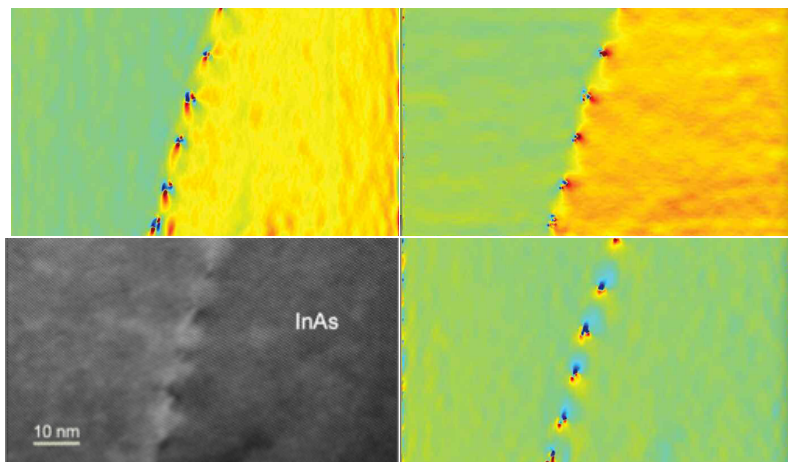


March 2022

PPA for DigitalMicrograph

Peak Pairs Analysis

*High-Resolution Peak Measurement
and Strain Mapping Analysis*



PPA User Manual v5.0

HREM Research Inc.

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Conventions

The typographic conventions used in this manual are described below.

Convention	Description
Bold	Used to denote specified elements of the user interface such as buttons, field names, menus, and menu options. For example, the New button.
Menu...MenuOption	Select the Menu from the Menu bar then select the Menu Option from the Menu. For example, File...Open would mean select the File Menu and then the Open Option.
CAPS	Used to denote the name of a key on the keyboard. For example, the ENTER key.
<i>Italics</i>	Used to denote emphasis, captions and the result of an action in a procedure.

Table of contents

<i>Introduction to Peak Pairs Analysis (PPA)</i>	5
Software Requirements	5
Software Installation	6
<i>Getting Started</i>	7
Image Pre-processing and Basis Vector Selection	7
Peak Detection (Simple Images)	10
Motif Detection (Complex Images)	13
Peak Pairs Determination	18
Displacement and Strain Maps Calculation	19
Setting the Reference Base Vectors	22
<i>Other Noise Filters</i>	24
Fourier Space Noise Filters / Wiener Filter	24
Real Space Noise Filters	26
Adaptive Wiener Filtering	26
Low Pass Filtering	27
Non-Local Noise Filters	28
<i>Advanced Topics</i>	35
Find Weak Peaks (using Find Peaks)	35
Correct Scan-Line Noise	37
Geometric Distortion Correction	39
Distortion Analysis	43
Analyze Peak Points	47
Analyze Equivalent Columns	48
Create Vector Maps	51
Show Ideal Positions	52
<i>Appendix:</i>	53
Technical Note	53
Some useful DM tricks	54
<i>Quick Reference Guide</i>	55

Introduction to Peak Pairs Analysis (PPA)

PPA stands for Peak Pairs Analysis, the DigitalMicrograph plug-in for High-Resolution Peak Measurement and Strain Mapping Analysis.

All results obtained by PPA are fully compatible with the other functions present in DM. For example, strain maps can be analyzed and/or manipulated with functions such as histograms, statistics (mean, standard deviation, min, max etc.), or using the corresponding buttons, such as the Profile utility.

