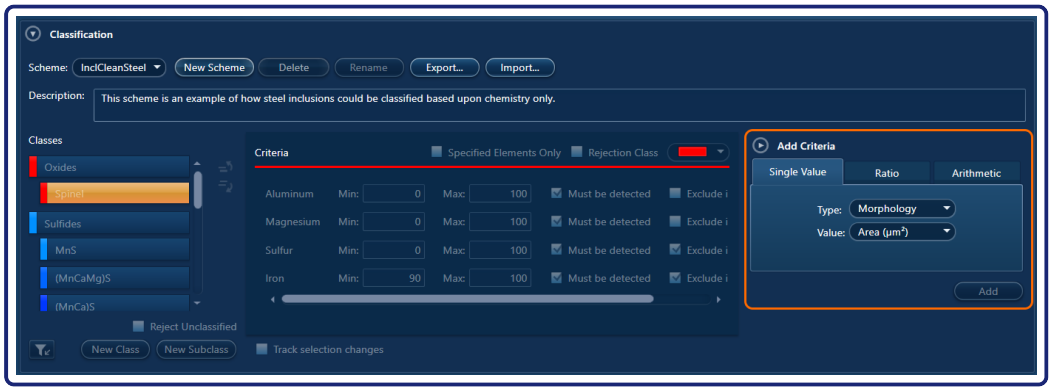
Criteria can be created using:

- Manual criteria creation.
- Assisted criteria creation.

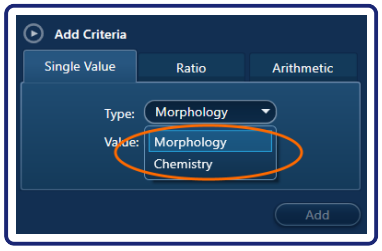
Manual Criteria Creation

To create a new criteria manually:

1. Expand the "Add Criteria" tab at the right of the "Classification" window to see the "Add Criteria" section of the window:



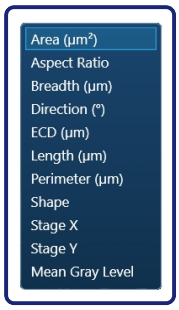
2. Select whether to create a criteria based on a single value, a ratio or arithmetic by clicking on the appropriate tab.
3. If available select between creating a morphology or a chemisty type criteria using the "Type" drop down menu.



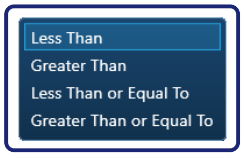
4. Select the measurement value for the criteria. Select the appropriate measurement from the "Value" drop down list.

   If "Chemistry" is selected, this list will be a list of elements or the total number of counts.

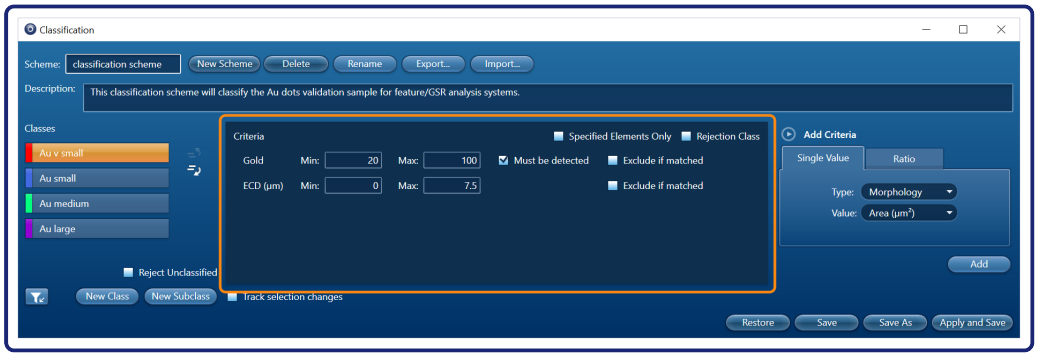
If "Morphology" is selected the values available will be:



If the arithmetic tab is selected, the type will be Wt% Expression and the values available will be:

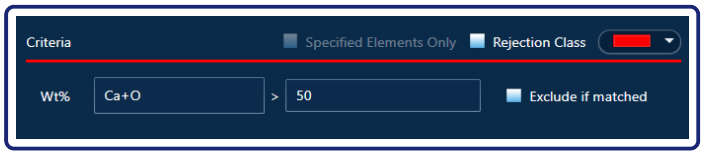


5. Click "Add" to add the criteria to the class set or sub-class. The criteria will now be added to the "Criteria" section in the center of the "Classification" window.



6. For each single value or ratio criteria that has been added, enter the minimum and maximum values for the search range for that criteria.

   For an arithmetic criteria, enter the criteria as a simple formula made up of element symbols and wt% values. For example, the arithmetic formula in the image below states that the weight percentage for the elements Ca and O must be greater than 50 wt%:

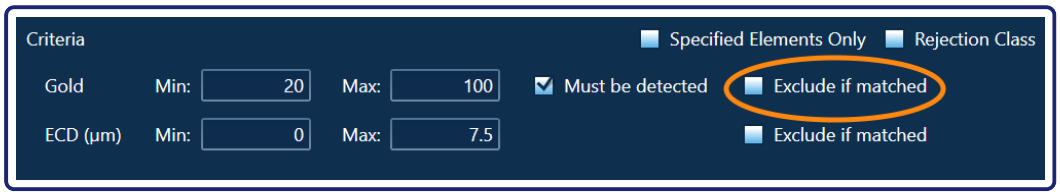


7. For each chemistry rule based on a single value, select whether or not to check the "Must be detected" option, to the right of the rule definition.

   If this option is active, then the result must be within the range defined by the criteria and also be statistically significant in the quant result to pass. If this option is off, then the result only needs to be within the range defined by the criteria to pass. The default is for this option to be selected.

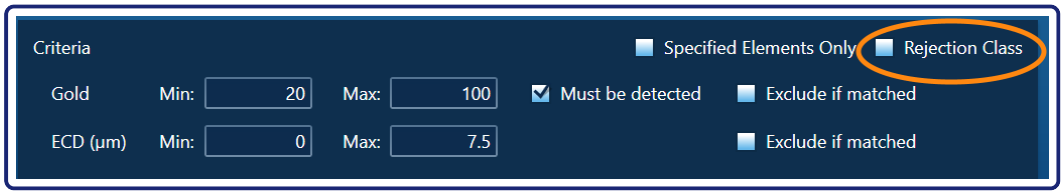
NOTE: *This relates to the sigma value for quant thresholding that is defined in the quant setup.*

8. For all criteria, choose whether or not to use the "Exclude if matched" option. If this option is active, any feature that meets the criteria is excluded from the class.

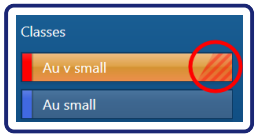


9. For all of the criteria within the current class or sub-class, select "Specified Elements Only", to specify that the feature must contain only the elements listed with the criteria and nothing else.

10. For all of the criteria within the current class or sub-class, select "Rejection Class", to specify that any feature meeting the criteria for that class or sub-class will be rejected.

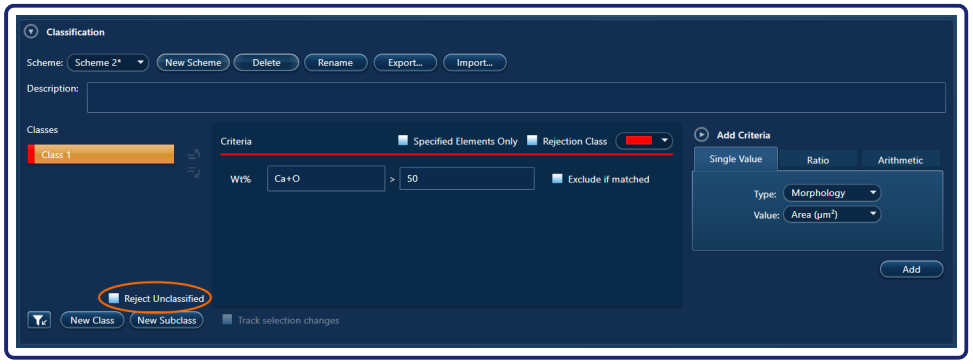


The class or sub-class label will have red stripes at the right end to signify that this option has been selected.



NOTE: *The data will still be acquired and kept for that feature. If this option is later un-selected, the data for this feature will be re-added to the data table. This behavior is different to manually rejected features.*

11. Choose whether to reject unclassified features.



If this option is selected any feature that hasn't been classified is rejected. It will no longer be shown in the general data table or images.

NOTE: *The data can be filtered so that only the rejected features are visible.*

Assisted Criteria Creation

AZtec's assisted criteria creation is designed to make defining criteria quick and intuitive. Simply select one or more features of the same type and the software displays the criteria that are common to all of the features in the selected group. These parameters include the morphological parameters "Aspect Ratio" and "ECD (µm)" and the concentrations of any elements present in all of the selected features.

To use assisted criteria creation:

1. Select one or more features that have common properties that are to be added to the class being defined. Features can be selected from both the image pane and the feature data viewer.

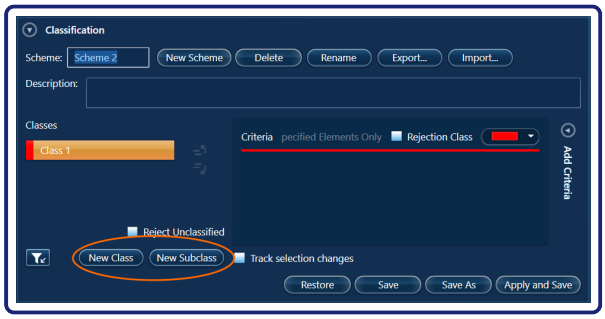
   To select multiple features from the image pane, select the feature selection tool:

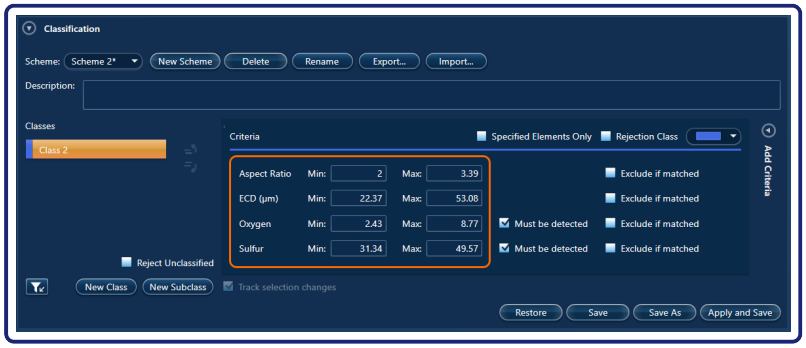
   To select features from the image pane, press the "Ctrl" key down on the computer keyboard and then select all of the relevant features.

   To select features from any of the feature data viewer tabs (i.e. one of the graphs or the data table) use the standard Windows keys (i.e. "Ctrl" to select a series of individual features or "Shift" to select a range of features) and select the relevant features.

2. Click the "New Class" or "New Subclass" icons in the "Classification" window to create a new classification based on the properties of the selected features:

   The morphological criteria "Aspect Ratio" and "ECD (µm) and chemical criteria for any elements that are present in all of the selected features are created and displayed in the "Criteria" section in the centre of the "Classification" window:

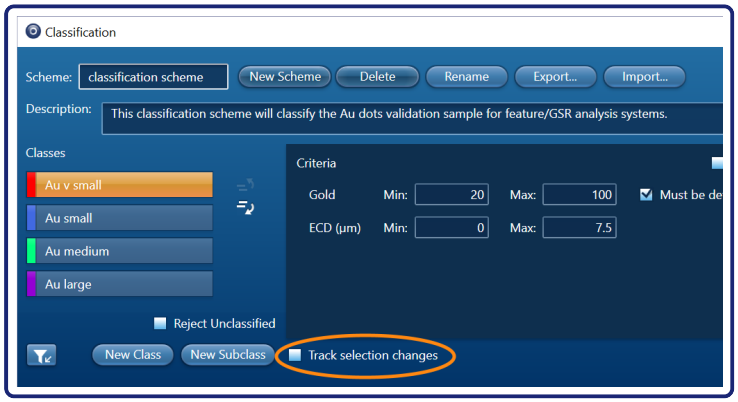
   

   The value ranges are based on the values of the features selected when the class or subclass was created. All other features fulfilling the same criteria will be classified and added to the class accordingly.

   NOTE: *The values displayed in the AZtecFeature Data Viewer are rounded to two decimal places. However, when determining whether a feature meets the criteria for a class the actual value is used. This*

rounding means that it is possible for a feature to appear to meet the criteria for a class, but to not be included in the class due to the actual value lying outside the acceptable range for the class. For example, a feature has an area of 1.009. This value is displayed in AZtec as 1.01. The area class has a minimum criteria value of 1.01. Because the feature area is actually 1.009, the feature does not meet the criteria for the class and is not included.

3. Refine the criteria manually by adding or removing criteria, editing the limits and specifying how the criteria must be considered (see steps 7-11 of the "Manual Criteria Creation" section above).
4. Choose whether to allow "Track Selection Changes". If this option is active, the value ranges and rules of the currently selected class will be updated, based on the features selected in the image pane or feature data viewer in the main AZtec software. As you select different features, the value ranges and element rules will be updated to correspond with those features.



Editing Criteria

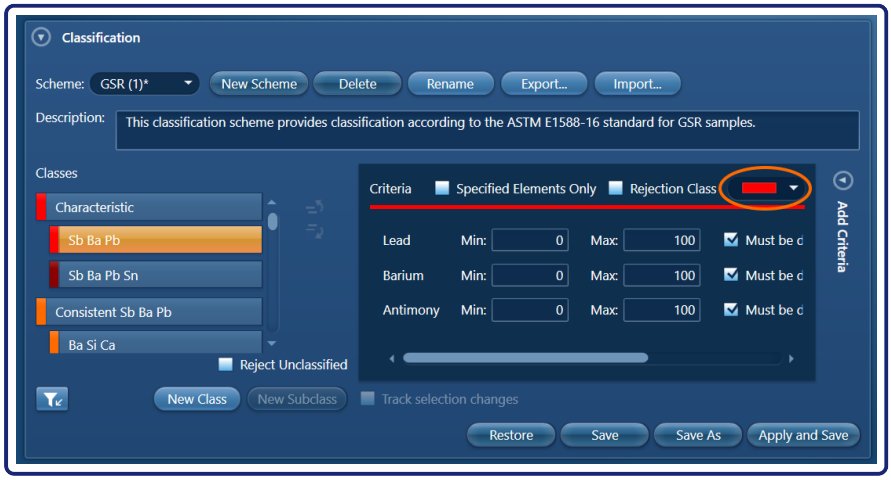
To edit a class:

- Selecting the class in the "Classification" window.
- Change any of its settings.

NOTE: *If the criteria are grayed, the classification scheme is read only. Click the "Save As" button to create a copy of the classification scheme that you can edit.*

For example, to change the class or sub-class color:

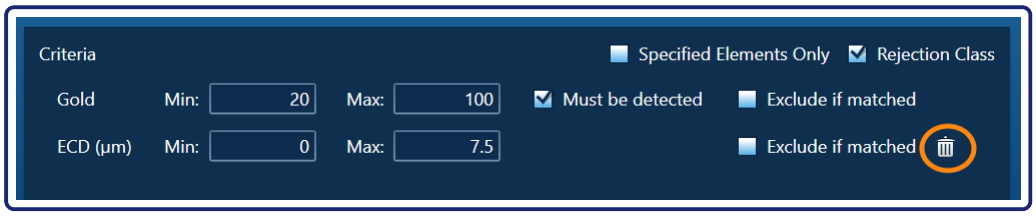
- Select the class or sub-class in the Classification window.
- Use the color drop down menu to change the color associated with the class or sub-class.



Deleting Criteria

To delete a criteria:

- Hover over the class until the trash can icon appears.



- Click the trash can icon. The criteria will now be deleted.

2.5.3. Creating a Classification Scheme from a Filter

If the project contains a set of filters that are similar to the classifications to be defined, then rather than having to define all of the filters manually, it is possible to create a filter rule set directly from the classes.

To create a classification scheme from a filter:

1. Click the "Create classes from filters" button in the bottom left hand corner of the edit filters window:

This will open the "Copy Filter Rules" window:

2. Select the filter scheme from which the rules are to be copied.
3. Check the tick boxes for the rules that are to be copied.
4. Click the "Copy" button to copy the rules and close the "Copy Filter Rules" window.

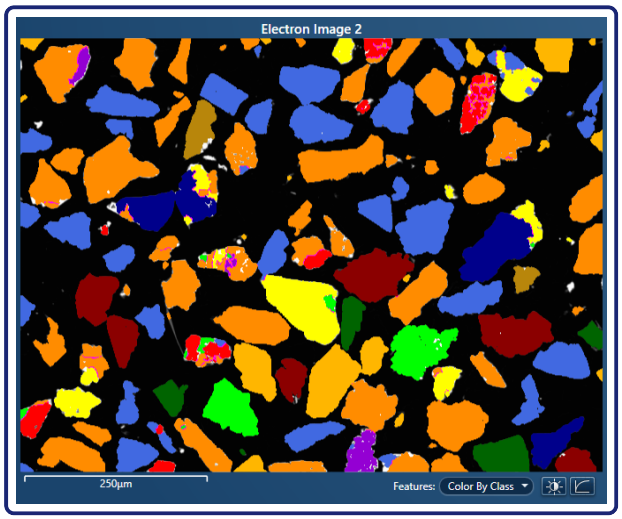
The "Classification" window will now show all of the filter rules and sub-rules that have been copied into the classification scheme as a series of classes and sub-classes with criteria. These classes and sub-classes can now be edited in the same way as classes that have been created manually.

> ***NOTE:*** *Once the filter rules have been copied into a classification scheme, the filter and classification scheme become independent of each other. Making a change to one will not affect the other.*

2.5.4. Viewing the Results of Applying a Classification Scheme

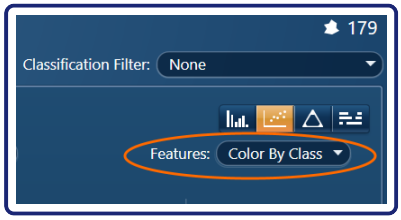
There are numerous ways in which the results of applying a classification scheme to the data can be visualized within the "Set Up Classification" step:

- In the image pane as a "Color by Class" or "Color by Subclass" map, where the features belonging to each class or subclass are displayed in the unique color assigned to that class or subclass:

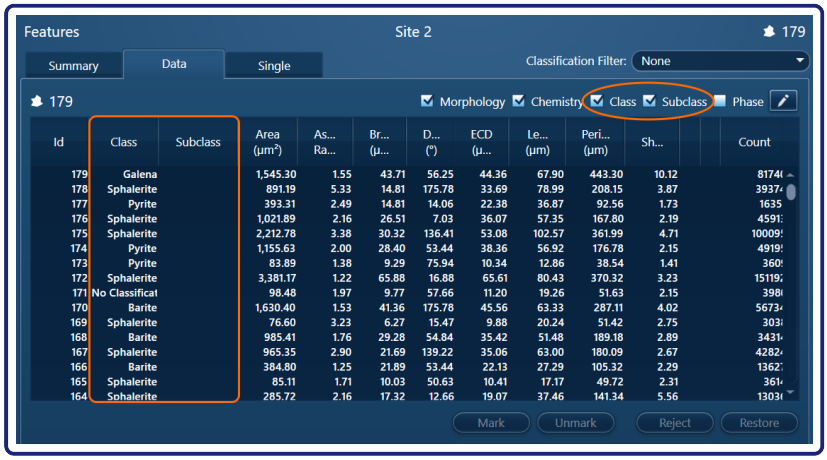


This map display is useful for visualizing which features belong to the different classes or subclasses and how they are distributed across the sample.

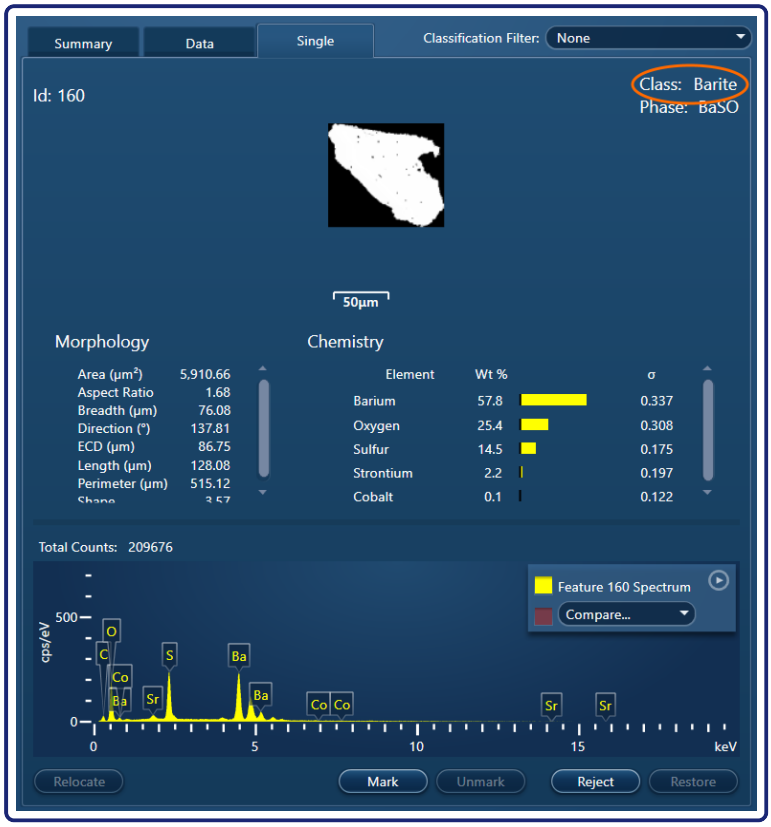
- In the Feature Data Viewer, Summary tab, scatter and ternary plots may be colored by class or subclass. This can be useful for helping to visualize common characteristics for the features belonging to a specific class or subclass within the plot:



- In the Feature Data Viewer, Data tab, where if the "Class" and "Subclass" options are selected it is possible to see which class or subclass each feature belongs to:



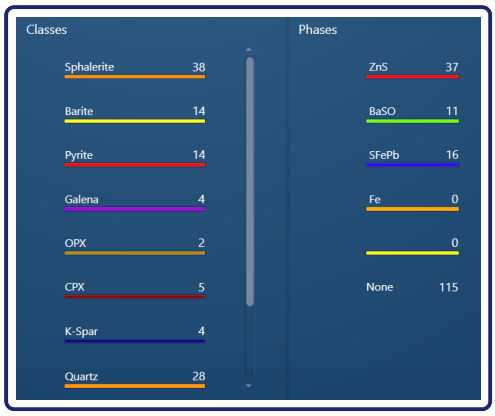
- In the Feature Data Viewer, Single tab, where it is possible to view which class or subclass that the specific feature belongs to:



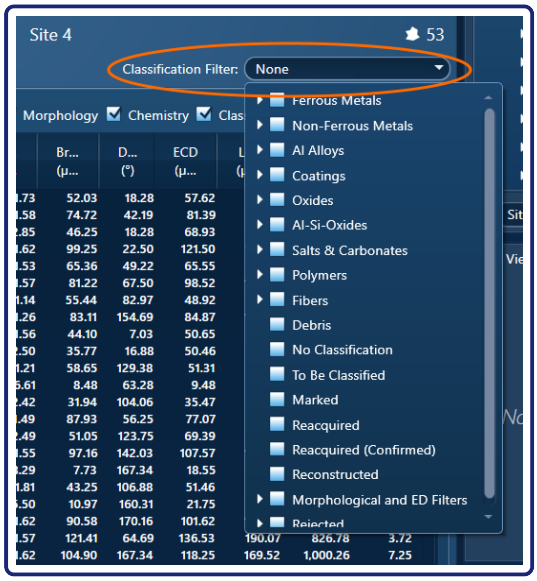
NOTE: *If either threshold phase detection or full field phase detection were used to detect the feature being displayed in the "Single" tab, then the Phase that the feature was detected as is listed below the class.*

- In the Classification Summary Pane below the Feature Data Viewer, where the number of features that have been detected in each class and subclass are displayed:

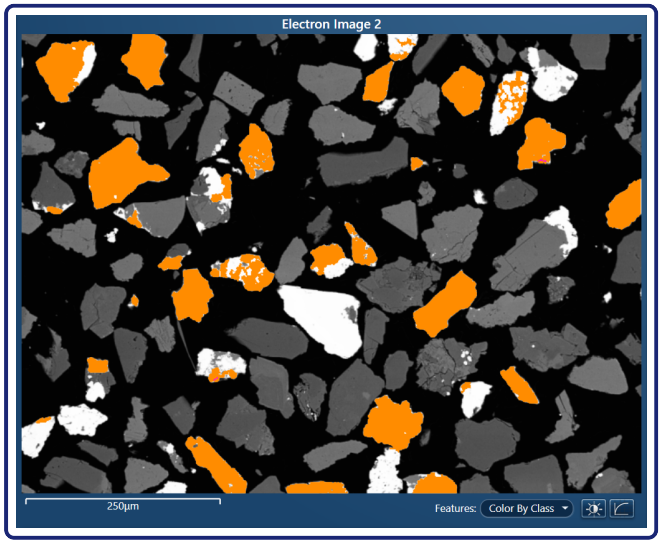
If either threshold phase detection or full field phase detection were used as part of the feature detection, then this pane will also include a summary of the phases detected and the number of features in each phase:

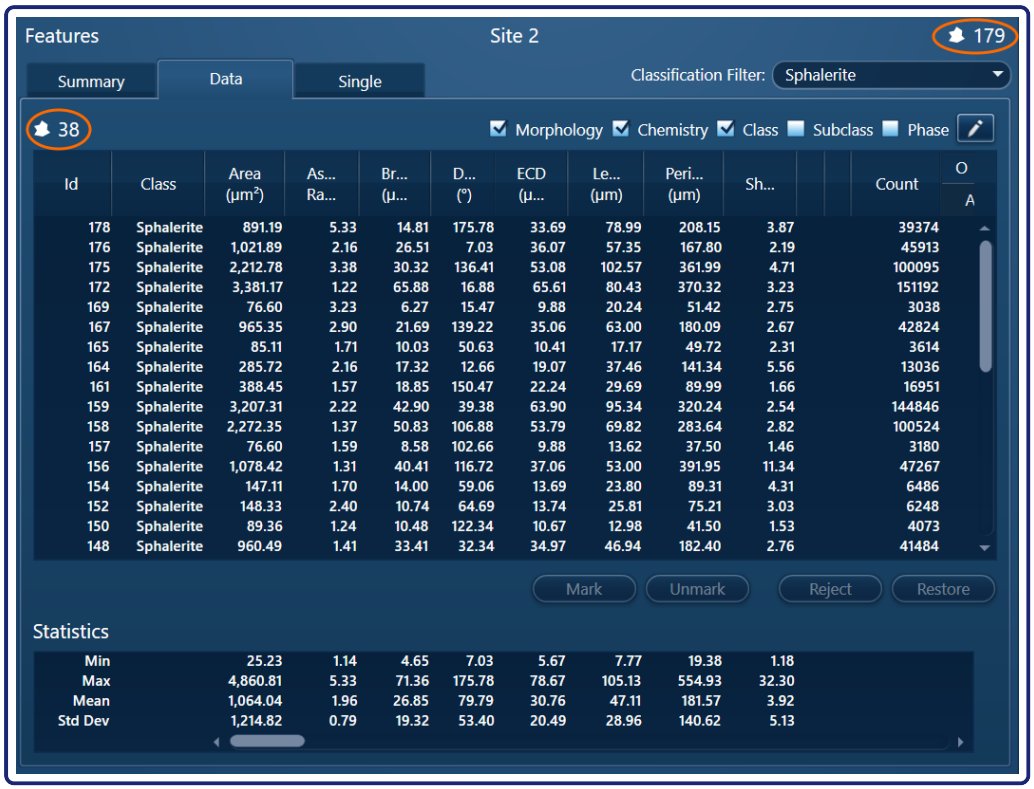


To allow the data for only the features that belong to a certain class or subclass to be visualized use the "Classification Filter" drop down menu to select the classes or subclasses of interest:



The data displayed in the Image pane and the Feature Data Viewer will now be updated to only display the data for the selected classes or subclasses. For example, if only the "Sphalerite" class is selected from the "Classification Filter" drop down menu, the electron image with the features colored by class and the Feature summary table will appear as:





NOTE: *The total number of features detected in the site was 179, however, the number of features displayed in the table is much lower (38). This is because only the Sphalerite features are displayed in the data table. The statistics are also updated to only be for the features listed in the table.*

2.6. Large Area Feature Acquisition

In the previous sections, for a single site of interest, the help has covered how to:

- Acquire an electron image and detect the features in that image.
- Acquire morphology and chemistry (EDS) data for the features.
- Set up a classification scheme to classify the features into groups with similar properties.

This section of the help describes how to proceed to set up to acquire and classify data by applying the same conditions for multiple fields spread over a larger area, including how to:

- Create an automated run.
- Use layouts to specify multiple areas (stubs) to be acquired.
- Set a consistent contrast and brightness for each run.
- Modify the settings

It also covers how to optimize a large area feature acquisition including using:

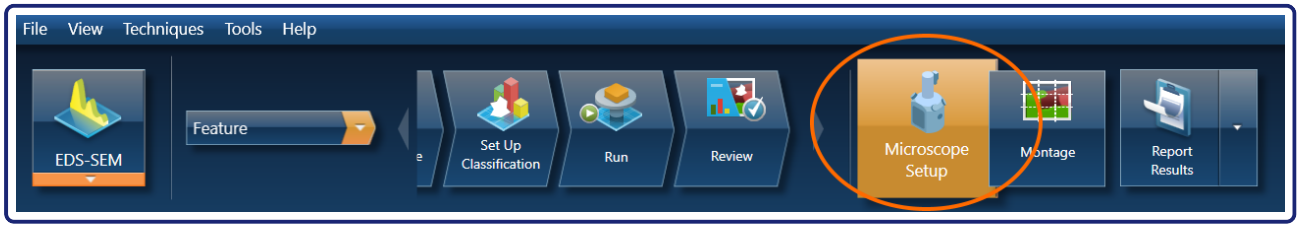
- Termination conditions to specify when sufficient data has been acquired and the acquisition of the site, area or specimen can be stopped.
- Field acquisition order to specify the order in which the fields should be acquired.
- Compensate for changes in the image brightness during a run.

2.6.1. Setting Consistent Contrast and Brightness for Each Run

Feature application specific profiles and user created profiles allow many of the settings that need to be defined for a feature acquisition to be saved and loaded as part of the profile. They can help to minimize the time it takes to set up an acquisition and ensure repeatability between multiple runs as they ensure that the same settings are always used.

One of the settings that can be contained within a profile are the gray-level thresholds which are used as part of detecting the features of interest. They work by specifying the gray-levels in the image that correspond to the features. This means that when the profile is loaded, if the gray-levels of the features are different to when they were defined, the gray-level threshold definitions are incorrect and that the features will not be detected correctly.

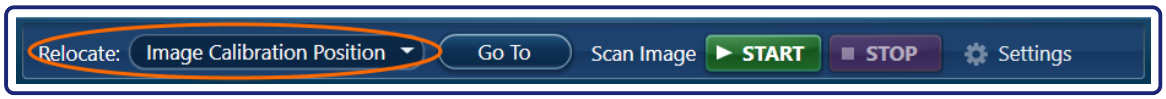
To resolve this, it is possible to acquire a reference image at the same time as setting the gray-level thresholds and to then set the contrast and brightness to the same levels at the start of every run. Both the reference image and the brightness and contrast levels for every run are set using the "Microscope Setup" mode to the right of the Feature steps:



To set consistent brightness and contrast at the start of a run:

1. If the gray-level markers and image settings for the reference image were saved as part of a user or application profile, load the profile.
2. Move to the area of the sample or imaging standard that was used to create the reference image and select the appropriate magnification to reproduce that image.

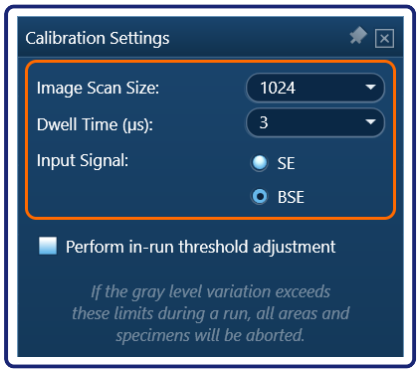
   If the position of this reference image has been stored as a "Point" using the Automate wizard, relocate to this position by selecting the stored position from the "Relocate" drop down menu in the acquisition toolbar of the "Microscope Setup" step and clicking the "Go To" button:



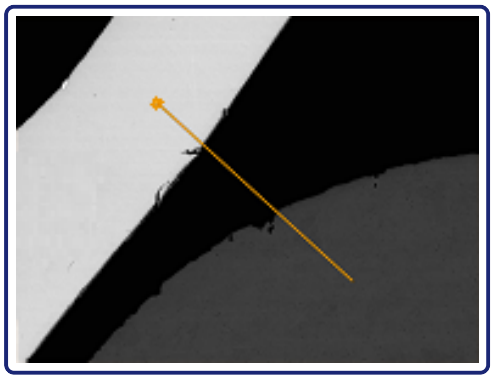
3. If the image settings were saved as part of a profile that has been loaded, start acquiring the image by clicking the "Start" button in acquisition toolbar.

   Otherwise, open the "Calibration Settings" window by clicking on the "Settings" icon in the acquisition toolbar:

   Select suitable settings for the image acquisition:



4. Select the Single Line Acquisition Tool and draw a line over the sample in the image viewer making it as similar as possible to the calibration line that was used when creating the initial calibration. Ideally the calibration line should cross features that cover the entire range of brightness including both the brightest and darkest features. i.e.:

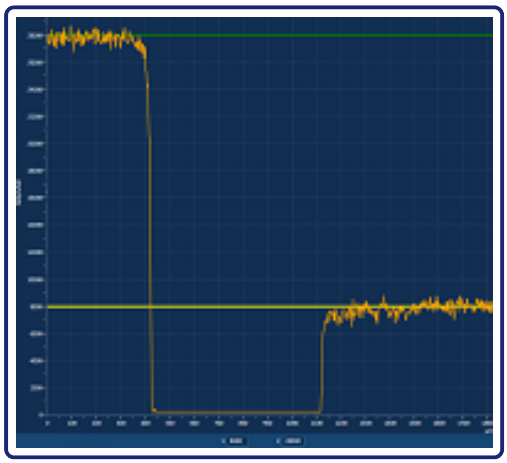


   A profile will appear on the graph to the right of the image showing the gray-levels along the image calibration line.

5. If the gray-level markers were saved as part of a profile that has been loaded, confirm that the markers are at the expected gray-level values. If not, set the markers to the correct gray-level values by either dragging

the markers up and down on the graph or by entering the correct gray-level values in the marker fields below the graph:

6. Adjust the brightness and contrast on the microscope until the gray-levels for the same features as in the reference image are on the markers. i.e.:

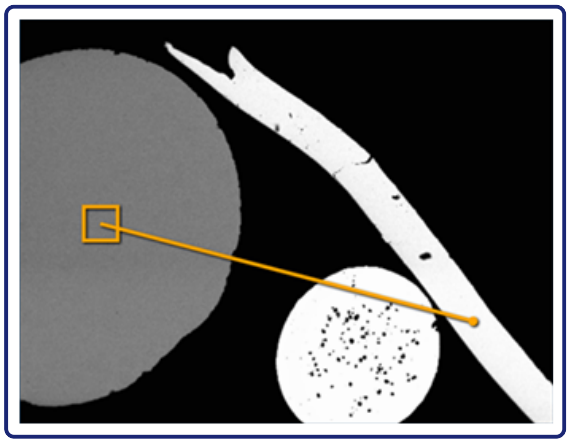


7. Click Stop to finish the scanning. The calibration will be saved in the data tree and will be available for reporting on.

Acquiring a Reference Image

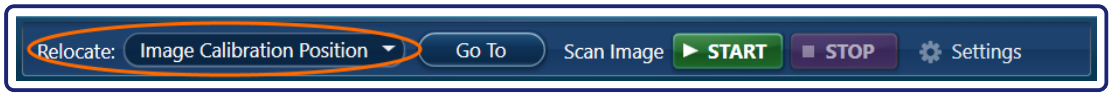
To acquire a reference image:

1. Select a suitable area of a sample or an imaging standard to be used to acquire an image before each run and adjust the magnification to an appropriate value. The region of sample within the field of view should have a good range of gray-levels including the brightest and darkest features that you wish to be detected, for example:

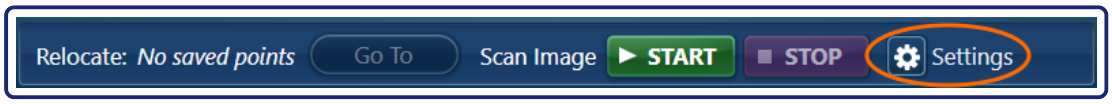


If the image is to be acquired from an imaging standard that is always mounted in the same position on the microscope stage, rather than manually relocating to it every time it is necessary to check the

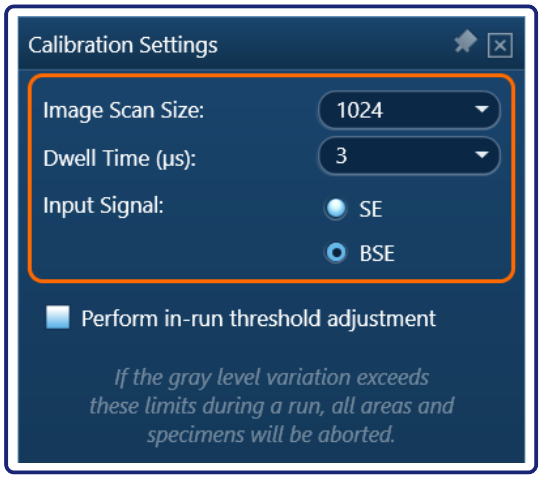
brightness and contrast of the image, the relevant stage position may be stored as a "Point" using the Automate wizard. This position may then be selected and moved to by selecting the stored position from the "Relocate" drop down menu in the acquisition toolbar of the Microscope Setup step and clicking the "Go To" button:



2. Open the "Calibration Settings" window on the Microscope Setup step by clicking on the "Settings" icon in the acquisition toolbar:

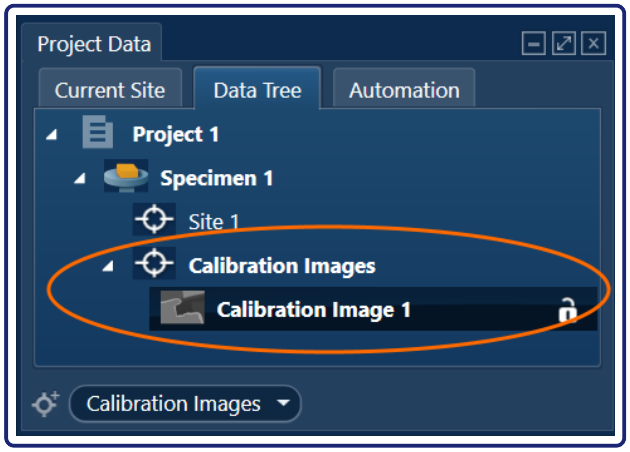


Select suitable settings for the image acquisition:

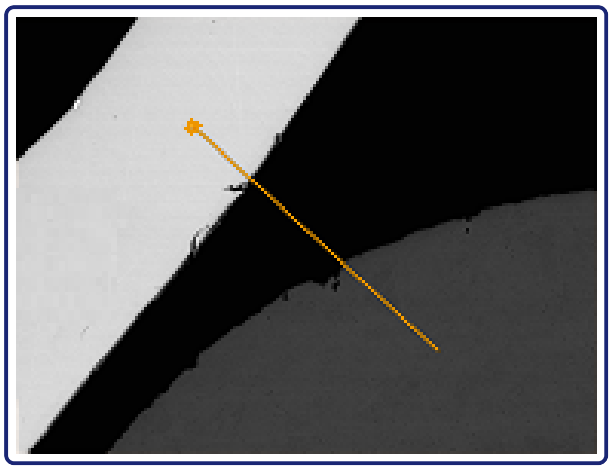


Ideally, the dwell time should be set to a similar value as for the main feature acquisition in order to give similar brightness levels and get a similar response from the backscatter detector. As such, to keep the acquisition time down for this process, reduce the resolution rather than the dwell time.

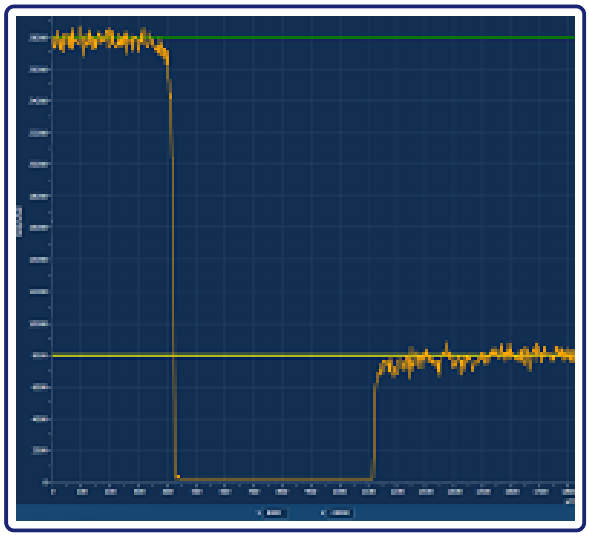
3. Click the "Start" button in the acquisition toolbar to start continually acquiring an electron image with the current settings. This will be the calibration image, which is saved to the data tree:



4. Select the Single Line Acquisition Tool and draw a line over the sample in the image viewer such that it crosses the different phases and range of gray-levels that you wish to detect. Ideally it should cross features that cover the entire range of brightness including both the brightest and darkest gray-levels, i.e.:



A profile will appear on the graph to the right of the image showing the gray-levels along the image calibration line:



5. Adjust the green and white markers on the graph by dragging them up and down so that they correspond to key gray-levels (which ideally are not saturated) along the reference line. Make a note of the features that the markers correspond to and their values:

It is this information that is used to identify whether the settings for brightness and contrast are the same for different runs.

6. Use the threshold histogram to see the gray-level values that the majority of pixels take and how they correspond to the threshold definitions. The markers in the histogram correspond to the markers in the main graph.
7. Click "Stop" to stop scanning the image. The calibration image will be automatically saved to the data tree.

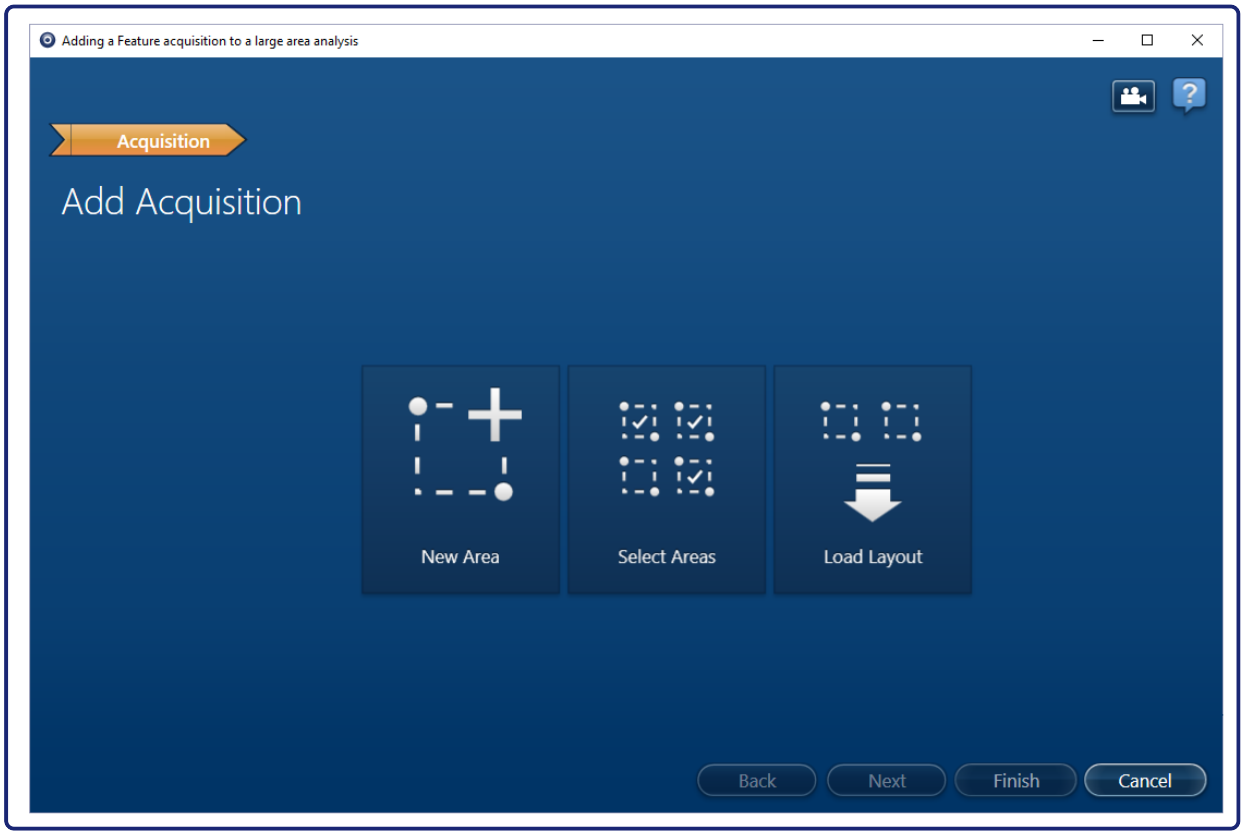
8. Save the user or application profile to save the marker positions and the image settings to that profile. When the profile is loaded for future runs, the settings will be automatically loaded and available to be used.
9. To assist with placing the calibration line in a similar position on the image and with reproducing the result for future runs, save the calibration as a report (for example using the Gray-level Calibration Report template).