The main reference for the algorithm is:

The Peak Pairs algorithm for strain mapping from HRTEM images

Pedro L. Galindo, Sławomir Kret, Ana M. Sanchez, Jean-Yves Laval, Andrés Yáñez, Joaquín Pizarro, Elisa Guerrero, Teresa Ben and Sergio I. Molina

Ultramicroscopy 107 (2007) 1186–1193 (doi: 10.1016/j.ultramic.2007.01.019)

The reference for the procedure of non-local noise filter is:

Evaluation of high-quality image reconstruction techniques applied to high-resolution Z-contrast imaging

G. Bárcena-González, M.P. Guerrero-Lebrero, E. Guerrero, A. Yáñez, D. Fernández-Reyes, D. González, P.L. Galindo

Ultramicroscopy 182 (2017) 283–291 (doi: 10.1016/j.ultramic.2017.07.014)

This manual will help you to use of the PPA package with some worked examples. There is also a quick reference guide at the end of this document.

Software requirements

The following is a list of the software requirements necessary to run the PPA plug-in:

- DigitalMicrograph (Gatan™)
- USB Key Driver
- HREM Mouse Tool Plug-in (freeware downloadable from www.hremresearch.com)
- IPU Plug-in (freeware downloadable from www.hremresearch.com)
- HREM-Filters Pro/Lite Plug-in (Lite is a freeware downloadable from www.hremresearch.com)

Software Installation

Installing USB Key Driver

The user key driver should be installed by following the instructions given by the key driver installer. You can find the key driver installer at the plug-in page on HREM Research web site.

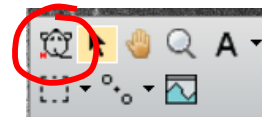
Installing DigitalMicrograph Plug-ins

The DigitalMicrograph Plug-in will be provided as Gatan compiled script file(s) (.gtk) and dynamic link library file(s) (.dll). All these files can be installed by copy-and-paste to the folder “PlugIns.” (The PlugIns folder should exist under a normal installation of the DigitalMicrograph).

When the DigitalMicrograph is launched after placing the plug-ins into the PlugIns folder, the PlugIns will appear as a new menu or an addition to the standard tools.

Installing HREM Mouse Tools

All the files relating HREM Mouse tool plug-in can be installed by copy-and-paste to the folder “PlugIns.” The Mouse tool will appear as an addition to the standard tools.



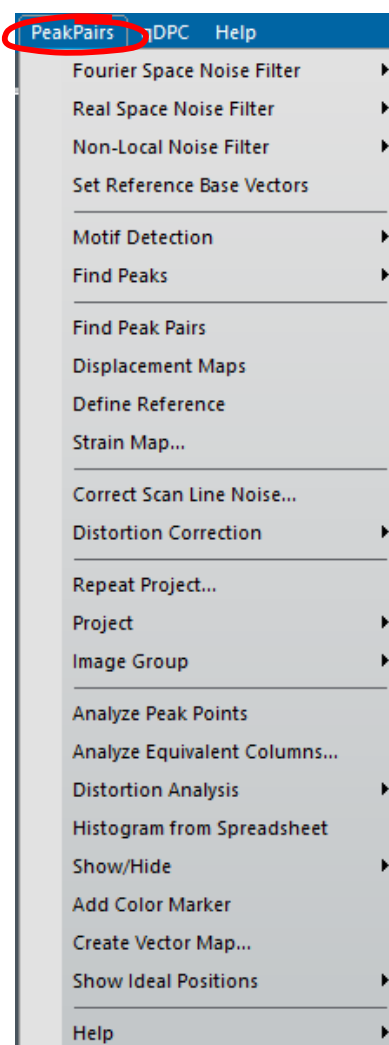
Installing IPU Plug-in

The PPA plug-in uses some functions based on the Intel' MKL (Math Kernel Library) provided by the IPU plug-in. All the files relating the IPU plug-in can be installed by copy-and-paste copy. The IPU plug-in will appear as under IPU menu. Please consult the ReadMe file that comes with the IPU plug-in.

Installing PPA

PeakPairs.gtk and PeakPairs.dll can be installed by drag-and-copy to the folder “PlugIns” (The PlugIns folder should exist under a normal installation of the DigitalMicrograph.)