2.6.2. Defining a Feature Large Area Acquisition

To define a Feature large area acquisition, from the "Run" step:

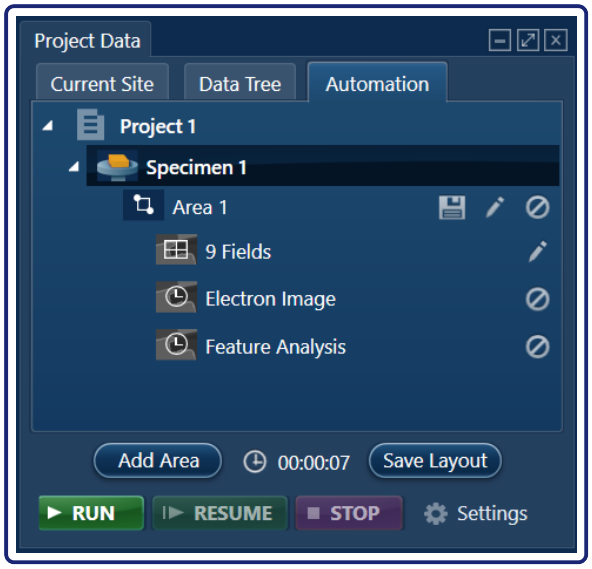
1. Click the Automate button in the acquisition toolbar:

2. This will open the Automate wizard which is used to define the main parameters for a large area acquisition.



3. Select whether to:
   - Create a new large area acquisition: Choose "New Area" to define a new area or "Load Layout" to load an existing area or layout. Confirm that the magnification and overlap settings are correct and adjust the z height to be appropriate.
   - Add an experiment to an area that has already been defined and added to the data tree: Choose "Select Areas" and then click "Next". Select the areas that the current recipe settings are to be applied to.

4. Click "Finish" to finish the large area definition and add the area to the data tree.



The feature experiment will use the current settings for the:

- Electron image and detecting the features - see the Detecting Features section.
- Eds acquisition - see the Acquiring EDS Data section.
- Feature automation run settings - see the Feature Automation Run Settings section.

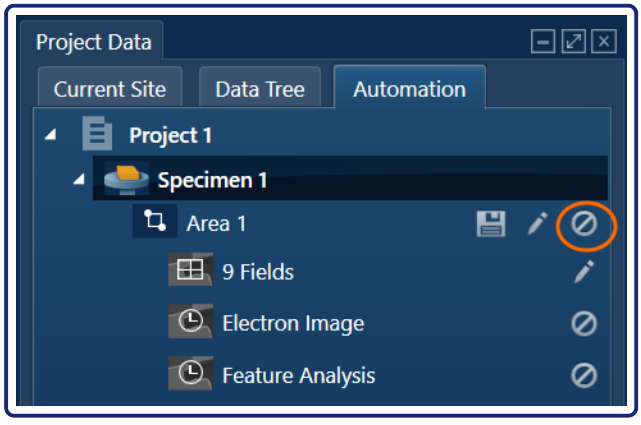
For additional help with using the Automate wizard, see the Working with Large Sample Areas section.

> ***NOTE:*** *When the area is defined by clicking the "Automate" button in the acquisition toolbar on the "Run" step, the large area definition will automatically include "Electron Image" and "Feature Analysis" experiments. If defined elsewhere in the AZtec software, these experiments may need to be added manually by following steps 1 and 2 and selecting the "Select Areas" option in step 2.*

5. Add additional areas to the acquisition by repeating steps 1 and 2.

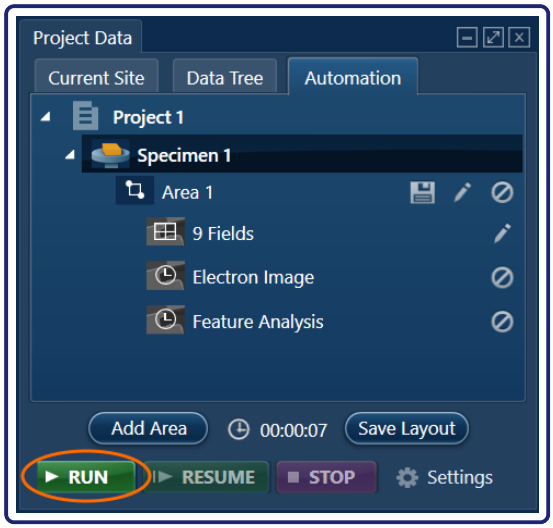
> ***NOTE:*** *Each area can have different experiments and settings to the other areas.*

6. To remove an area or experiment, click the icon at the end of its row in the Automation tab.



7. Start the acquisition of all of the defined areas by either:
   - Clicking the "Run" button in the acquisition toolbar of the "Run" step.

- Clicking the "Run" button at the bottom of the Automation tab in the Data Tree.

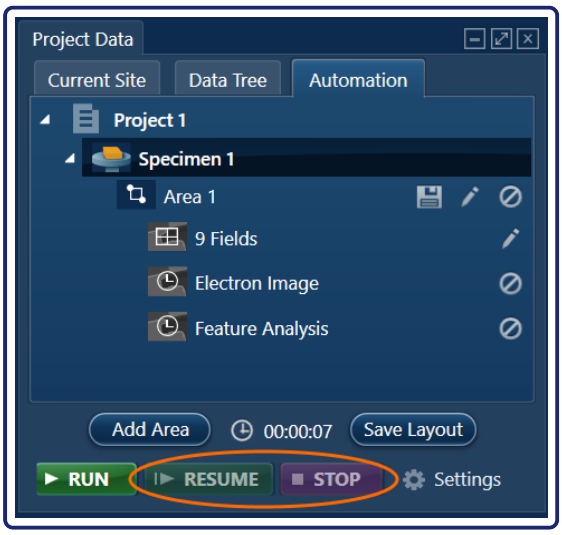


The software moves the microscope stage to the first stage position and starts acquiring the electron image. The areas are scanned in the order that they appeared in the Automation tab.

The data for each field is added to the Data Tree as a site, in numerical order. Each site contains data such as an electron image or feature data, which can be viewed as it is being acquired. (See "Site 4" in the examples.) A green bar indicates the progress.

> ***NOTE:*** *If brightness and contrast are set to automatically adjust during the run, the image might appear to flicker. If fields are set to align automatically during the run, the image might appear to flicker and move. During long acquisitions, long pauses might occur.*

8. The run can be stopped at any time, and resumed later, using the STOP and RESUME buttons in the "Automation" tab of the Data Tree.

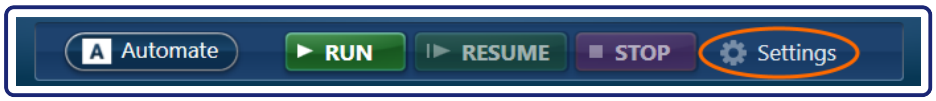


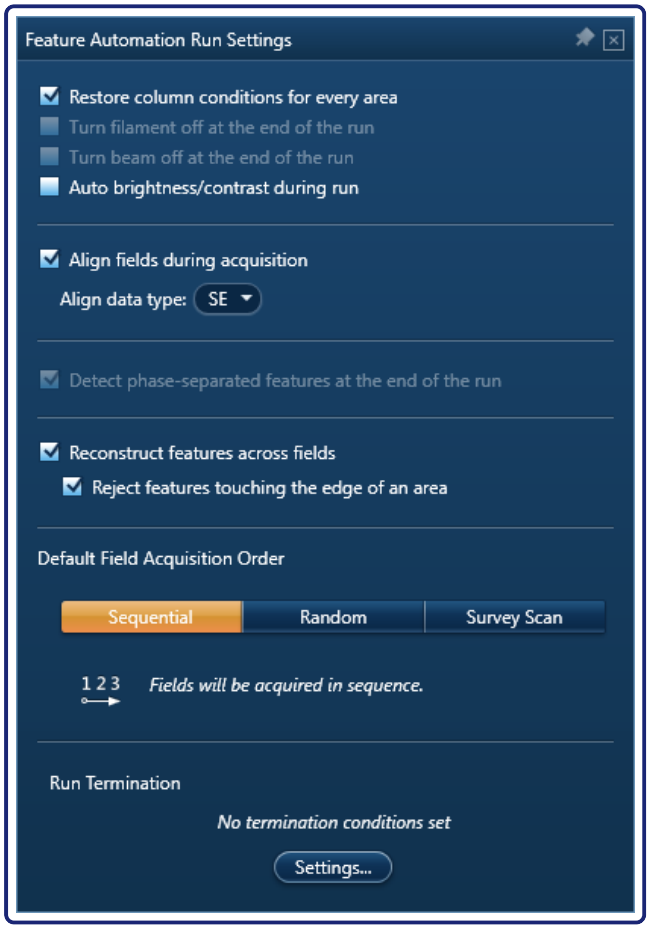
9. After all the data has been acquired, the fields can be combined into a single map or image, called a montage, which allows the data to be analyzed as a single unit.

   If any data was not acquired, because for example the microscope filament failed, some fields may appear empty, faint or black. If you act straightaway, it is possible to recover the missing data without needing to run the entire scan again.

Feature Automation Run Settings

The "Feature Automation Run Settings" window can be accessed from the acquisition toolbar in the "Run" step by clicking on the settings icon:





The settings window contains the standard options for a large area map acquisition including:

- Controlling the beam during and at the end of an acquisition.
- Performing automatic brightness and contrast adjustment during the acquisition.
- Performing automatic field alignment during the acquisition.

It also contains options that are specific to a Feature experiment including:

- Automatically reconstructing features that cross the boundaries of fields as a single feature.
- Specifying the order in which to acquire each of the fields.
- Performing a survey scan to prioritize the order that the fields should be acquired.
- Setting conditions to specify when the acquisition can be stopped.

Unless stated otherwise, all of the settings will affect all of the areas currently defined and not run in the Automation tree.

Microscope Controls

Specify whether to:

- Restore the columns conditions for every area.

  Ensures that for a single area, the microscope settings at the start of every field are the same, and for multiple areas, the settings at the start of each area are changed to those defined for the area.

  > ***NOTE:*** *If this option is not selected, the automated run will use the current microscope settings rather than the settings defined for an area. This means that if there are multiple areas, each with different microscope conditions (i.e. at different magnifications), all of the areas will be acquired with the current microscope settings, not those defined.*

- Turn the beam off (blank the beam) or filament off (set the beam to 0 keV) at the end of the run.
- Perform automatic brightness and contrast adjustment at the start of every field during the run.

  This gives a good brightness and contrast range for the entire area and ensures that all fields have a consistent brightness level.

Align Fields During Run

Specify whether the software should attempt to automatically align the fields during the acquisition.

Use the drop down menu to select the image type that the alignment should be based on. The images must have sufficient detail (i.e. a high number of features) in order for the software to be able to align them. The options are typically SE (secondary electron) or BSE (backscatter electron) images for Feature.

This options works well for samples with a high number of features (i.e. mineral samples with a high concentration of particles). It does not work so well on samples where there are few features on the borders of the fields that can be used for the alignment.

> ***NOTE:*** *For large area maps with a high number of fields selecting this option can slow down the acquisition. In these cases it may be better to use guided align afterwords.*

Detect Phase Separated Features at the End of the Run

Specify whether to automatically detect phase-separated features at the end of the run.

If selected and used with either threshold phase detection (see Separating Phases with Similar Gray-Levels into Individual Features) or full field phase detection (see Separating Features from Backgrounds with Similar Gray-Levels), when the EDS part of the large area acquisition is run, the EDS data is collected but not processed with AutoPhase until the end of the run.

> ***NOTE:*** *If this option is not selected, for example because of a very high field count. AutoPhase detection can be manually triggered from the "Review" step, after any field alignments have been performed.*

Reconstruct Features Across Fields

Specify whether to automatically reconstruct features across fields.

During a feature acquisition, if a feature is located in more than one field, it is counted and analyzed as multiple separate features (one feature per field that the feature is found in). This can give misleading

results, because, especially for very large features, the same feature can be counted multiple times and the morphology information for that feature will be incorrect.

When the “Reconstruct Features Across Fields” option is selected, feature reconstruction is done automatically after the feature acquisition has been completed and “Auto Align” (if selected) has been run. During the reconstruction any features in two (or more) separate fields that touch each other and have the same threshold are reconstructed as a single feature. This is important for achieving accurate morphology measurements and to have a single quantification per feature.

It is also possible to automatically "Reject features touching the edge of an area". When this option is selected, the feature reconstruction is completed and then any features that are found to touch the edge of the acquisition area are rejected.

NOTE: *If manually aligning the fields, for example, because of a very high field count, then rather than selecting to use automatic feature reconstruction at this point, it may be better to manually run feature reconstruction and to reject any features touch the edge of the area from the "Review" step, after the field alignments have been adjusted.*

For more information about reconstructing features see the Reconstructing Features Across Fields section.

Default Field Acquisition Order

Specify the default field acquisition order.

Option	Description
Sequential	The fields in an area are acquired in a sequential order.
Random	The fields in an area are acquired in a random order until the whole area has been completed or the termination conditions have been satisfied. This method is useful for sampling, where not all fields are expected to be acquired.
Survey Scan	A pre-scan of the area is undertaken and the number of features in each field is estimated so that the fields in the main run can be prioritized in order of most to least populated. This method is commonly used with termination conditions (i.e. to acquire 50% of particles) and is designed to allow the termination conditions to be met in the most efficient manner. For more information on using Survey Scan see the Survey Scan section.

NOTE: *The selected option will be the default field acquisition order for any new areas that are defined and will be the default option when completing the "Area Layout" step of the "Automate" wizard. It can be overridden by selecting a different field acquisition order in either the Automate wizard or the editing multiple areas window which can be accessed from the "Run Summary" or the Data View.*

Run Termination

Termination conditions are used to specify when sufficient data has been acquired and the acquisition can be stopped. They may be specified for a field, area or sample. When the termination conditions have been met, the software will stop the current acquisition and move on to the next field, area or sample, as appropriate until all of the defined Feature experiments are complete. For more information on using termination conditions see the Termination Conditions section.

Changing the termination conditions in the Feature Automation Run Settings will affect all future large area acquisition definitions. It will not affect any existing areas. To change the termination conditions for an existing area either:

- Use the editing multiple areas window
- Delete the experiment, change the settings and then recreate the experiment.

Both methods are described in the Modifying Feature Experiment Settings section.

2.6.3. Using Layouts to Define Multiple Areas

In addition to defining areas made up of multiple fields, it is also possible to define layouts which consist of multiple areas. These layouts are particularly useful for situations where multiple areas with the same dimensions and layout are mapped repeatedly. This is because rather than having to create or load a series of areas, it is possible to create the areas once and then save them as a layout. These layouts can then be loaded into projects as a single item. Different experiments can be added to the areas within the layout.

Some examples of applications where layouts can be beneficial are:

- Multiple stub holders where data is acquired for a given area on each stub.
- Very large samples where data is acquired for several different areas spread across the sample.

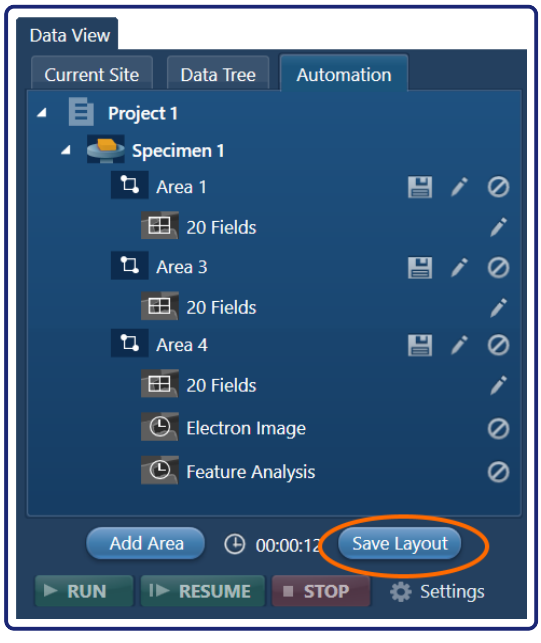
The following sections describe how to:

- Save multiple areas as a layout.
- Use a layout.

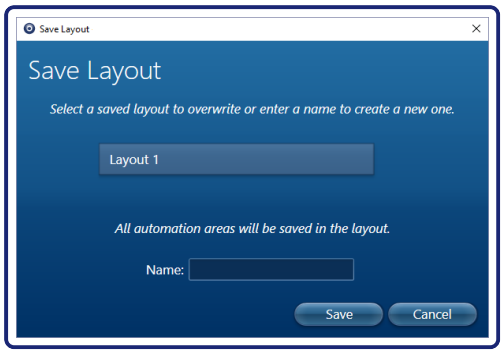
Saving Layouts

To create and save a layout, in the Automation tab of the Data View:

1. Define multiple areas.
   The areas may be defined for the same or different specimens. For example:



2. Click the "Save Layout" button to save the layout. This will open the Save Layout window:

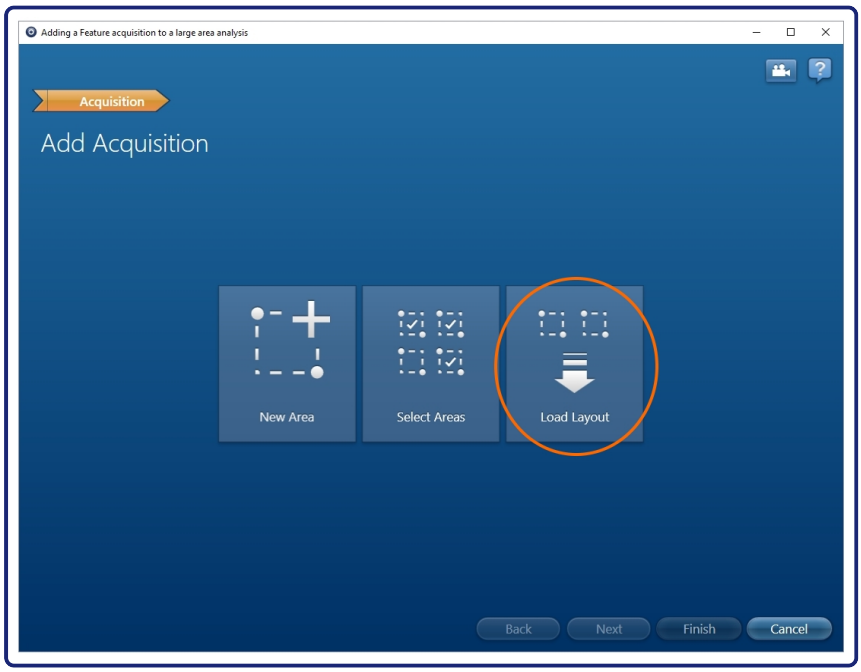


3. Select an existing layout to overwrite or enter a name to save the layout to as a new layout.
4. Click "Save" to save the layout and close the "Save Layout" window.

The layout can now be loaded from the "Automate" wizard - see the "Using Layouts" section.

Using Layouts

Layouts can be loaded through the Automate wizard by clicking on the "Load Layout" button in the Acquisition step:

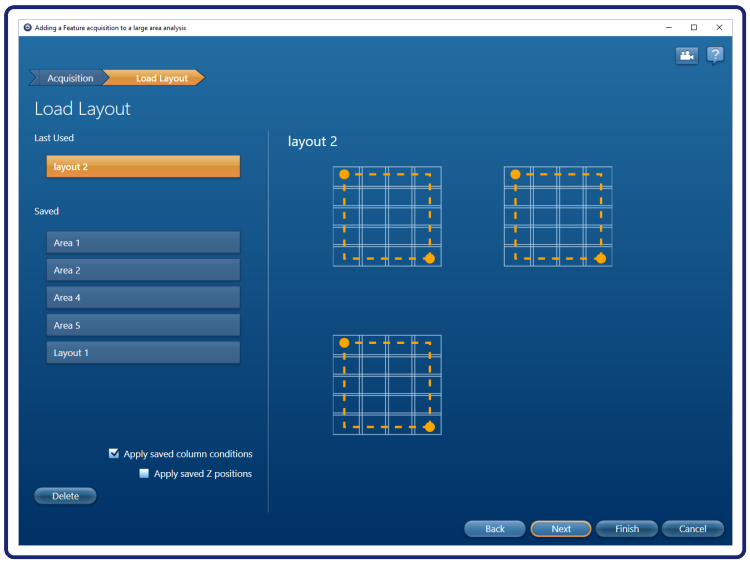


There are four steps to setting up to use a layout:

1. Load Layout: Select the layouts to be loaded.
2. Select Areas: Select the areas of a layout to acquire data for.
3. Definition: View and edit the acquisition areas.
4. Layout: View and edit the settings for each area.

Load Layout

The "Load Layout" step of the Automate wizard is used to select the layouts or areas to be loaded:



For a selected area, hover the mouse over the image for that area to view its details.

For a selected layout, hover the mouse over the image for an area in the layout to view its details.

For the selected area or layout choose whether to:

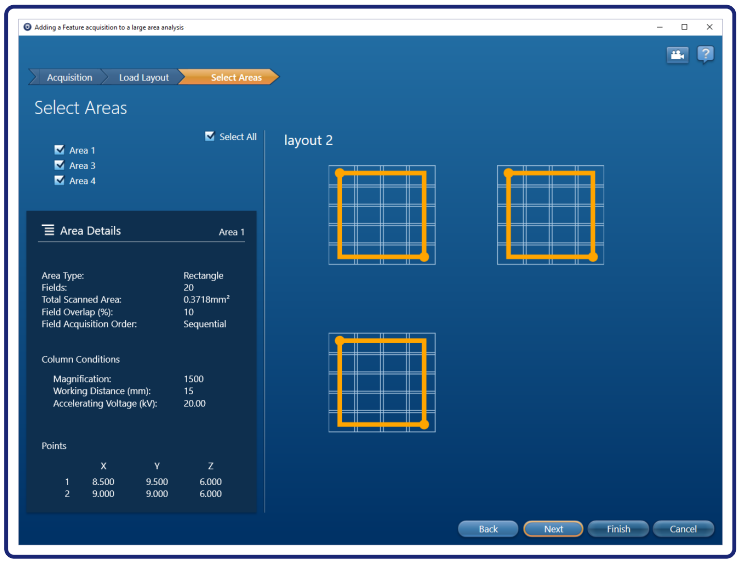
- Apply saved column conditions.
- Apply saved z positions.

> ***NOTE:*** *To avoid a collision between the specimen and the pole-piece of the microscope, by default, the Z position used for each of the area's stage positions is the current stage Z position and not the original Z position. Select the "Saved Z positions" options, to use the saved Z positions. When selecting this option, be very careful, especially when the sample is tilted, as there is the potential for the sample to collide with the pole piece. If the saved Z positions are not used, the Z position can be set in the "Area Definition" step.*

Click "Next" to proceed to the "Select Areas" step.

Select Areas

The "Select Areas" step of the wizard is used to select which of the areas of the layout are to be used:

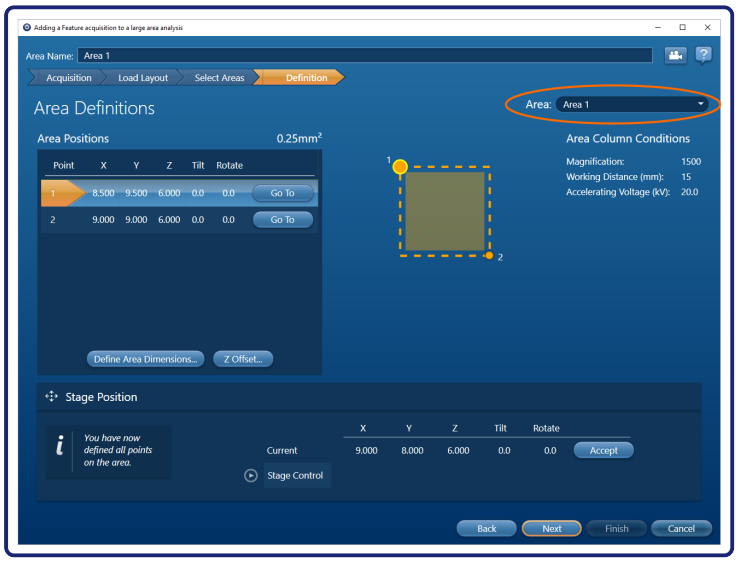


When an area has been selected it will be shown by a solid orange line (unselected areas have a dashed line). The details for the different areas can be viewed by hovering the mouse over the areas.

Click the "Next" button to proceed to the "Area Definitions" step.

Area Definitions

The "Area Definitions" step of the Automate wizard is used to view and edit the acquisition areas that were selected in the "Select Areas" step:



Use the "Area" drop down menu to switch between the different areas that were selected in the previous "Select Areas" step and view the stage positions that have been defined for that area.

Test the stage positions using the "Go To" buttons next to each stage position in the "Area Positions" section of the window:

To edit a stage position:

1. Select the stage position using the "Area Positions" section of the window.
2. Change the stage position using either the "Stage Control" in the "Stage Position" section of the window or using the microscope.
3. Click "Accept" to overwrite the currently highlighted stage position.

To edit the area dimensions:

1. Click the "Define Area Dimensions..." button to open the "Define Area Dimension" window.
2. Edit the values for the width and height in mm.
3. Click "Ok" to close the window and return to the Automate wizard.

For more information on editing stage positions and area dimensions, see the Area Definition section in "Creating a New Area".

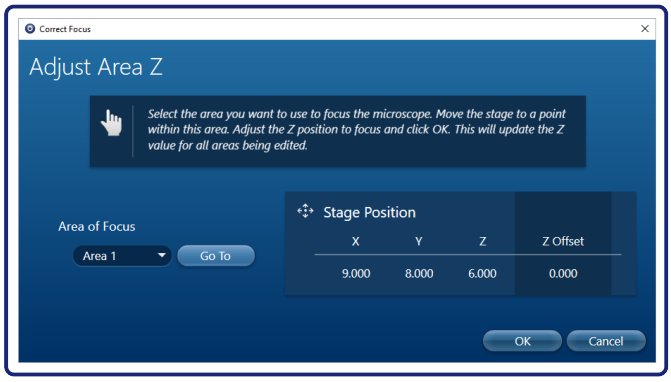
If "use saved Z positions" was not selected in the Load Layout step, the Z position can be set now. To adjust the Z position:

1. Ensure that the specimen is at a height where it will not collide with the pole-piece.
2. For the first stage position listed in the "Area Positions" section of the "Area Definition" step, click the "Go To" button for the first area position. The stage will drive to the saved X and Y positions, keeping the Z position the same.
3. Bring the specimen into focus by adjusting the Z position.
4. Click "Accept" to save the new stage position.
5. Follow this procedure for each of the stage positions.

To allow for sample holders to be mounted at slightly different heights, it is possible to load an existing layout and then calculate the z offset (the difference between the original z position of the sample and the new z position) for the sample. This offset can then be applied to all of the areas within the layout so that they are at the correct height for acquisition and in focus at the recommended working distance.

To calculate and apply a z offset to a layout:

1. Click the "Z Offset..." button in the Area Positions section to open the "Adjust Area Z" window:



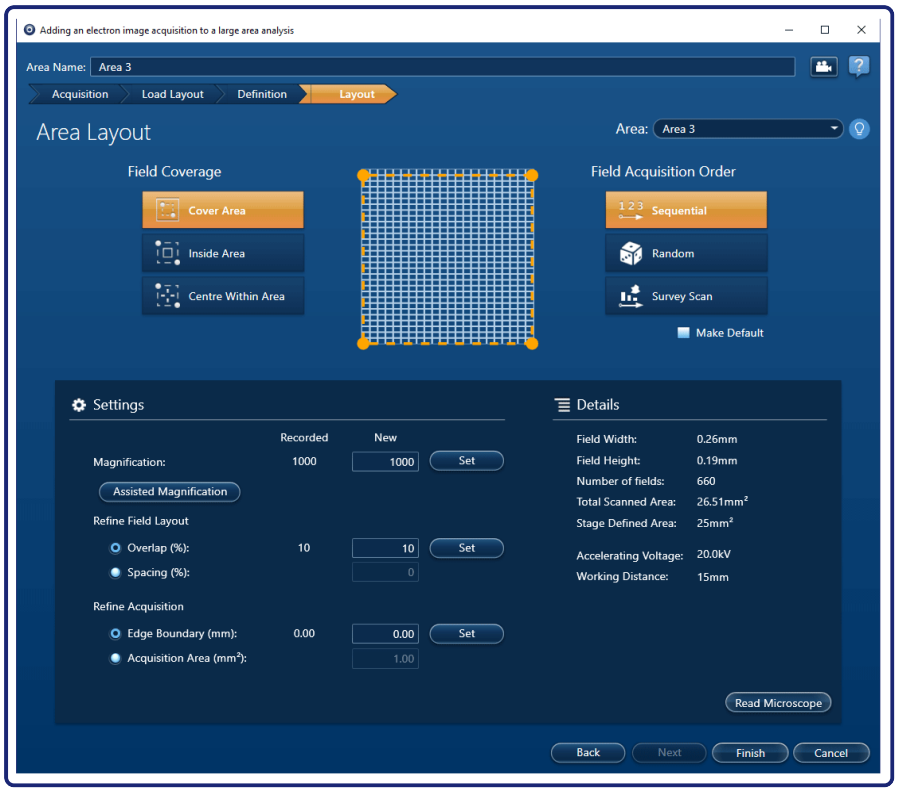
2. Select the "Area of Focus" for which the z stage position is to be edited from the drop down menu.
3. Click "Go To" to automatically move the stage to the center of the area or manually move the stage to a point within that area.
4. Adjust the z position to bring the sample into focus.
5. Click "OK" to submit the new z position.

   The software will calculate the difference between the original z position and the new z position and apply that value to all areas within the layout.

Once finished making changes, click the "Next" button to proceed to the Area Layout step.

Area Layout

The last step of loading a layout using the Automate wizard, is the "Area Layout" step. This step is the same as the Area layout step in the "Creating a New Area" section of Working with Large Sample Areas:



Use the Area drop down menu to select each area in turn and define the settings to be used for that area.

When applying the same settings to multiple areas, it may be quicker to use the "Edit Multiple Areas" window, which can be accessed from the "Run" step. For more information on using the "Edit Multiple Areas" window, see the "Modifying Feature Experiment Settings" section.

Click the "Finish" button to complete the layout setup and close the Automate wizard.

2.6.4. Optimizing a Feature Large Area Acquisition

This section describes the different methods available for optimizing feature acquisitions including:

- Using Termination Conditions to Stop the Acquisition: Specify when sufficient data has been acquired and the acquisition of the site, area or specimen can be stopped.
- Optimizing the Field Acquisition Order: Specify the order in which the fields should be acquired.
- Compensating for Changes in Image Brightness During a Run: Specify the gray-levels that should be maintained to get consistent feature detection and results.

Using Termination Conditions to Stop the Acquisition

Termination conditions can be used to specify when sufficient data has been acquired and the acquisition of the site, area or specimen can be stopped. They are designed to:

- Avoid excessively large amounts of data being collected.
- Reduce the amount of time spent analyzing samples.
- Minimize disk storage space.

They can be defined for a field, area or specimen.

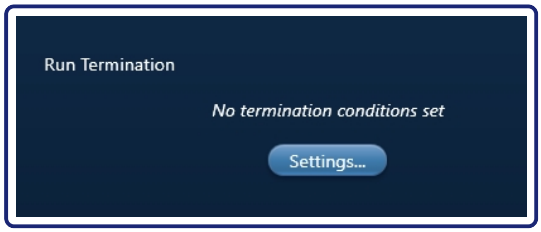
They can be based on:

- The number of features acquired.
- The number of features that fall in to a certain class or subclass.
- The time that data has been acquired for.

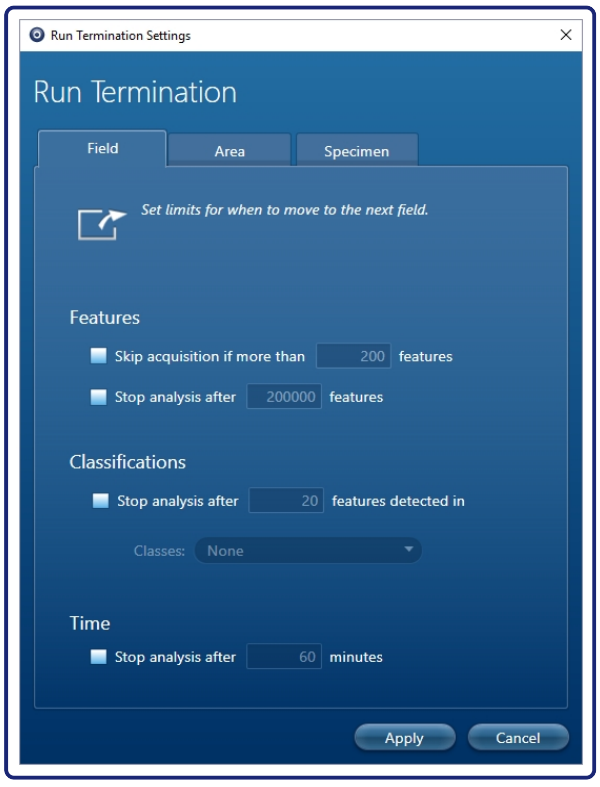
When the termination conditions for the acquisition have been met, the software will stop the current acquisition and move on to the next field, area or sample, as appropriate until all of the defined Feature experiments are complete.

To specify termination conditions prior to creating a feature experiment:

1. In the "Feature Automation Run Settings" window, click the "Settings..." button in the "Run Termination" section:



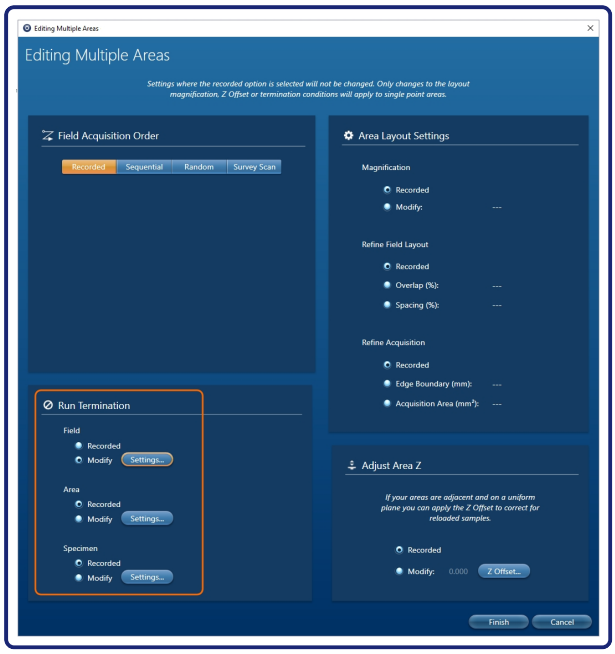
This will open the "Run Termination" window which has separate tabs for defining the termination conditions for a field, area and specimen:



2. Select the relevant tab and edit the settings as described in the sections:
   - Field Termination Conditions.
   - Area Termination Conditions.
   - Specimen Termination Conditions.

To edit the termination conditions for an already created feature experiment:

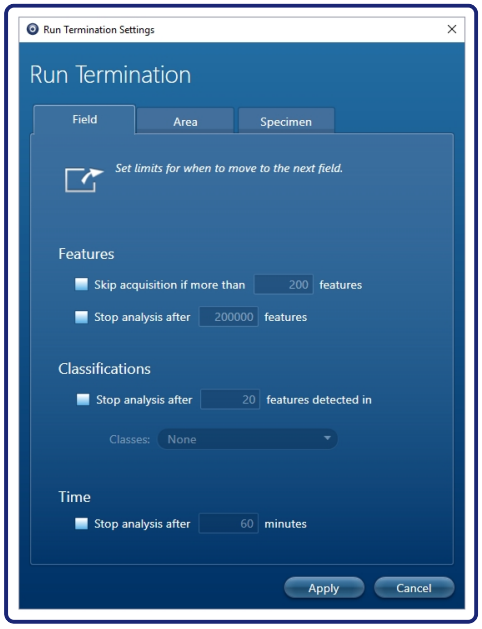
1. In the Run Summary pane of the Run step, select the area to be edited.
2. Click the edit button to open the "Editing Multiple Areas" window:



3. Edit the settings in the "Run Termination" section as described in the sections:
   - Field Termination Conditions.
   - Area Termination Conditions.
   - Specimen Termination Conditions.

Field Termination Conditions

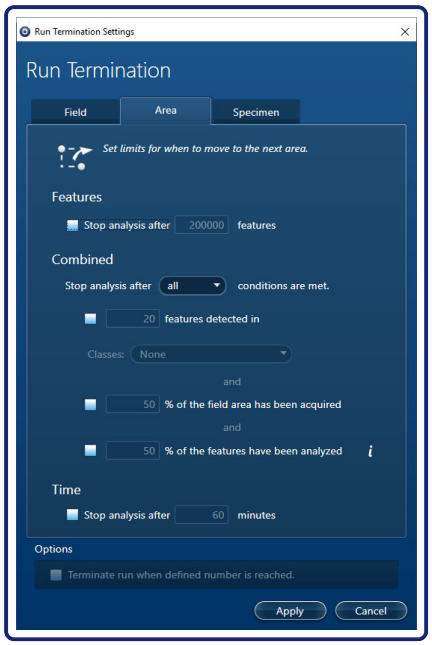
The field run termination settings window is used to specify the termination conditions for the acquisition of a field. When the termination conditions are met, the data is saved and the data acquisition moves onto the next field.



Termination Condition	Description	Example Application
Features		
Skip acquisition if more than "x" features	If more features are detected in a field than the number defined here (x), EDS acquisition is not performed on the field. The software moves on to the next field.	Fields with a lot of contamination will have a much higher number of features than other fields. Use this termination condition to specify the maximum acceptable number of features in a field and that the contaminated fields with greater numbers of features should be skipped.
Stop analysis after "x" features	Once EDS acquisition of the defined number of features (x) has been performed, the acquisition of the field is stopped. The software moves on to the next field.	If a field has more than a certain number of features of a certain type it is a "bad" field. Analyze the defined number of features to characterize the field and then move on to the next.
Classifications		
Stop acquisition after "x" features detected in Classes "y"	Once the software has detected the defined number of features (x) within the selected classes (y), the acquisition of the field is stopped and the software moves on to the next field.	For samples where a certain number of a particular feature type in a field are required for the sample to pass or fail, there is no benefit to acquiring data for additional features in the field. Use this termination condition to set the number and move on to the next field once reached.
Time		
Stop analysis after "x" minutes	Once the specified time (x) has been reached, the software will complete the current feature acquisition. It will then stop the acquisition of the field and move on to the next field.	If a field has a lot of charging (i.e. from contamination), the EDS detector dead time and hence the acquisition time can become very high. Rather than waste time trying to collect EDS data for these fields, specify a time after which most fields will have been acquired to move on.

Area Termination Conditions

The area run termination settings window is used to specify the termination conditions for the acquisition of an area. When the termination conditions are met, the acquisition is stopped at the end of the current field and the software either moves on to acquire data in the next area (if present) or if the "Terminate run when defined number is reached" option is selected, the acquisition is stopped. If multiple conditions are specified in the Combined section, the acquisition will only stop when all of the combined options are met.

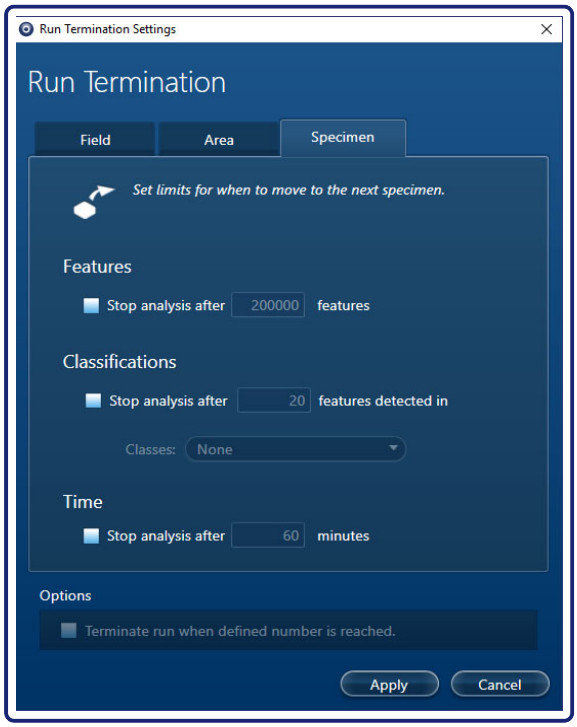


Termination Condition	Description	Example Application
Features		
Stop analysis after "x" features	Once EDS acquisition of the defined number of features (x) has been performed, the acquisition of the area is stopped.	Only a set number of features are required to be analyzed in order to characterize the sample. Analyzing a greater number of features is not necessary and only adds to the time overhead.
Combined		
Stop acquisition after "x" features detected in Classes "y"	Once the software has detected the defined number of features (x) within the selected classes (y), the acquisition of the area is stopped.	For samples where a certain number of a particular feature type are required in an area for the sample to pass or fail, there is no benefit to acquiring data for additional features in the area. Use this termination condition to set this number and move on to the next area once reached.
"x"% of the field area has been acquired	When the defined percentage (x) of the area has been acquired, the acquisition of the area is stopped. This is often used in conjunction with the random field acquisition order.	This condition is useful for sampling, where data for a specific percentage of the sample is required.
"x"% of the features have been analyzed	When the defined percentage (x) of the total number of features in the field area have been acquired, the acquisition of the area will be stopped. This option will only be enabled when a	This condition is useful for ensuring high throughput where the data is analyzed for "x"% of the features.

Termination Condition	Description	Example Application
	survey scan is to be performed, as the survey scan is used to estimate the number of particles present in the entire field area.	
Time		
Stop analysis after "x" minutes	Once the specified time (x) has been reached, the software will complete the current feature acquisition. It will then stop the acquisition of the area.	
Options		
Terminate run when defined number is reached	When the termination condition is reached terminate the run. Do not move to the next area.	

Specimen Termination Conditions

The specimen run termination settings window is used to specify the termination conditions for the acquisition of a specimen. When the termination conditions are met the acquisition is stopped at the end of the current field and the software either moves on to acquire data for the next specimen (if present) or if the "Terminate run when defined number is reached" option is selected, the acquisition is stopped.



Termination Condition	Description	Example Applications
Features		
Stop analysis after "x" features	Once EDS acquisition of the defined number of features (x) has been performed, the acquisition is stopped and the software moves on to the next specimen.	Multiple areas within the specimen may be part of the same sample. Once a sufficient number of features within the specimen have been analyzed, move on to the next specimen.
Classifications		
Stop analysis after "x" features detected in Classes "y"	Once the software has detected the defined number of features (x) within the selected classes (y), the software moves on to the next specimen.	For samples where a certain number of a particular feature type are required for the sample to pass or fail, there is no benefit to acquiring data for additional features in the area. Use this termination condition to set this number and move on to the next specimen once reached.
Time		
Stop analysis after "x" minutes	Once the specified time (x) has been reached, the software will complete the current feature acquisition before moving on to the next specimen.	Set the time allocated per specimen (collection of samples) to maximize throughput.
Options		
Terminate run when defined number is reached	When the termination condition is reached terminate the run. Do not move to the next area.	

Optimizing the Field Acquisition Order

The order in which the fields in an area are acquired can be specified and optimized to allow the acquisition to be completed in the most efficient manner. There are three different options available:

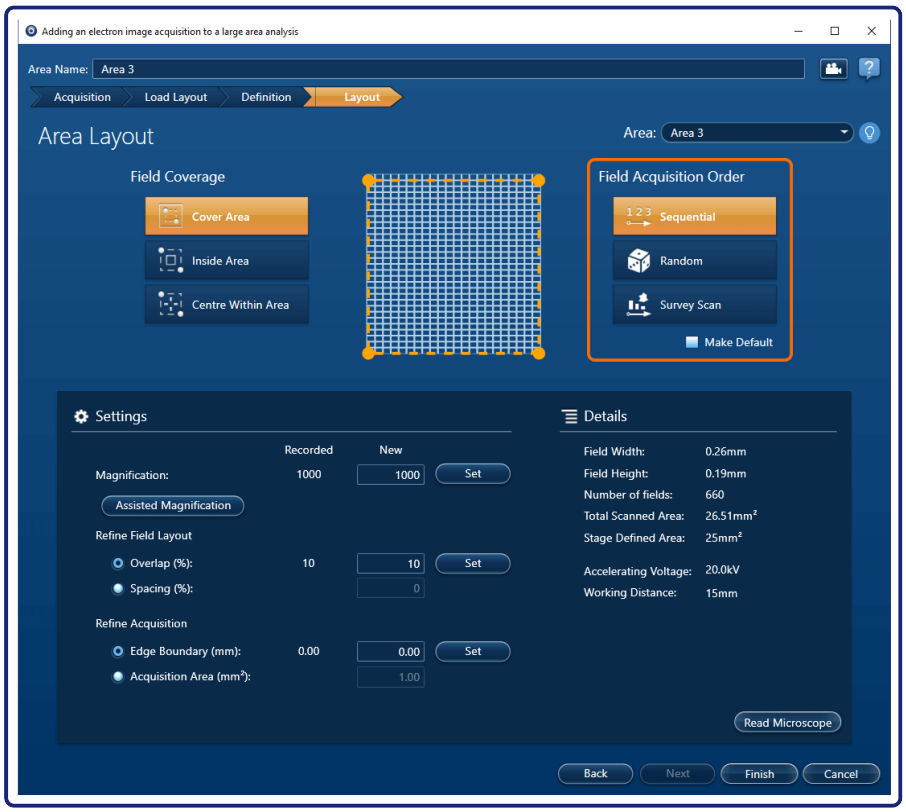
1. **Sequential:** Adjacent fields are analyzed one after the other in a traditional order.
2. **Random:** The software selects a random order for the fields to be acquired in. The fields are acquired until the whole area has been completed or the termination conditions have been satisfied. This method is useful for sampling, where not all fields are expected to be acquired.
3. **Survey Scan:** A pre-scan of the area is undertaken and the number of features in each field is estimated so that the fields in the main run can be prioritized in order of most to least populated. This method is commonly used with termination conditions (i.e. to acquire 50% of particles) and is designed to allow the termination conditions to be met in the most efficient manner. For more information on setting up a survey scan, see the Survey Scan section.