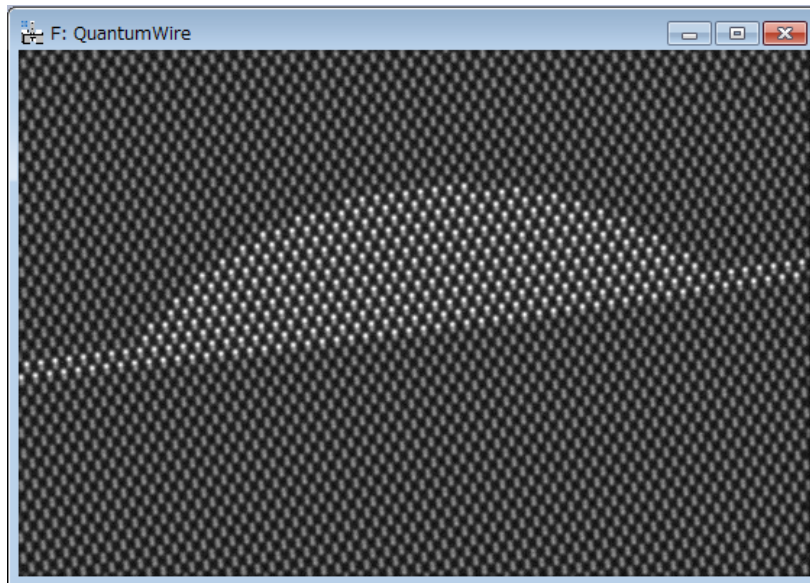
When the DigitalMicrograph is launched after placing the plug-ins into the PlugIns folder, **PeakPairs** menu commands shown right will appear.



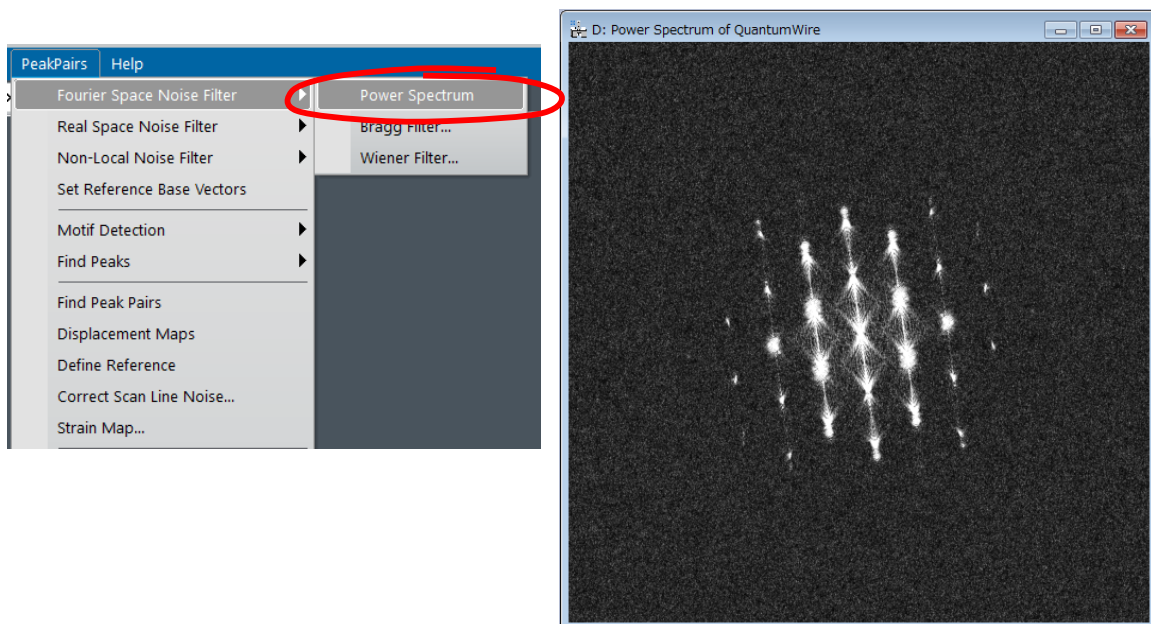
Getting Started

Image pre-processing and Basis Vector Selection (Bragg Filter)

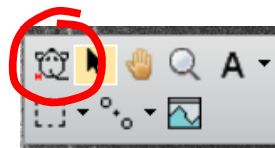
Open the file *QuantumWire.dm3* using the DM command File...Open. The image below represents a capped InAs quantum wire on GaAs. Composition was considered to be uniform inside the quantum wire and across the wetting layer.