Defining the Field Acquisition Order

The field acquisition order can be defined from:

- The Feature Automation Run Settings accessed from the acquisition toolbar in the Run navigator step:

- The Area Layout step of the "Automate" wizard:



NOTE: *If the same field acquisition order is to generally be used, it may be set as the default by checking the "Make Default" option below the Survey Scan option.*

NOTE: *If Survey Scan is selected here, its settings cannot be changed (the current settings in the "Featured Automation Run Settings" window will be used).*

Editing the Field Acquisition Order

Once a feature experiment has been created, it is still possible to go back and change the field acquisition order for the experiment prior to starting the acquisition by:

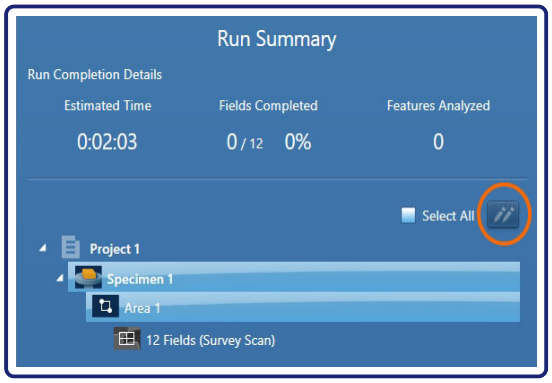
- Editing the “Area” definition from the Automation data tree. With this method the field acquisition order can only be changed from the Automate Wizard.

  > ***NOTE:*** *If the “Survey Scan” option is selected, it will take the settings that were current when the feature experiment was created, which may not be the same as the values currently shown in the “Feature Automation Run Settings” window.*

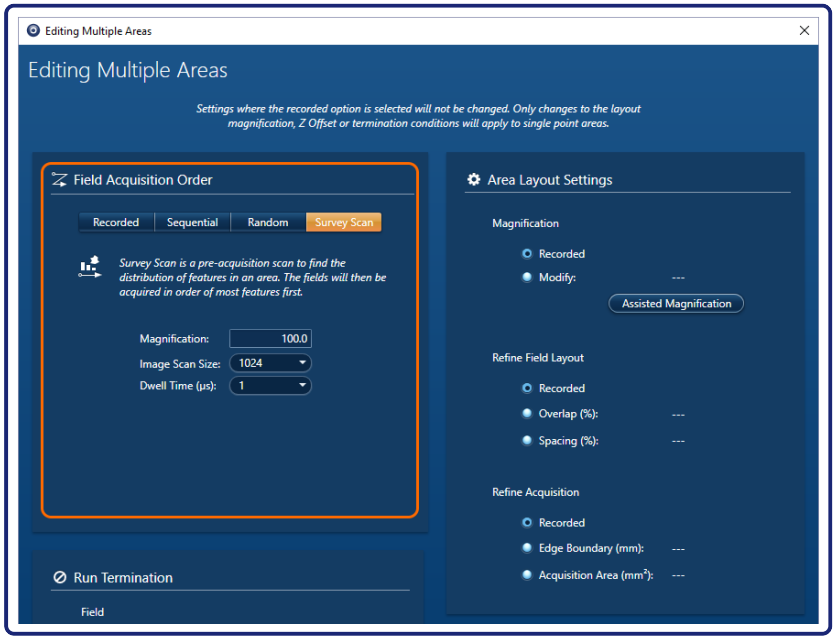
- Deleting the feature experiment (“Feature Analysis”) from the data tree and then creating a new feature experiment by clicking the “Automate” button.

  The advantage of this method, is that prior to creating the new feature experiment, the survey scan settings can be viewed and edited in the “Feature Automation Run Settings” window.

- Edit the feature experiment settings from the editing multiple area option in the “Run Summary” on the left of the screen:



The advantage of this method over the other two, is that all of the settings for the survey scan can be viewed and edited without having to delete and then recreate the feature experiment.



The bulk edit window can also be used to change the termination conditions, the area layout settings and to adjust for any z offset between samples.

Prioritizing Fields with the Highest Number of Features

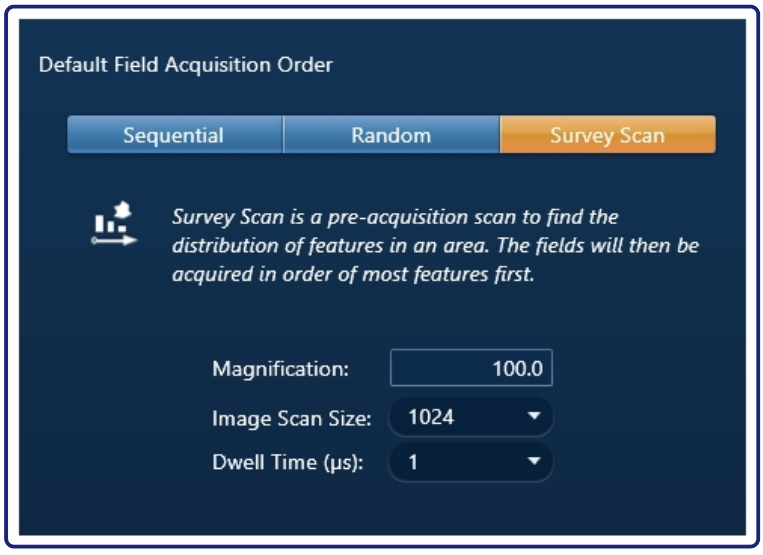
Some Feature samples may have a heterogeneous distribution of features, where there is a high number of features concentrated in some areas of the sample and a very low number in others. For these samples acquiring the fields in a sequential order may not be the most optimal method of acquiring the data as a significant amount of time can be spent acquiring data for fields with few or no features.

The survey scan option is a powerful and efficient way of analyzing these types of samples because it allows the order that the fields are acquired in to be prioritized by the number of features present. It works by acquiring images for every field in the defined large area acquisition prior to the full feature acquisition and uses the number of features detected in each of these fields to prioritize the fields with the highest number features so that they are acquired first.

It is particularly effective when used in conjunction with termination conditions, where you only want to analyze a certain number of the features on the sample. In particular it allows you to:

- Acquire the EDS data for the maximum number of features in the minimum time by acquiring data over the minimum number of fields. This saves time by reducing the number of stage moves and image acquisitions necessary to achieve the given number of features.
- Specify that you would like to analyze a certain percentage of features. This is not available with the sequential and random acquisition orders because the survey scan is required to determine the total number of features present.

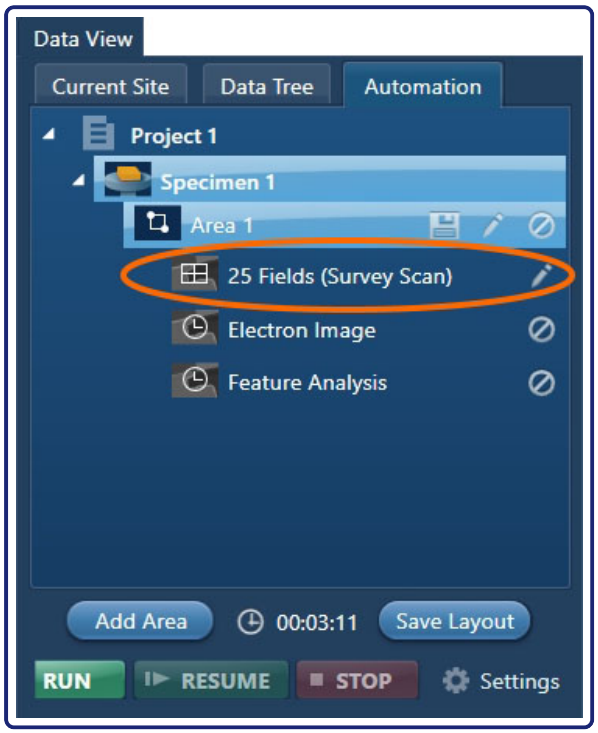
The simplest method to set up to use a survey scan, is using the “Default Field Acquisition Order” section of the “Feature Automation Run Settings” window to select “Survey Scan” as the default field acquisition order:



The settings that are used to acquire the images for the survey scan are also defined here. They must be specified prior to the feature experiment being created in order for the feature experiment to take the values. Otherwise they may be changed after the feature experiment has been created as described in the Optimizing the Field Acquisition Order section.

The settings for the survey scan may be different to those specified for the full feature acquisition. For example, it may be desirable to use a lower magnification and dwell time to the main acquisition in order to cover the acquisition area more quickly. These settings should allow the most to least populated fields to be effectively located. However, fewer features may be detected than if the higher quality image settings of the main acquisition were used.

When a feature experiment that will use the survey scan is created, the automation tab in the data view will show that a feature experiment has been created for an area and that a survey scan has been specified within the "Fields" entry. For example:



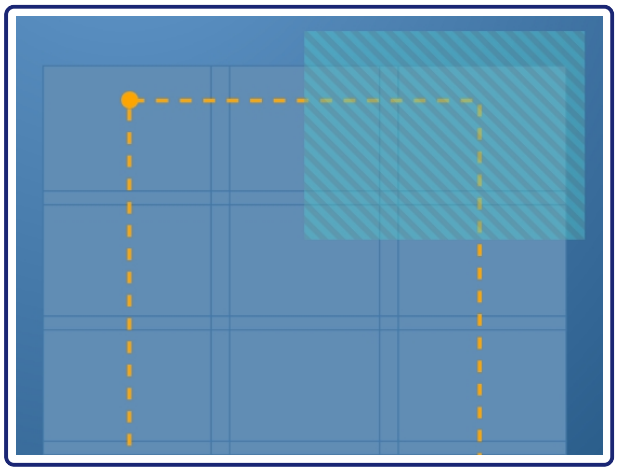
NOTE: *The number of fields shown in the "Fields" entry relates to the number of fields in the full feature acquisition and not the survey scan.*

When a feature acquisition with survey scan is run, the acquisition starts with the survey scan, during which:

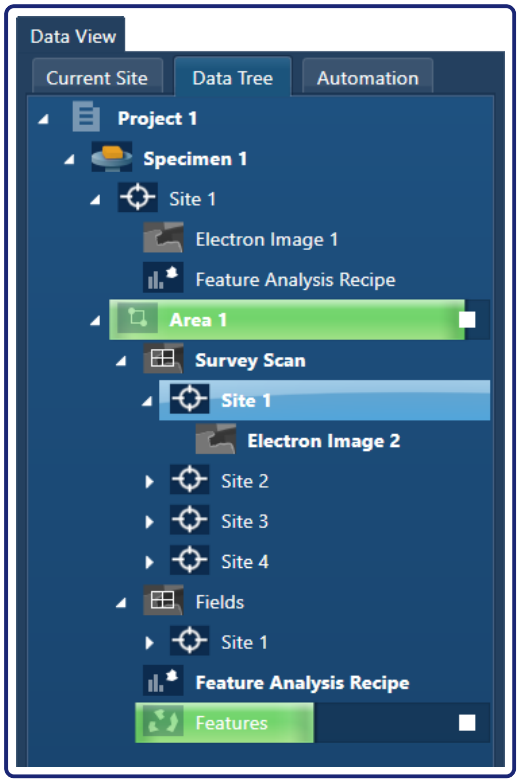
1. An image is acquired for each field.
2. The number of features present in each field is estimated.
3. The fields in the full feature acquisition are prioritized in order of highest to lowest number of features in a field.

The full feature acquisition will then proceed as normal using the prioritized fields.

To signify that a field is being acquired as part of the survey scan, the field is marked on the full acquisition area definition using blue hatching. The example below shows a field being acquired as part of a survey scan at a different magnification to that which will be used fur the full feature acquisition:

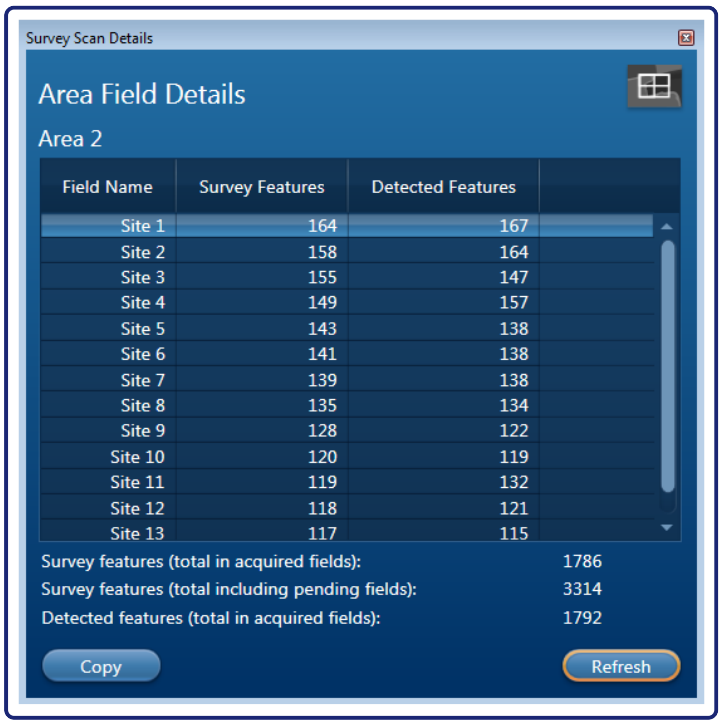


Electron images acquired as part of the survey scan are saved in the data tree under "Survey Scan":



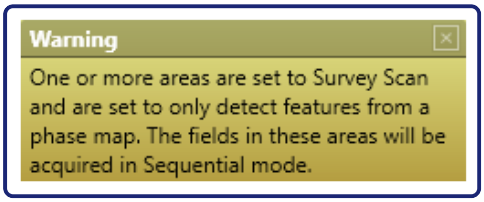
A summary of the number of features detected as part of the survey scan and from the full feature acquisition is displayed in the "Survey Scan Details" window, which is accessed by right clicking on "Fields" in the data tree and selecting "Details...". The "Survey Scan Details" window (shown below) displays:

- The number of features detected as part of the survey scan for each field.
- The number of features detected by the full feature acquisition for each field.
- Some summary information the number of features detected in the survey scan to be compared to the full feature acquisition for all of the acquired fields.



NOTE: *If the details window is displayed while the data is being acquired, periodically click refresh to update the information displayed.*

NOTE: *If using threshold phase detection or full field phase detection, the survey scan will not work in the same way. For threshold phase detection, the survey scan will run but will only be based on the image, i.e. it will take the number of features detected before threshold phase detection is performed. For full field phase detection, the survey scan will not run. Instead the fields will be acquired sequentially. A warning message will be displayed:*



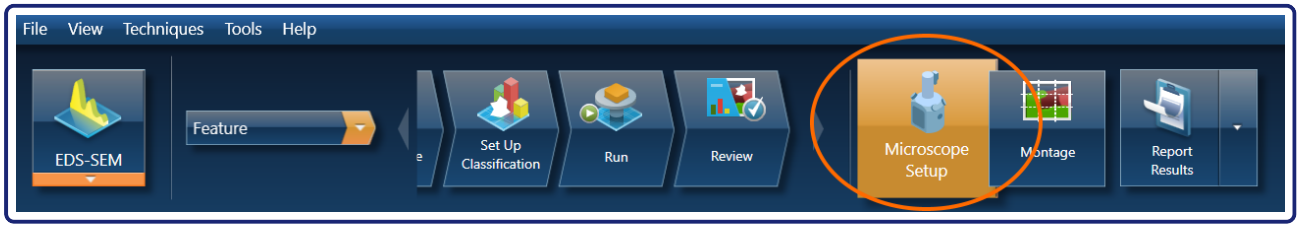
Compensating for Changes in Image Brightness During a Run

As described in the Detect Features section, the feature detection from the electron image is reliant on the gray-level thresholds that have been defined. If the microscope electron beam varies in brightness during a run, the electron images that are acquired for each field for feature identification will also vary in brightness. This can cause the features in different images to have different gray-level values and mean that some features that were within the gray-level thresholds set prior to starting the run, fall outside of these levels and not be detected.

To monitor and compensate for any changes in the brightness and contrast of the electron images during a run, AZtecFeature offers in-run threshold adjustment. This feature uses a small reference area, which may either be on the sample or on an imaging standard to periodically acquire and check the brightness of the image against an original reference image and then adjusts the gray-level thresholds to compensate for the changes in image brightness accordingly by:

- Pausing the acquisition at the end of the field after the specified time interval has been reached.
- Moving to the stage position saved with the reference image and changing to the specified magnification.
- Acquiring an image with the specified settings.
- Calculating the mean gray-level within the specified sample area.
- Comparing the mean gray-level to the mean gray-level calculated for the sampled area on the reference image. If the two values differ the difference between them is calculated.
- Adjusting the gray-level thresholds used for feature detection accordingly.
- Returning to the next field in the Feature large area acquisition.

The in-run threshold adjustment is set up from the Microscope Setup mode to the right of the Feature steps:



The following sections describe how to:

- Set up an in-run threshold adjustment.
- View the results of an in-run threshold adjustment.

Setting Up In-Run Threshold Adjustment

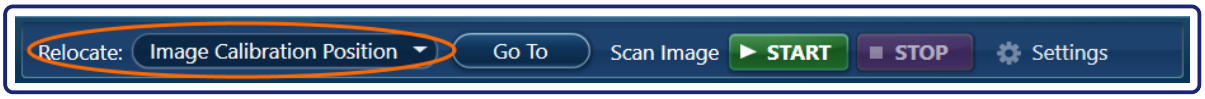
There are two parts to setting up an in-run threshold adjustment:

1. Selecting suitable image conditions and acquiring the reference image.
2. Defining the in-run threshold adjustment settings.

To select suitable image conditions and acquire a reference image:

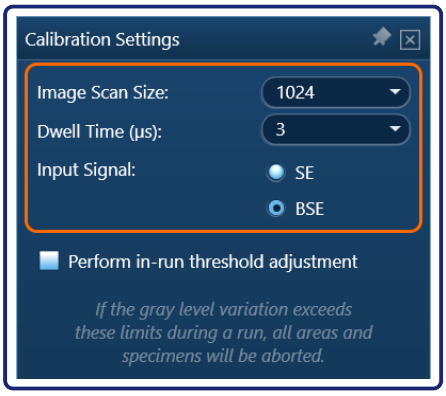
1. Select a suitable area of a sample or imaging standard to acquire images periodically throughout the large area run. The region of sample within the field of view should have mid-range gray-levels (i.e. not be saturated black or white) to ensure that any variation in brightness and gray-level is picked up.

   If the reference images are acquired from an imaging standard that is always mounted in the same position on the microscope stage, rather than manually relocating to it every time a reference image needs to be collected, the relevant stage position may be stored as a "Point" using the Automate wizard. To relocate to this "point", select the stored position from the "Relocate" drop down menu in the acquisition toolbar of the "Microscope Setup" step and click "Go To":



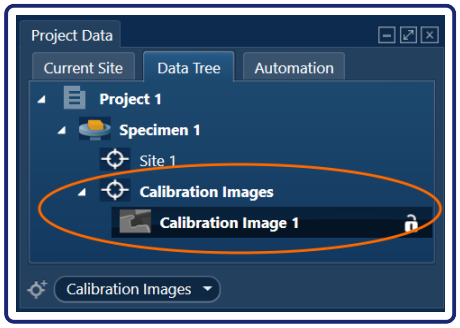
2. Open the "Calibration Settings" window by clicking on the "Settings" icon in the acquisition toolbar:

   Select suitable settings for the image acquisition:



   Typically the image settings should be optimized for speed while maintaining consistent noise and gray levels for constant beam conditions.

3. Click the "Start" button in the acquisition toolbar to acquire an electron image with the current settings. This will be the reference image, which is saved to the data tree:



The stage position, magnification and acquisition conditions for the image are also saved so that equivalent images can be acquired as part of the in-run threshold adjustment.

> ***NOTE:*** *If using a stored stage position and move away from this position before acquiring the reference image, the current stage position will be saved for the reference image and not the stored stage position.*

> ***NOTE:*** *If a project has more than one calibration image, the latest calibration image will be used.*

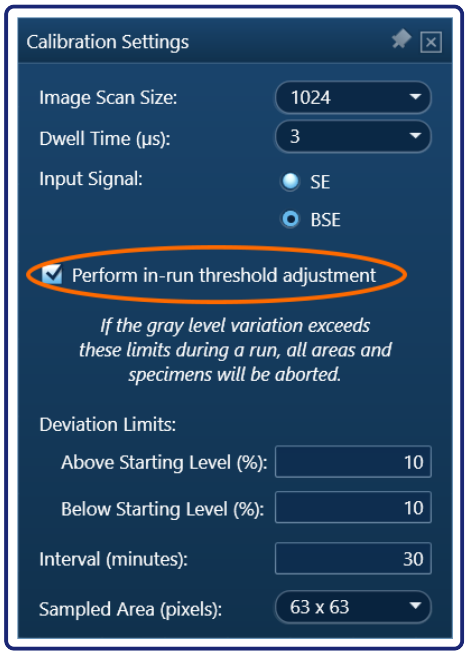
4. Select the Single Line Acquisition Tool from the toolbar on the left of the screen:

Draw a line over the image displayed in the image viewer pane. The in-run threshold adjustment uses the square box at the end of the line, rather than the line itself. It is important that this square box covers an area of the image that is not saturated black or white (this can be confirmed from the profile in the histogram) and that a consistent gray-level average value within the box can be achieved as long as the beam conditions and brightness do not change.

To define the in-run threshold adjustment settings:

1. Open the "Calibration Settings" window by clicking on the "Settings" icon in the acquisition toolbar:

2. Check the "Perform an in-run threshold adjustment" option:



The fields below this check box should now appear active as shown above.

3. Enter values for the deviation limits, as a percentage of the total gray-level range (0 - 32767).

These limits specify how much adjustment is allowed to be made to the gray-level thresholds before the run is canceled. The maximum allowed value is 100%, where the run will never be stopped.

> ***NOTE:*** *If one of the limits of one of the gray-level thresholds is either 0 (black) or 32767 (white), then this limit will not be adjusted when the threshold is adjusted, only the other limit will be adjusted.*

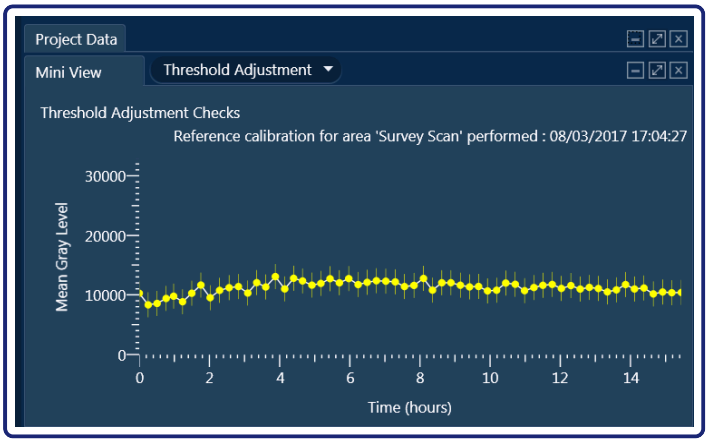
4. Enter a value for the interval in minutes. This value specifies how often the in-run threshold adjustment should be run.

   NOTE: *If this value is reached part of the way through a field, AZtec will continue to the end of the field before proceeding to do the in-run threshold adjustment. Once the adjustment has been completed AZtec will continue with acquiring the data for the next field in the Feature acquisition.*

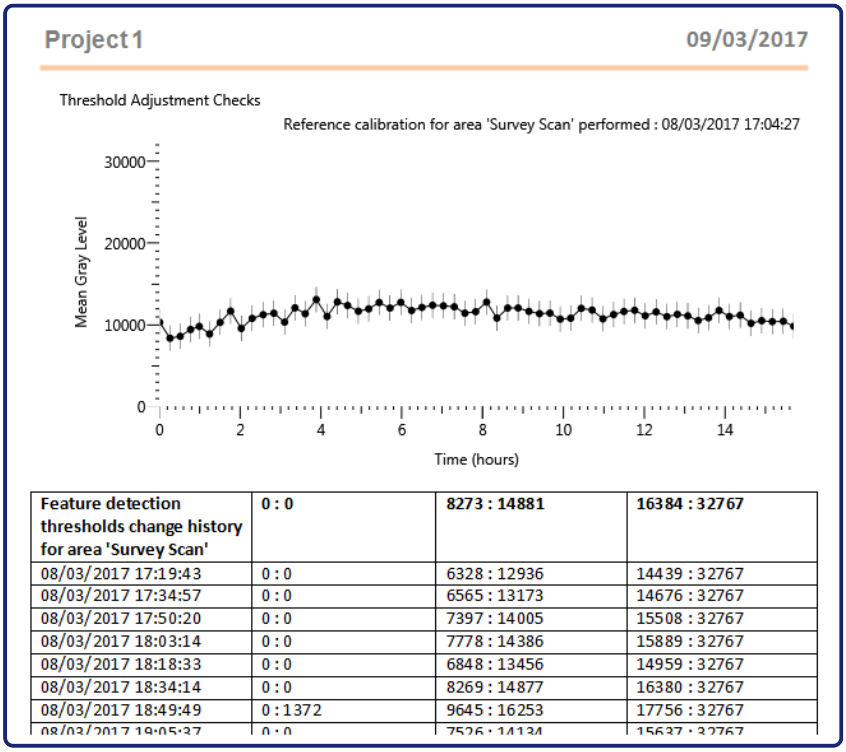
5. Select the size of the sampled area in pixels upon which the in-run threshold adjustment will be carried out (i.e. the size of the square box on the reference image). It is important that this box is large enough to have sufficient pixels to get a good average gray-level value.

View the Results of an In-Run Threshold Adjustment

The in-run threshold adjustment can be monitored from the Mini View "Threshold Adjustment" display:



The results of the threshold adjustment can also be seen in more detail via the dedicated report template:



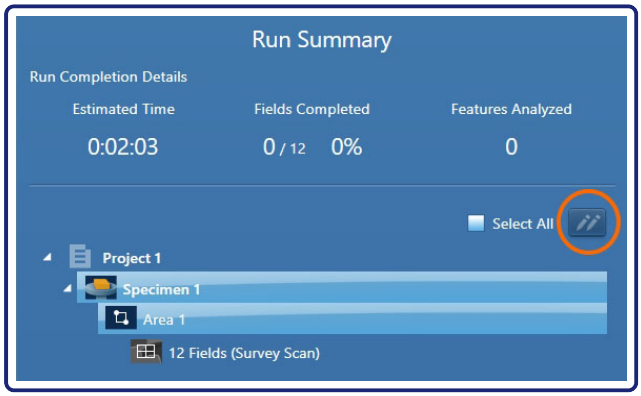
Feature detection thresholds change history for area 'Survey Scan'	0 : 0	8273 : 14881	16384 : 32767
08/03/2017 17:19:43	0 : 0	6328 : 12936	14439 : 32767
08/03/2017 17:34:57	0 : 0	6565 : 13173	14676 : 32767
08/03/2017 17:50:20	0 : 0	7397 : 14005	15508 : 32767
08/03/2017 18:03:14	0 : 0	7778 : 14386	15889 : 32767
08/03/2017 18:18:33	0 : 0	6848 : 13456	14959 : 32767
08/03/2017 18:34:14	0 : 0	8269 : 14877	16380 : 32767
08/03/2017 18:49:49	0 : 1372	9645 : 16253	17756 : 32767
08/03/2017 19:05:37	0 : 0	7526 : 14134	15637 : 32767

2.6.5. Modifying Feature Large Area Acquisition Settings

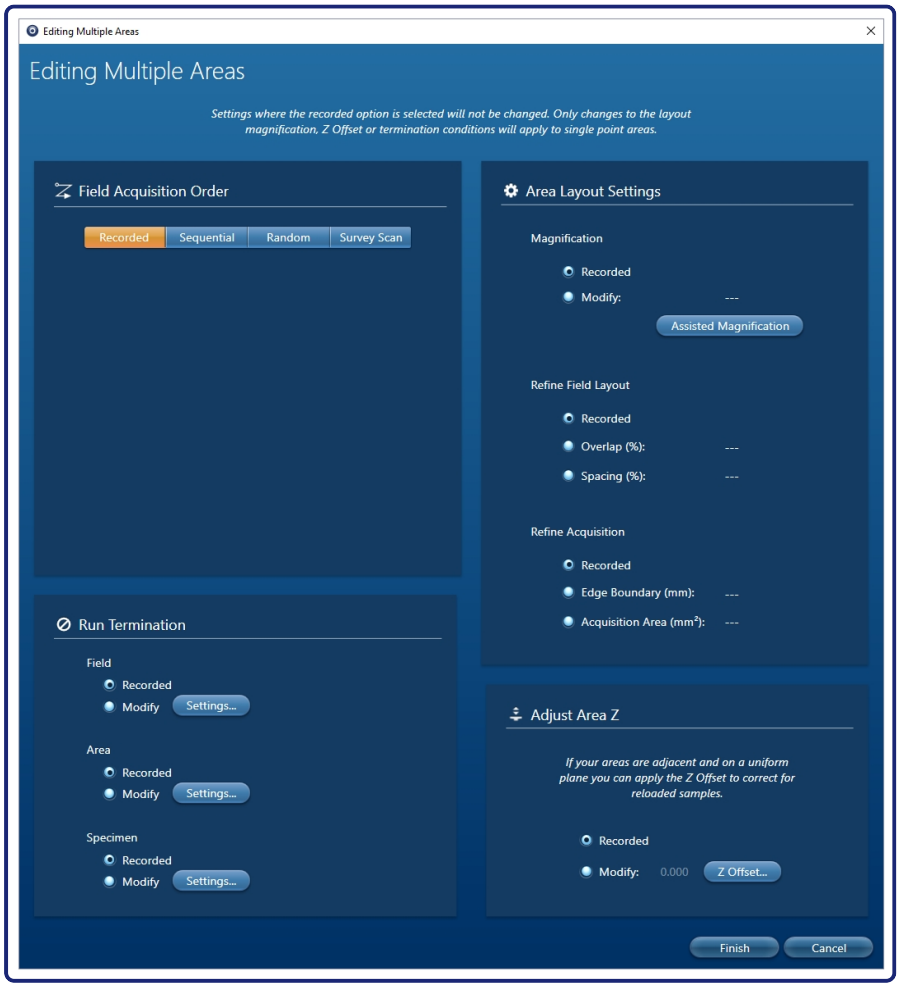
When a Feature Experiment is created, it takes the settings that are current at the time. To change any of these settings after the Feature experiment has been created, for example to change the survey scan magnification and dwell time or the edit termination conditions:

- Delete the experiment, change the settings and then recreate the experiment.
- Use the "Editing Multiple Area" window which can be accessed from the Run Summary.

To use the "Editing Multiple Area" method, in either the "Run Summary" or the Data View, select the areas for which the settings are to be edited. This may be one area or several, and then click the edit icon:



This will open the "Editing Multiple Area" window:



This window can be used to view and edit the settings for:

- The field acquisition order.
- The termination conditions.
- The area layout settings.
- The z offset.

For any settings that are not to be edited, select the "Recorded" option.

Any settings that are changed will affect all of the areas that were selected when opening this window.

When happy with the settings, click the Finish button to save the changes and close the "Editing Multiple Areas" window.

Field Acquisition Order

Change the field acquisition order by choosing between the "Sequential", "Random" and "Survey Scan" options. When the Survey Scan option is selected, the current survey scan settings will be displayed and can be edited. For more information on the different field acquisition orders see the Feature Automation Run Settings and Prioritizing Fields with the Highest Number of Features sections.

Run Termination

Change the termination conditions for a field, area or specimen by selecting the "Modify" option and then clicking the relevant "Settings" button. This will open the run termination settings window for the field, area or specimen. Modify the termination conditions and then click "Close" to make the changes, close the run termination settings window and return to the "Editing Multiple Areas" window. For more information on termination conditions see the Termination Conditions section.

Area Layout

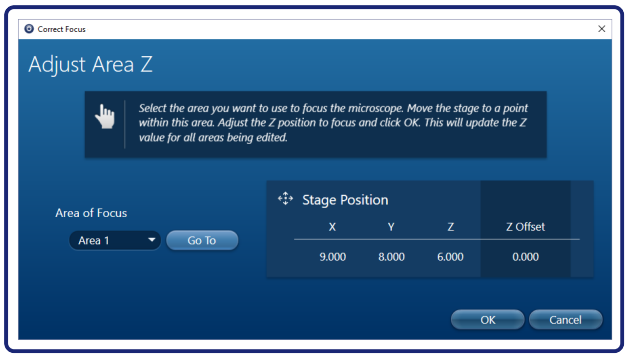
Use the area layout section to modify the settings for the acquisition area by changing:

- The magnification on the microscope.
- The assisted magnification where the magnification is calculated based on the minimum size feature that you would like to resolve and the number of pixels that it must have.
- The amount of overlap or spacing between fields.
- The size of the edge boundary, which is used to specify a border inside the defined area, from which you do no wish to collect data.
- The acquisition area, which is used to define a specific size area around the center of the automation area to acquire data from.

For more information on defining field spacing, using edge boundaries and acquisition areas, see the Area Layout section in Feature Layouts.

Adjust Area Z

Apply a z position offset to the selected areas, by selecting the "Modify" option and then clicking the "Z Offset..." button. This will open the "Correct Focus" window:

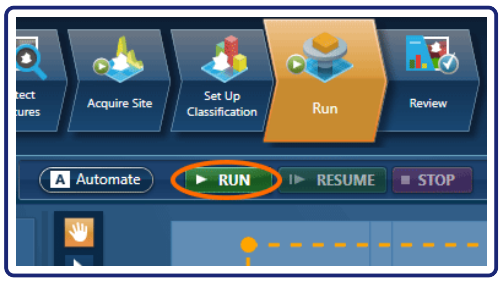


1. If editing multiple areas, select the "Area of Focus" for which the z stage position is to be edited from the drop down menu.
2. Click "Go To" to automatically move the stage to the center of the area or manually move the stage to a point within that area.
3. Adjust the z position to bring the sample into focus.
4. Click "OK" to submit the new z position. The software calculates the difference between the original z position and the new z position and applies that value to all areas.

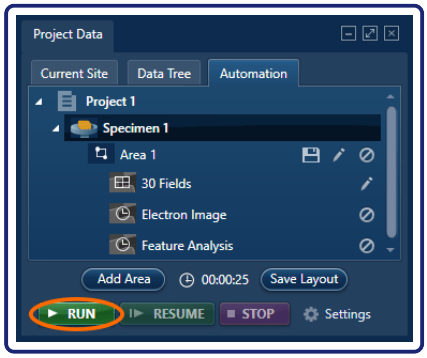
2.6.6. Acquiring Large Area Data

Once a AZtecFeature large area acquisition has been defined and optimized, the data may be acquired by either:

- Clicking Run on the acquisition toolbar of the navigator step:



- Clicking Run from the bottom of the Automation tab in the Project Data pane:



The microscope will move to the first position and start acquiring the data for that field.

The large area acquisition may be stopped at any time by clicking the "STOP" button in either the acquisition toolbar or the Automation tab of the Project Data pane. The button will flash "STOPPING" and the acquisition will stop when it reaches the end of the current field.

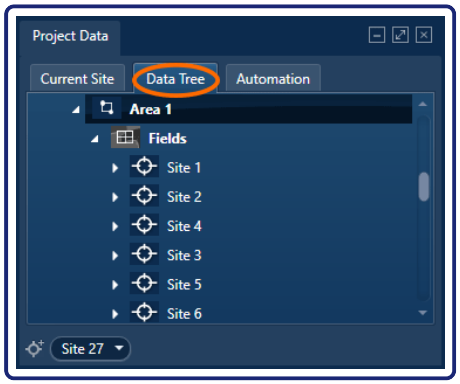
To stop the acquisition immediately, click the "STOP" button twice.

The acquisition can be continued by clicking the "RESUME" button in either the acquisition toolbar or the Automation tab of the Project Data pane. The acquisition will resume with the next field for which no data has been acquired.

The data for a partially acquired field, or for a field in which the data does not appear acceptable (i.e. it has a different brightness due to fluctuations in the beam current, or appears black due to a blown filament) may be reacquired by deleting the "bad" fields and then resuming the acquisition, so that the fields are acquired again.

The "bad" fields may be deleted from either:

1. The Data Tree tab in the Project Data pane:



   - Select the "bad" site.

     NOTE: *To select multiple sites, hold down the Ctrl key on the computer keyboard while selecting the sites.*

   - Right click the site and select the delete option from the context menu.

2. The Review navigator step by:
   - Selecting the "Move and Select" tool from the palette toolbar.
   - Clicking on the field in the Image pane.
   - Pressing delete on the computer keyboard.

   NOTE: *To select multiple sites, hold down the Ctrl key on the computer keyboard while selecting the sites.*

Once the fields have been deleted, select the "RESUME" option from either the acquisition toolbar or the Automation tab of the Project Data pane. The fields will now be reacquired.

NOTE: *In order to reacquire the data for a field, the data must be reacquired immediately after the large area acquisition has been stopped or has completed. If any changes are made to the area or layout, the experiment settings or the project is closed and reopened, then the fields may no longer be reacquired.*

2.7. Processing Feature Data

Once the Feature data has been acquired there are a number of ways in which it can be processed, including:

- Requantifying the data.
- Separating the phases.
- Reconstructing features.

> ***NOTE:*** *If either threshold or full field phase detection has been used, separate phases should be run before reconstructing features.*

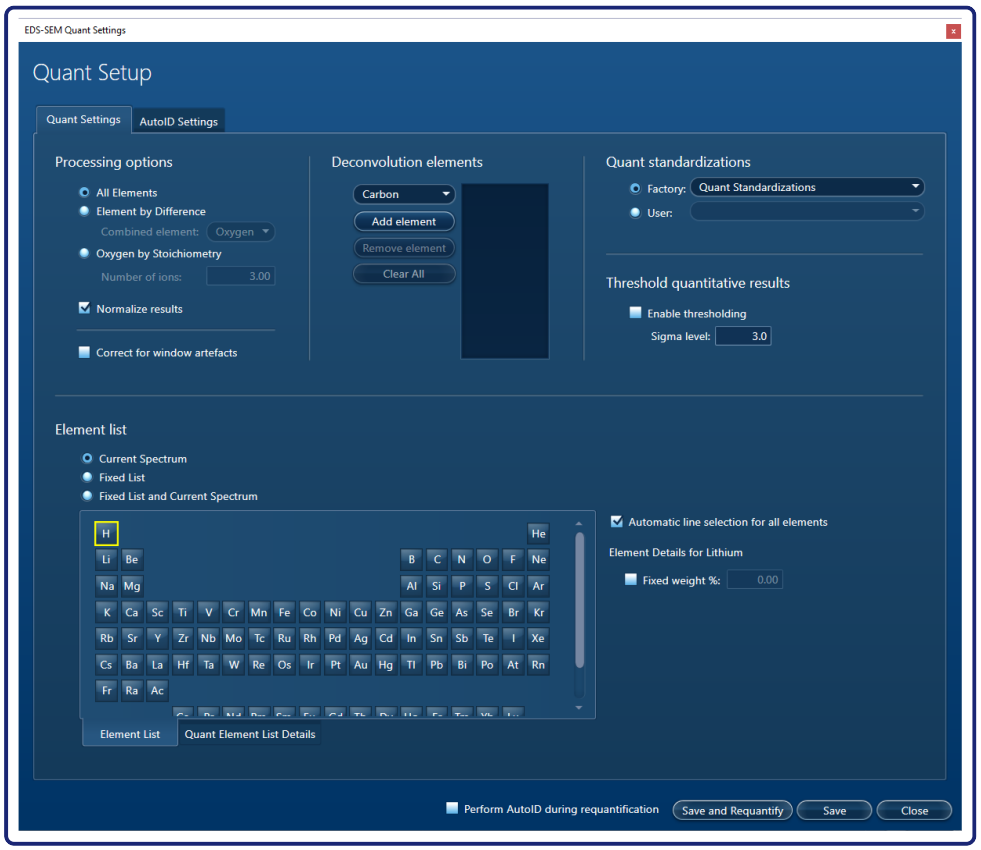
2.7.1. Editing the Quant Settings

As AZtecFeature acquires the EDS data, it quantifies the EDS spectrum for each feature using the current quant settings. The result is displayed in the feature data viewer data table and is used to determine whether a feature meets the criteria to be accepted or rejected into a class or by a filter. Once the acquisition has completed, it may be necessary to adjust the quant settings.

To change the Quant Settings:

1. Click on the "Quant Setup" button in the acquisition toolbar of the "Review" step:

2. This will open the standard EDS Quant Settings window where the quant settings can be edited:



2. Make any changes to the quant settings. For more information on the quant settings that you can edit, see the Quant Settings section.
3. Select whether or not to "Perform AutoID during requantification".
4. Click "Save and Requantify" to save the new quant settings and requantify all of the feature data or click "Save" to save the quant settings and close the quant setup window without applying the changes to the data.

NOTE: *Once the quant settings have been edited and the data requantified, it is recommended that if applicable, the phase separation and reconstruct feature processing options are re-run as the quant settings might affect the result of these processing tools.*

2.7.2. Separating Features Using Phase Data

If either threshold phase detection (see Separating Phases with Similar Gray-Levels into Individual Features) or full field phase detection (see Separating Features from Backgrounds with Similar Gray-Levels) has been used, when the EDS part of the large area acquisition is run, the EDS data is collected and temporary features are extracted from the phase maps. However, the data is not processed with AutoPhase until the end of the run. This is because in order to run, AutoPhase needs to know all of the elements that are present in all of the fields.

When setting up to acquire a large area feature dataset with either threshold phase detection or full field phase detection, it is possible to either:

- Run the phase separation automatically at the end of the acquisition.

  This is the default method and is specified from the settings menu on the "Run" step as described in the Feature Automation Run Settings section.

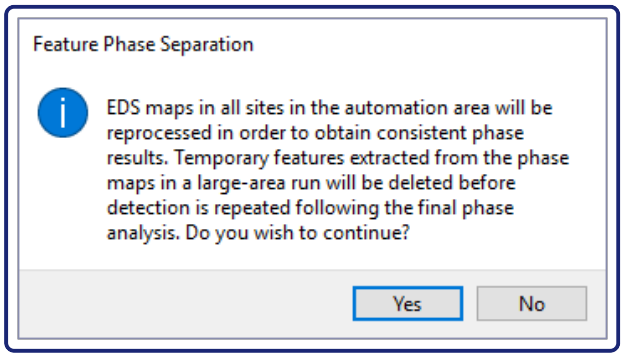
- Manually run the phase separation after the run has completed.

  This method may be more suitable if there is a very high field count or number of areas that have been acquired. It allows any alignments and processing to be performed after all of the data has been acquired. It may also be used if some changes have been made to the quantification settings that could affect the phase separation.

To trigger the manual AutoPhase detection:

1. On the "Review" step, click the "Phase Separation" button in the acquisition toolbar:

   If phase separation has not already been applied, this will open the "Feature Phase Separation" warning window:



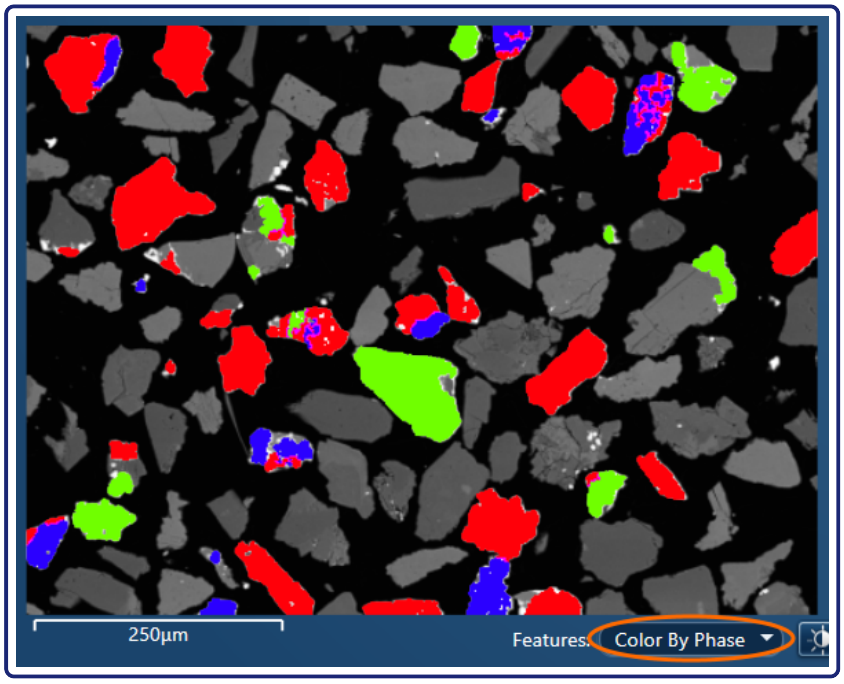
2. Click "Yes" to reprocess the data using AutoPhase. Click "No" to cancel.

   If phase separation has previously been run on the dataset, the phase separation will automatically run without any prompt.