All the commands related to PPA are located in the menu **Peak Pairs**. The first command to be applied to a new image is the **Power Spectrum** command to calculate the power spectrum of the image:

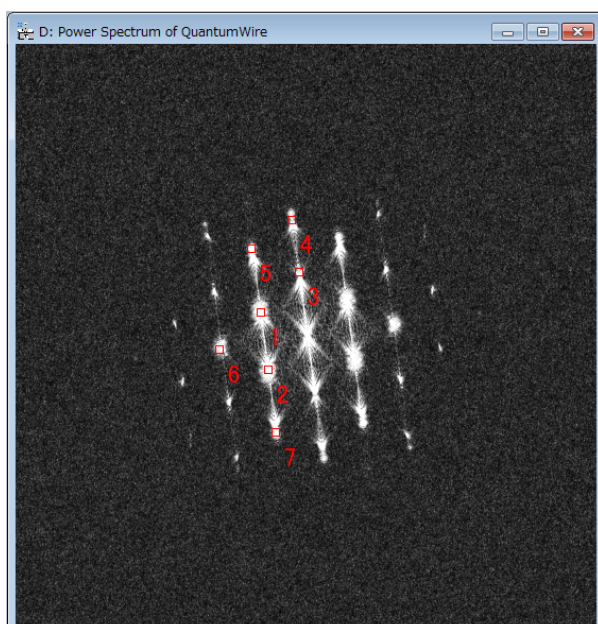
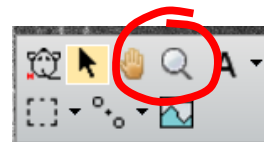


Now, select the **HREM mouse** tool, and click on desired spots to apply Bragg filter. The usual choice is to select the brightest spots in the spectrum, but those corresponding to higher harmonics can also be selected:



The user doesn't need to hit the spot exactly, because PPA looks for the local maxima near the selected point.

Anyway, if necessary, you can zoom in the spectrum before hitting peaks using the **DM zoom** tool:



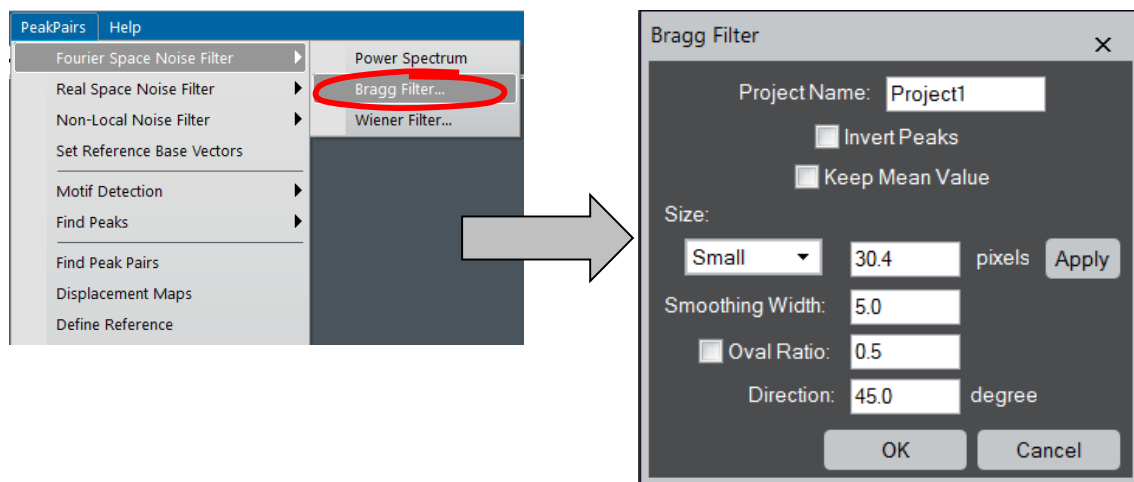
Hint: if you wish to delete any spot, just click on the mouse mark again with the **SHIFT** key down.