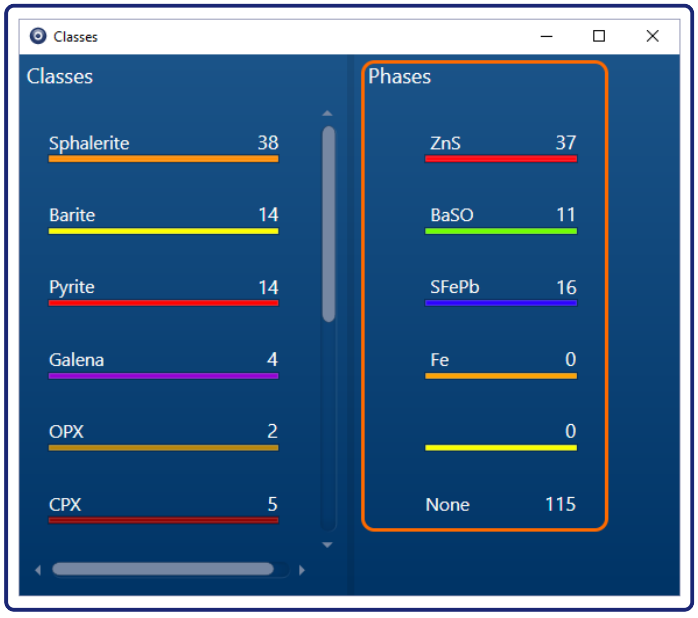
   As the phase separation progresses a progress bar is displayed in the acquisition toolbar showing the current progress of the phase separation:

The results of the phase separation can be viewed:

- On the electron image, using the "color by phase" coloring:

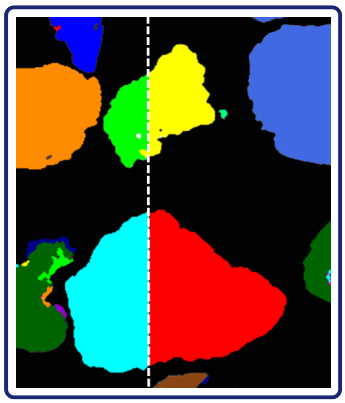


- In the phases list below the feature data viewer:



2.7.3. Reconstructing Features Across Fields

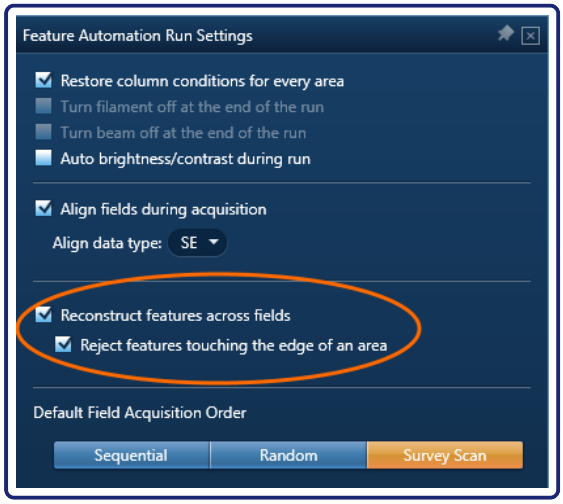
During a feature acquisition, if a feature is located in more than one field, it is counted and analyzed as multiple separate features (one feature per field that the feature is found in). This can give misleading results, because, especially for very large features, the same feature can be counted multiple times and the morphology information for that feature will be incorrect. An example of how features located in multiple fields are treated as separate features is shown by the image below. The features are displayed using "Color by Feature" coloring (available in the Review step) and the field boundary is marked by the white dashed line:



AZtec has the ability to reconstruct these features as single features either:

1. Automatically at the end of the acquisition from the "Run" step.
2. Manually from the "Review" step.

To run feature reconstruction automatically at the end of the acquisition from the "Run" step, select the “Reconstruct Features Across Fields” option in the "Feature Automation Run Settings" window which is accessed from the settings icon in the "Automate" toolbar. If "Auto Align" has also been selected, the reconstruction will be done after the automatic field alignment.



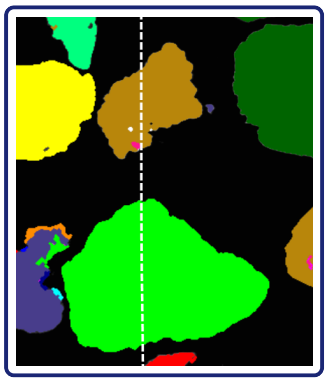
To run feature reconstruction manually from the "Review" step, click the "Reconstruct" button in the toolbar after doing any field alignments. This method should be used if you select to do manual field alignment, for example, because you have a very high field count.

When the feature reconstruction is run, any features in two (or more) separate fields that touch each other and either:

- belong to the same gray-level threshold
- have the same phase if one of the phase feature detection methods has been used

are reconstructed as a single feature. The constituent features that make up the large feature are rejected and a new feature with a new feature Id is created to represent the feature as a whole. The EDS data for each of these constituent features is weighted according to their area and combined. For each new feature, the morphology is measured, Auto-Id run, and the feature quantified and classified.

The image below shows the results of running the reconstruction on the image above. The features are displayed using "Color by Feature" coloring and the field boundary is marked by the white dashed line:



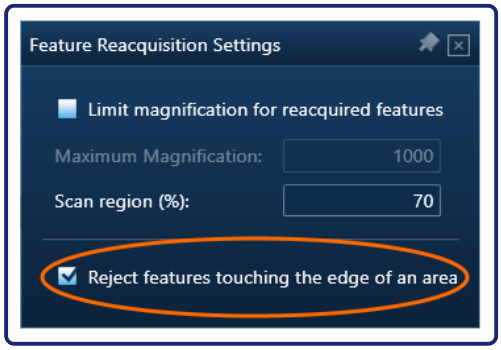
In the original image, before reconstruction, the features appeared in different colors in each field signifying that they are treated as separate features. After reconstruction, the same features appear as single larger features in a single color.

Rejecting Edge Touching Features

When reconstructing features, there is also the option to choose to automatically "Reject features touching the edge of an area". When this option is selected, the feature reconstruction is performed and then any features that are found to touch the edge of the acquisition area are rejected.

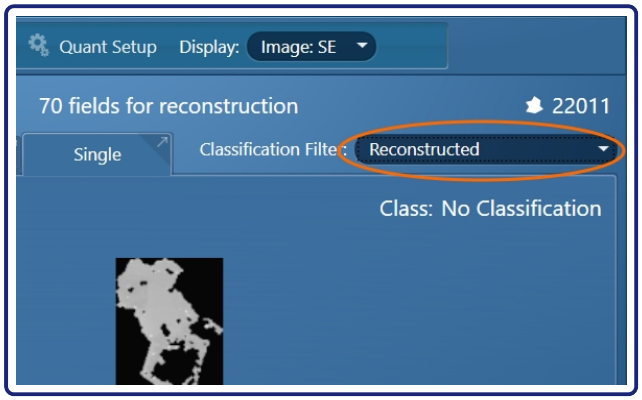
To reject edge touching features either:

- In the "Run" step, check the "Reject features touching the edge of an area" option which is available when the “Reconstruct Features Across Fields” option is selected in the "Feature Automation Run Settings" window.
- In the "Review" step check the "Reject features touching the edge of an area" option which is available in the Settings window.



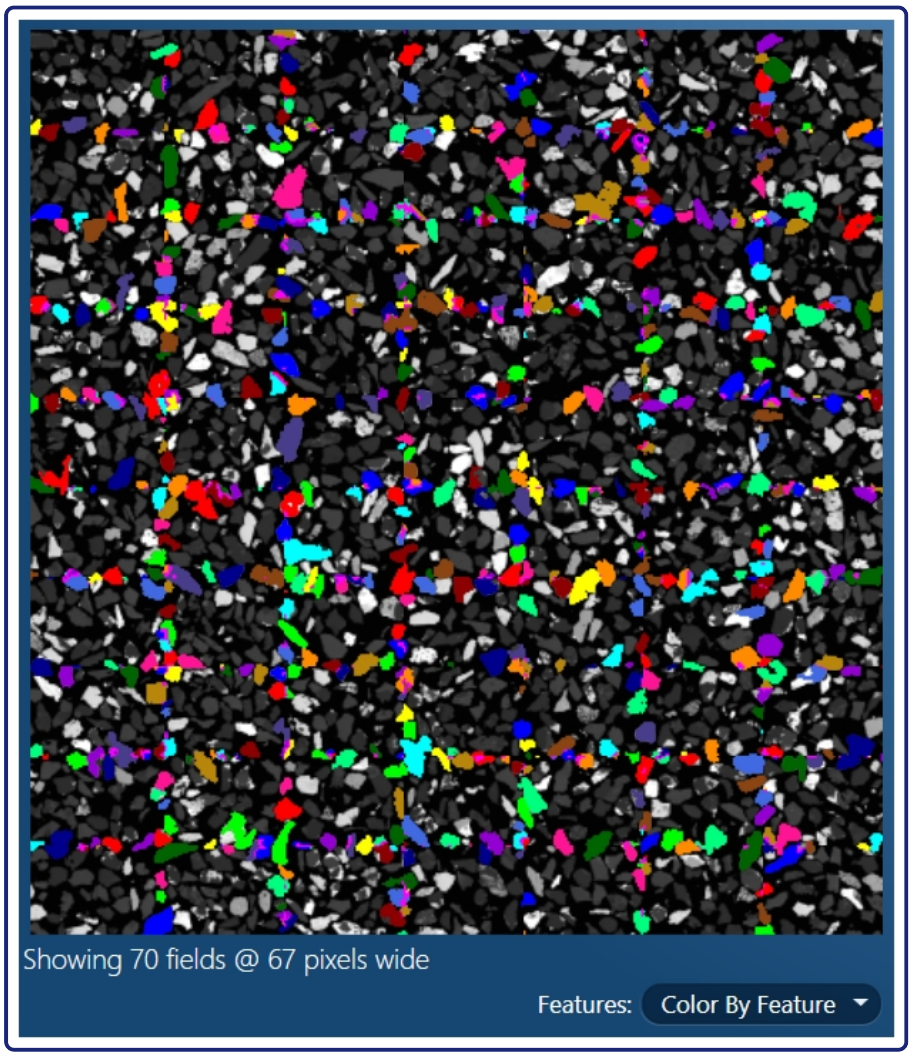
Viewing the Results of Feature Reconstruction

To view the results of the feature reconstruction, select the "Reconstructed" option from the classification filter drop down menu:



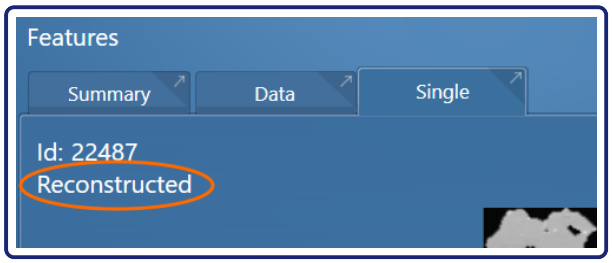
This option, will filter the entire dataset so that only the features that have been reconstructed are displayed.

For example, in the image below, only the reconstructed features are shown in "Color by Feature" coloring overlaid on the BSE electron image.



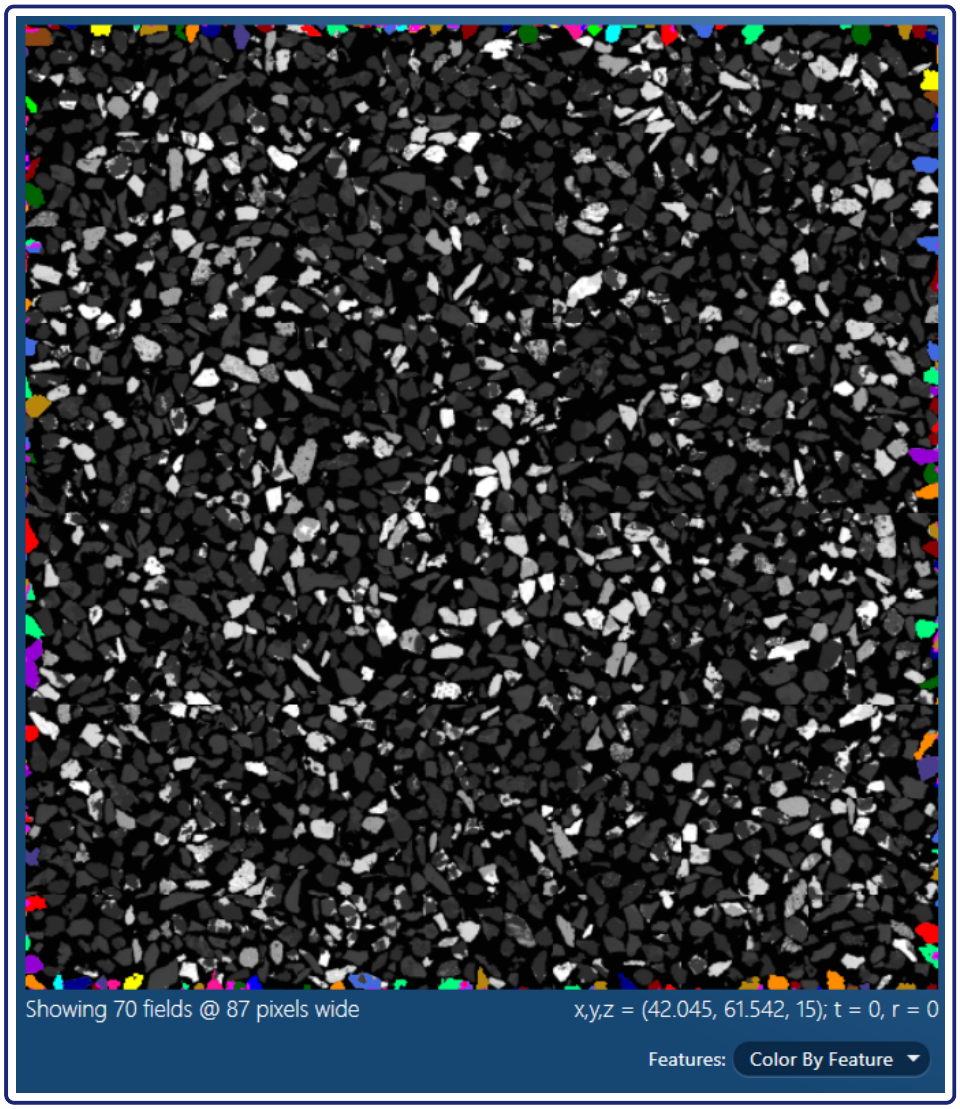
This type of data display can be useful for confirming the features that have been affected by the feature reconstruction and that the results are acceptable.

It is also possible to verify whether an individual feature has been reconstructed from the "Single" Features tab:



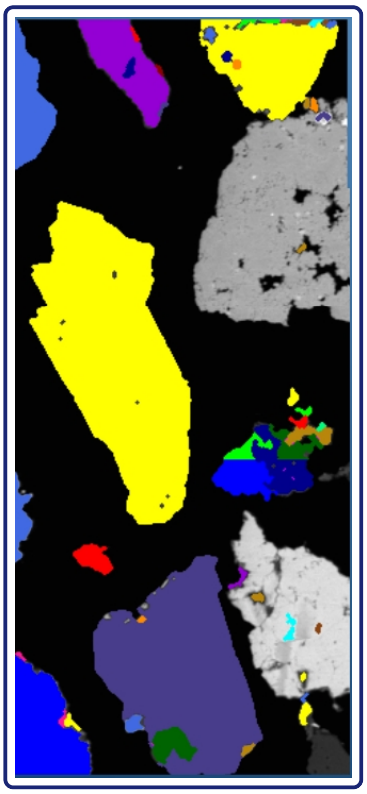
To view only the features that have been rejected for touching the edge of the acquisition area select the Rejected (Touching Edge) option from the classification filter drop down menu. This can be useful for visualizing the effects of the edge touch rejection filter and ensuring that the results are acceptable.

The data displayed in the "Summary" and "Data" tabs and in the image is updated to only include the rejected features. For example, in the image below, only the rejected features are shown in "Color by Feature" coloring overlaid on the BSE electron image.



The results of rejecting edge touching features can also be visualized in the image on the "Review" step by selecting the "Reconstructed" option from the classification filter drop down menu and using the "Color by Feature" coloring:

Features detected during acquisition



Features after feature reconstruction and edge touch rejection

2.8. Interrogating Feature Data

Once all of the feature data has been acquired it can be viewed, interrogated and analyzed. This is most commonly done from the "Review" step, where if the feature data was acquired over a large area, the entire area can be viewed and considered. However, the data for a single site can also be interrogated from the "Set Up Classification" step.

This section of the help describes the typical steps followed when interrogating Feature data, including:

- Viewing the data to:
  - Identify trends and outliers in the data.
  - Create classes based on the trends observed in the data.
  - Confirm that the classes defined in the loaded classification scheme are correct.
- Filtering the data to focus on specific features:
  - Highlight features of interest for further evaluation.
  - Reject features that are observed to be outliers from the analysis.
- Further evaluation of specific features.
  - Relocating to a feature for further non-feature investigation.
  - Reacquiring the data for a feature.

2.8.1. Viewing the Data

Within AZtecFeature, the data is updated dynamically and can be reviewed as it is acquired. There are numerous tools for visualizing and interrogating the data, allowing any measured parameter to be plotted and reported. They include:

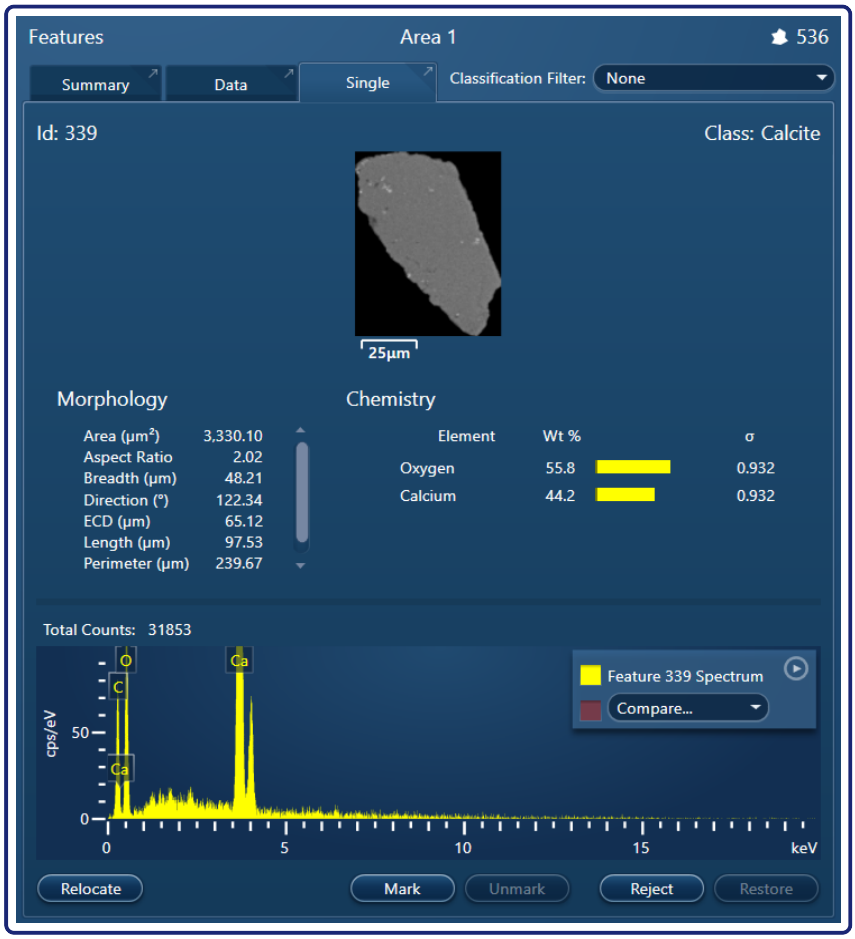
- Feature Data Viewer, Summary tab: The data for a number of features can be viewed using a number of different plots such as using quant bars. These charts can be particularly useful for identifying trends and outliers in the data.

- Feature Data Viewer, Data tab: The data for a number of features can be viewed in table form. This table is useful for viewing a summary of the data in table form for all features.

Id	Class	ECD (µm)	Count	O Wt%	Na Wt%	Mg Wt%	Al Wt%	Si Wt%	P Wt%	S Wt%
2	Quartz	21.50	40353	53.95			0.99	45.07		
3	No Classific	6.57	26362	47.55		11.30	3.89	5.63		3.65
4	Quartz	19.05	33757	47.85		0.92	2.79	44.18		1.13
5	Calcite	52.09	30184	55.62			0.68			0.50
6	No Classific	38.07	33513	40.15		2.53	8.47	18.01		12.43
7	Calcite	44.38	29030	55.29						
8	Quartz	56.88	38214	53.40				43.58		
9	Quartz	33.73	37612	52.86				47.14		
10	Feldspar	23.67	32246	48.78	7.80		10.99	30.97		
11	Quartz	56.69	37988	52.08				47.92		
12	Dolomite	25.95	25666	55.84		14.06		0.88		
13	Quartz	27.38	35056	51.96				38.28		3.42
14	Dolomite	16.39	27896	52.36		11.90				3.78
15	OPX	41.71	34594	48.06	0.88	1.16	11.54	29.07		2.07
16	Dolomite	15.32	25392	51.49		12.30		0.98		0.92

Min	4.44	1.59	0.52	0.41	0.39	0.45	0.55	0.40
Max	101.08	61.82	8.79	16.09	19.17	55.11	0.90	56.19
Mean	33.44	40.80	4.91	5.16	6.38	25.68	0.74	20.51
Std Dev	21.84	17.45	2.93	5.13	4.68	16.59	0.17	17.26

- Feature Data Viewer, Single tab: The data for a single feature can be viewed in detail.



- Electron image: The features can be colored according to different criteria (for example by class). This is useful for visualizing the spatial distribution of different types of features.

Identifying Trends and Outliers

There are numerous ways of viewing feature data with the Feature Data Viewer to identify trends and outliers. Some typical methods include:

- **Histograms:** Shows how the features are grouped.

  This chart type is particularly useful for seeing distributions of features in the morphological or EDS data.

- **Scatter plots:** Highlights trends and outliers in the data being plotted.

  This chart type is particularly useful for visualizing and selecting features with particular characteristics. For example, for selecting features that are deemed to be interesting or that appear to be outliers that should be rejected and excluded from the general analysis.

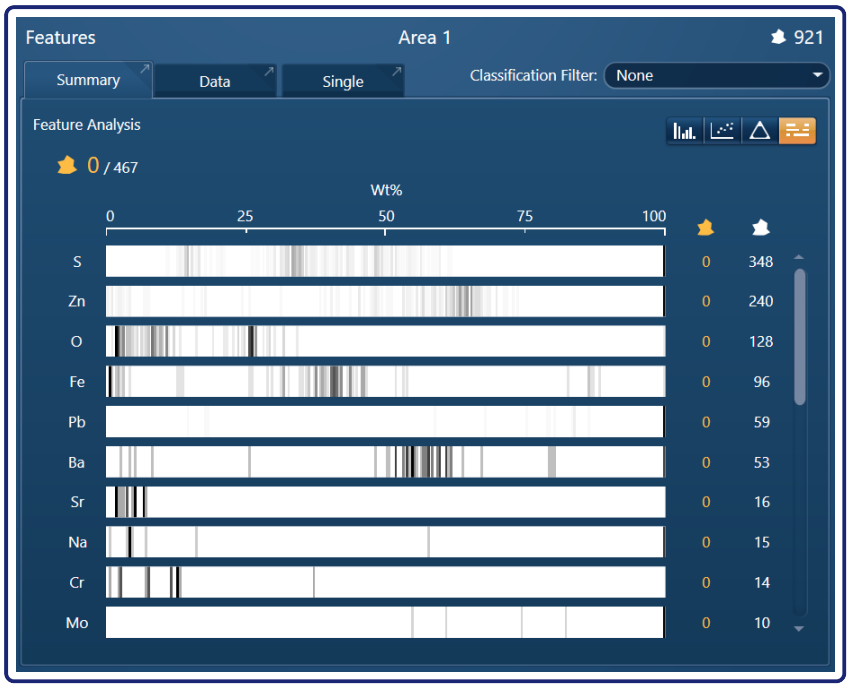
  It is also useful for visualizing trends and selecting features with similar characteristics (i.e. all features which contain a certain element and have an area within a certain range).

- **Ternary plots:** Displays the proportion of three variables that sum to a constant.

  This chart type is useful for visualizing data where more than two elements are being examined.

- **Quant distribution chart:** Shows the distributions in chemistry for all elements at the same time.

  This chart type is useful for visualizing how the elements in the sample relate to each other on a feature by feature basis:



This chart can be useful for selecting all features with a particular composition. For example, all features with a similar Wt% of an element (i.e. 60% zinc) could be selected and then all features which also have another element in a certain range (i.e. >10% oxygen) could be deselected.

It can also be useful for identifying the populations of features within the sample.

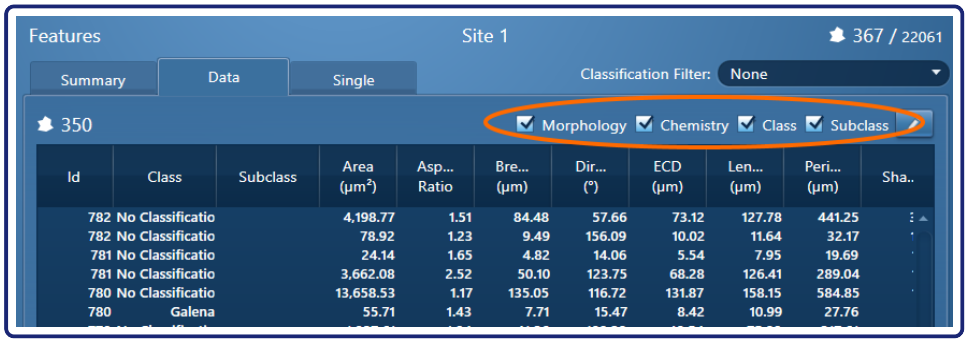
Sorting Data Using the Data Table

The data table is used to display all of the feature data at once:

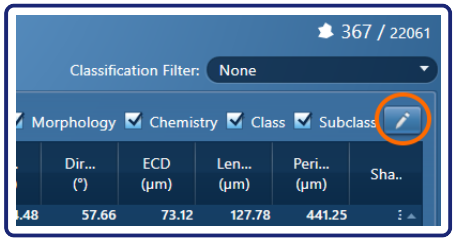
The types of data to be displayed in the main table can be specified using the:

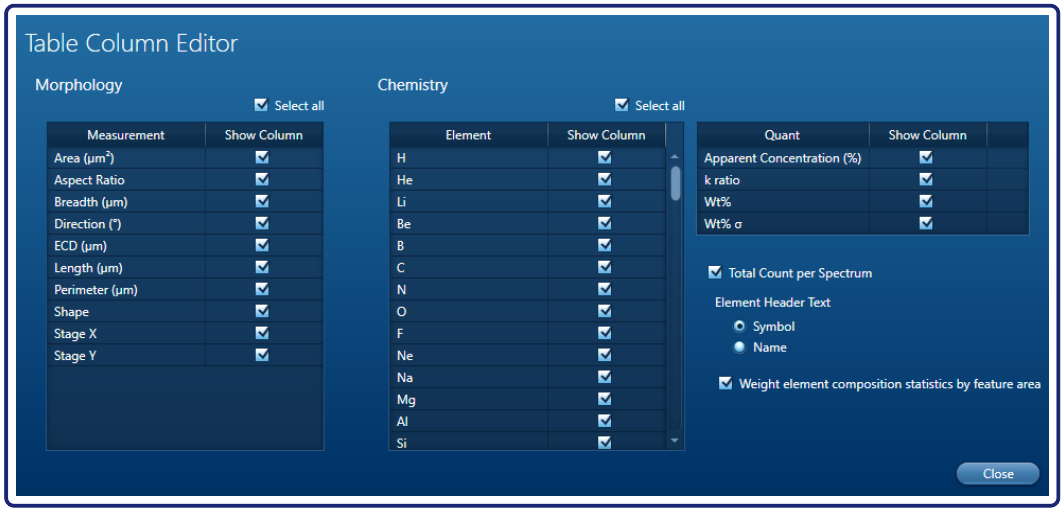
- Classification Filter drop down menu:

- The check boxes immediately above the main table:

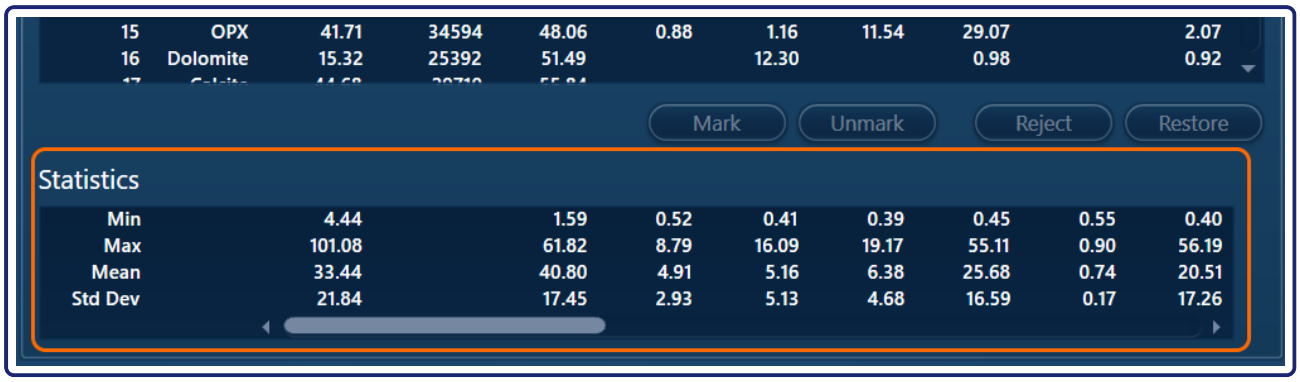


- The Table Column Editor:





Below the main data table are the statistics for the data displayed in the main data table:



The data table can be particularly useful for sorting data by a particular parameter (for example, to sort features by class, area or by the presence of a particular element). To sort the table by a particular parameter in alphabetical or ascending order:

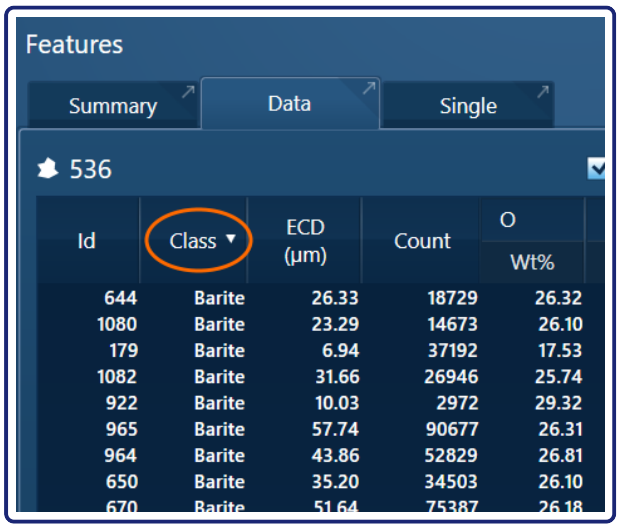
- Click on the column header for that parameter.

  A down arrow will be displayed in the column header to show that the data in the table has been ordered in terms of that parameter in ascending or alphabetical order.

- To reverse the sort order, for example to use descending order, click the column header a second time.

  The arrow displayed in the column header will now point upwards to demonstrate that this is the sort order being used.

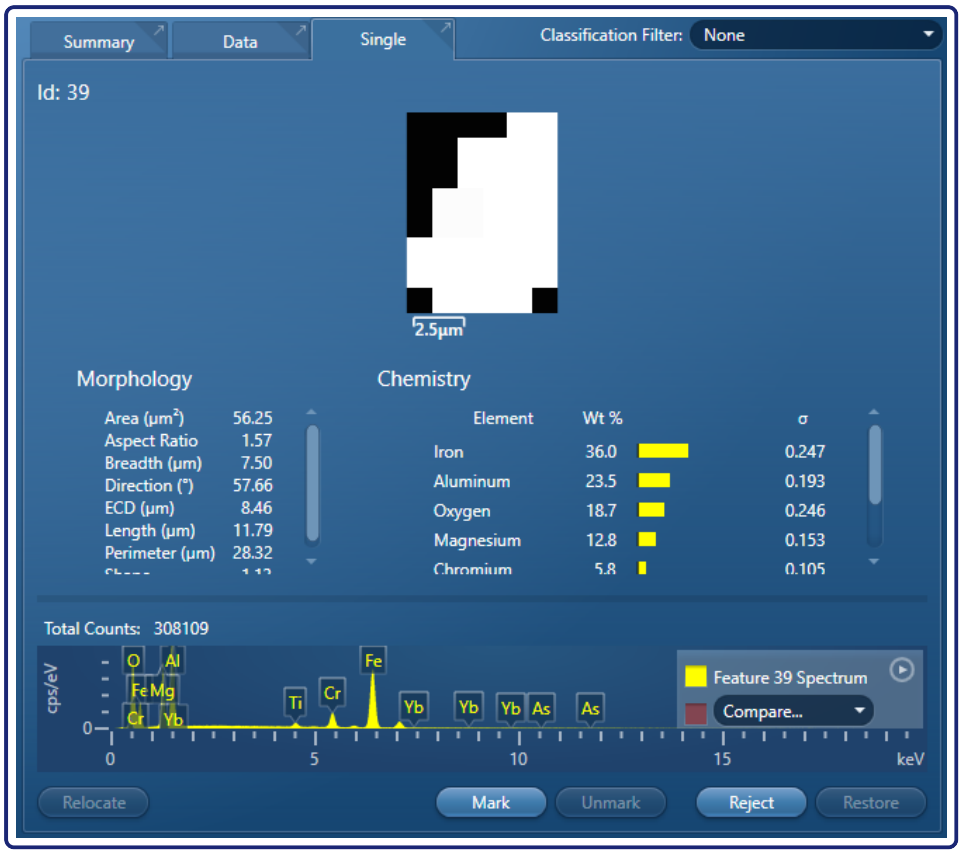
For example, to sort the data by class (in alphabetical order), click the class column header once. The data in the table will now be sorted according to this parameter and a down arrow will be displayed in the column header to indicate that this is the case:



When the data for one or more features is selected in the data table, the corresponding features are highlighted on the electron image. This can be useful for visualizing the size and position of the features that the data corresponds to.

Visualizing Single Feature Details

The "Single" tab in the feature data viewer displays the feature image, the morphological and quantitative data and the EDS spectrum for a particular feature.



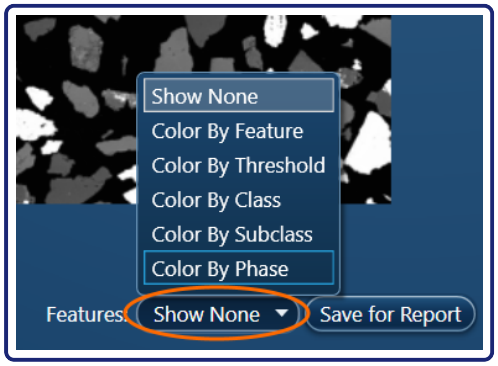
Some examples of where this information is useful is for:

- Seeing the detailed data for a feature.
- Creating and editing classes based on the feature data.
- Determining why a specific feature does or does not meet the criteria of a specific class.

When the data for a feature is selected in either the data table or from the electron image, the corresponding feature details are displayed on the Single tab. This can be useful for fully interpreting the data for the feature by linking its morphological and EDS data with the size and position of the feature in the electron image.

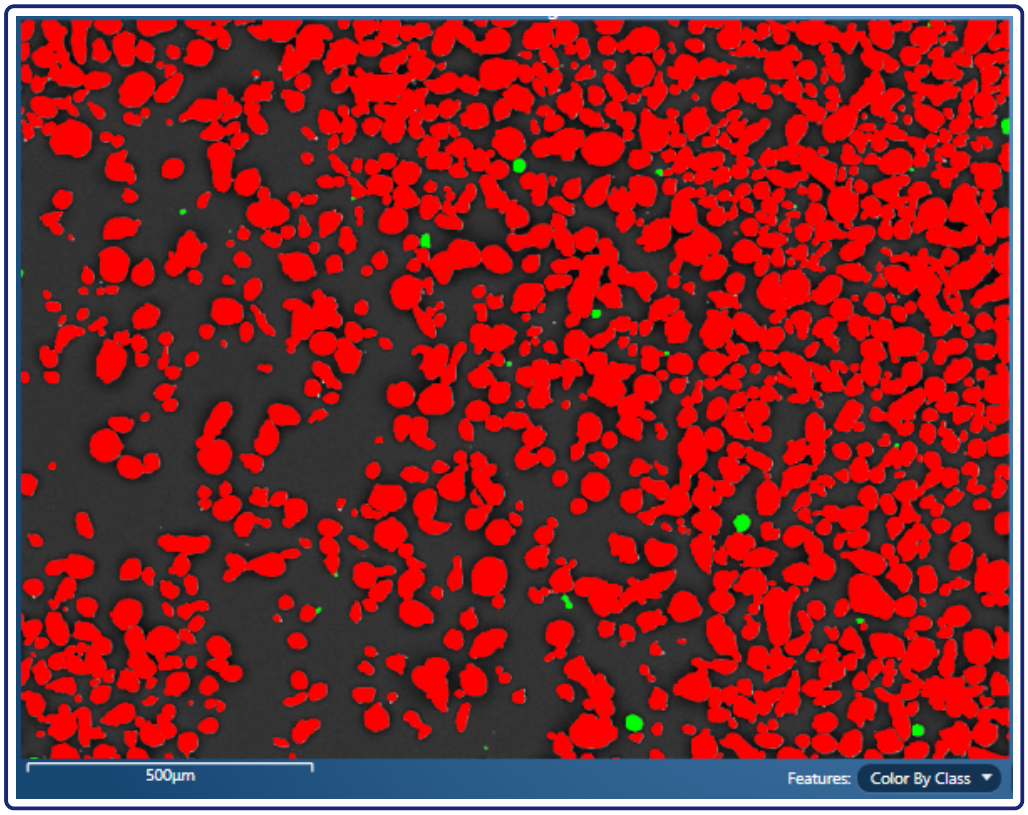
Visualizing Trends in Physical Space

The electron image allows the location of the different features on the sample to be visualized. The feature "Color by" drop down menu below the electron image is used to specify which characteristics (i.e. class or phase) the features should be colored by:



This coloring allows different feature trends to be observed in physical space.

For example, in a sample where all features should contain aluminum and silicon within a certain ratio, if a class is created with this definition (red color), then it is possible to select "color by class" and see which features do not fit this class (green color) and whether they are distributed evenly across the sample:



The select feature tool may then be used to select each of the features that do not fit the class in turn so that their details can be viewed within the feature data viewer and it can be determined why they do not fit the defined class.

2.8.2. Selecting Features from the Different Data Views

Depending on the way in which the data is being viewed there are different methods available to select data. Once the features have been selected, it is possible to:

- Look at the selected features using the different data views to gain a better understanding of the data.
- Relocate the stage to the feature, so that it may be examined in more detail (i.e. at higher magnification).
- Use assisted criteria creation to create a class based on the selected features.
- Reject the selected features.

The ways in which the features can be selected include from:

- The electron image.
- The Summary tab.
- The data tab.

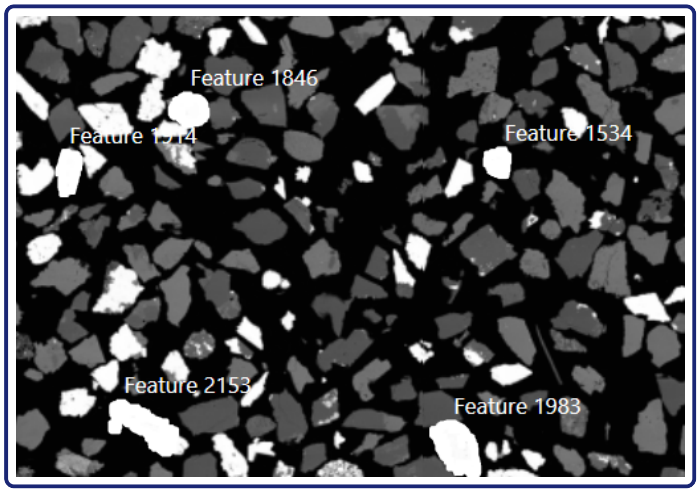
Select Features from the Electron Image

To select features from the electron image:

- Select the select feature tool from the toolbar on the left of the screen:

- Click on a feature on the electron image to select it. To select multiple features hold down the "Ctrl" key on the computer keyboard and click on all of the features to be selected. The selected features will be highlighted in the electron image:

  The corresponding rows of data for the selected feature(s) will also be highlighted in the data table.

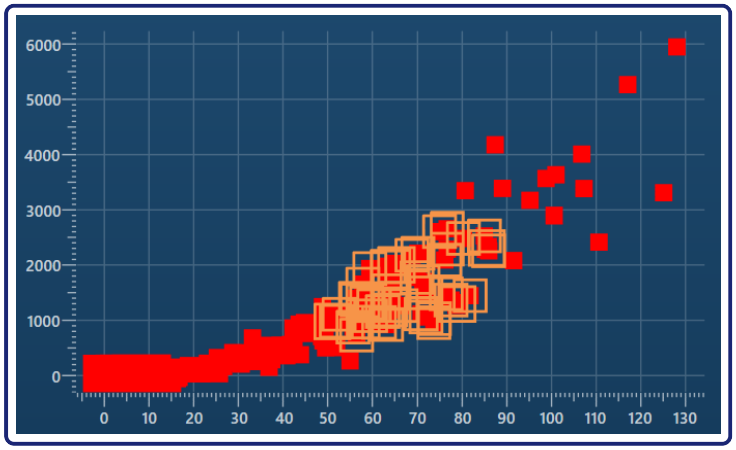
Select Features from the Summary Tab

Features can be selected from the scatter plot, ternary plot and quant bar chart types.

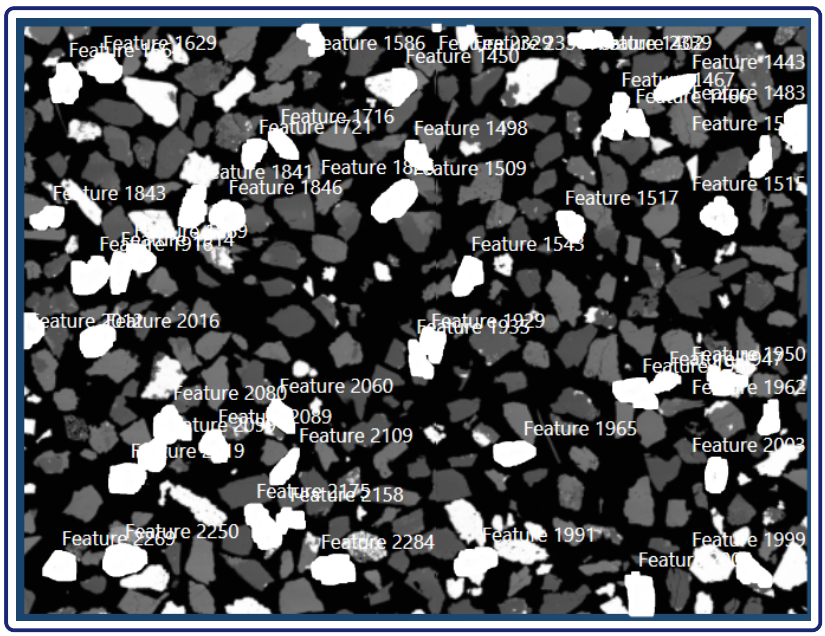
To select data from the scatter and ternary plots:

- Hold the "Ctrl" key down on the computer keyboard and then press the left mouse button down.
- Drag the mouse over the range of data to be selected.
- Release the "Ctrl" key and left mouse button to complete the selection.

The selected features will be highlighted on the plot:



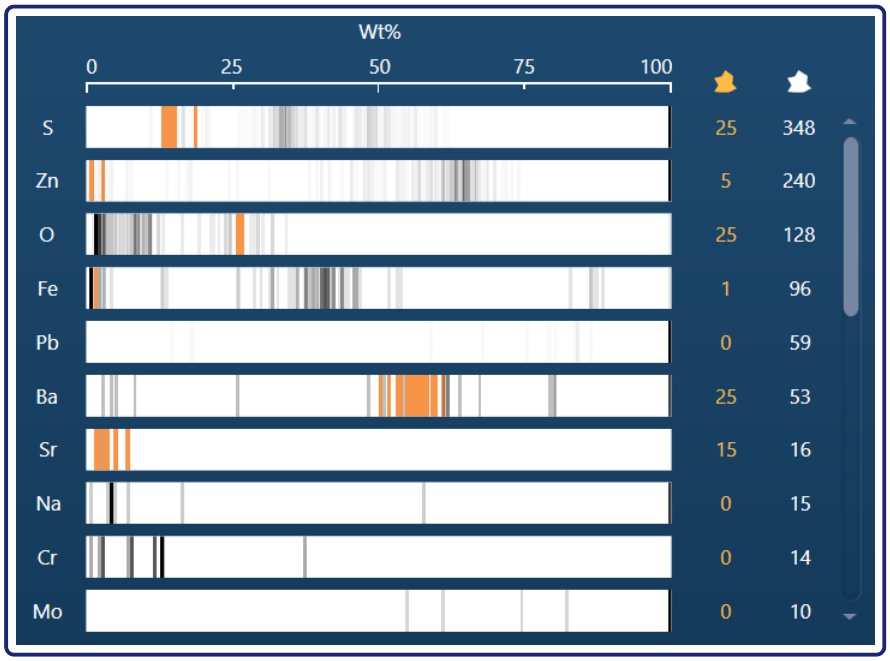
They will also be highlighted on the electron image:



To select a single range of data for a specific element on the quant bar plot:

- Press the left mouse button down and drag the mouse over the range of data to be selected.
- Release the left mouse button to complete the selection.

  The selected data range will be highlighted in orange for all of the elements present in the selected features:



To select multiple ranges of data from the quant bar plot:

- Hold the "Ctrl" key down on the computer keyboard.
- Drag the mouse with the left mouse button held down over the different data ranges to be selected.
- Release the "Ctrl" key to complete the selections.

Select Features from the Data Tab

To select features from the data table on the data tab:

- To select a single feature from the data table, click on the feature in the table.

  The same feature will be visible on the "Single" tab and be highlighted on the electron image.

- To select multiple, separate rows in the "Feature Data" viewer, hold the "Ctrl" key down on the computer keyboard, while clicking on the row for each feature to be selected.

  NOTE: *To deselect a feature, hold the "Ctrl" key down and click the feature in the table.*

- To select a number of adjacent features in the "Feature Data" viewer, click on the first feature so that it is highlighted, then hold the "Shift" key down on the computer keyboard and click on the last feature.

  Alternatively, place the cursor over the first row, hold the left mouse button down and drag the mouse until all of the features have been highlighted.

  Release the left mouse button to complete the selection.