Hint: Symmetry in the selection for each spot is assumed.

IMPORTANT: *First* and *second* chosen spots (numbered as 1 and 2) will define the lattice basis vectors. These spots should be apart from the vertical or horizontal of the central spot, in order to obtain maximum resolution.

Don't be surprised if the central spot is not present in the power spectrum. It just indicates that the mean intensity of the image is zero.

We are now ready to apply **Bragg Filter**. This process creates an image where the contrast resulting from the ordered regions is clearly distinguishable from the background intensity.

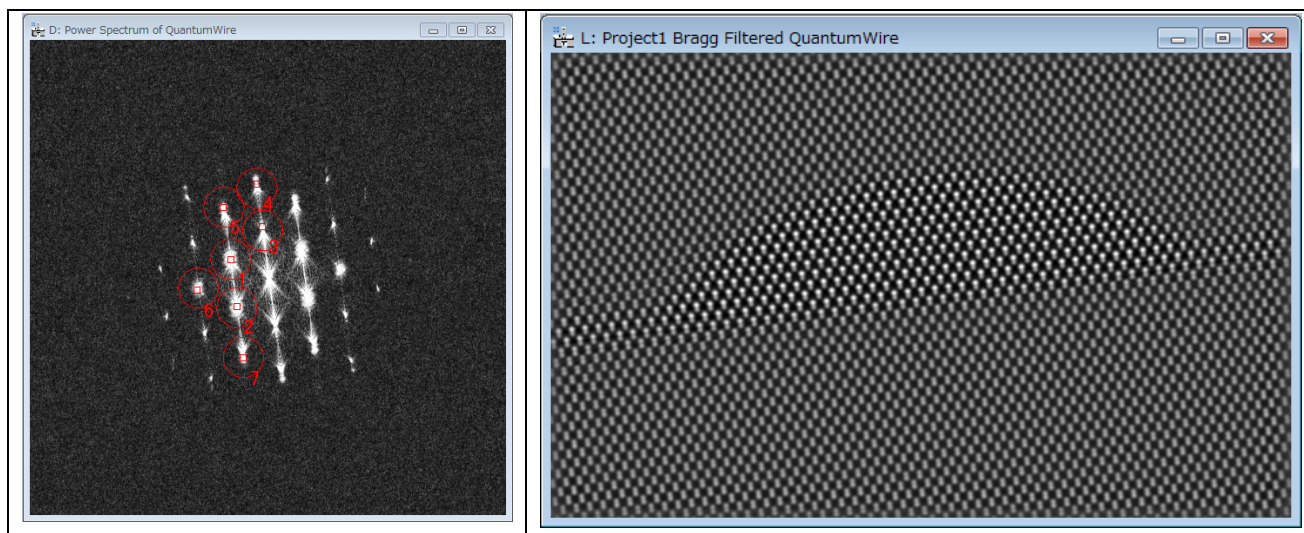


NOTE: If you are interested in *black* spots, the **Invert Contrast** will be checked.

The shape and size of the Bragg filter must be adjusted such that no loss of information occurs. In this dialog box we can determine the size (in pixels), smoothing width (in pixels), oval *axis* ratio and direction (in degrees) of oval masks. When you change any parameters, we recommend you to check an actual mask shape by pressing the **Apply** button.