  NOTE: *To deselect the selection, click any row.*

- To select multiple sets of adjacent features, for example:

Id	ECD (µm)	Count	N	O	F	Na	Mg	Al	Si	S	K
			Wt%	Wt%	Wt%	Wt%	Wt%	Wt%	Wt%	Wt%	Wt%
2288	2.64	154									
2289	2.16	123									
2290	51.64	75387		26.18						14.54	
2291	1.52	54									
2292	1.76	82									
2293	31.46	34659		3.04						32.80	
2294	2.49	194								26.09	
2298 (1390)	0.05	8									
2300 (1390)	0.05	8									
2325 (1387)	0.07	37704									
2326 (1387)	0.09	37704									
2327 (1387)	0.07	37704									
2329 (1387)	49.70	5846628			9.65		6.41	9.68			
2330 (1388)	0.07	37704									
2331 (1388)	0.09	37704			4.68				0.61		
2332 (1388)	0.07	37704							0.60		
2333 (1388)	0.58	37716	23.01								
2334 (1388)	49.70	5846628					7.14	10.85			
2335 (1391)	0.07	37704									
2336 (1391)	0.09	37704							0.73		
2337 (1391)	0.07	37704									

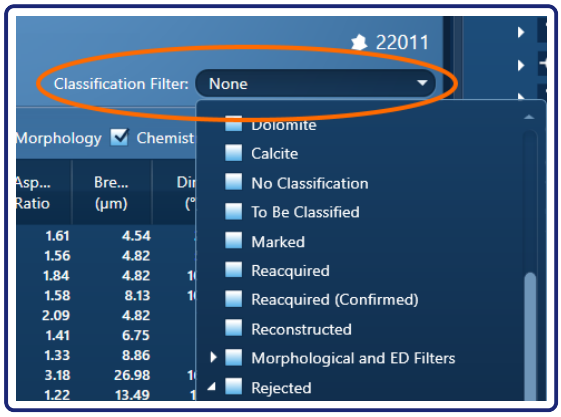
  Hold the "Ctrl" key down on the computer keyboard and then follow the process for selecting a number of adjacent features.

2.8.3. Filtering the Data to Focus on Specific Features

Large area feature data sets can contain tens of thousands of features. When analyzing data, it is not very practical or efficient to consider this number of features in one go, especially if a number of them are not of any importance for the analysis.

To assist with focusing on the specific types of features that are relevant to the current analysis, within AZtecFeature it is possible to filter the features by a specific characteristic, for example, by class or by phase. Then only features that meet this filter are colored on the electron image and displayed in the feature data viewer.

Data can be filtered using the Classification filter drop down menu which appears in the top right corner of the feature data viewer:



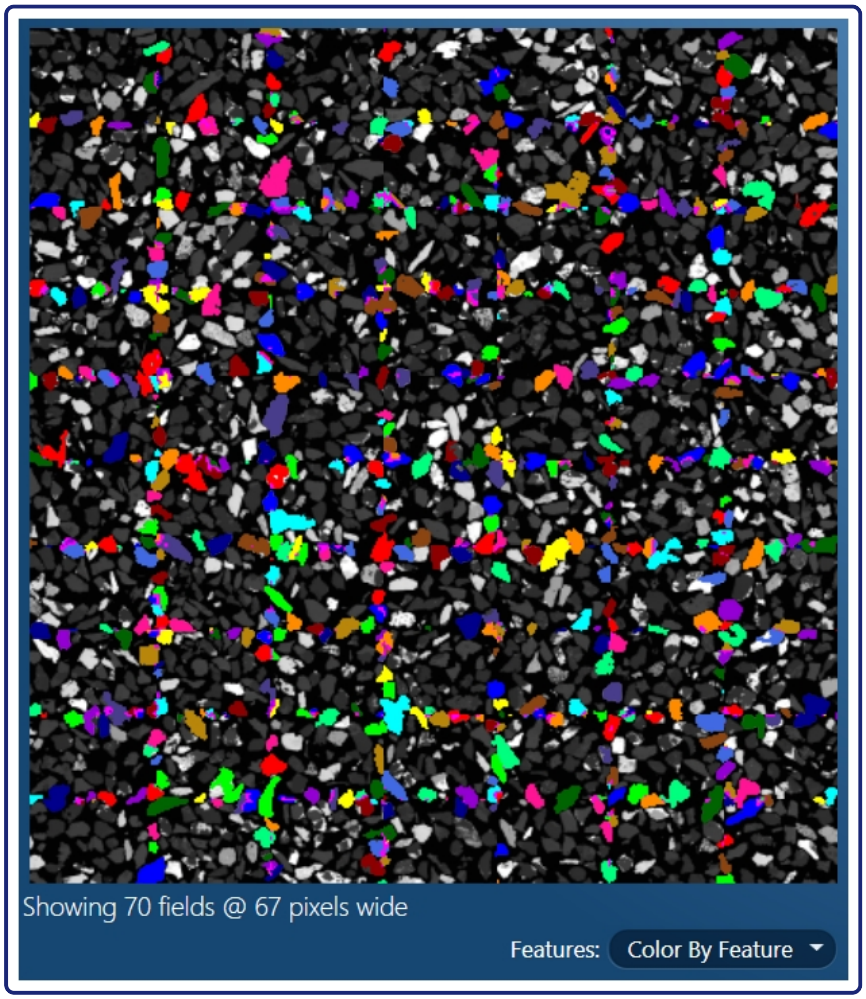
It is possible to select to filter the data and display features that have been:

Classification Filter	Use
Assigned to a particular class (i.e. Calcite) or not classified (No Classification)	Allows the data to be filtered so that only features of interest that belong to a certain class or collection of classes are worked upon. Filtering by class can also be useful for reviewing the features in the class to verify that the class definition is correct and as expected.
Marked	Allows data to be filtered so that only features that have been manually marked (have an asterisk next to the feature Id in the data table) are displayed. Generally features are marked for some reason, for example because they of particular interest and it is desirable to analyze them in more detail.
Reacquired or Reacquired (Confirmed)	Allows the data to be filtered so that only features that have been reacquired, but not yet confirmed or features that have been both reacquired and confirmed are displayed. This filter is useful for concentrating on the reacquired features to see the extra data that has been acquired for them.
Reconstructed	Filter the data so that only features that have been reconstructed are displayed. This filter is useful for viewing only these features to ensure that the result of the reconstruction is acceptable.
Morphological and ED Filters	Filter the data to display only the features that have passed either a specific morphological or ED filter or any of them. This filter is useful for verifying that the filters are behaving as expected. For example, to see why a feature passed or failed a filter and to see which features met which filters.
Phase	This option is only available when either full-field or threshold phase detection have been used to detect the features. It can be used to show all of the phases

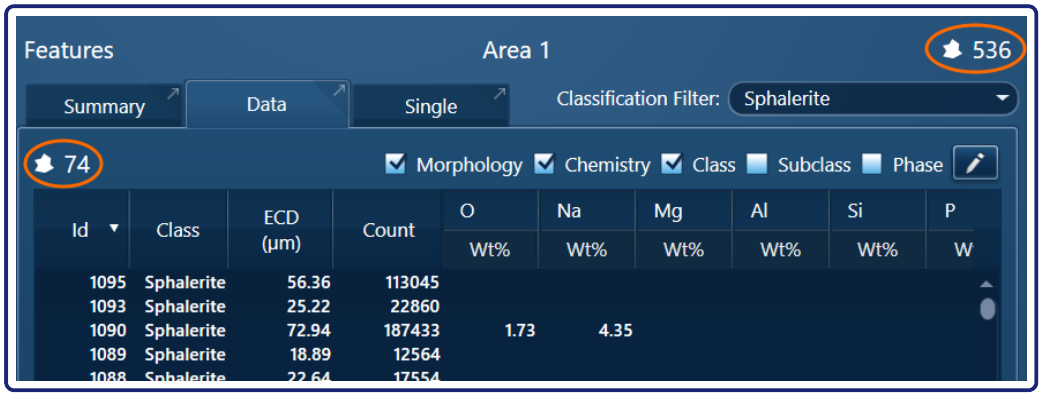
Classification Filter	Use
	that have been identified or only select ones. This filter allows the result of the phase grouping from the autophase algorithm to be reviewed and can be used to see all features that contain a particular phase without having to create a classification for it.
Rejected (all) or by a particular tool	This filter is used to display features that have been rejected and to see which features were rejected by a particular tool or action (e.g. features that were rejected manually by the user or by a tool such as the reconstruct tool which rejects the source features). This filter is useful for viewing the rejected features so that they can be restored or unrejected. It can also be useful for exploring the data for the rejected features to see why they were rejected.

Once one or more filters have been selected, the data displayed in the electron image and in the data viewer is filtered to only display the features that meet that filter.

Viewing the filtered data on the electron image is useful for seeing the physical location of the features that meet the filter. For example, if the reconstructed classification filter is selected and the "color by feature" coloring is selected for the electron image, it is possible to easily see the features that have been reconstructed on the electron image:



In the data tab of the feature data viewer, the number of features that belong to that filter is displayed at the top left of the table, while the total number of features in the project are still displayed above the classification filter drop down menu:



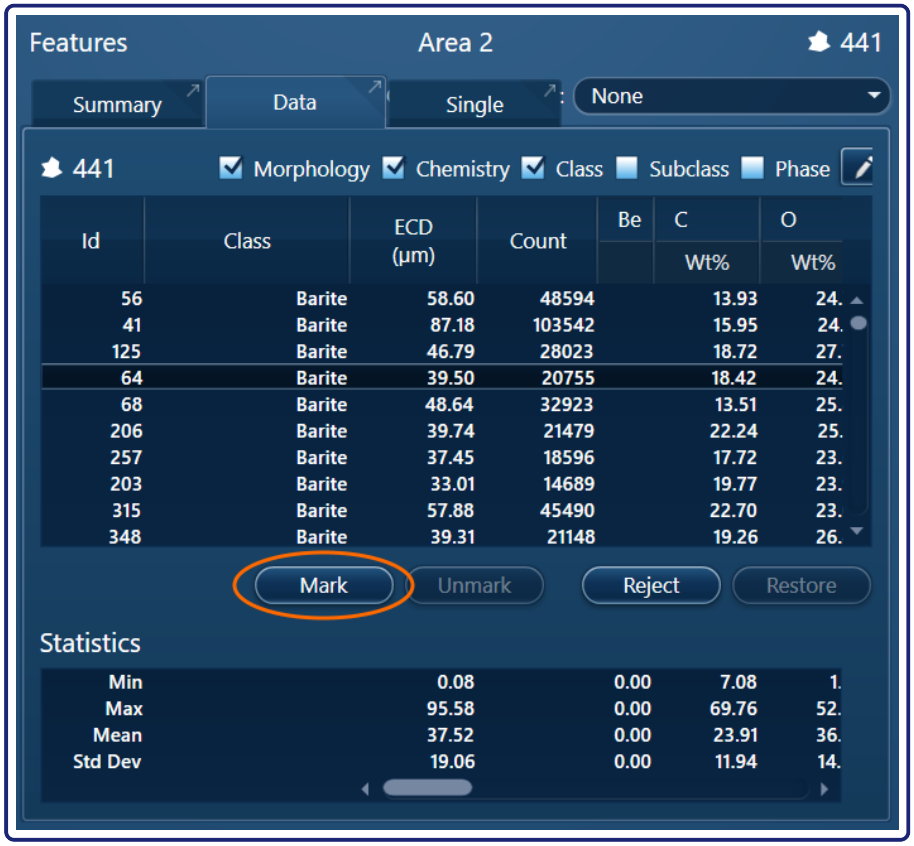
The data table and statistics table below now also only display the features that belong to the filter allowing the analysis to be concentrated on the filtered data.

Highlighting Features of Interest for Further Evaluation

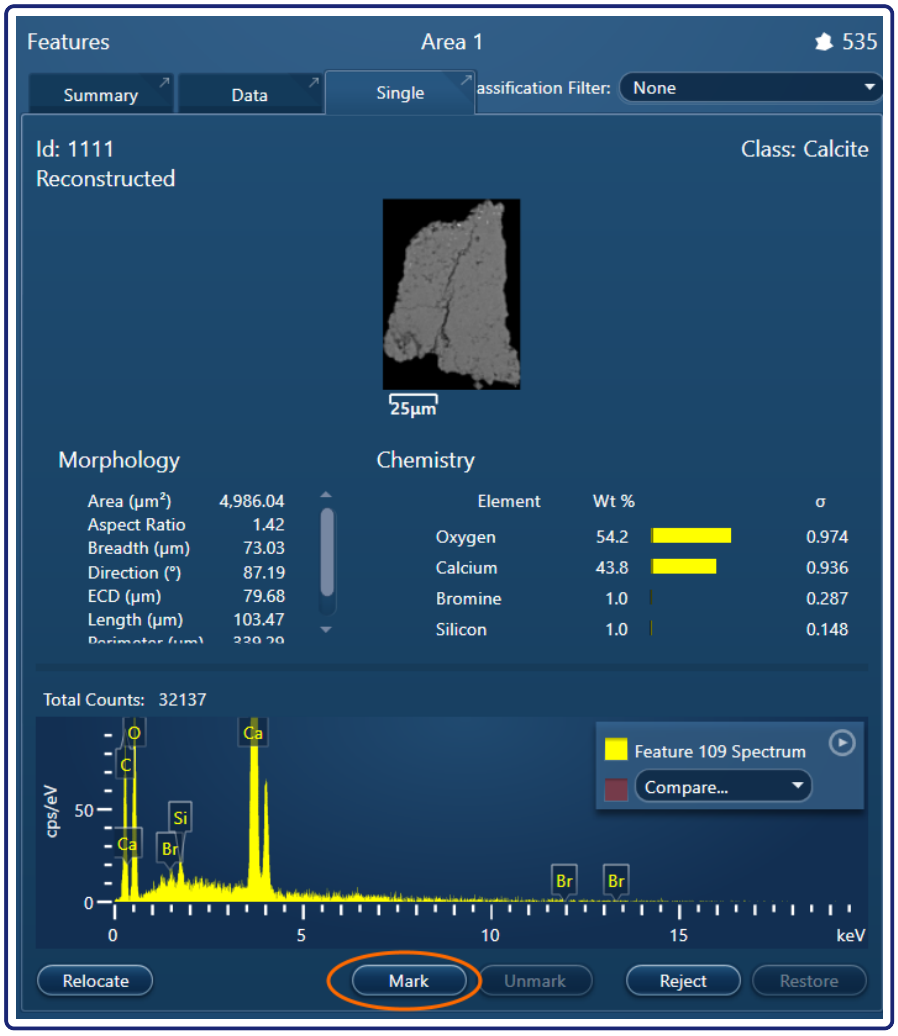
A useful tool for highlighting multiple features of special interest in the Data tab of the Feature Data Viewer for further evaluation is the "Mark" tool. Once the features have been highlighted, the data can then be filtered to only display these features.

To use the mark feature tool:

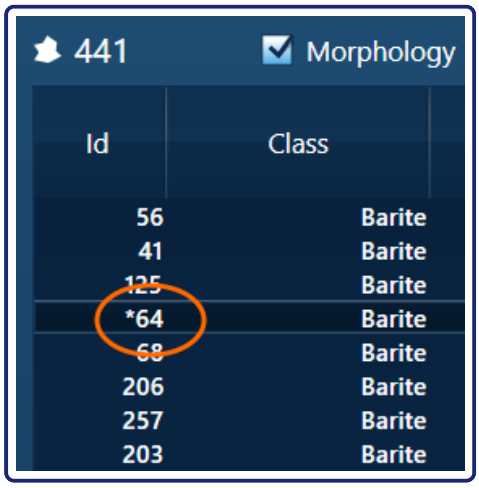
1. Select one or more features in the data table or in the image viewer.
2. Click the "Mark" button below the data table:



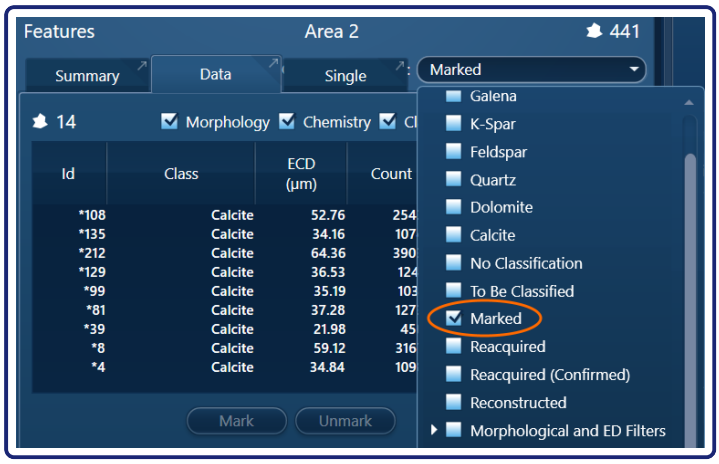
Or below the EDS spectrum in the Single tab:



In the data table the selected features will be marked by an asterisk before the feature Id number:

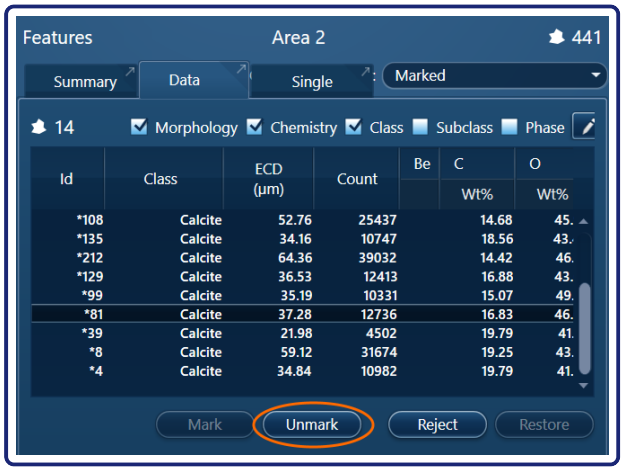


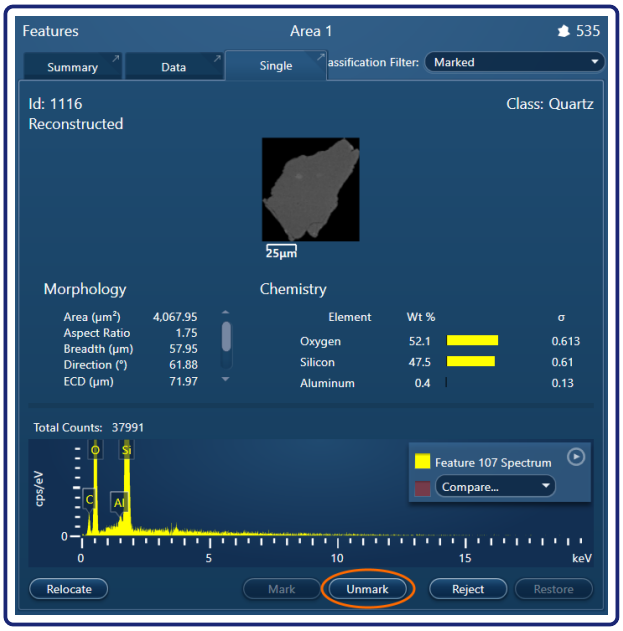
3. Repeat this process as many times as required until all of the features to be highlighted have been marked.
4. To work with only the highlighted (marked) features, filter the data table to display only the "Marked" features:



To unmark one or more features:

1. Select the features in the Data table or in the image viewer.
2. Click the "Unmark" button below the data table or below the EDS spectrum in the Single tab:





Removing Specific Features from the Analysis

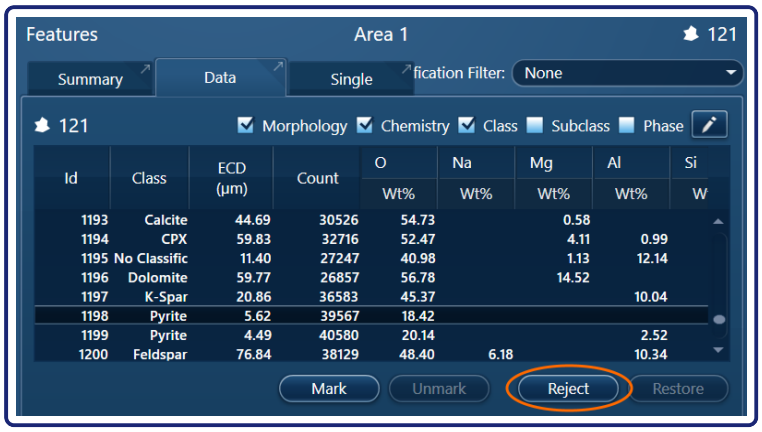
Some features in the current area or site might be found to not fit with the general data trend or not be of interest. These features can be rejected to remove them from the main analysis and statistics. For example, large features that are characteristic of contamination, or features that contain elements that are not of interest can be rejected.

> ***NOTE:*** *When features are rejected, they are removed from the "Feature Data" viewer. They are not included in the graphs or the statistics on the Summary tab. However, the feature data for these features remains saved in the project and can be restored.*

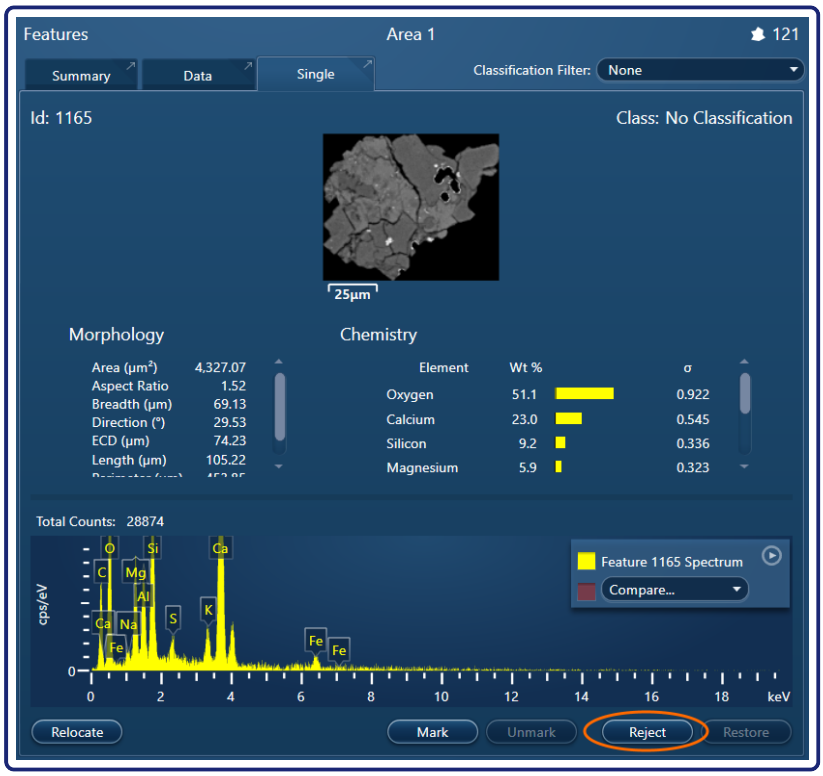
To use the reject feature tool:

1. Select one or more features in the data table or in the image viewer as described in the Selecting Features from the Different Data Views section.

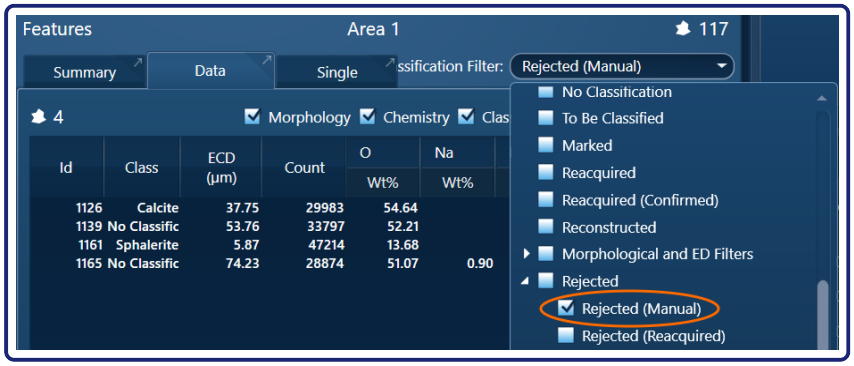
2. Click the "Reject" button below the data table:



Or below the EDS spectrum in the Single tab:

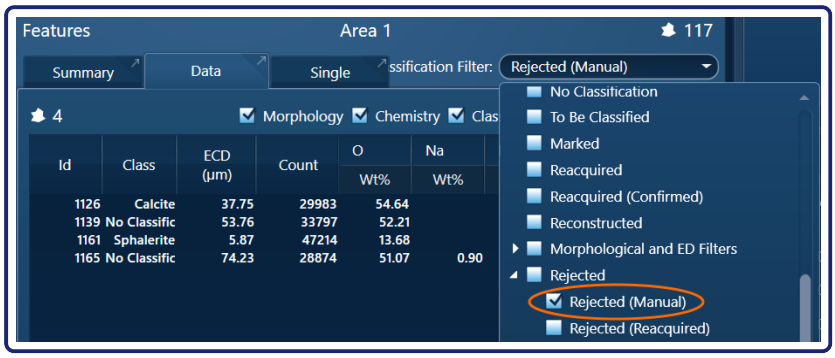


3. Repeat this process until all of the features to be rejected have been rejected.
4. To view the rejected features in either the "Summary" or "Data" tabs, filter the data to display only the "Rejected" features:

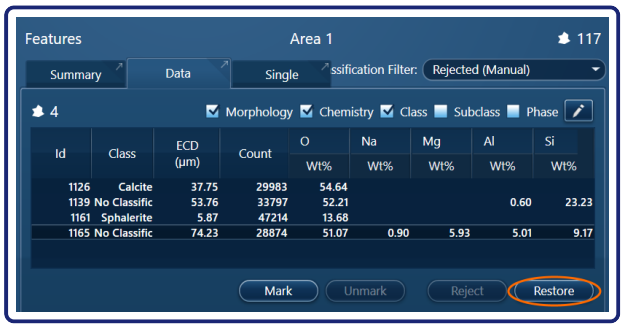


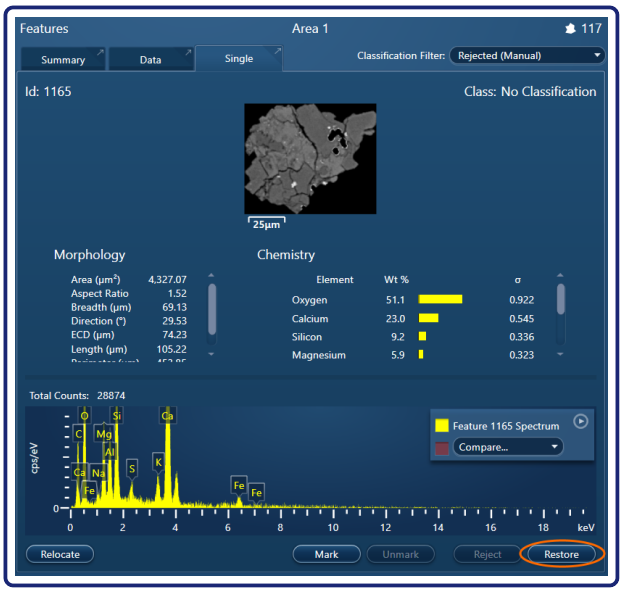
To restore a rejected feature:

1. Use the "Classification Filter" to select to view the "Rejected (Manual)" features:



2. Select the features that are not to be rejected from the Data table or Single tab.
3. Click "Restore" button below the data table or below the EDS spectrum in the Single tab:





2.8.4. Relocating to a Feature for Further Analysis

If a feature detected during a large area acquisition is of special interest, it is possible to relocate the microscope stage to that feature from either the Single or Data tabs of the Feature Data Viewer so that it may be further examined (for example at higher magnification).

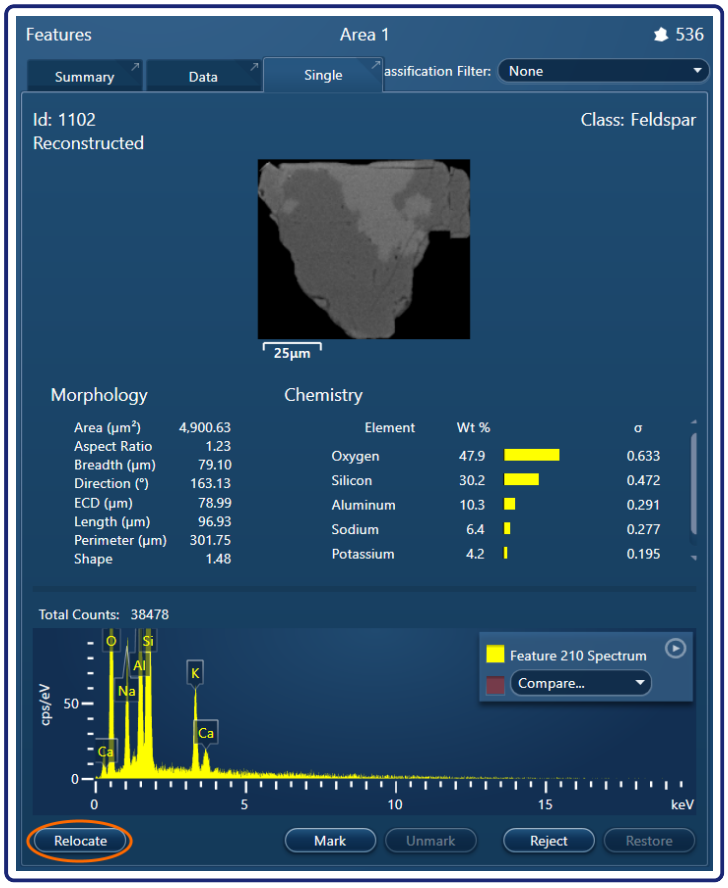
To relocate to a feature using the Data tab of the Feature Data Viewer:

1. In the Data tab, select the row for the feature.
2. Right click the feature to access the context menu.
3. Select "Relocate to Feature" to move the microscope stage such that the feature will appear in the center of the field of view.

   Select "Relocate to Field" to move the microscope stage such that the feature will appear in its original position within the field of view.

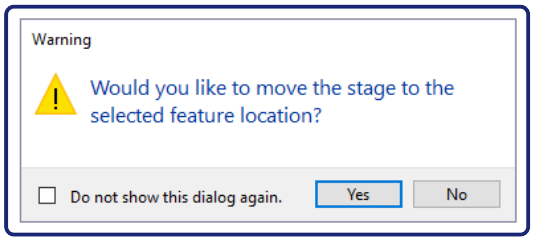
To relocate to a feature using the Single tab of the Feature Data Viewer:

1. Select the feature from either the electron image or from the feature data viewer.
2. Select the "Single" tab in the feature data viewer:



3. Click the "Relocate" button below the EDS spectrum.

   A warning message will be displayed:



   Click "Yes" to relocate the microscope stage to the center position of the feature, or "No" to cancel.

4. Manually acquire any additional data for the feature.

2.8.5. Creating and Updating Classification Schemes

While interrogating the data, if any trends or outliers were identified, they may be used to either create a new classification scheme for the project or update the classification scheme currently being used.

If the project contains an existing classification scheme, it is possible to:

- Manually edit existing classes.
- Add new classes to the scheme using either the manual or assisted criteria creation mode.

If a new classification scheme is to be created, it is possible to create the classes:

- Using manual criteria creation.
- Using assisted criteria creation.
- Using a mix of both.

It is possible to work on the classification scheme in either the "Set Up Classification" or "Review" steps. Both steps contain the same classification tools, however, in the "Set Up Classification" step, it is only possible to view the data for a single site, while in the "Review" step, it is possible to view the data for an entire area.

2.8.6. Reacquiring Feature Data

When analyzing the data from a Feature acquisition, it may be necessary to reacquire data for a number of features. For example for:

- Features with an unusual shape.
- Features that contain unexpected elements.
- Features that contain some interesting elements in low quantities.

By reacquiring the data for these features at a higher magnification and with a longer acquisition time, higher quality data is collected and gives better confidence in the result.

In AZtecFeature features can be reanalyzed using:

- Automatic Reacquisition: Automated reacquisition of multiple features that can be triggered by clicking a single button, making further analysis of key features fast and easy.
- Manual Reacquisition: Manually optimize the microscope settings before reacquiring the data for each feature. This step ensures that the optimum settings for reacquiring the data for each feature are used.

Once the reacquisition has been completed, the confirmation wizard is used to review and confirm the data to keep quickly and efficiently, whilst ensuring that data integrity is maintained. See the Confirming Reacquired Feature Data section.

There are also numerous ways in which the reacquired data can be viewed and interrogated. See the Viewing Reacquired Feature Data section.

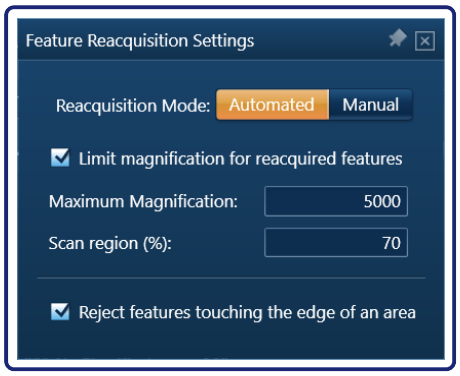
> ***NOTE:*** *If either threshold or full field phase detection has been used, phase separation must be applied before any data can be reacquired.*

Automatic Reacquisition

This is the general method that is used to reacquire Feature data for specific features. It uses a higher magnification along with the current image and EDS settings to acquire higher quality data than in the initial run. Once the reacquisition has completed the data to be kept can be confirmed using the method described in the Confirming Reacquired Feature Data section.

The method used for automatic reacquisition is:

1. In the "Detect Features" step, select the image and threshold settings to be used for the reacquisition.
2. In the "Acquire Site" step, select the EDS settings to be used for the reacquisition.
3. In the "Review" step, click on the "Settings" icon in the acquisition toolbar to open the "Feature Reacquisition Settings" window:



4. Select the "Automated" reacquisition mode.
5. Select whether to limit the maximum magnification that the microscope can be set to when reacquiring a feature using the "Limit magnification for reacquired features" check box. If limiting the magnification, enter the value of the maximum magnification that is to be allowed.

   When reacquiring the data for a feature, AZtec aims to increase the magnification on the microscope (up to the maximum specified in the Feature Reacquisition Settings window) to make the size of the feature two-thirds of the field of view. This allows a high quality image and EDS data to be acquired for that feature. However, depending on the accuracy of the stage relocation, this magnification may result in part or all of the feature not appearing in the field of view. To ensure that this does not happen, the maximum allowed magnification can be specified and limited using the "Limit magnification for reacquired features" option.

6. Specify the scan region (%).

   This is the region within the field of view that AZtec will scan. Any features that are inside or touching the edge of this region will be reacquired.

   The size of this region needs to be defined as it is dependent on the accuracy of the stage relocation. The more accurate the stage repositioning, the smaller the region can be and the fewer the number of features that will be detected and reacquired.

7. Select the original features that data will be reacquired for.

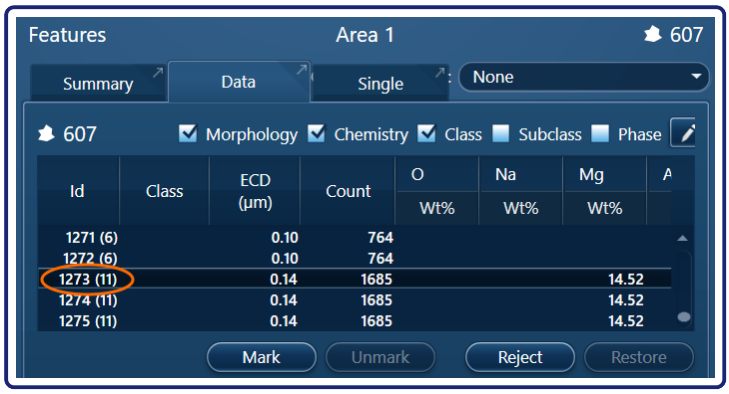
   The features may be selected from the electron image using the select feature tool or from the Data and Summary tabs in the Feature Data Viewer.

   To assist with marking features in the data view, a useful tool is the "Mark" tool. For information on how to use this tool, see the Marking Features section.

8. Click the "Start" button in the acquisition toolbar to start reacquiring the data for the selected original features. For each original feature AZtec:
   - Automatically rejects the original feature.
   - Moves the stage to the coordinates that correspond to the centre of the original feature.
   - Increases the magnification until it reaches the maximum magnification or the original feature is two-thirds the size of the field of view, whichever is sooner.
   - Acquires an electron image and identifies all child features that lie within or touch the edge of the scan region. For each of these child features, AZtec will:

- Assign a new feature Id to the feature:
- Acquire the EDS data.

The new child features are added to the data table:



NOTE: *The feature Id of the original feature is shown in brackets after the new child feature Id number.*

9. Once the reacquisition has completed, the data that has been acquired can be reviewed and the data to be kept selected using the method described in the Confirming Reacquired Feature Data section.

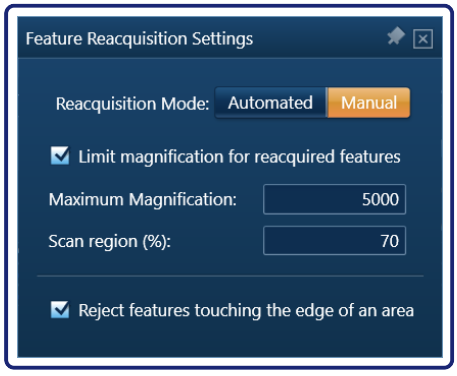
Manual Reacquisition

Manual reacquisition allows the user to optimize the settings before reacquiring the data for each feature. As for automatic reacquisition, it uses the current image and EDS settings and attempts to use the highest magnification that it is allowed. However, rather than automatically acquiring the data, with manual reacquisition AZtec drives the stage to each feature and then stops allowing the SEM to be manually optimized by adjusting the magnification, stage position and focus before the data for the feature is reacquired.

Once the reacquisition has completed the data to be kept can be confirmed using the method described in the Confirming Reacquired Feature Data section.

The method used for manual reacquisition is:

1. In the "Review" step, click on the "Settings" icon in the acquisition toolbar to open the "Feature Reacquisition Settings" window:



2. Select the "Manual" reacquisition mode.
3. Select whether to limit the maximum magnification that the microscope can be set to when reacquiring a feature using the "Limit magnification for reacquired features" check box.

   If this option is selected, enter the value of the maximum magnification to be allowed.

When reacquiring the data for a feature, AZtec aims to increase the magnification on the microscope (up to the maximum specified in the Feature Reacquisition Settings window) so that the feature fills two-thirds of the field of view. This allows a high quality image and EDS data to be acquired for that feature. However, depending on the accuracy of the stage relocation, this magnification increase may result in part or all of the feature not appearing in the field of view. To ensure that this does not happen, the maximum allowed magnification can be specified and limited using the "Limit magnification for reacquired features" option.

4. Specify the scan region (%). This is the region within the field of view that AZtec will scan. It is a letterbox shape, centered on the middle of the image with a width and height defined as a percentage of the field dimensions. Any features inside or touching the edge of this region will be reacquired.

   NOTE: *The size of this region needs to be defined because it is dependent on the accuracy of the stage relocation. The more accurate the stage repositioning, the smaller the region can be and the fewer the number of features that will be detected and reacquired.*

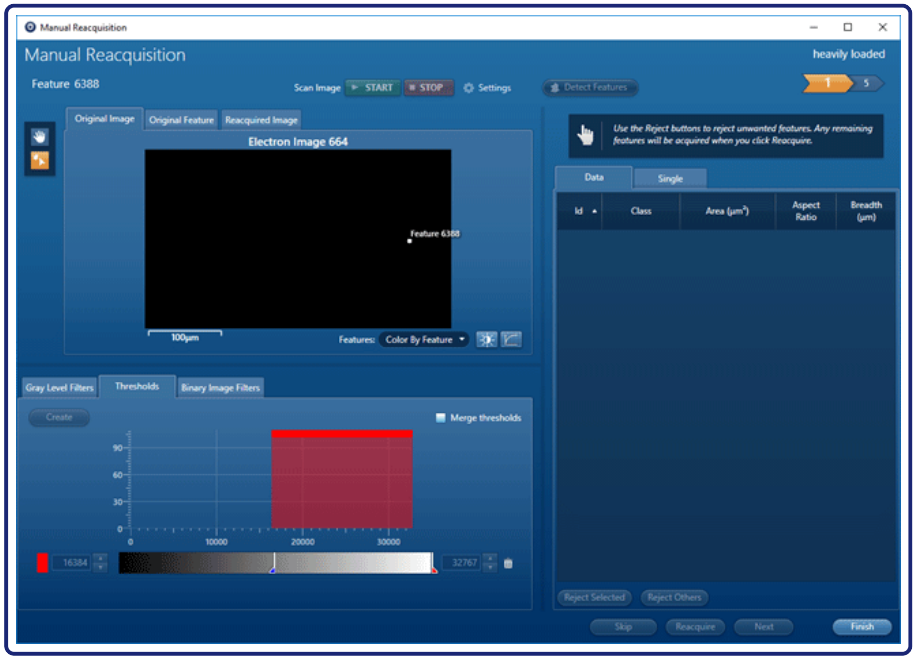
5. Select the original features that data will be reacquired for.

   They may be selected from the electron image using the select feature tool or from the Data and Summary tabs in the Feature Data Viewer.

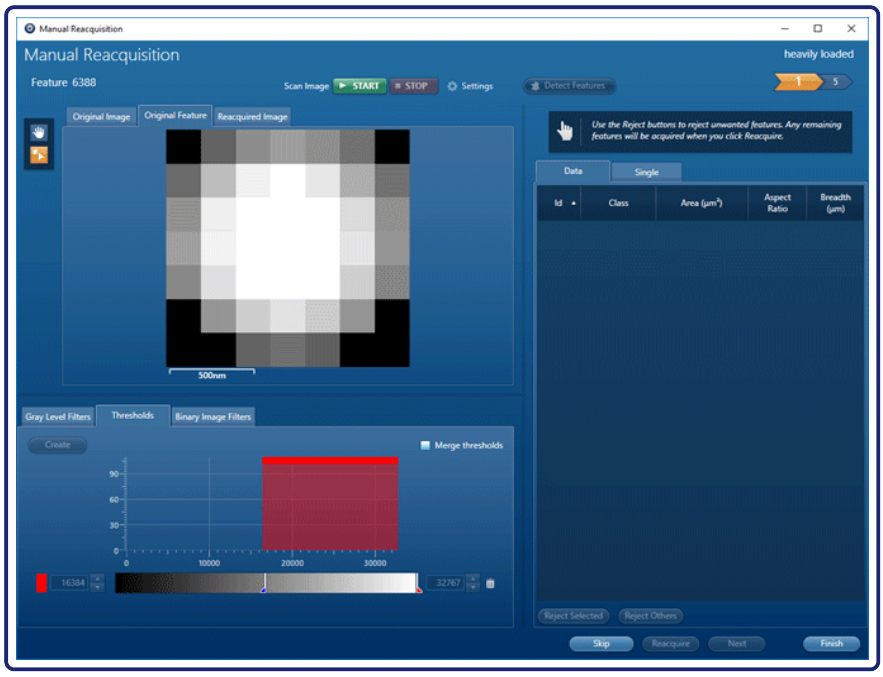
   To select multiple separate features hold down the Ctrl key on the computer keyboard while selecting the features. To select multiple features together select the first feature, hold down the Shift key and select the last feature, all of the features in between will also be selected.

   Features of interest may be highlighted in the data view, using the "Mark" tool. For information on how to use this tool, see the Marking Features section.

6. Click the "Start" button in the acquisition toolbar to open the Manual Reacquisition window. For the first feature to be reacquired, AZtec:
   - Moves the stage to the coordinates that correspond to the center of the original feature.
   - Increases the magnification until it reaches the maximum magnification or the original feature is the two-thirds the size of the field of view, whichever is sooner.
   - Automatically rejects the original feature.



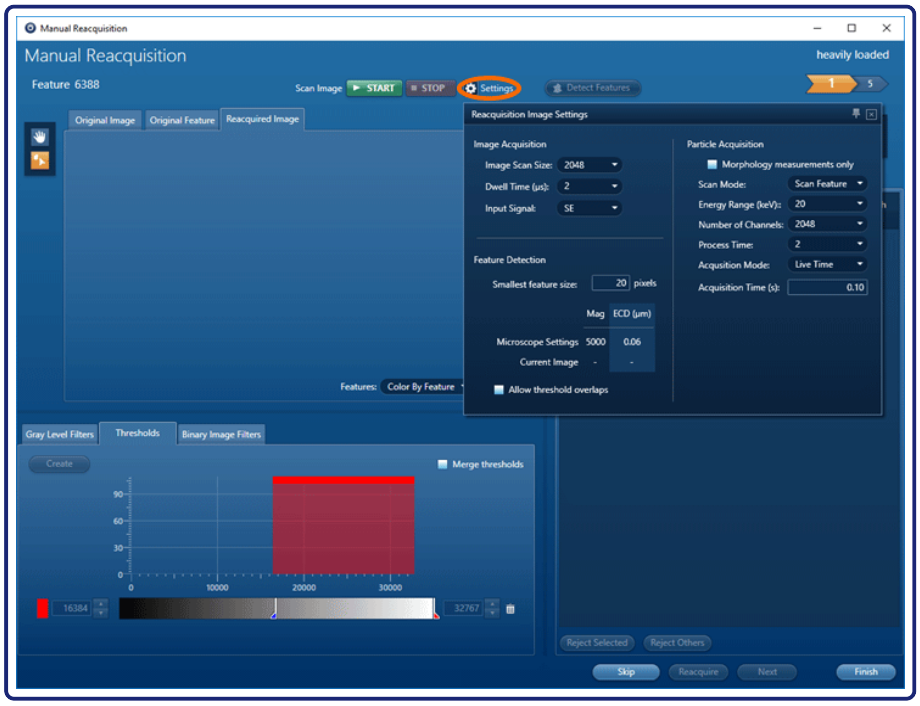
The Start button will become available once AZtec has reached the correct stage position for the feature and adjusted the magnification. For example:



7. Use the microscope to adjust the focus, magnification, image settings and stage position as required.

   NOTE: *It is possible to override the magnification limit set in AZtec here.*

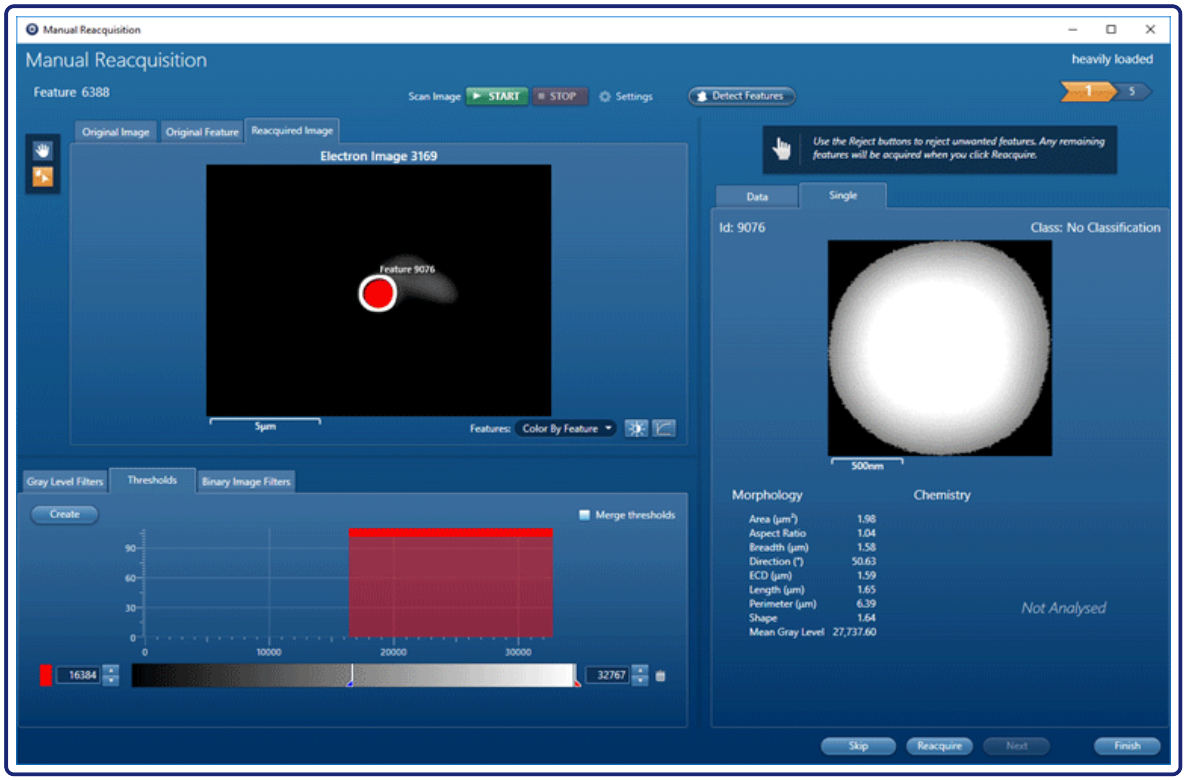
8. Use the Settings in the Manual Reacquisition window to change any of the image or particle acquisition settings as required.



NOTE: *Any changes to the settings in the Manual Reacquisition window will persist for the remainder of the reacquisition. Any changes to these settings are lost when the manual reacquisition is closed.*

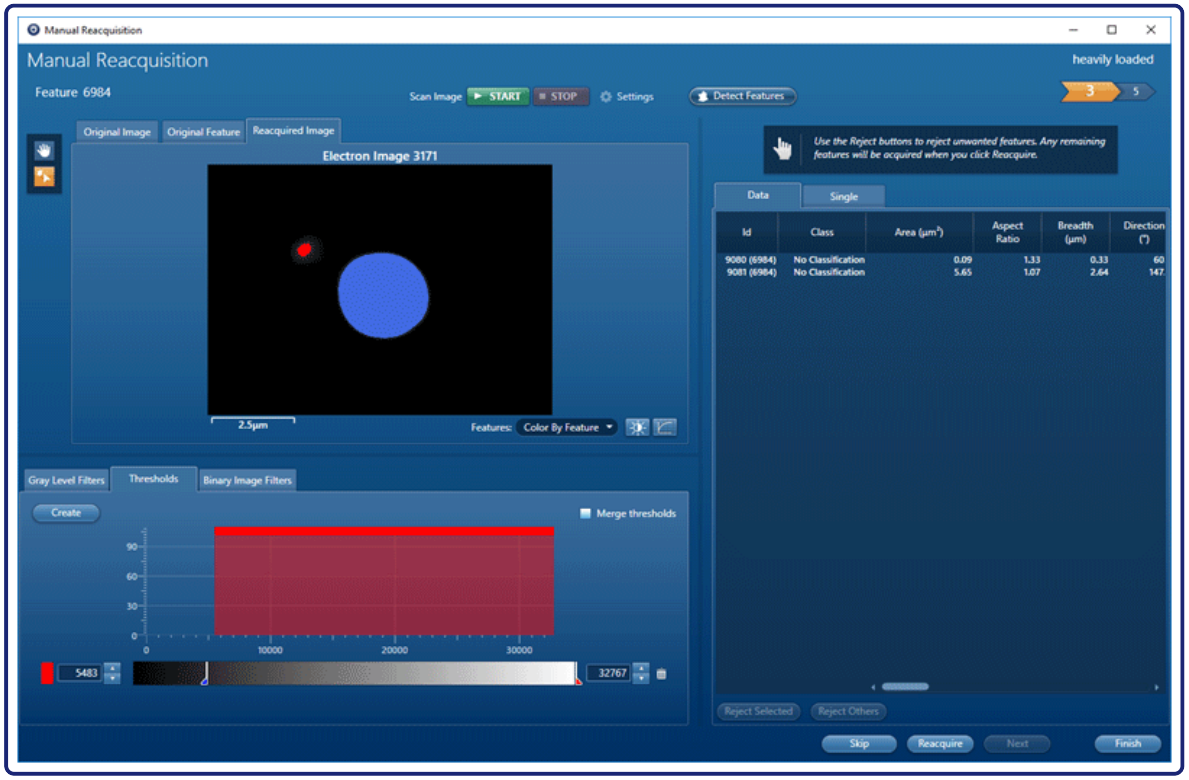
9. Click "Start" to acquire a new electron image for the feature.

   For example:

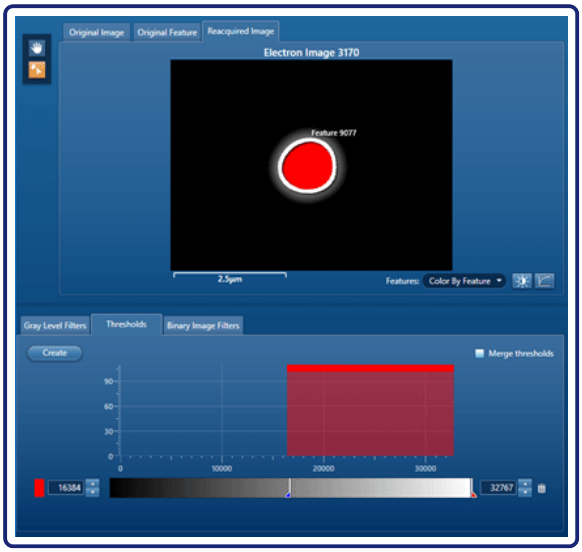


If any additional (child) features are detected when reacquiring the image for the original feature, AZtec will add them under the Data tab. Each feature will be assigned its own feature ID.

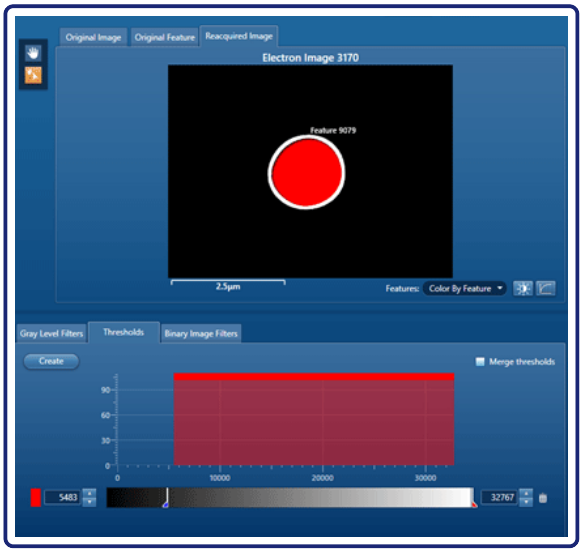
For example:



10. Use the Thresholds tab in the lower left pane of the Manual Reacquisition window to adjust the thresholds for detecting the feature as required (i.e. if the feature has been detected inaccurately). For example:

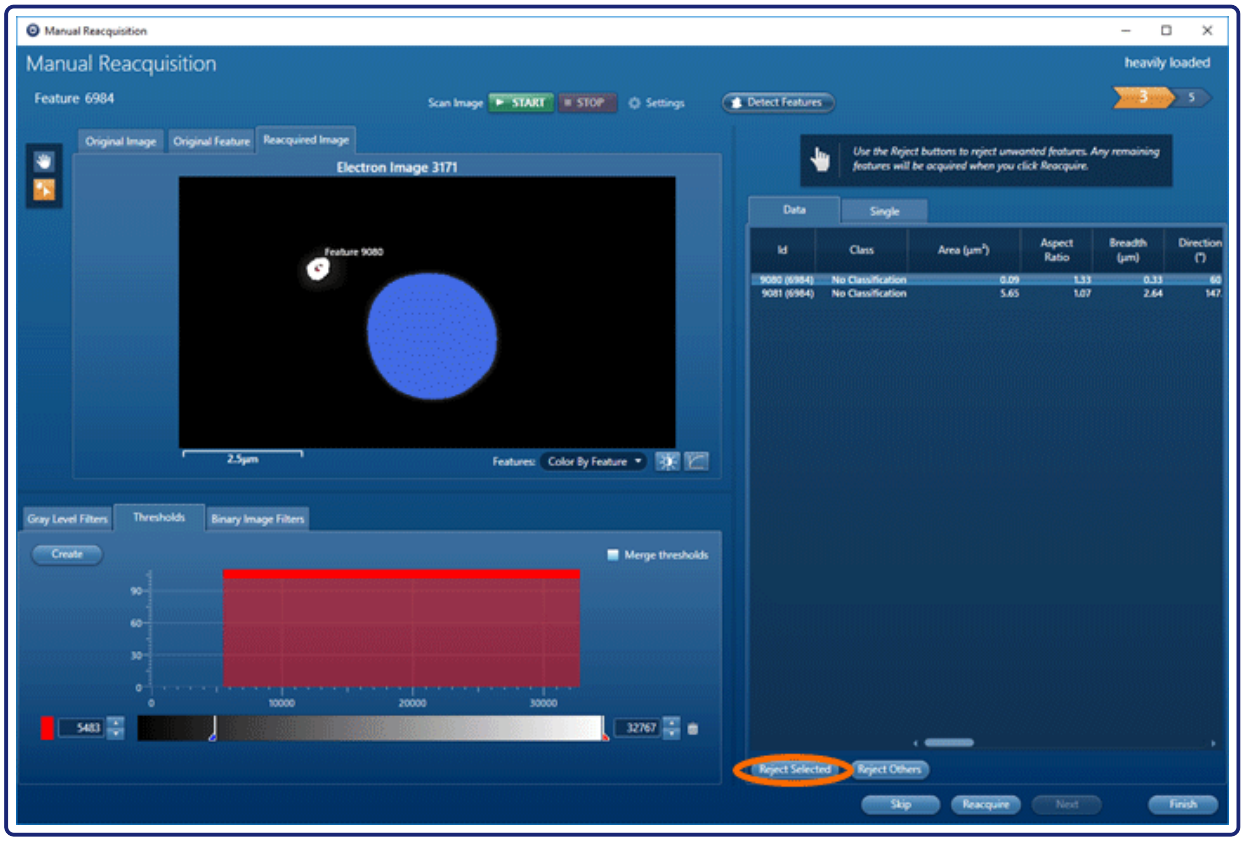


Before threshold adjustment



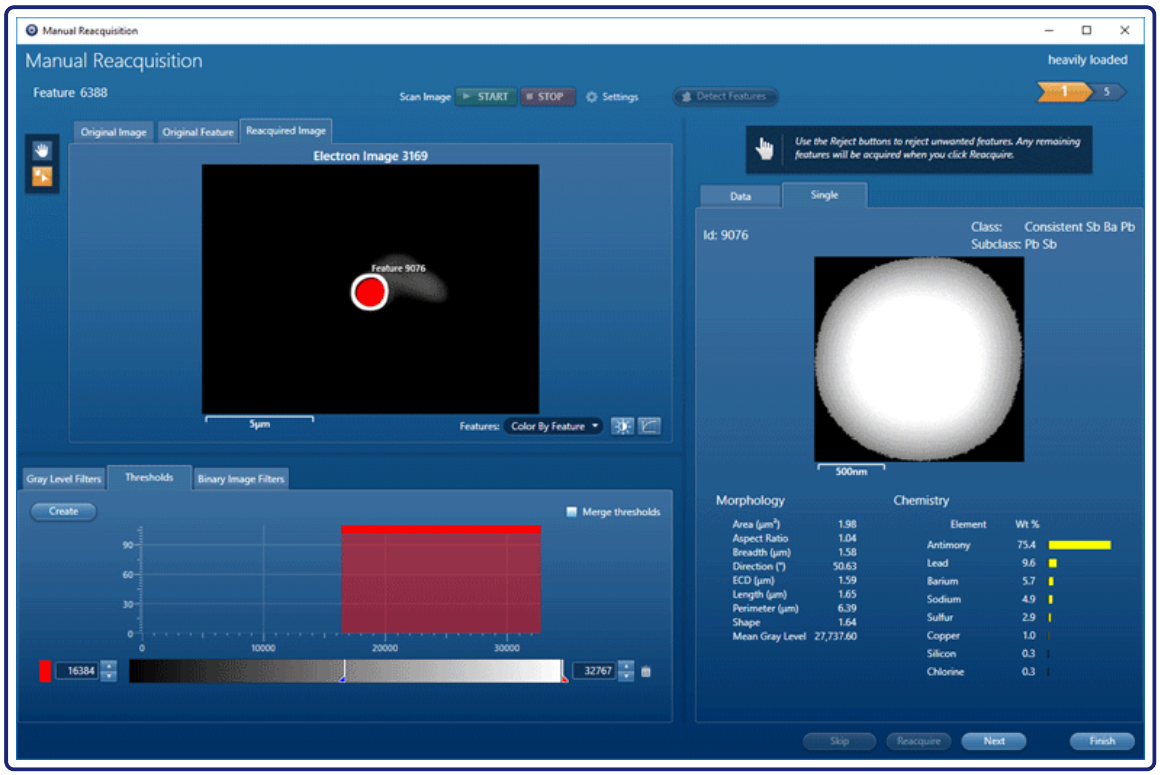
After threshold adjustment

11. Any unwanted features may be rejected from the analysis by selecting the feature and clicking the "Reject Selected" button at the bottom of the Data tab:



12. Click the "Reacquire" button in the "Manual Reacquisition" window to reacquire the EDS data for the current feature with the current settings or click the "Skip Feature" button to move straight to the next feature without reacquiring any data.

When the reacquisition of the EDS data, quantification and classification has completed, the "Manual Reacquisition" window will update to show the details of the EDS data for the original feature:

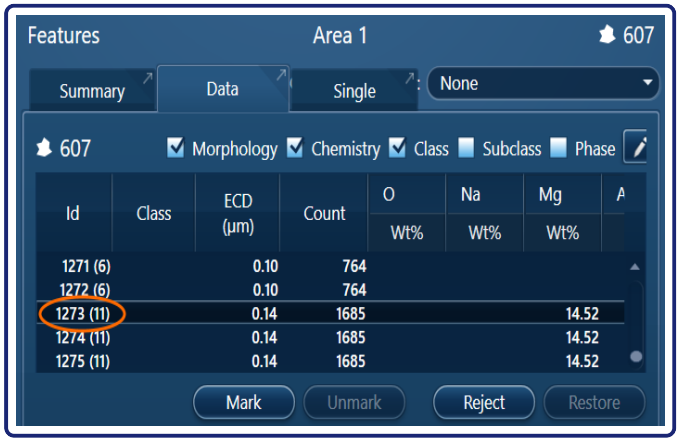


13. Click "Next" to proceed to the next feature or "Finish" to finish the reacquisition and close the Manual Reacquisition window without reacquiring all of the features.

    When the data for all of the original features has been reacquired, the "Manual Reacquisition" window will automatically close.

    Once the manual reacquisition has been completed and the "Manual Reacquisition" window closed, the data table will automatically be filtered to show the reacquired features. The child features can then be viewed in the normal way.

14. View the data in the data table, where the feature Id of the original feature is shown in brackets after the new child feature Id number:



15. All of the data that has been acquired can be reviewed and the data to be kept can be confirmed using the method described in the Confirming Reacquired Feature Data section.

Viewing Reacquired Feature Data

It is possible to view and interrogate reacquired data in a number of ways, including with the:

- Data Table: using filters to select the type of data to be displayed.
- Single View: where the details of the reacquired data is displayed.
- Mini View: using the "Reacquired Features" view to display the reacquired electron image and position of the child features.
- Review Reacquired Features window: see the Confirming Reacquired Feature Data section.

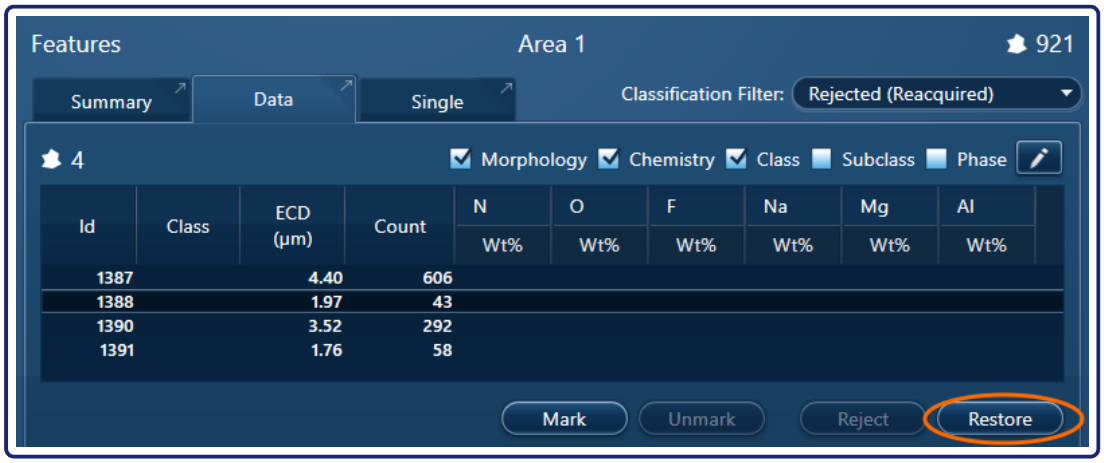
Data Table

The data table allows either all of the feature data or specific categories of feature data selected using filters to be viewed.

There are four filters that are useful for viewing reacquired data:

- Reacquired: displays all features that have been reacquired but not rejected. It includes all features that have been confirmed.
- Reacquired (confirmed): displays all features that have been reacquired, confirmed as being correct (see the Confirming Reacquired Feature Data section) and selected for inclusion in the main data set. These are generally the features that you are most interested in as the data for them has been reacquired in more detail and they have been confirmed as being correct.
- Rejected (reacquired): displays the original features that were rejected prior to being reacquired.
- Rejected (manual): displays all of the child features that were reacquired and then rejected by the user.

The data for a rejected feature can be restored by selecting the feature in the data table and then clicking the "Restore" button below the data table:



NOTE: *Restoring an original feature does not automatically remove the child features. They need to be rejected manually.*

It is possible to see whether a feature has been reacquired from its Feature Id. In the data table all reacquired features have the child feature Id with the original feature Id in brackets after so that it is possible to see from which original feature the child feature originates:

Single View

The single feature view in the feature data viewer is used to view the electron image and the details of the morphology and EDS data acquired during the reacquisition of a feature. The feature is identified using its child feature Id.

This single data view can be used to "Mark", "Reject" or "Restore" the reacquired feature being currently viewed:

Mini View

The mini view on the right hand side of the AZtec software can be used to show the position of the child features that have been reacquired on the reacquired electron image. This is useful for seeing how the reacquired features are laid out next to each other.

Confirming Reacquired Feature Data

Once the data for the original features has been reacquired, it is possible to review it and confirm its validity, selecting which data to keep and which to reject. For each child feature, the electron image, and the morphology and EDS data can be viewed and the child feature confirmed or rejected. For cases where a single original feature was selected to be reacquired, but more than one child feature was reacquired because more than one child feature was detected within or touching the edge of the scan region, this process can be used to determine which of the child features is the correct feature to replace the original feature.

To review the reacquired data:

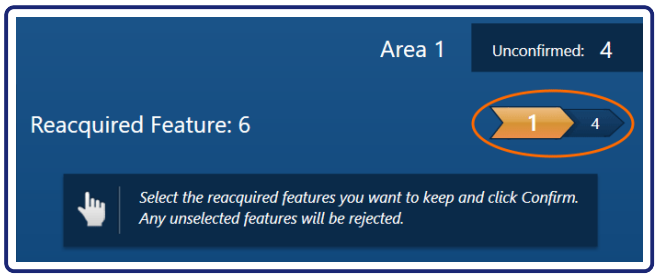
1. Click the "Confirm" button in the acquisition toolbar on the "Review" step:

This will open the "Review Reacquired Features" window:

Within the window, the data will be displayed for the first original feature that was reacquired. It can be viewed as:

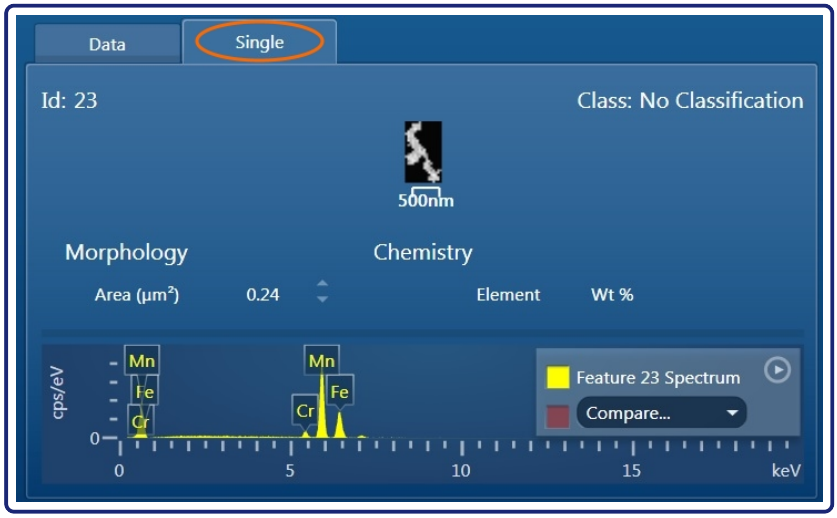
- The electron image that was acquired for the original feature that was selected to be reacquired. All child features that were detected within the scan region and acquired as part of reacquiring the original feature are shown on the image.

- The feature Id number of the reacquired feature.
- The current number of the original feature out of the total number of features that were reacquired:



- A data table showing the data for all of the child features that were detected and analyzed as part of reacquiring the data for the current original feature:

- The detailed data for the feature currently selected in the data table:



- The Confirm Elements tab, which can be used to add or remove elements from the spectrum for the current feature reacquisition.

2. For each original feature that was reacquired, select whether to:
   - **Confirm the reacquired feature data that is correct:** Select the data for the child feature that is correct and to be kept in the data table and then click the "Confirm" button.

> ***NOTE:*** *More than one child feature can be selected.*

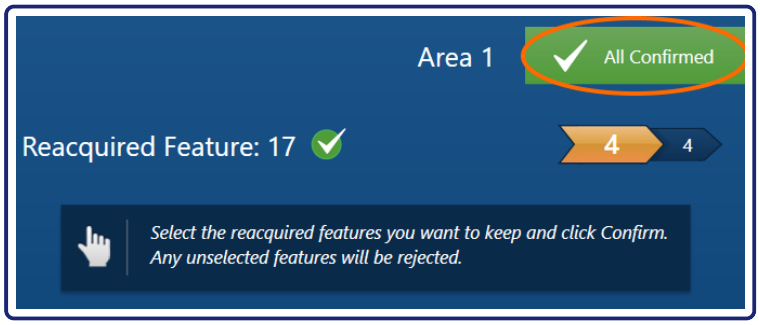
The selected child features are now confirmed as being correct and all other child features are rejected:

To show that the reacquired data for the original feature has been reviewed and confirmed a green tick is added to the right of the original feature number and the number of unconfirmed original features in the top right corner of the "Review Reacquired Features" window will drop by one.

- **Reject all of the reacquired features:** Click the "Reject All" button to reject all of the child features that were reacquired for a single original feature.

  All of the child features will be rejected and hidden from the main data display, a green tick and " (rejected)" will be added to the right of the original feature number to show that the feature has been reviewed and the data rejected. The number of unconfirmed features will drop also by one:

3. To change the data that has been confirmed or rejected for an original feature, click the "Restore" button to repopulate the data table with all of the child features for the original feature.
4. Click "Next" to move on and review the next feature or "Previous to return to the previous feature. Alternatively, click the "Previous Unconfirmed" or "Next Unconfirmed" buttons to jump to the previous or next feature that has not been confirmed.
5. When all of the reacquired data for the original features has been confirmed, the top right corner of the "Review Reacquired Features" window will be updated to show that all of the features have been confirmed:



6. Click "Finish" to close the "Review Reacquired Features" window and return to the main AZtec software.
7. Reacquired child features that have been confirmed are added to the end of the data table in the Feature Data Viewer. They are displayed with the new child feature Id with the original feature Id in brackets afterward.

   To view only these features in the data table use the drop down menu to filter the display by "Reacquired" or "Reacquired (Confirmed)".

   Reacquired features that were rejected can be viewed in the main data table by selecting to display the "Rejected (Reacquired)" features from the drop down menu.

> ***NOTE:*** *It is possible to restore these features by selecting the feature and clicking the "Restore" button below the data table.*

2.9. Extracting Feature Data from SmartMaps

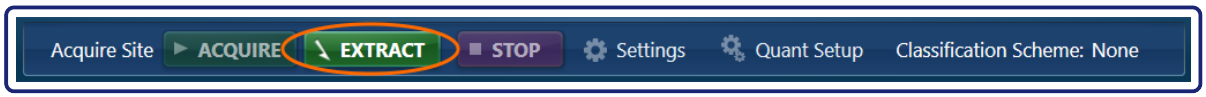
If you have a sample that you have acquired SmartMap data for and would now like to acquire feature data for. Rather than having to acquire the data again as feature data, it is possible to extract feature data directly from the saved SmartMap data.

To extract feature data from a SmartMap

1. In the Data Tree, select the SmartMap, site or field from which the data is to be extracted.
2. Use the Feature "Detect Features" step to identify the features.

   NOTE: *For information on detecting features, see the Detecting Features section of the help.*

3. Extract the feature data from the SmartMap data:
   - Ensure the appropriate site or area is selected in the data tree.
   - Click the "Extract" button in acquisition toolbar of the "Acquire Site" step:

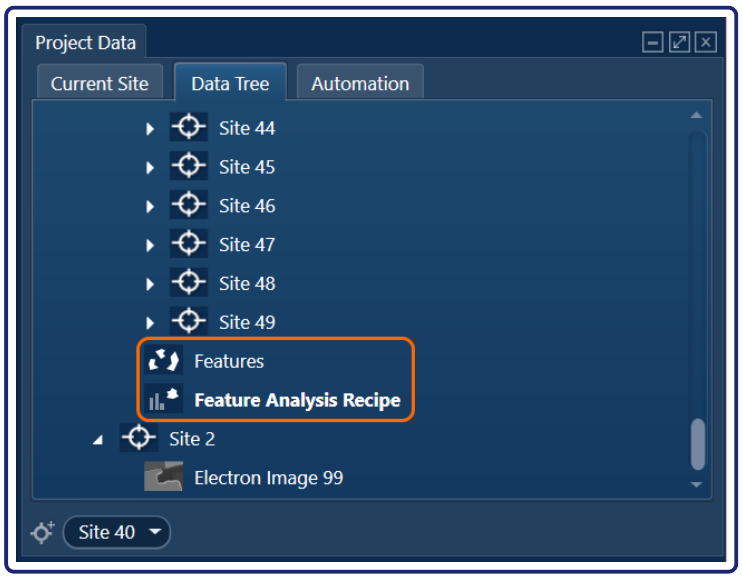
     

     As the data is extracted, a green progress bar is displayed in the acquisition toolbar showing the progress of the extraction:

     If data is being extracted for an area, select the "Run" or "Review" step to view the data for the field that is currently being extracted.

     Two new feature items are also added to the data tree:

Once the extraction has completed the data may be treated the same as for any conventionally acquired feature data.

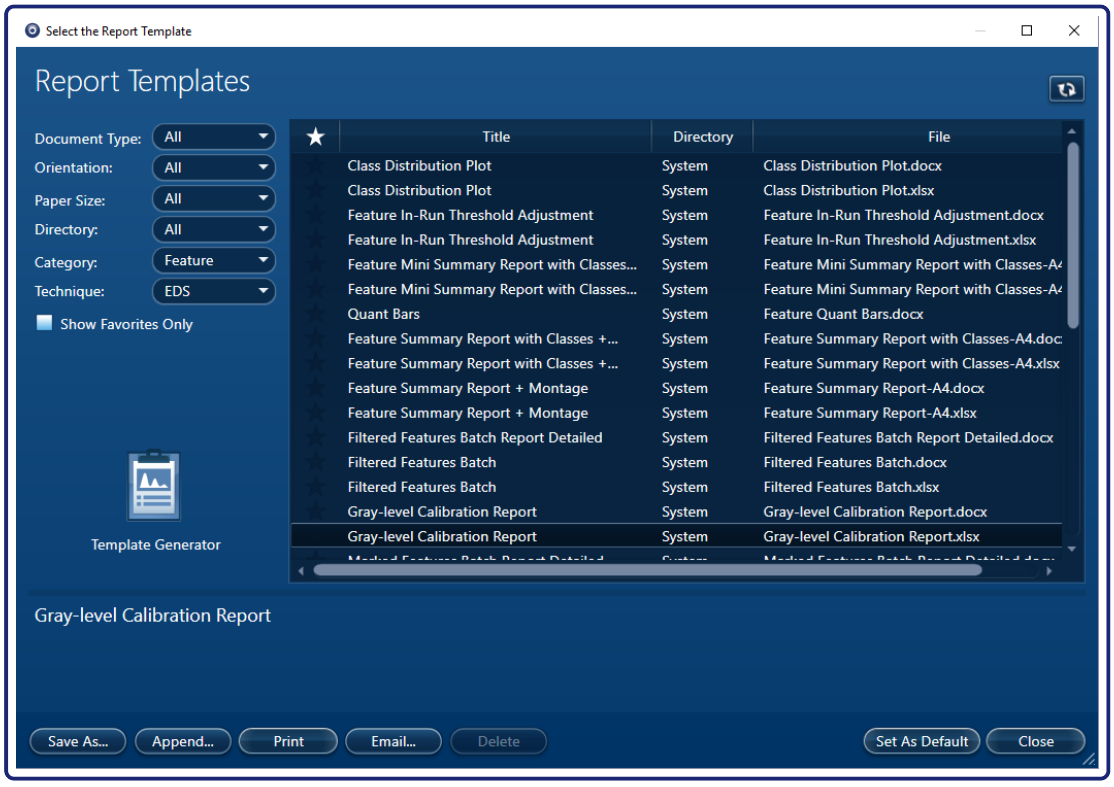
2.10. Feature Reporting

To assist with reporting feature data, AZtec has a collection of dedicated Feature report templates that are built in. They are customizable and designed to allow feature data to be reported quickly and with ease.

To view the Feature report templates:

1. Select the "Report Templates..." option from the "Report Results" drop down menu:

This will open the "Select the Report Template" window:

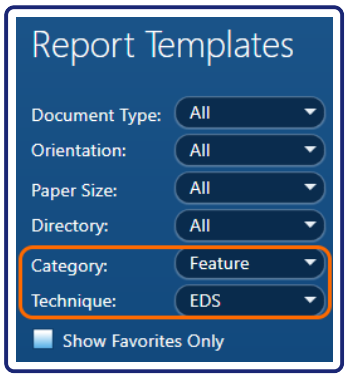


The templates available within the Report Template window include the options to report:

- Run summaries: include run completion and classification details (i.e. Feature Summary Report).
- Plots from the feature data viewer: detailed plots as displayed on the summary tab (i.e. Ternary Plot).
- Detailed feature information: batch reports giving all details of selected features (i.e. Filtered Features Batch Report).

- System validation: report the feature calibration results (i.e. Feature In-Run Threshold Adjustment or gray-Level Calibration, Pre & Post Run Beam Measurements).

2. Select the "EDS" option from the Technique drop down menu and the "Feature" option from the Category drop down menu:



   Now only Feature specific report templates will be displayed in the table.

3. Select the appropriate template.
4. Select how the template should be added to the report (i.e. Set as Default, Save As.., or Append...).

2.11. Exporting Feature Data

Feature data can be exported in several formats.

From the Data Tree

The possible export options available include:

- **Export (Inclusion Classifier):** Export the full feature data to the application, Inclusion Classifier for further analysis.

  This is intended for use with Feature Data on non-metallic inclusions in steel.

- **Export (Full Analysis):** Export the full data table including all areas within a specimen into a file with the extension ".fullexport".

  This can be useful for post processing multiple areas of Feature Data simultaneously.

- **Export (Classification Summary):** Export a summary of the classified and unclassified features for multiple areas in a specimen. The data is saved into a file with the file extension ".csummaryexport".

  This is useful for quickly understanding the number of features classified in multiple runs.

- **Export (Specimen Summary):** Export a summary for all of the classes for each area in the selected specimen. The number of features and fields analyzed for each area is given. The data is saved into a file with the file extension ".ssumaryexport".

To use one of these export options:

1. On the Data Tree, right-click the site, specimen or area to access the context menu.
2. Select the appropriate export option.
3. Type a file name, then click "Save".

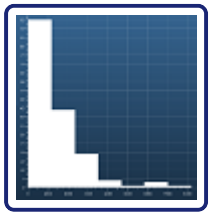
For spreadsheets

All of the data in the "Feature Data" viewer can be copied so that it can be pasted into other programs such as Microsoft ® Excel® or Notepad.

1. In the "Feature Data" viewer, right-click then select "Copy".
2. Open the program into which the data is to be pasted and paste the data.

For files, documents and email

An image of the histogram can be saved as a graphic file, or pasted into a document or email.



1. On the "Summary" tab, right-click, then select "Export".
2. To make a copy of the image, select "Copy". Open the document or email, and paste the image.
3. To create an image file, select "Save As". Type a file name, then click "Save".

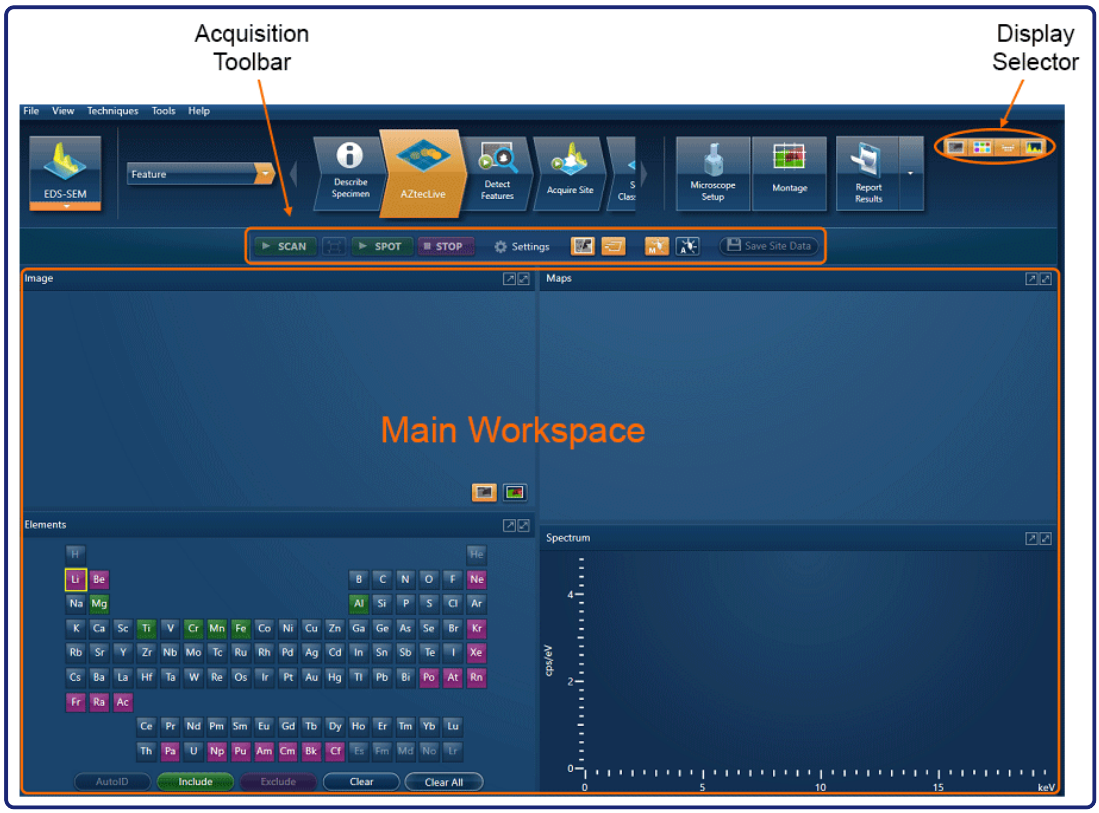
3. Feature Workspace

This section contains help for the AZtecFeature workspace. It explains the functionality available for each AZtecFeature step.

It includes the sections:

3.1. The AZtecLive Workspace

The AZtecLive navigator step has the structure shown below:



Item	Description	
Acquisition Toolbar	Contains the settings and acquisition controls for the current navigator step.	
Display Selector	Select the items to be displayed in the main workspace:	
		Display the Image pane.
		Display the EDS Maps pane.
		Display the Elements pane. Use to view the elements detected, select elements to be included or excluded and whether to use AutoID.
		Display the spectrum pane.
Main Workspace	Displays the items currently selected using the Display Selector as up to four panes. Use the arrows in the top right corner of each pane to undock or maximize each pane.	

It can be used in conjunction with the Live Trace Mini View.

3.1.1. Acquisition Toolbar

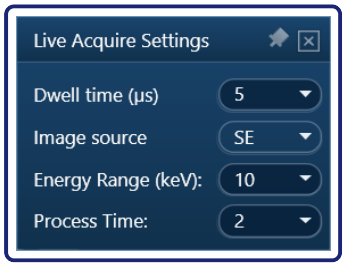
The acquisition toolbar contains the tools used to control AZtecLive:

Item	Description
SCAN	Start simultaneous acquisition of the electron image and EDS data.
	Switch to reduced area scan. This feature can be useful when focusing the sample.
SPOT	Puts the beam into spot mode. The spot is marked by a yellow cross on the electron mode. This feature can be useful for viewing the EDS spectrum for a single spot, rather than the entire field of view.
STOP	Stop the acquisition.
Settings	Access the Live Acquire settings.
	Improve the quality of the EDS data when the sample is stationary. Select this option to allow AZtec to improve the quality of the image and maps by integrating the data during periods where the microscope stage is stationary and there are no changes to the image settings. As soon as any changes to the microscope stage position or the image settings are detected the image and map data will be constantly refreshed.
	Motion detection sensitivity. This option is available when the "Improve quality when stationary" option is selected. By default it should be selected (orange). When active (orange), AZtecLive will monitor the image for changes. When a change in the image is detected, AZtecLive will switch out of the "Improve quality when stationary" mode and refresh the image and map data every frame. In cases where the image quality or stability is poor (i.e. there are fluctuations in brightness and contrast, high image noise or vibration), apparent changes in the image may cause AZtecLive to switch out of "Improve quality when stationary" mode even though no real change in the image has occurred. In this situation, this option should be disabled (button appears blue). AZtecLIVE will then remain in the "Improve quality when stationary" mode as long as no stage movements or changes in either the working distance or magnification are read through the microscope communications.
	Apply manual brightness and contrast adjustment.

Item	Description
	Apply automatic brightness and contrast adjustment.
Save Site Data	Save the displayed image, maps and spectrum.

3.1.2. AZtecLive Acquire Settings

The Live Acquire Settings window is used to define the settings to be used by AZtecLive:



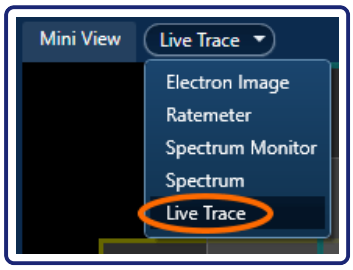
Select:

- **Dwell time (µs):** The amount of time that the beam spends on each pixel.
  The greater the dwell time, the greater the amount of data acquired from each pixel will be. However, the longer it will take to acquire an image.
- **Image source:** Select the image input source.
  The SE image input source will allow the image source currently selected on the microscope to be displayed. The BSE image input signal is only available on certain systems, where it is connected.
- **Energy Range (keV):** The energy range used to collect the EDS data.
  The most suitable energy range depends on the microscope accelerating voltage. It should be set so that all energy lines that are likely to be excited are displayed. For example, if the microscope is set to 10 keV, the 0-10 keV energy range is most suitable as plotting higher energies will not reveal any additional data as no energy lines above 10 keV will be excited. If the microscope is set to 15 keV, the 0-20 keV energy range is likely to be more suitable as it will allow the energy lines between 10 and 15 keV to be revealed.
- **Process Time:** The length of time spent processing the X-ray signal coming from the EDS detector and removing noise from the data.
  If the process time is set to “default”, the process time will be set to a fixed general purpose process time. For the fastest acquisition rates, with some loss in resolution, select a low process time. To improve the resolution of the spectrum or resolve elements that have similar energies use a higher process time.

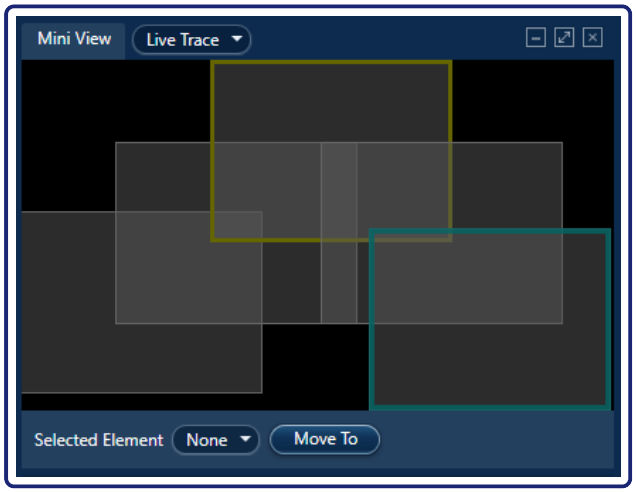
3.1.3. Live Trace Mini View

The Live Trace Mini View is a useful tool that may be used in conjunction with the AZtecLive navigator step. It allows the areas of the specimen that have been visited to be visualized. It can also provide a visual assessment of which locations contain an element of interest.

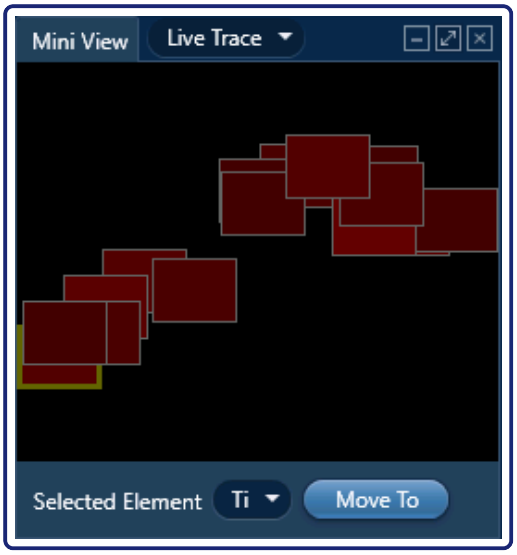
The Live Trace Mini View is automatically selected whenever the AZtecLive navigator step is selected. It can also be accessed by selecting the Live Trace option from the drop down menu at the top of the Mini View pane:



It has the layout:



Item	Description
Main Workspace	Represents the size and position of each scanned field on the specimen using white rectangles. The current field of view is highlighted in blue. The currently selected field is highlighted in yellow. ***NOTE:*** *If the project contains a registered image, then this image will automatically be displayed as a background image in the Live Trace mini view, where it can be used to help navigate around the sample.*
Selected Element	Use the selected element drop down menu to select an element to be displayed. All fields containing the element will be shown in red. The brighter the shade of red, the greater the weight % of the element in that field. For example:

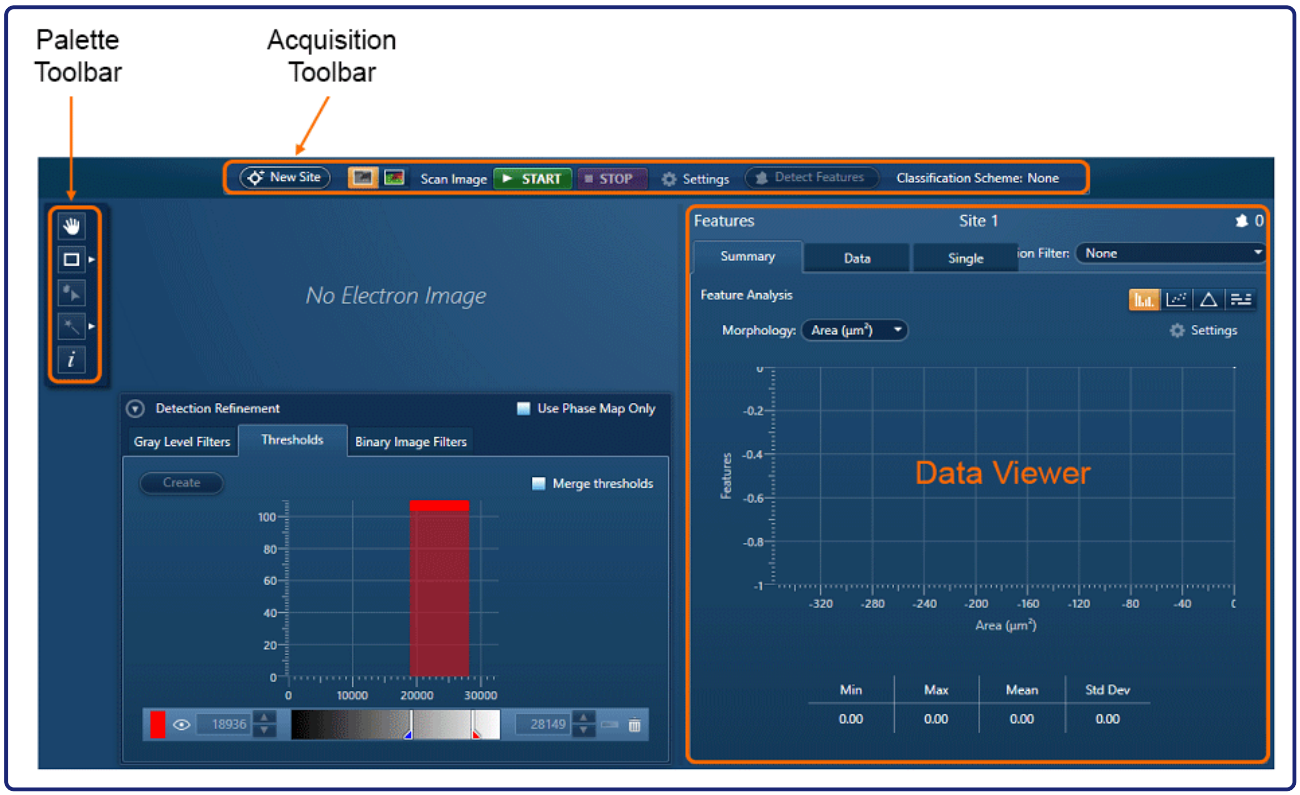
Item	Description
	
Move To	Select a field from the main workspace (highlighted in yellow) and then click "Move To" to move the microscope stage to that field of view.