NOTE: When the check box for Oval Ratio is **OFF**, the parameters for the oval are not applied.

Let us select the window size as shown below and press the **OK** button, and the Bragg filtered image will appear immediately.



If Bragg filter parameters are properly chosen for a sufficient number of peaks, the resulting filtered image will preserve the location of maxima. The great advantage in using the filtered image is the reduction of noise.

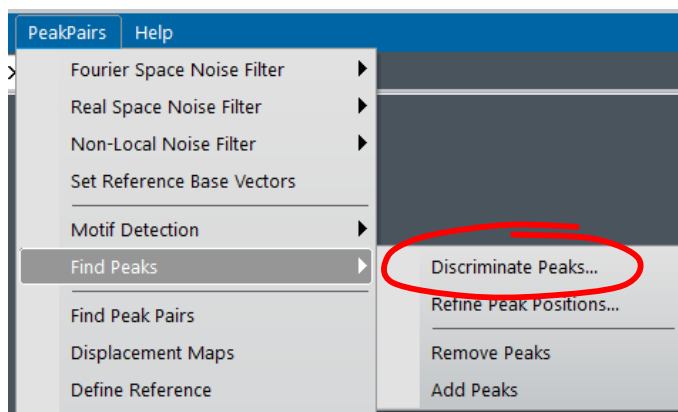
Peak Detection (for a simple structure)

IMPORTANT: Peak Detection uses two base vectors information (unit cell) to find a set of good intensity peaks. Thus, when the base vectors have not been defined yet, they should be defined manually using the **Set Reference Base vectors** command.

NOTE: The Bragg filter or Wiener filter defines the two base vectors automatically.

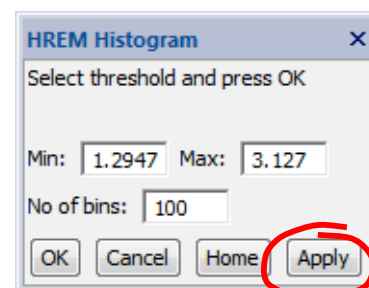
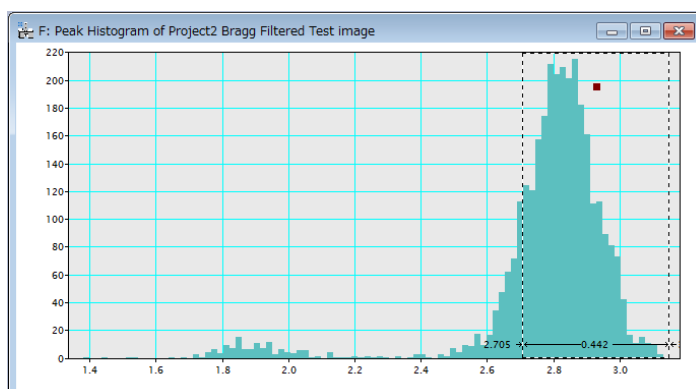
Once we have a Bragg filtered image, the next step is to locate peaks of intensity in the image by using the **Find Peaks** menu commands.

The first step of peak detection is peak identification based on their intensities. The **Find Peaks...Discriminate Peaks** command detects all local intensity maxima in the image, and calculates the histogram of peak intensities.



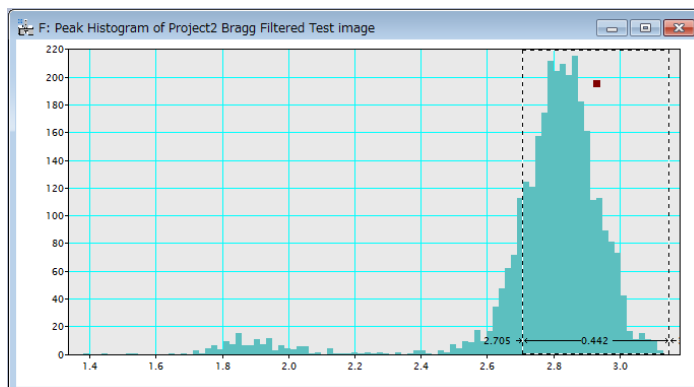
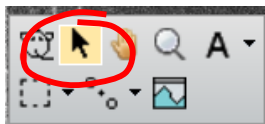
Here, we use *Test image.dm3* as a sample data. First, we apply the Bragg filter using all the spots in the Power Spectrum. When the command **Discriminate Peaks** is selected, a new window showing the histogram of all the peaks found in the image will appear. The histogram allows the user to locate different sets of peaks, based on their intensities. All peaks of intensity lower than this threshold are discarded.

The **Discriminate Peaks** will also open the HREM Histogram control tool. If you want, you can change the histogram range as well as the number of bins. The default range of the histogram is set to the maximum and minimum of the peaks. When you change these values, push the “Apply” button.

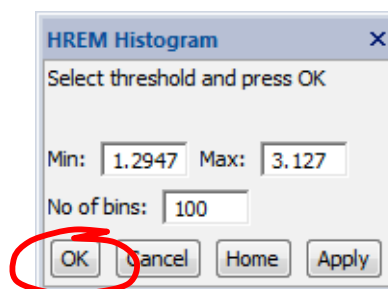
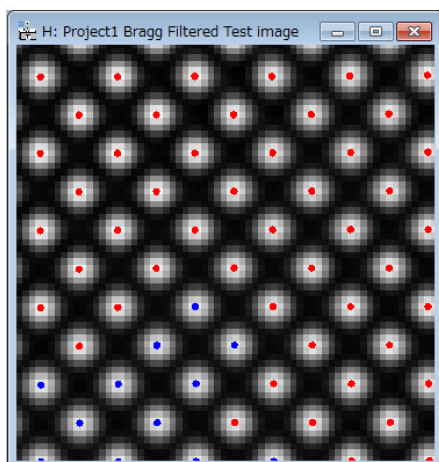


TIPS: If you want to analyze *black* spots (hollows or dips), you have to check **Invert Contrast** when you create a project.

Once the histogram is shown, the user should select the intensity threshold for identifying which peaks will be used in further analysis. To do so, just click the mouse on the histogram, and select the desired range of peaks. The left side of the selection made in the histogram will be used in the following **Refine Peak Positions** command.

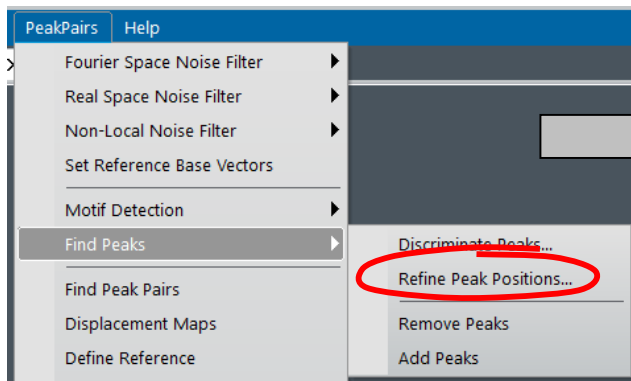


The discovered peaks will be classified to red or blue depending on the peak values: red indicate the peak that is higher value than the selected threshold, while blue indicate the peak equal to or lower than the threshold. The peak color will be dynamically revised by changing the threshold (the left-edge of the Range ROI).

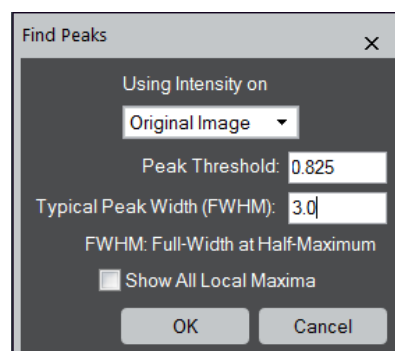


When you satisfy the threshold by looking the motif markers (red or blue), push the “**OK**” button of the **Histogram** tool, or the “**Cancel**” button to stop the process.