The field of view in the Live Trace should automatically re-size as the specimen is explored showing the full extent of the fields scanned. To investigate the area it is possible to:

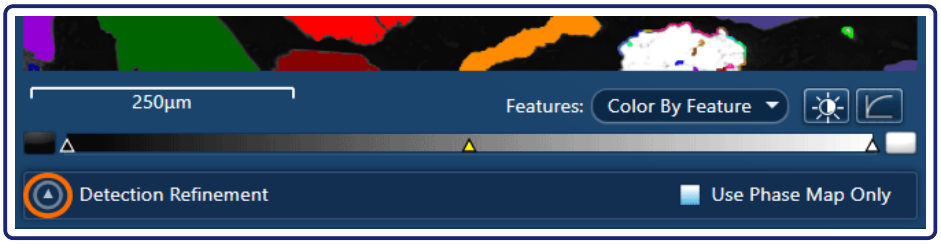
- Zoom in and out on the field of view using the mouse wheel.
- Pan around by holding the left mouse button down while moving the mouse.
- Return to the full field view by right clicking on the main workspace and selecting "Fit Image to Display".

3.2. The Detect Features Workspace

The Detect Features navigator step has the structure shown below:



Item	Description
Palette Toolbar	Contains tools relevant to the current workspace.
Acquisition Toolbar	Contains the settings and acquisition controls for the current navigator step.
Main workspace	The main workspace can be split into three panes: 1. The upper left pane contains the Image Viewer pane and is used to display the current electron image. Depending on the option selected in the Features drop down menu below the electron image, it may also show the detected features. 2. The lower left pane contains the detection refinement controls for: • Defining the gray-level thresholds. • Optimizing the image using gray-level filters. • Optimizing the how the features are detected using binary image filters. If this pane is not visible, click the up arrow to the right of the Detection Refinement tab at the bottom left of the main workspace:

Item	Description
	 3. The right pane contains the Data Viewer which can be used to view all of the Feature data for the current site or area.

3.2.1. Palette Toolbar

The Palette toolbar contains the tools that are relevant to the current workspace.

Item	Description
	**Pan:** Allows images to be panned (moved) around and zoomed in and out. For more information on panning and zooming images, see in The Detect Features Workspace section section of Imaging the Sample.
	**Annotate:** Allows images to be annotated. For more information on annotating images, see in The Detect Features Workspace section.
	**Select Feature Tool:** Allows individual features to be selected on the electron image and the corresponding data in the "Feature Data" viewer to be highlighted and vice versa. To select several features, press the "Ctrl" button down on the computer keyboard while selecting the features.
	**Wand Tool:** Used to select an area of pixels from which the gray-levels will be set as part of assisted thresholding.
	**Show Data Value Tool:** To view the information for a specific data point: 1. Select the "Show Data Values" tool from the palette toolbar. 2. Hover the mouse over the data point. The data for that point will be displayed.

Pan and Zoom Tool

To assist with viewing and interrogating electron images or maps, AZtec has the functionality to allow images to be panned (moved) around and also zoomed in and out. To access these facilities click the pan tool icon in the palette toolbar on the left of the screen:

When in display modes with multiple images and maps, prior to starting to zoom or pan, it is recommended to select whether to zoom in or out on a single image or map using the link tool:

NOTE: *The individual images and maps are linked when the button has an orange background.*

There are two methods that can be used to zoom in and out on an image or map:

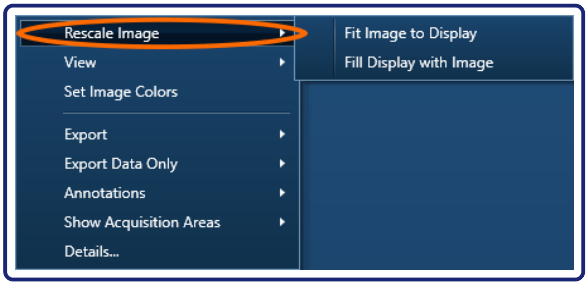
1. Using the scroll wheel on the mouse while hovering the mouse over the image or map.
2. Simultaneously holding down the "Ctrl" key on the computer keyboard and the left mouse button on the image or map. Move the mouse to the right to zoom in and to the left to zoom out.

To move images or maps around, with the pan tool selected, press the left mouse button down and drag the image about. Release the left mouse button to stop moving the image.

Images can be returned to their original size by:

1. Right click on the image to access the context menu.
2. For an individual image or map in the Display pane select "Reset Image Scales".

   For an electron image, layered image or map displayed in the Image pane, select "Rescale Image" and then select either "Fit Image to Display" or "Fill Display with Image".

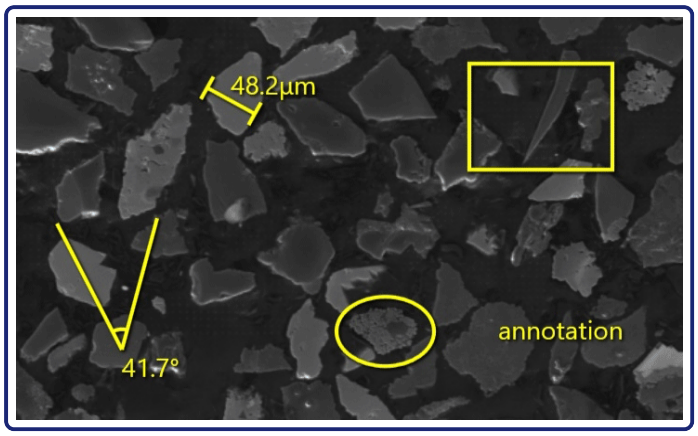


Annotation Tool

The annotate tool can be found in the palette toolbar:

It allows images and spectra to be annotated including:

- Features and angles to be measured.
- Rectangular and elliptical markers to be created to highlight features.
- Text to be added.



To create an annotation, click on the arrow to the right of the annotation tool in the palette toolbar. This will maximize the list of annotation tools available:

To create a rectangular or elliptical marker:

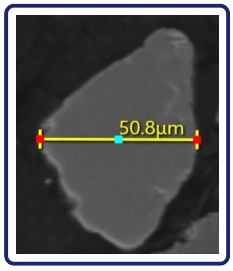
1. Press the left mouse button down at the start point.
2. Drag the mouse to draw out the shape.
3. Release the left mouse button to complete the annotation.

To add text:

1. Click the left mouse button at the point where you would like the text to be displayed.
2. Add the text.
3. Click again to complete the action.

To delete or edit an annotation:

1. Select the pan tool (hand symbol) from the palette toolbar.
2. Click on the annotation so that it is selected (highlighted by red dots).

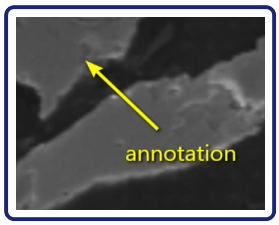


3. Press delete on the computer keyboard to delete it, or click and drag the red dots to move or resize it.

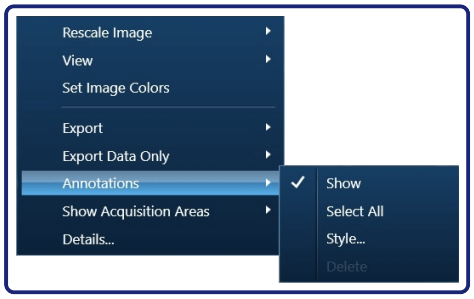
To add an arrow to a text annotation:

1. Select the text by clicking on it.
2. Press and hold the left mouse button down on the red dot where the arrow will be added.
3. Drag the dot to form an arrow.

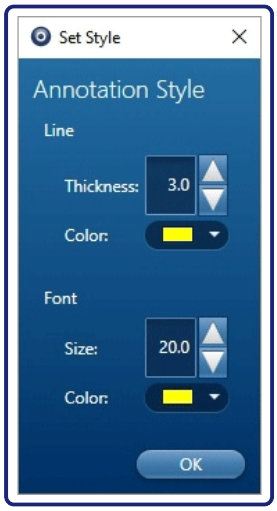
4. Release the mouse button to complete the action.



The style of an annotation can be configured by right click on the image or map to access the context menu and selecting "Annotations" and "Style...".



This will open the Set Style window where the line and font size and color can be specified:



All annotations made after changing these settings and existing annotations selected when changing the style, will displayed in the new style. Existing annotations that were not selected will be displayed in the old style.

The annotation display can be changed using the context menu and checking or unchecking the "Annotations", "Show" option.

3.2.2. Acquisition Toolbar

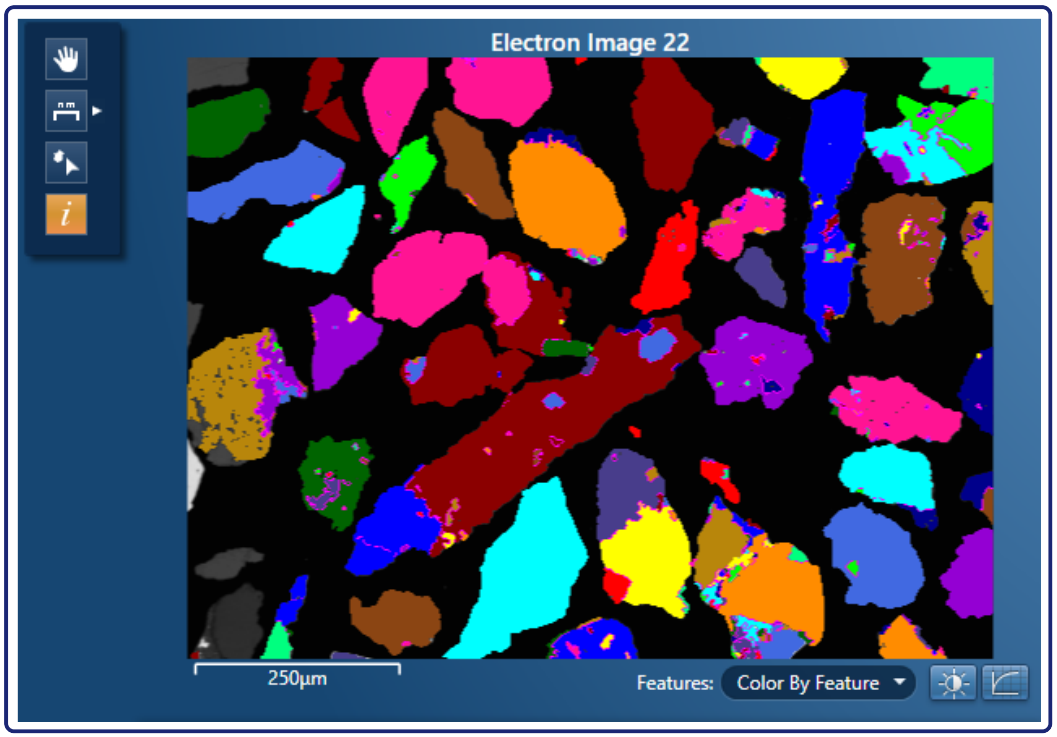
The acquisition toolbar contains the acquisition tools and settings relevant to the navigator step.

Item	Description
New Site	Create a new site of interest in the data tree.

Item	Description
	Specify that an electron image is to be acquired.
	Specify that both an electron image and EDS data are to be acquired. For more information on using this feature, see the Separating Features from Backgrounds with Similar Gray-Levels section.
START	Start acquiring either the electron image or the electron image and EDS data.
STOP	Stop acquiring.
Settings	Opens the Feature Image Settings window where the following settings may be found: • Electron image acquisition settings. • EDS map acquisition settings (where required for Separating Features from Backgrounds with Similar Gray-Levels). • Basic feature detection settings.
Detect Features	Forces the features to be redetected using the current settings. ***NOTE:*** *Every time the electron image is reacquired or a setting is changed, the features are automatically redetected. Therefore, this option is only applicable when a large area map is loaded and it is required to detect the features using the current settings.*

3.2.3. Feature Overlay Options

The detected features can be displayed as a color overlay on the electron image in the Image Viewer pane on most of the navigator steps.



The color scheme that is used for displaying the features may be selected from the "Features" drop down menu in the bottom right corner of the image viewer. The options available include, Color by:

- **Feature:** Each feature is displayed using a different color.

  This color scheme is useful for initial analysis and exploratory work. It generally provides a clear view of the detected features with neighboring features being displayed using contrasting colors.

- **Threshold:** Colors the features according to which gray-level threshold they lie in.

  This color scheme is useful for identifying which threshold each feature lies in. It can also be used to visualize the distribution and frequency of the features belonging to each gray-level threshold.

- **Class:** Colors the features according to which class they have been categorized as.

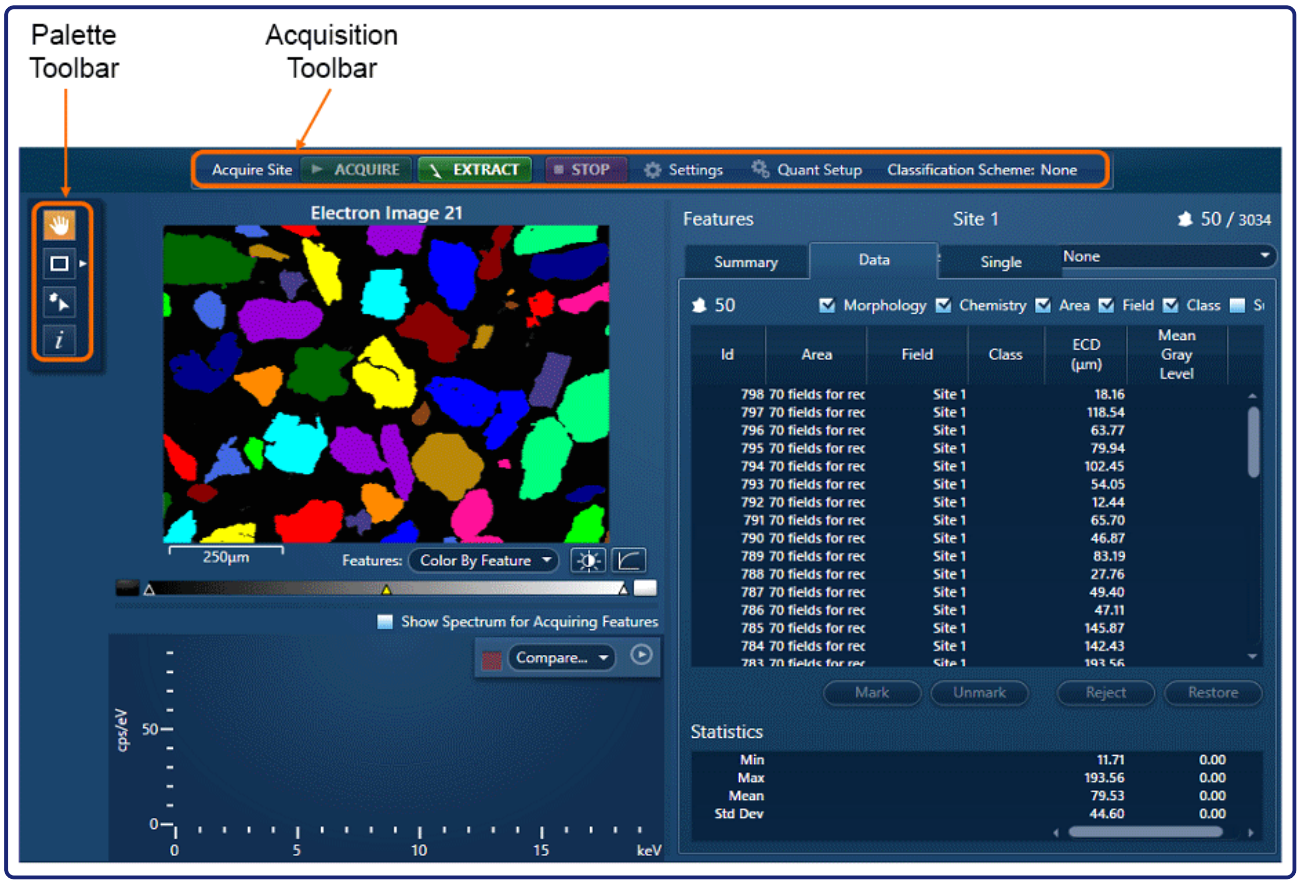
  This color scheme is useful for identifying the distribution and frequency of the features that belong to each class. It can also be used to visualize the interactions between features belonging to each of the classes.

- **Subclass:** Colors the features according to the sub-classes that they have been categorized as.
- **Phase:** Colors the features according to their phase.

  This color scheme is useful for visualizing the distribution of the different phases in the sample. Similar phases are assigned similar coloring, allowing significant changes in the chemistry of the features to be easily observed.

3.3. The Acquire Site Workspace

The Acquire Site navigator step has the structure shown below:



Item	Description
Palette Toolbar	Contains tools relevant to the current workspace.
Acquisition Toolbar	Contains the settings and acquisition controls for the current navigator step.
Main workspace	The main workspace can be split into two panes: 1. The left pane contains the electron image (top) and the spectrum (bottom) for either the currently acquiring feature, or the feature currently selected in the Data Viewer. 2. The right pane contains the Data Viewer which can be used to view all of the Feature data for the current site or area.

3.3.1. Palette Toolbar

The Palette toolbar contains the tools that are relevant to the current workspace.

Item	Description
	**Pan:** Allows images to be panned (moved) around and zoomed in and out. For more information on panning and zooming images, see in The Detect Features Workspace section section of Imaging the Sample.
	**Annotate:** Allows images to be annotated. For more information on annotating images, see in The Detect Features Workspace section.
	**Select Feature Tool:** Allows individual features to be selected on the electron image and the corresponding data in the "Feature Data" viewer to be highlighted and vice versa. To select several features, press the "Ctrl" button down on the computer keyboard while selecting the features.
	**Show Data Value Tool:** To view the information for a specific data point: 1. Select the "Show Data Values" tool from the palette toolbar. 2. Hover the mouse over the data point. The data for that point will be displayed.

3.3.2. Acquisition Toolbar

The acquisition toolbar contains the acquisition tools and settings relevant to the navigator step.

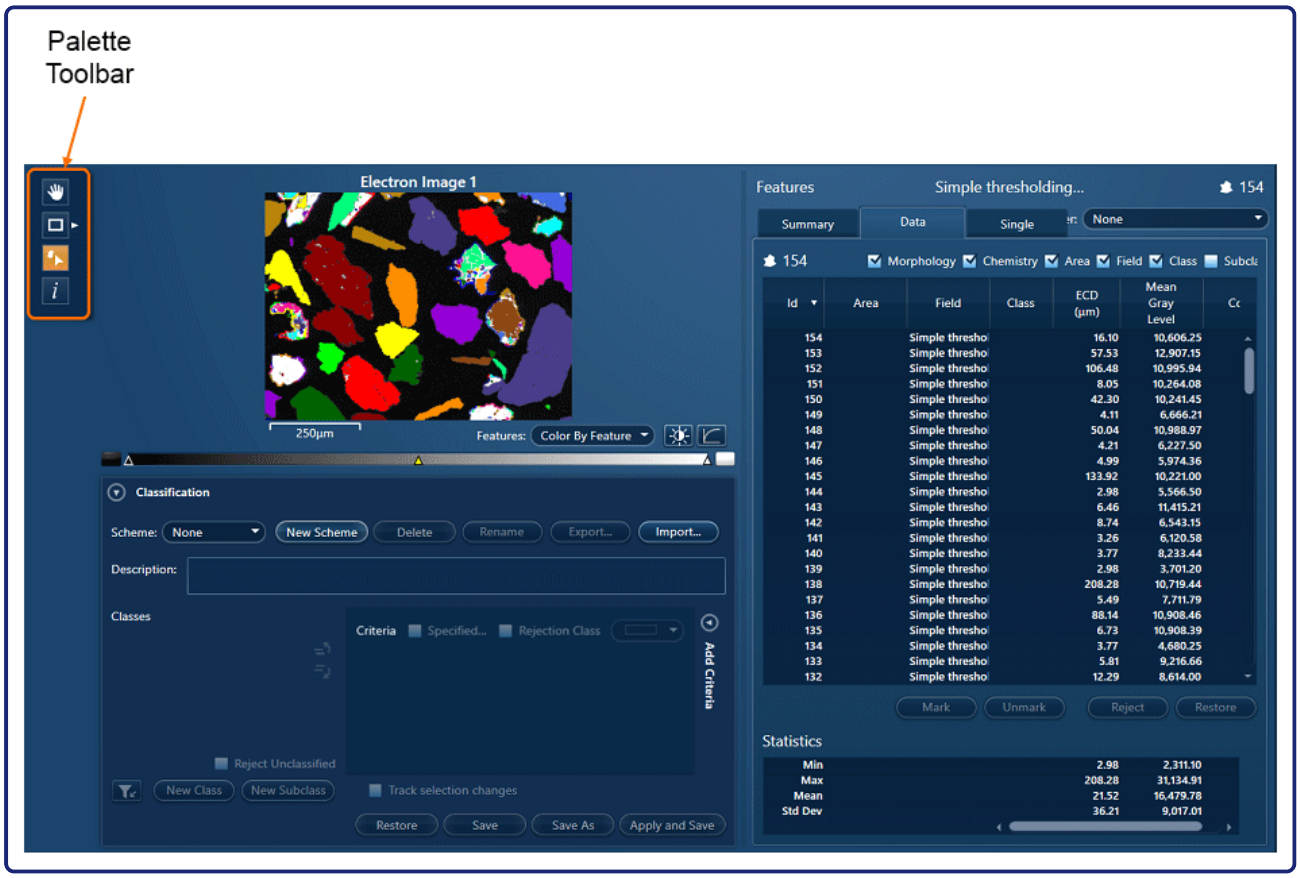
Item	Description
ACQUIRE	Acquire EDS data.
EXTRACT	Extract EDS data from an EDS map.
STOP	Stop acquiring EDS data.
Settings	Opens the Feature Analysis Settings window where it is possible to specify: • Whether to acquire second pass images. • The EDS acquisition settings. • Any morphological or EDS filters and further EDS analysis to be performed
Quant Setup	Opens the Quant Settings window where the quantitative analysis settings are specified.

3.4. The Set Up Classification Workspace

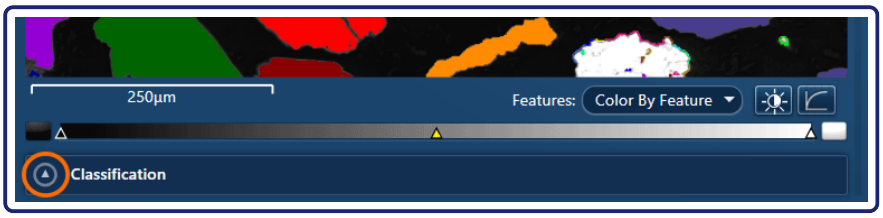
The Set Up Classification Workspace is used to:

- View and interrogate the feature data for the current site using the Feature Data Viewer.
- Create classification schemes and see the result on the data in the current site.
- Create and save classification schemes that will be used for analyzing further specimens.

The Acquire Site navigator step has the structure shown below:



Item	Description
Palette Toolbar	Contains tools relevant to the current workspace.
Main workspace	The main workspace can be split into three panes: 1. The upper left pane is the Image Viewer pane and displays the current electron image. Depending on the option selected in the Features drop down menu (described in The Detect Features Workspace section) below the electron image, it may also show the detected features. 2. The lower left pane is the Classification pane. This pane is used to load, import, create and edit classification schemes as described in the Classifying Features section. If this pane is not visible, click the up arrow to the right of the Classification tab at the

Item	Description
	bottom left of the main workspace:  3. The right pane contains the Data Viewer which can be used to view all of the Feature data for the current site or area.

3.4.1. Palette Toolbar

The Palette toolbar contains the tools that are relevant to the current workspace.

Item	Description
	**Pan:** Allows images to be panned (moved) around and zoomed in and out. For more information on panning and zooming images, see in The Detect Features Workspace section section of Imaging the Sample.
	**Annotate:** Allows images to be annotated. For more information on annotating images, see in The Detect Features Workspace section.
	**Select Feature Tool:** Allows individual features to be selected on the electron image and the corresponding data in the "Feature Data" viewer to be highlighted and vice versa. To select several features, press the "Ctrl" button down on the computer keyboard while selecting the features.
	**Show Data Value Tool:** To view the information for a specific data point: 1. Select the "Show Data Values" tool from the palette toolbar. 2. Hover the mouse over the data point. The data for that point will be displayed.

3.4.2. Classification Pane

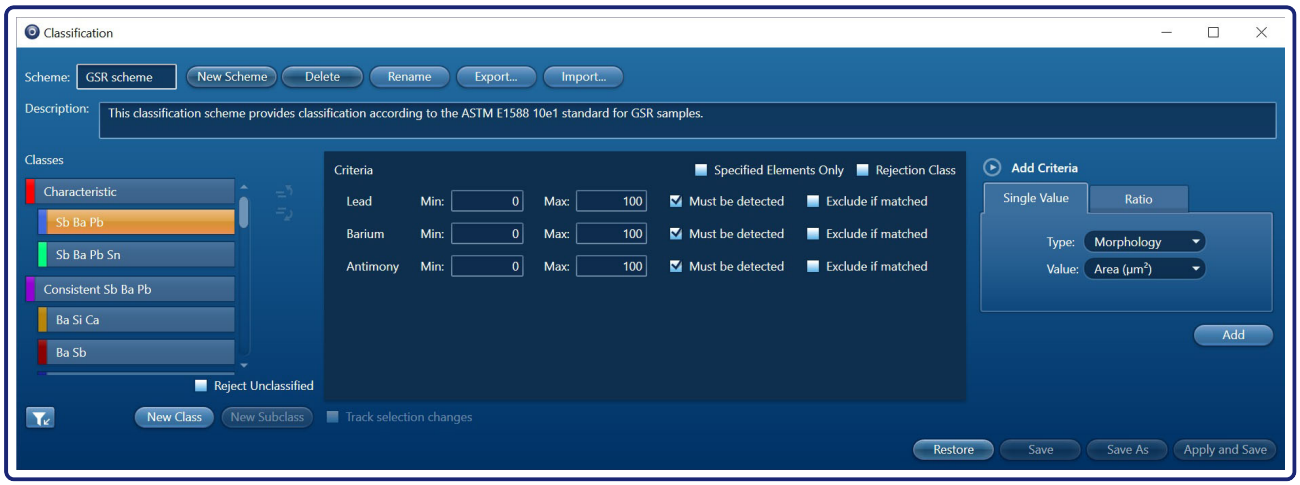
The Classification pane allows:

- New classification schemes to be created.
- Classification schemes to be shared between multiple systems, by exporting a scheme from the system on which it was created and importing it onto multiple other AZtec systems.

- Existing classification schemes to be edited

  NOTE: *They must be in an editable format (i.e. created on the current system).*

- Copies to be made of read only classification schemes and for the copies to be edited (i.e. a factory classification scheme or one that was created on another system and loaded onto the current system as part of the AZtec project).



Item	Description
Scheme	Select an existing classification scheme from the Scheme drop down menu.
New Scheme	Create a new classification scheme. Clears any currently loaded classification scheme.
Delete	Delete the currently loaded classification scheme.
Rename	Rename the currently loaded scheme using the Scheme field.
Export	Export the currently loaded classification scheme by saving the classification scheme in .oif format. The classification scheme can now be shared between multiple AZtec systems in editable format.
Import	Import an AZtec classification scheme that has been saved in .oif format.
Description	Enter a description for the classification scheme.
Classes	Within the "Classes" sub-section, all of the classes and sub-classes in the current classification scheme are listed. ***NOTE:*** *The order of the list is important.*
Reject Unclassified	When this option is selected, any feature that hasn't been classified is rejected. It will no longer be shown in the general data table or images.
	Create Classes from Filters: Import a filter into a classification scheme. See the Creating a Classification Scheme from a Filter section.
New Class	Create a new class in the current classification scheme.

Item	Description
New Sub-Class	Create a new sub-class in the current classification scheme.
Criteria	Within the "Criteria" sub-section, all of the criteria for the currently selected class or sub-class are listed.
Special Elements Only	If this option is selected, the feature must contain only the elements listed with the criteria. If any other elements are present, the feature is excluded.
Rejection Class	If this option is selected, any feature meeting the criteria for the selected class or sub-class will be rejected.
Must be Detected	If this option is selected, the result must be within the range defined by the criteria and also be statistically significant in the quant result to pass. If this option is not selected (i.e. off), then the result only needs to be within the range defined by the criteria to pass. The default is for this option to be selected. ***NOTE:*** *This setting relates to the sigma value for quant thresholding that is defined in the quant setup.*
Exclude if Matched	If this option is selected, any feature that meets the criteria is excluded from the class.
Track Selection Changes	If this option is active, the value ranges and rules will be updated, based on the features selected in the data table in the main AZtec software. As you select different features, the value ranges and element rules will be updated to correspond with those features.
Add Criteria	Use this sub-section to define a criteria to be added to the current class or sub-class.
Single Value tab	Specify criteria based on a single value.
Ratio tab	Create a criteria based on a ratio.
Type	Select to create either morphology or chemistry criteria from the drop down menu.
Value	Select the value type that the criteria will be based on using the drop down menu.
Add	Add the criteria to the current class or sub-class.
Restore	Restore all settings in the classification scheme to those that were last saved.
Save	Save the classification scheme under the current scheme name.
Save As	Save the classification scheme as a new name. Use this option to save a copy of a read only classification scheme which you can then edit.
Apply and Save	Save the current classification scheme and apply it to the current site or area.

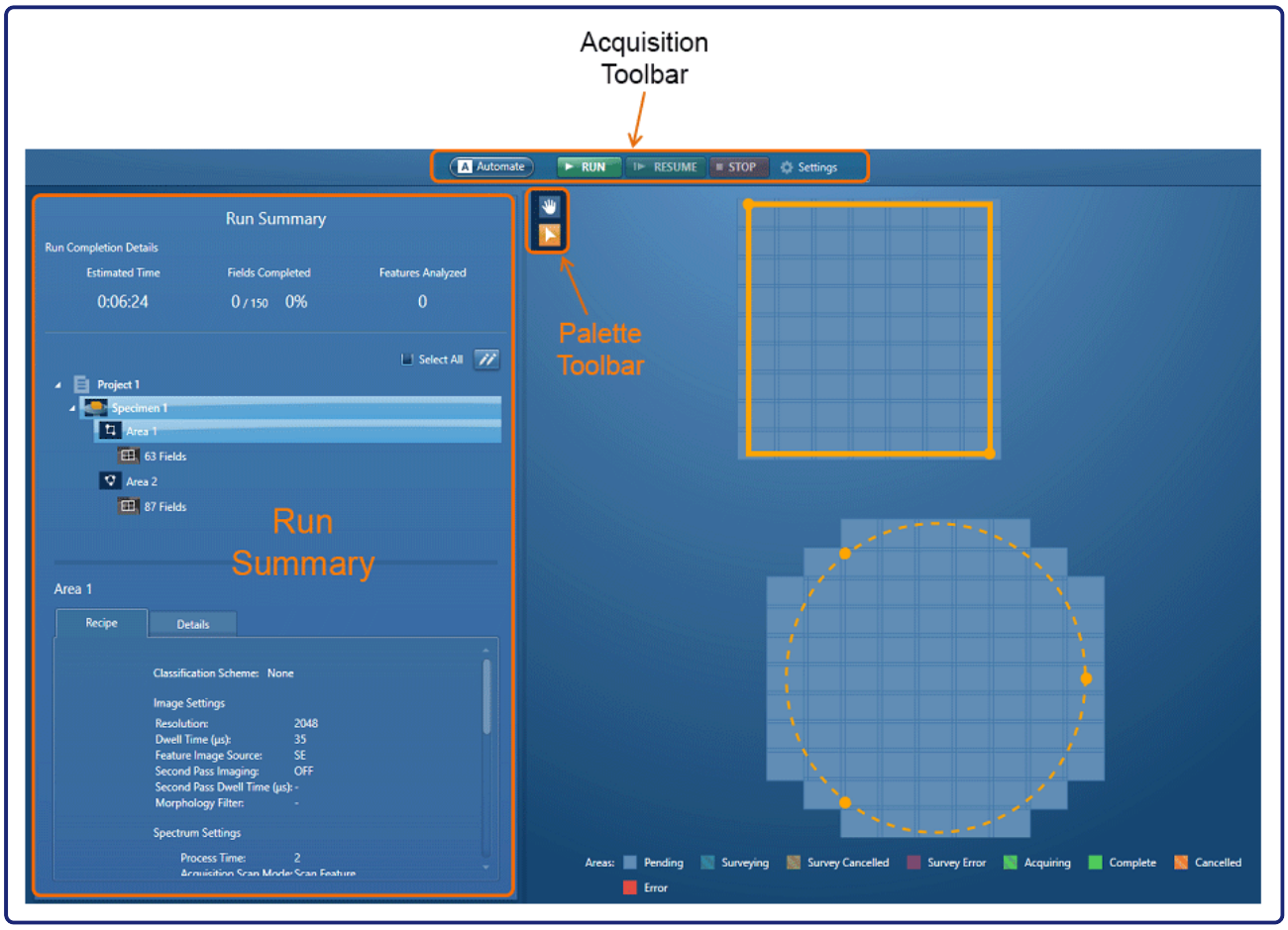
For more information on using Classification schemes, see the Classifying Features section.

3.5. The Run Workspace

The Run navigator step is used to:

- Access the Automate wizard to define large area Feature data acquisitions.
- Specify and modify the settings for large area Feature data acquisitions.
- Control the acquisition of large area Feature data acquisitions.

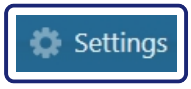
The Run workspace has the layout shown below:



Item	Description
Palette Toolbar	Contains tools relevant to the current workspace.
Acquisition Toolbar	Contains the acquisition controls for the current navigator step.
Main workspace	The main workspace can be split into two panes: 1. The left pane is the Run Summary pane. It displays a useful summary of the currently defined Feature large area acquisitions and allows their settings to be edited. 2. The right pane is the main workspace. It displays the areas for the current defined large area acquisition.

3.5.1. Acquisition Toolbar

The acquisition toolbar contains the acquisition tools and settings relevant to the navigator step.

Item	Description
	Opens the Automation wizard where large area acquisitions can be defined.
RUN	Starts acquiring data from all the fields that are listed in this window.
RESUME	Resumes data acquisition of the current run. ***NOTE:*** *This button becomes available once an acquisition has been stopped.*
	Stop acquiring data. Click once to stop the acquisition at the end of the current field. The button will change to read STOPPING to show that the acquisition will stop at the end of the current field. Click twice to stop the acquisition immediately.
	Opens the Feature Automation Run Settings window where the following settings may be found: • The standard options for a large area map acquisition. • Field alignment settings. • Feature detection and reconstruction settings. • The default field acquisition settings. • Run termination settings to specify when the acquisition can be stopped.

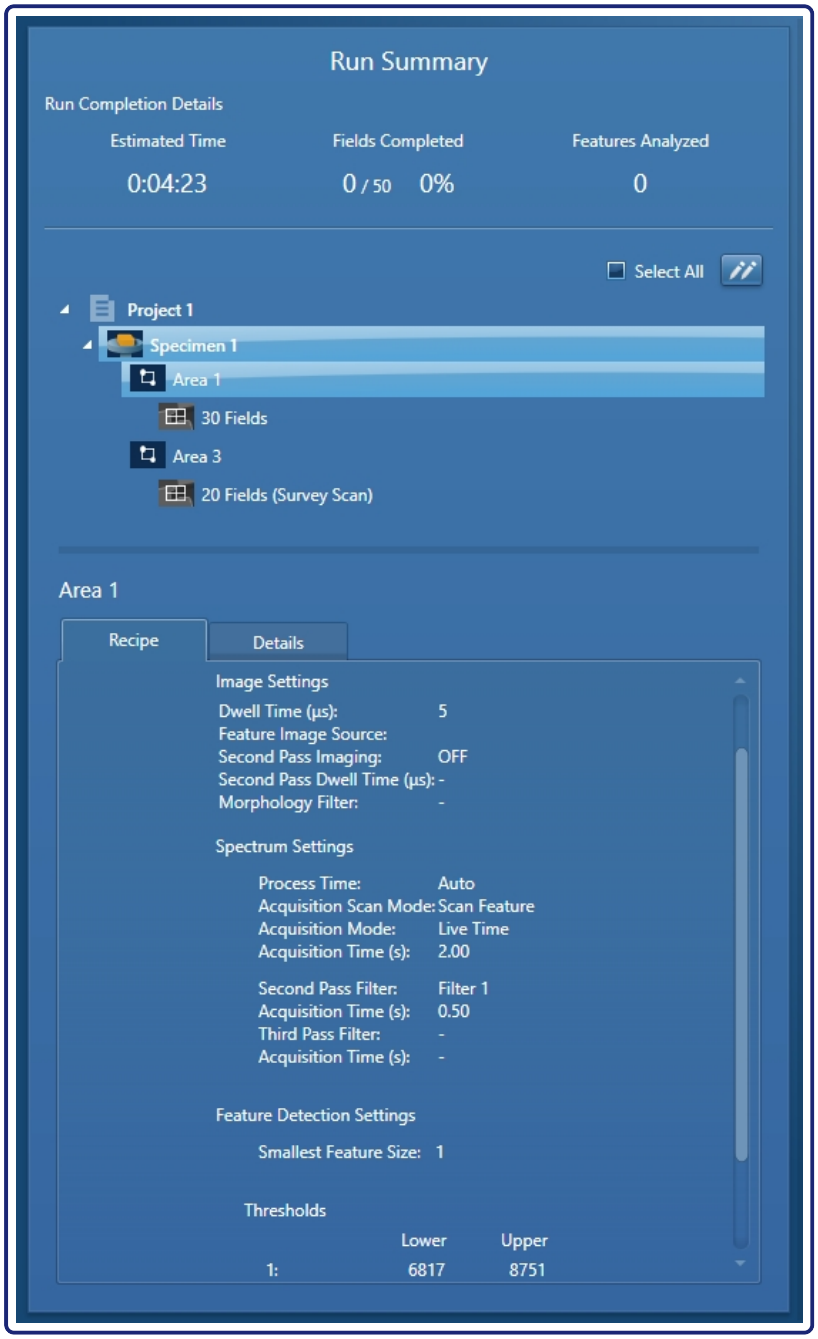
3.5.2. Palette Toolbar

The Palette toolbar contains the tools that are relevant to the current workspace.

Item	Description
	**Pan:** Allows images to be panned (moved) around and zoomed in and out. For more information on panning and zooming images, see in The Detect Features Workspace section section of Imaging the Sample.
	**Move and Select Tool:** Allows the areas displayed in the main workspace to be selected and moved. The currently selected area, will be displayed in the main workspace with a bold orange line and its details will be displayed in the Run Summary pane.

3.5.3. Run Summary

The "Run Summary" section of the "Run" step provides a useful summary of the Feature experiments that have been defined:



The top section of the Run Summary displays a summary of how the acquisition is progressing for all of the areas that have been defined including:

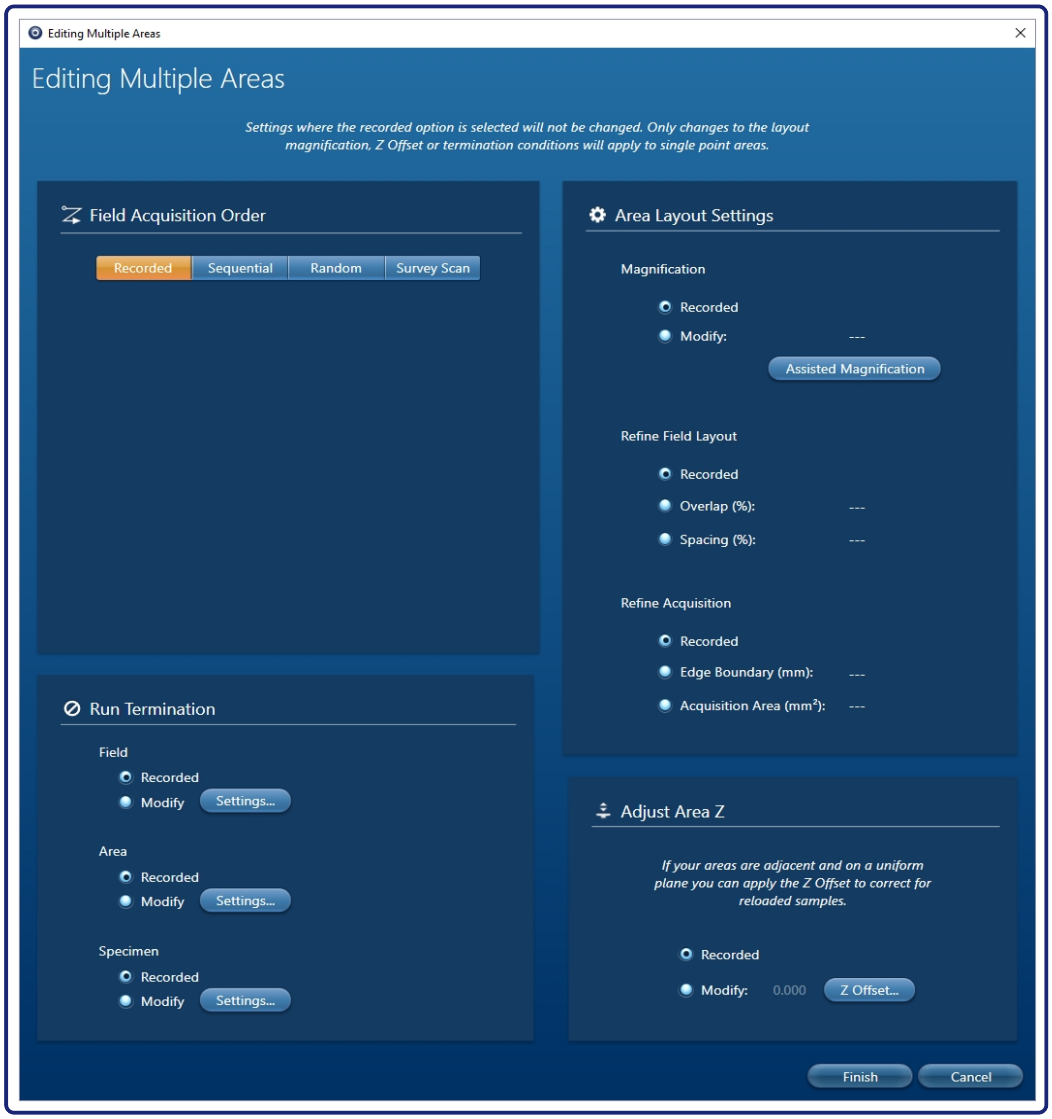
- The estimated time left to acquire all areas.
- The number of fields that have been acquired as a fraction of the total number of fields and as a percentage.
- The number of features analyzed.

The middle section of the Run Summary shows all of the areas that have been defined in the project. The settings for one or more of the areas in this list can be edited by:

1. Selecting the areas to be edited from either this Run Summary or the Data View.
2. Clicking the edit settings button:

This will open the "Editing Multiple Areas" window, which can be used to change the settings for:

- The field acquisition order including the Survey scan settings.
- The termination conditions.
- The area layout settings.
- Correcting the z-offset between acquisition areas.



For information on using the "Editing Multiple Areas" window see the **Modifying Feature Large Area Acquisition Settings** section.

If a single area is selected in the middle section of the Run Summary, then at the bottom of the section of the Run Summary, the recipe information and detailed area information for that area will be displayed in the

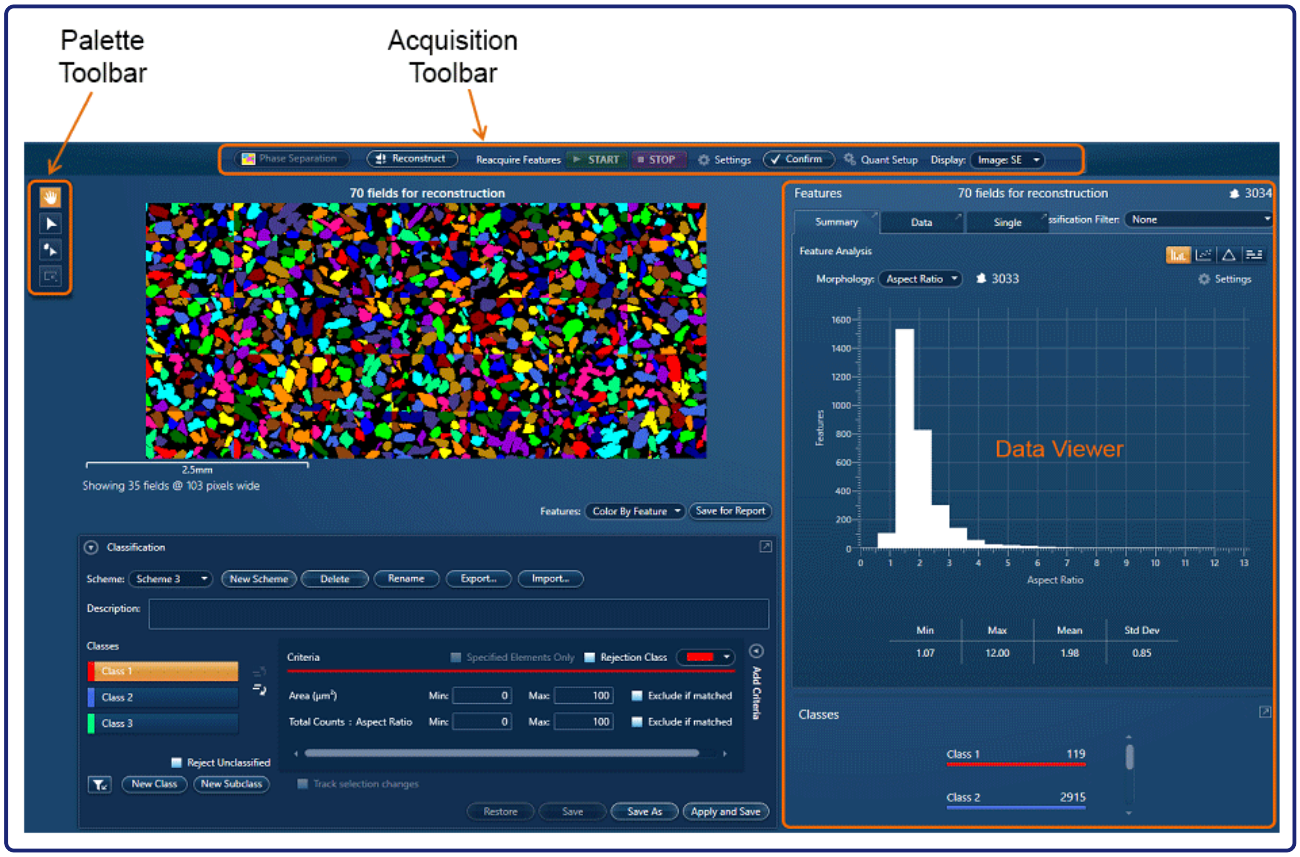
"Recipe" and "Details" tabs. This section is useful for easily checking the current settings that have been defined for that area.

3.6. The Review Workspace

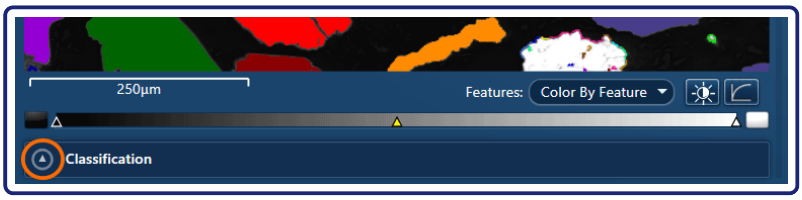
The Review navigator step is used to:

- Review individual features or groups of features (Classes).
- Reject unwanted features and mark features of special interest for further analysis.
- Modify existing classes or add new ones as described in the Classification Schemes section.
- Reconstruct features that cross multiple fields.
- Reacquire data for selected features.
- Create reports using the report templates.

The Review has the layout shown below:



Item	Description
Palette Toolbar	Contains tools relevant to the current workspace.
Acquisition Toolbar	Contains the acquisition controls for the current navigator step.
Main workspace	The main workspace can be split into three panes: 1. The upper left pane contains the Image Viewer pane and is used to display the montaged electron image for all of the fields in the current large area map.

Item	Description
	Depending on the option selected in the Features drop down menu (described in The Detect Features Workspace section) below the electron image, it may also show the detected features. 2. The lower left pane is the Classification pane described in The Set Up Classification Workspace section). This pane is used to load, import, create and edit classification schemes as described in the Classifying Features section. If this pane is not visible, click the up arrow to the right of the Classification tab at the bottom left of the main workspace:  3. The right pane contains the Data Viewer which can be used to view all of the Feature data for the current site or area.

3.6.1. Palette Toolbar

The Palette toolbar contains the tools that are relevant to the current workspace.

Control	Description
	**Pan:** Allows images to be panned (moved) around and zoomed in and out. For more information on panning and zooming images, see in The Detect Features Workspace section section of Imaging the Sample.
	**Move and Select Tool:** Allows the areas displayed in the main workspace to be selected and moved. Click on a field to select it. Press the left mouse button down and drag the mouse to move a field. To select several fields, hold down the Ctrl key while selecting the fields.
	**Select Feature Tool:** Allows individual features to be selected on the electron image and the corresponding data in the "Feature Data" viewer to be highlighted and vice versa. To select several features, press the "Ctrl" button down on the computer keyboard while selecting the features.
	Relocate the stage to a specific field in the montage for closer examination. With the tool selected, double-click on the field to which the stage should relocate. When the stage has reached the selected position, an electron image is acquired for the field.

3.6.2. Acquisition Toolbar

The acquisition toolbar contains the acquisition tools and settings relevant to the navigator step.

Item	Description
	Reconstruct features that lie in multiple fields as a single feature.
Start	Start reacquisition of the selected features.
Stop	Stop reacquisition of the selected features.
Settings	Specify the Feature Reacquisition Settings as described in the Reacquiring Feature Data section.
	Opens the Review Reacquired Features window where it is possible to accept or reject the reacquired data for a feature. For more information, see the Confirming Reacquired Feature Data section.
Quant Setup	Specify the quantitative analysis settings.
Display	Use the Display drop down menu to select the type of image to be displayed (i.e. SE or BSE).

3.7. Feature Data Viewer

The Feature Data Viewer is used to view all of the Feature data for the current site or area. It can be accessed from the following steps:

- Detect Features
- Acquire Site
- Setup Classification
- Review

It can be used to:

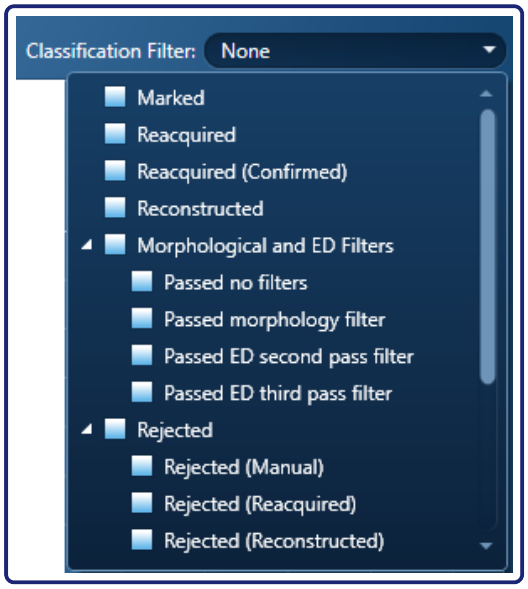
- Interrogate the results for a site or area.
- View the results of applying a classification scheme on a site or area.
- Mark and reject features.
- Select features for further interrogation (Review step).

The Feature Data Viewer contains three main tabs:

- The Summary tab: The data can be viewed as a histogram, scatter plot, ternary plot or as quant bars, with a summary of the statistics displayed below.
- The Data tab: The data is displayed in a table.
- The Single tab: For a single feature, view the image, morphology and chemistry results and the EDS spectrum.

At the bottom of the data viewer is the classification summary. It shows all of the classes in the currently applied classification scheme including the color of the class and the number of features in it.

The classification filter drop down menu is used to select which features to view and work with in the data view:



It is useful for focusing on the different types of features in the data viewer.

The number of features displayed in the top right hand corner above the Classification Filter drop down menu, is the number of features in the area.

The number of features displayed within the data tabs, is the number of features being currently displayed.

3.7.1. The Summary Tab

The Summary Tab allows the statistical feature data to be viewed. There are four different ways in which the data can be displayed:

Item	Description
	Data is presented as a Histogram.
	Data is presented as a Scatter Plot.
	Data is presented as a Ternary Plot.
	Data is presented as a Quant Distribution Chart.

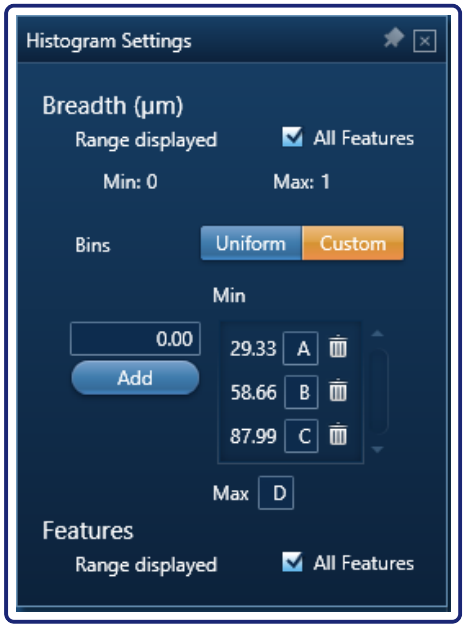
Data presented as a Histogram

Feature data may be summarized as a Histogram where the data is categorized into a number of bins.

To view the data in a histogram, click the Histogram icon on the Summary tab of the Feature Data Viewer:

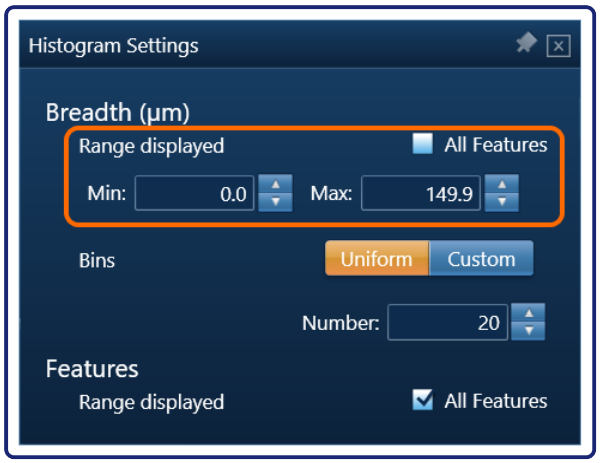
Select between plotting Morphology and Chemistry data and the type of morphology measurement or the element as relevant.

Use the Settings menu to specify the histogram display settings:

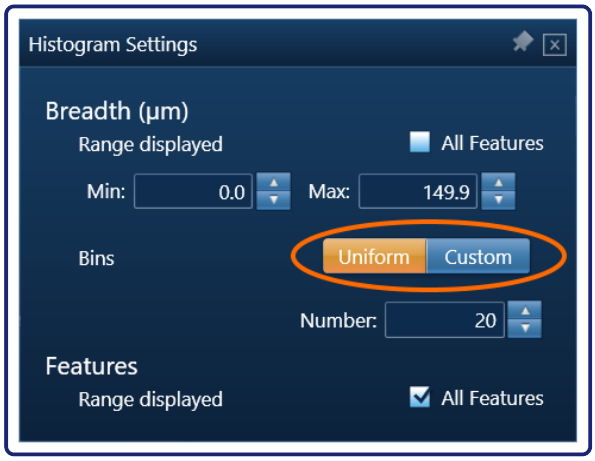


Choose between:

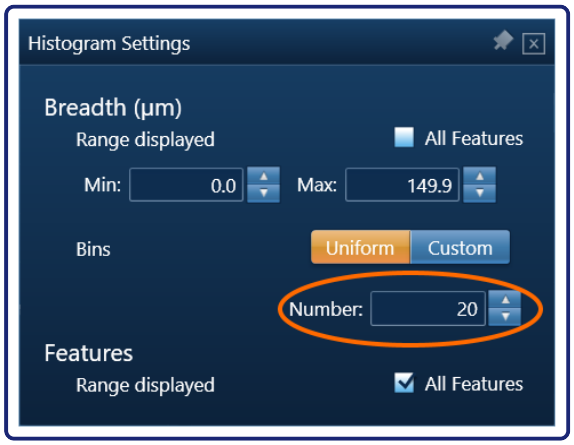
- Displaying the data for "All Features" or only features within a certain data range.



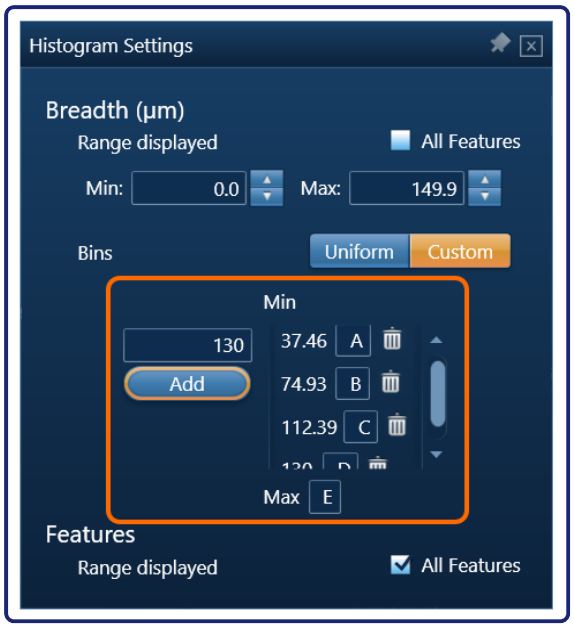
- Using Uniform or Custom defined bins of varying widths.



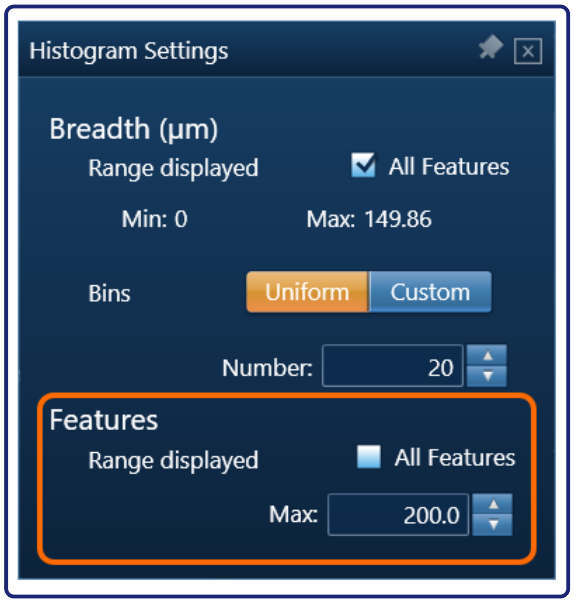
For "Uniform" bins specify the number of bins.



For "Custom" bins specify the number of bins and their sizes.



- Whether to set the y-axis to display all features or only a certain range.



Below the histogram is the statistics for the data measurement currently being displayed. It includes the minimum, maximum, mean and standard deviation values.

Interrogating the Data in a Histogram

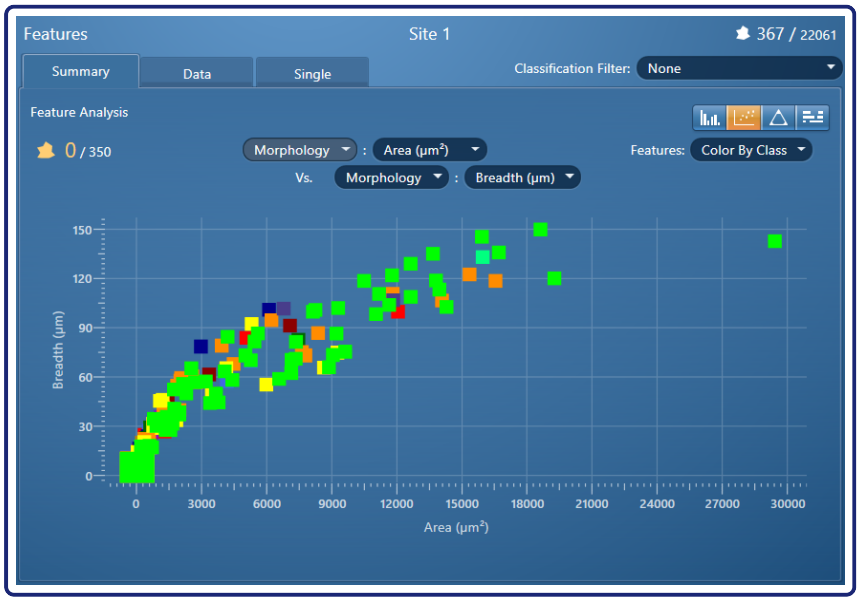
To zoom in on the histogram, either use the middle mouse wheel or press the Shift button on the computer keyboard and press the left mouse button down. Drag the mouse to select the area to zoom to.

When zoomed in on the histogram, press and hold the left mouse button down to drag the histogram around and focus on different parts of the histogram.

Right click and select "Reset Scales" to return to the full view of the histogram.

Data Presented as a Scatter Plot

Feature data may be summarized as a Scatter Plot, where one parameter is plotted against another.



To view data as a Scatter Plot:

1. Click the Scatter Plot icon on the Summary tab.
2. Select the measurement type to be plotted on each axes. Choose between plotting morphology and chemistry data as well as the type of morphology measurement or the element as relevant.
3. Select whether to color the data by class or sub-class using the Features drop down menu.

Interrogating the Data in a Scatter Plot

Zoom in on the scatter plot by either using the middle mouse wheel or press the Shift button on the computer keyboard and press the left mouse button down. Drag the mouse to select the area to zoom to.

When zoomed in on the scatter plot, press and hold the left mouse button down to drag the scatter plot around and focus on different parts of the data.

Right click and select "Reset Scales" to return to the full view of the scatter plot.

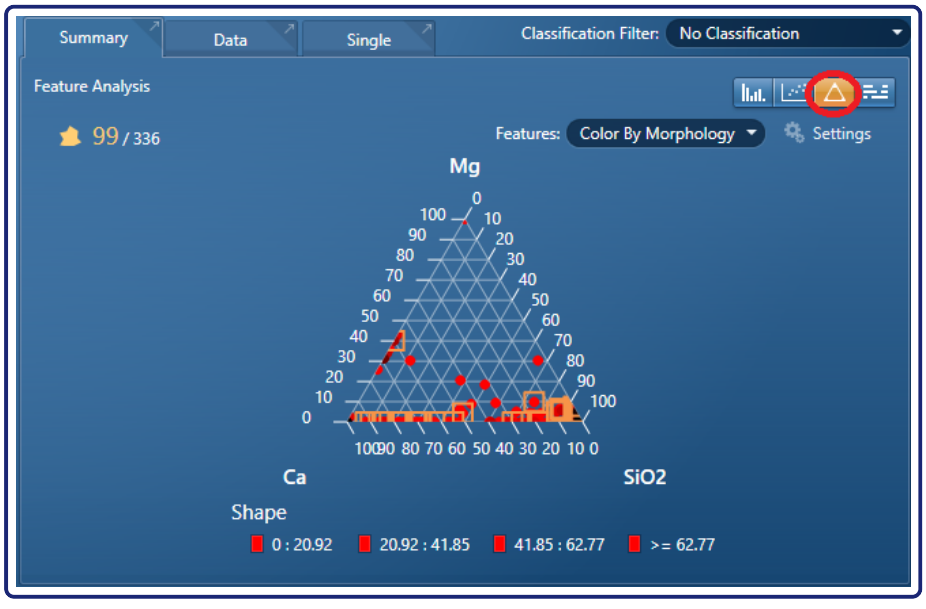
To select a single feature in the scatter plot click once on it. The feature will also be highlighted in the image. Click on an empty space in the plot to clear the selection.

To select multiple features, hold down the 'Ctrl' button on the computer keyboard and click once on each of the features to be selected. Alternatively, to select a number of features that are close together, hold down the 'Ctrl' button on the computer keyboard and then press the left mouse button down and drag the mouse to select all of the features within the selected range.

To deselect specific features when multiple features have been selected, hold down the 'Alt' button on the computer keyboard and click once on each feature to be deselected. To deselect a number of features close together while leaving other features still selected, hold down the 'Alt' button on the computer keyboard and then press the left mouse button down and drag it to deselect all of the features within the selected range.

Data presented as a Ternary Plot

Feature data may be summarized as a Ternary Plot that displays the proportion of three variables that sum to a constant. It is useful for visualizing data where more than two elements are being examined:



To view a Ternary plot:

1. Click on the Ternary Plot icon on the Summary tab.
2. Click on the settings icon.

   This will open the ternary plot settings window:

3. Select the element(s) to be assigned to each corner.

   Additional elements may be added to each corner by clicking the "Add" button at that corner.

4. Select the anion for each corner.

   If there are multiple elements in a corner, select which elements are to be assigned to the compound formed between the element and the selected anion by clicking the appropriate check box.

5. Select whether to group features by morphology.
6. Click "Close" to save the settings and close the Ternary Plot Settings window.

In the main window select whether to color the features by Class, Subclass, or custom Morphology Bin.

Interrogating the Data in a Ternary Plot

Zoom in on the ternary plot by either using the middle mouse wheel or pressing the Shift button on the computer keyboard and pressing the left mouse button down. Drag the mouse to select the area to zoom to.

When zoomed in on the ternary plot, press and hold the left mouse button down to drag the ternary plot around and focus on different parts of the data.

Right click and select "Reset Scales" to return to the full view of the ternary plot.

To select a single feature in the ternary plot click once on it. The feature will also be highlighted in the image. Click on an empty space in the plot to clear the selection.

To select multiple features, hold down the 'Ctrl' button on the computer keyboard and click once on each feature to be selected. Alternatively, to select a number of features that are close together, hold down the 'Ctrl' button on the computer keyboard and then press the left mouse button down and drag the mouse to select all of the features within the selected range.

To deselect specific features when multiple features have been selected, hold down the 'Alt' button on the computer keyboard and click once on each feature to be deselected. To deselect a number of features close together while leaving other features still selected, hold down the 'Alt' button on the computer keyboard and then press the left mouse button down and drag the mouse to deselect all of the features within the selected range.

Useful Information on Ternary Plots

Ternary Plot Calculations

Each data point displayed in the ternary plot is calculated for a single feature and is calculated from the Weight % quant results acquired for the feature.

The position in the chart is determined by the value calculated for each of the three ternary plot components where each component is defined by between 1 and 4 assigned elements or compounds.

Ternary component assignments

Each component can have any element in the atomic table assigned to it and then each of these selected assignments can be modified by having a selected anion assigned to it to effectively change this assignment from an element to the compound formed between the element and the selected anion.

Supported anions

Currently Oxygen, Sulfur and Carbon are the three elements that can be designated as anions to form compound assignments with. E.g. combining the selected element Calcium with Oxygen forms Calcium Oxide which is the assignment to this corner component. The calculation for the component is modified when a compound selection is made as described below.

Calculating the ternary components for a feature

Each component is calculated from the sum of the quant results acquired for the feature for the list of elements and compounds assigned to the component.

For example, for a corner component comprised of Cu + MgO, the unnormalized component is calculated from: Sum = Wt% of Cu + Compound modification (MgO Wt%).

Finally, once each component has been obtained for a feature, the three components are normalized so that the three values sum exactly to 1.0. This allows for the data to be plotted in the ternary diagram as each corner represents a value of 1.0 for one of the components. A feature with equal values in each of the components would be plotted directly in the center of the diagram. This can be demonstrated when a user applies the same element to each of the three components.

> ***NOTE:*** *A feature which has a value of 0% for all the quant results specified will not appear in the plot as there is no data to perform the calculation. A feature that contains a non-zero value in any of the assigned elements will be included in the plot.*

The Compound Modification

The Wt % value for a compound is calculated from the formula:

Compound Wt % = Assigned element Wt % * Compound Factor (assigned element, assigned anion).

Where the Compound Factor is calculated from :

CF = 1 + (Valency of the element * Atomic Number of the compound) / (Valency of the compound * Atomic Number of the element).

Unnormalized Quant Results

To perform the above calculations, it is necessary for all the initial Wt% quant results to be positive as the final result is to calculate the normalized ternary components in the range 0 - 1. With unnormalized quant results, the Wt% values can be negative.

Before the ternary plot components are normalized, the three component values are incremented by the same positive value equal to the modulus of the smallest negative initial value. This effectively shifts all the data into a positive range before the normalization is performed.

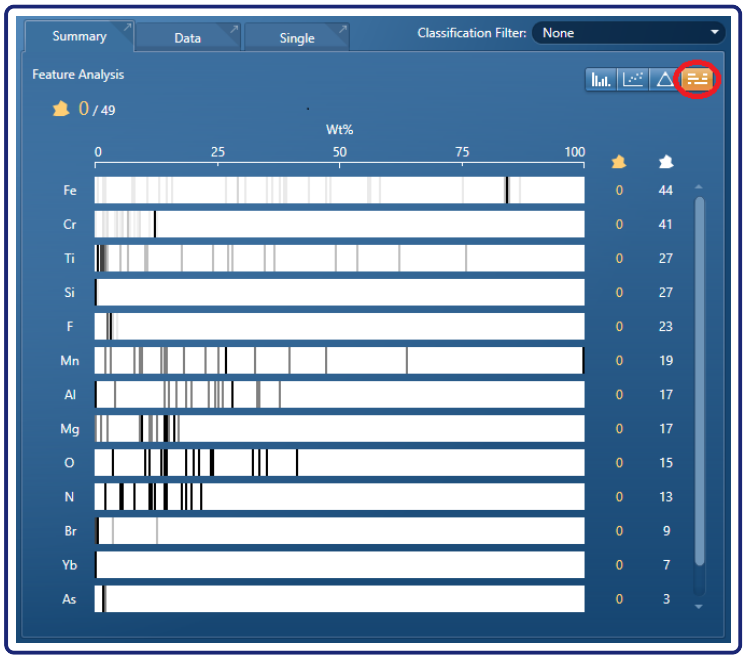
Restrictions

The ternary plot is not updated when invalid selections are made in the settings. Examples of this are when the same element is applied to the same corner component more than once (this is a pretty meaningless operation as you wouldn't want to duplicate the same data in one of the components) and when the user tries to create an invalid compound (e.g. combine Sulfur with Sulfur to make Sulfur Sulphide or combine Argon with Oxygen).

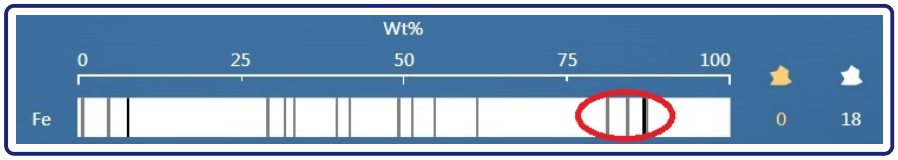
Data presented as a Quant Distribution Chart

Feature data may be summarized as a quant distribution chart that shows distributions in chemistry for all elements at the same time.

To view the quant distribution chart click the Quant Bar icon on the Summary tab:



The distribution chart lists those elements found within the features in the sample. It then expresses the concentration of each element as weight percentage (Wt%). The following example illustrates iron content:



Here, 18 particles were found containing iron. Each particle is represented by a single bar. So, in the above example 18 bars are used to show the distribution of iron particles in the sample. The three particles circled are composed of more than 75% iron.

Interrogating the Data in a Quant Distribution Chart

To examine a single concentration of an element, click on a single bar. A selected bar will appear orange. When a single bar is selected, full details about the feature will be available on the "Single" tab.

To select a range of concentrations, hold down the "Ctrl" key while clicking or dragging each one. When several bars are selected, full details for those features will be available on the "Data" tab.

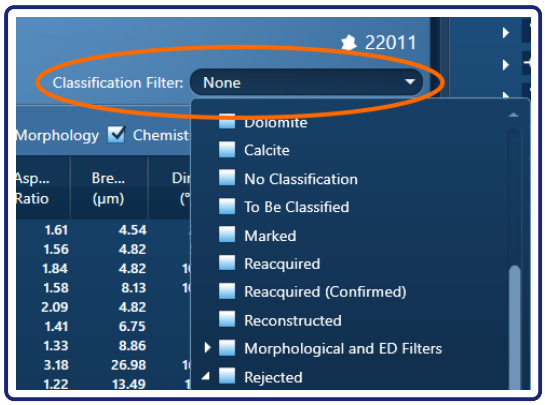
To undo any selection, hold down the "Alt" key while clicking or dragging each one.

To cancel all selections, click on a white area in any bar.

3.7.2. Data Tab

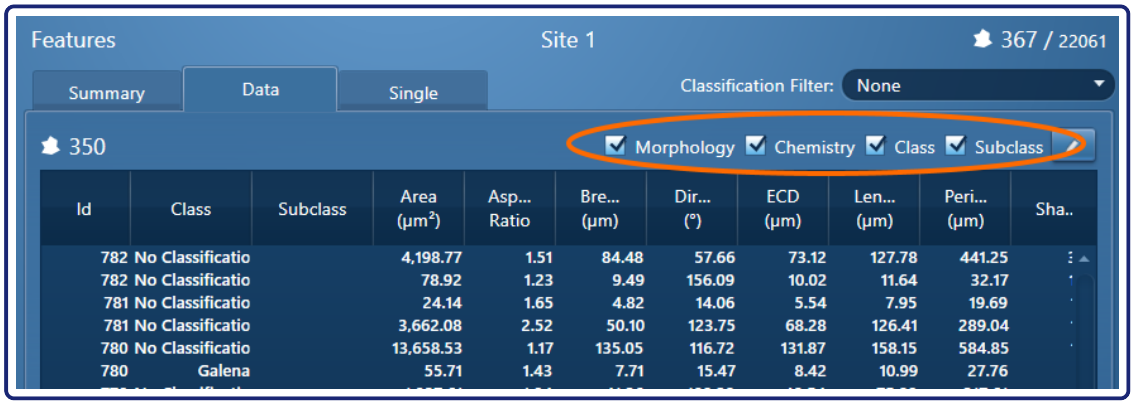
The Data Tab shows the feature data and statistics for the current site or if present, area. It is useful for interrogating data and for marking and rejecting features. It may also be used to select the features that data is to be reacquired for.

Use the "Classification Filter" drop down menu to filter the feature data displayed:



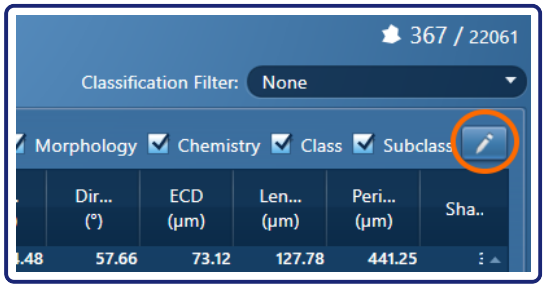
The information displayed in the table can be changed by either:

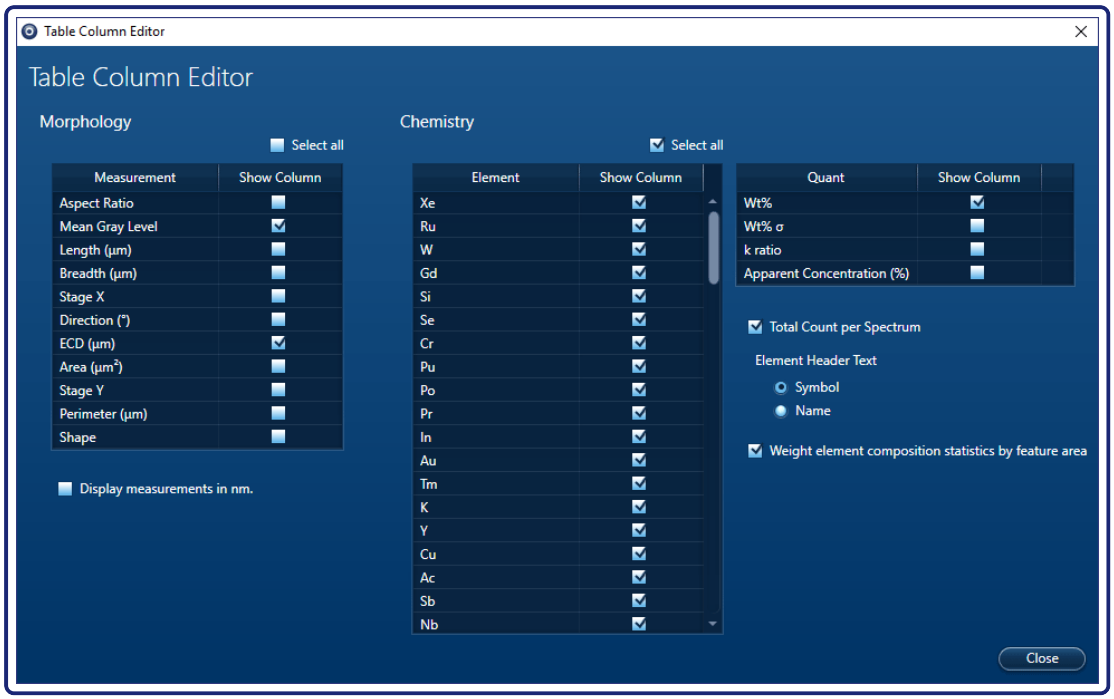
- Selecting to hide or show the different types of data using the check boxes:



Display Option	Description
Morphology	Check to display all morphology data (i.e. Area, Aspect Ratio, Breadth etc)
Chemistry	Check to display all chemistry information for each element detected. To select the type of chemistry information that should be displayed (apparent concentration, k ratio, Wt% and Wt% σ) use the Table Column Editor which can be accessed from the pen icon.
Class	Check to display the classes that the features belong to.
Subclass	Check to display the sub-classes that the features belong to.

- Selecting each column individually using the Table Column Editor, which is accessed from the pen icon in the top right corner of the Data tab:





Display Option	Description
Morphology	Select to display all morphology measurements or only certain measurements.
Chemistry	Select to display all elements or only certain elements.
Quant	Select the types of quant data that should be displayed (apparent concentration, k ratio, Wt% and Wt% σ)
Total Count per Spectrum	Select to display the total number of counts in the spectrum for a feature.
Element Header Text	Choose to display either the element symbol or element name as the column header for the element data.
Weight element composition statistics by feature area	Select to weight the element composition statistics by feature area. Calculates the mean and standard deviation of the quant results as weighted by feature area. For example: Mean = ∑ (Concentration x Area of feature)/(Total area of features). The calculated values appear wherever the statistics are displayed: • In the table under "Statistics" in the "Feature Data" viewer. • In the table below the histogram on the "Summary" tab. • In the chemistry data in reports. ***NOTE:*** *The column headers of the table indicate that the statistics are weighted by area.*
Display measurements in nm	Select to display the measurements in the data viewer in nm, rather than the default µm.

For any feature:

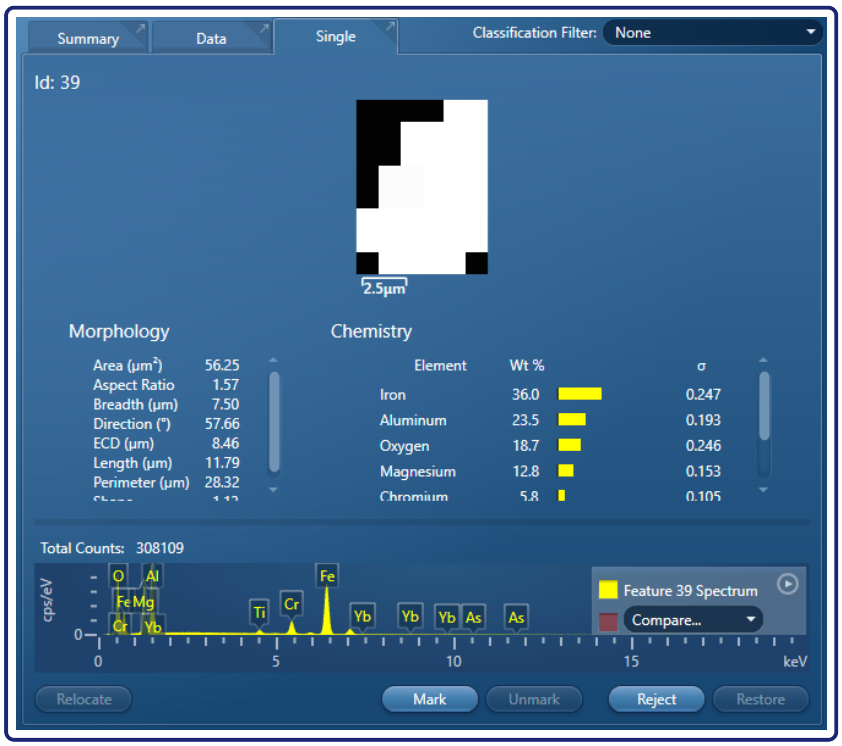
- Select it in the data table and see it highlighted in the image or vice versa.
- Select it in the data table and choose whether to mark or unmark it, reject it or restore it:

Field	Description
Mark Button	Mark the feature for easy reference in the future. Marked features can be identified in the data table by an asterisk next to the feature Id. They can also be filtered by selecting the "Marked" option in the classification filter drop down menu.
Unmark Button	Unmark the feature.
Reject Button	Reject the feature. Rejected features will be removed from the data table and statistics. They can be viewed by selecting "Rejected (Manual)" from the classification filter. ***NOTE:*** *When a feature is rejected, its data is not permanently deleted. This means that it is possible to restore the original data at a later point.*
Restore Button	Undoes any rejection that has been applied since the data was acquired.

3.7.3. Single Tab

The Single tab is used to show detailed information for single features. It can also be used to mark, reject and relocate the microscope stage to the feature. The items displayed will include:

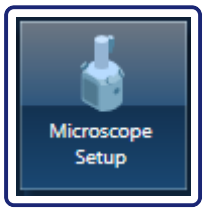
- An image of the feature.
- The morphology and chemistry data.
- The EDS spectrum including the total number of counts in the spectrum.



Field	Description
Relocate Button	Relocate the microscope stage to the feature.
Mark Button	Mark the feature for easy reference in the future. Marked features can be identified in the data table by an asterisk next to the feature Id. They can be filtered by selecting the "Marked" option in the classification filter drop down menu.
Unmark Button	Unmark the feature.
Reject Button	Reject the feature. Rejected features will be removed from the data table and statistics. They can be viewed by selecting to view "Rejected (Manual)" features from the classification filter. ***NOTE:*** *When a feature is rejected, its data is not permanently deleted. This means that it is possible to restore the original data at a later point.*
Restore Button	Undoes any rejection that has been applied since the data was acquired.

3.8. Microscope Setup

The microscope setup can be accessed by clicking on the Microscope Setup icon to the right of the Feature navigator steps:



The Microscope Setup step has two applications:

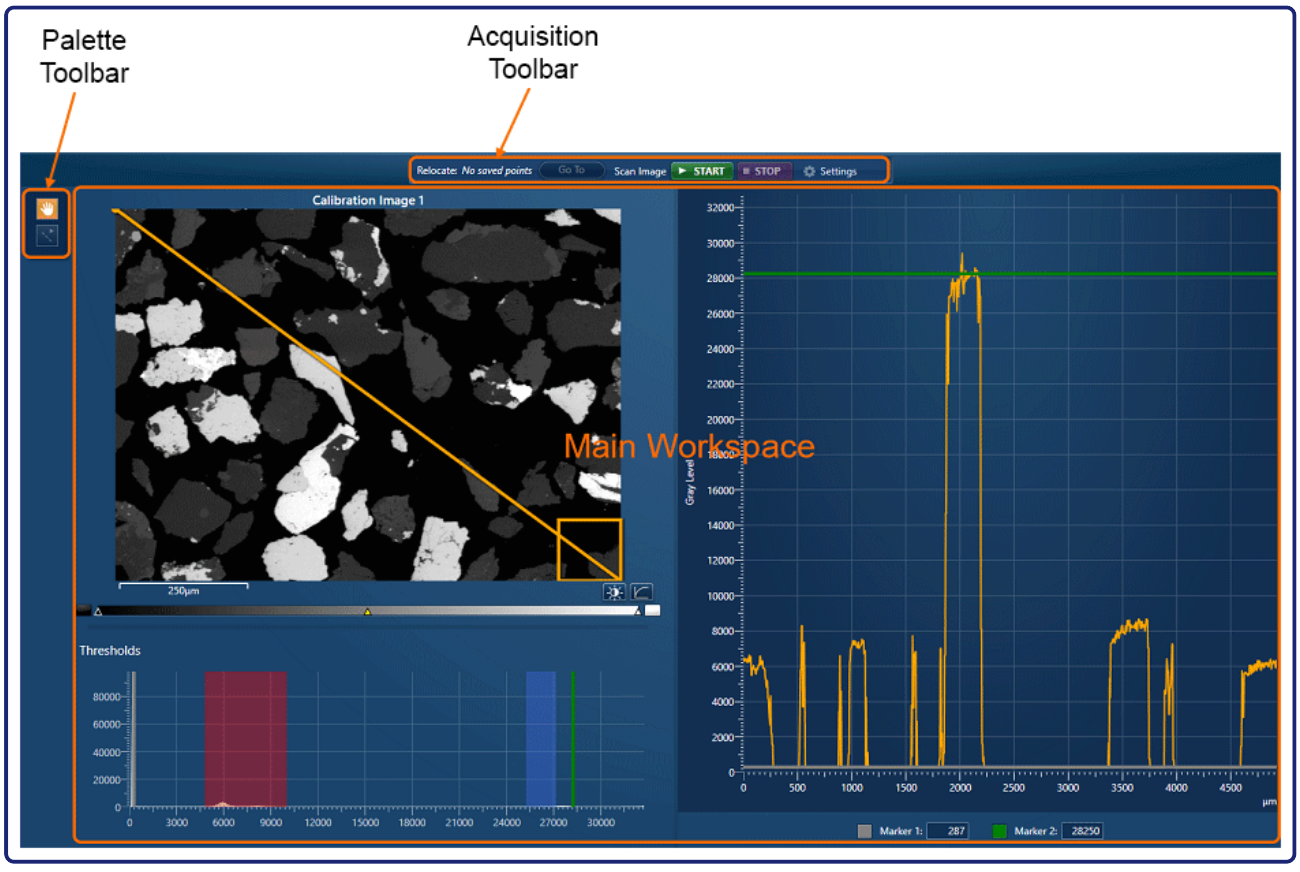
1. In-run threshold adjustment: Used to monitor and compensate for any changes in brightness and contrast of the electron images during a large area acquisition.

   This is important to ensure that the features can always be detected correctly.

2. Set brightness and contrast before a large area acquisition: Used to set the same brightness and contrast levels for each run such that they same thresholds may always be used for feature detection.

   This is important to ensure that there is consistency between acquisitions performed at different times.

The Microscope Setup has the structure shown below:



Item	Description
Palette Toolbar	Contains tools relevant to the current workspace.
Acquisition Toolbar	Contains the settings and acquisition controls for the current step.
Main workspace	The main workspace can be split into three panes: 1. The upper left pane contains the electron image. It may be overlaid with a yellow line marker upon which the gray-level calibration is performed. If the in-run threshold adjustment option is selected, at the end of the line with be a yellow box. This is the region used to perform the in-run threshold adjustment. 2. The lower left pane is the Thresholds pane. This pane is used to graphically display the number of pixels for each brightness level. The current gray-level thresholds as defined in the Detect Features navigator step and the two markers used to set the white and black gray-levels are also overlaid on this graph. 3. The right pane displays the gray levels along the yellow marker line graphically. A gray and a green marker are overlaid and may be adjusted to set two gray level markers for the image. The current gray level for each marker are displayed at the bottom of this pane. For more information on setting the markers see the Setting Consistent Contrast and Brightness for Each Run section.

3.8.1. Palette Toolbar

The Palette toolbar contains the tools that are relevant to the current workspace.

Item	Description
	**Pan:** Allows images to be panned (moved) around and zoomed in and out. For more information on panning and zooming images, see in The Detect Features Workspace section section of Imaging the Sample.
	**Single Line Acquisition Tool:** Define the line along which the gray-levels will be displayed in the right hand pane of the main workspace.

Pan and Zoom Tool

To assist with viewing and interrogating electron images or maps, AZtec has the functionality to allow images to be panned (moved) around and also zoomed in and out. To access these facilities click the pan tool icon in the palette toolbar on the left of the screen:

When in display modes with multiple images and maps, prior to starting to zoom or pan, it is recommended to select whether to zoom in or out on a single image or map using the link tool:

NOTE: *The individual images and maps are linked when the button has an orange background.*

There are two methods that can be used to zoom in and out on an image or map:

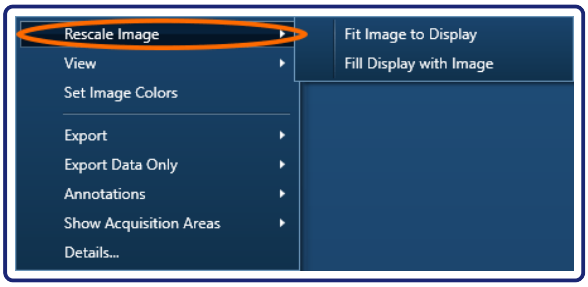
1. Using the scroll wheel on the mouse while hovering the mouse over the image or map.
2. Simultaneously holding down the "Ctrl" key on the computer keyboard and the left mouse button on the image or map. Move the mouse to the right to zoom in and to the left to zoom out.

To move images or maps around, with the pan tool selected, press the left mouse button down and drag the image about. Release the left mouse button to stop moving the image.

Images can be returned to their original size by:

1. Right click on the image to access the context menu.
2. For an individual image or map in the Display pane select "Reset Image Scales".

   For an electron image, layered image or map displayed in the Image pane, select "Rescale Image" and then select either "Fit Image to Display" or "Fill Display with Image".



3.8.2. Acquisition Toolbar

The acquisition toolbar contains the acquisition tools and settings relevant to the navigator step.

Item	Description
Go To	Move to saved stage position selected from the drop down menu. ***NOTE:*** *To save a stage position, it must first be created as an area using the Automate wizard. It must then be saved from the Automation data tree.*
START	Start continuous electron image acquisition.
STOP	Stop acquiring.
Settings	Opens the Calibration Settings window where the following settings may be found: • Electron image acquisition settings. • In-run threshold adjustment settings.