Once the range of peaks is selected, the next step is to refine the peak positions using the **Refine Peak Positions** based on the intensity of the image.



The following dialog box appears:



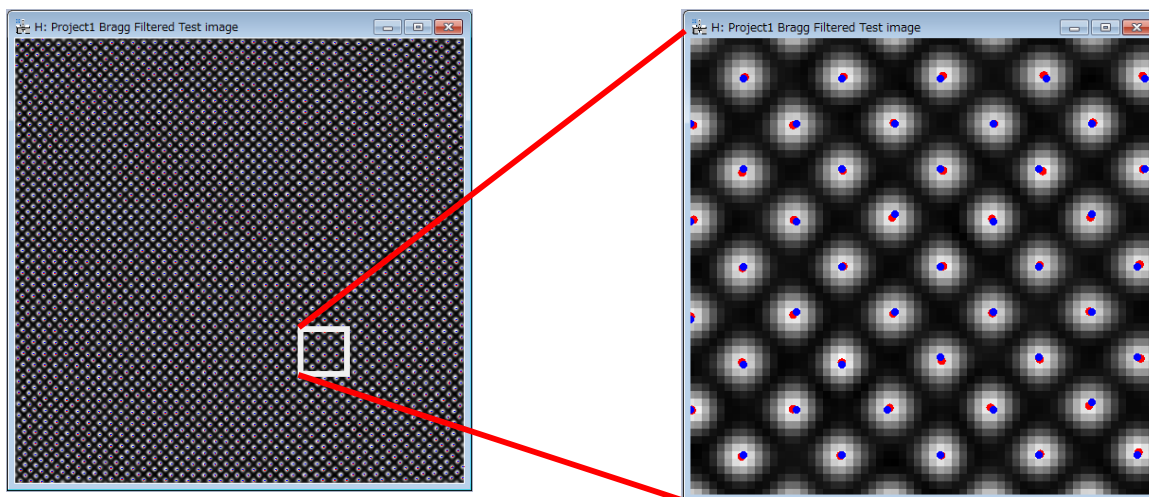
The image used to refine the peak positions can be selected from the images listed by **Using Intensity on**.

Peak Threshold indicates the minimum intensity of a point to be considered as a valid peak. Peak threshold value is automatically read from the left side of the selection made in the histogram. However, the user can manually modify this value, if necessary.

Typical Peak Width indicates the size (FWHM) of the typical peak in pixels. The peaks (columns) within this value will be merged into a single peak.

When **Show All Local Maxima** is checked, all the peaks at the local maxima is also displayed in blue in addition the refined peaks (in red).

By pressing OK, we get a first set of peaks shown as colored spots over the filtered image. *Blue* dots represent local maxima (8-neighbourhood) on a pixel basis. *Red* dots represent refined maxima at sub-pixel resolution. Sub-pixel resolution is achieved by fitting a 2D quadratic function and calculating the maxima, as described in the reference for the algorithm in the Introduction section.

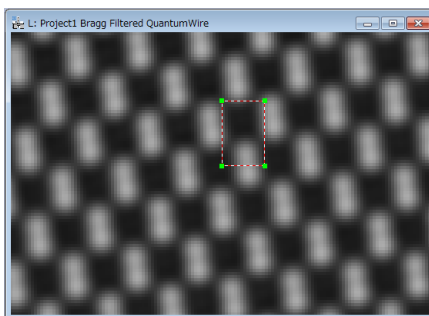
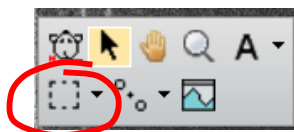


Sometimes, extra peaks are obtained in this automatic Peak Finding process, especially at the borders of the image. Repeating the Find Peaks command with a new Peak Threshold, all peaks in the border of the image will be discarded and won't be considered in any further calculations.

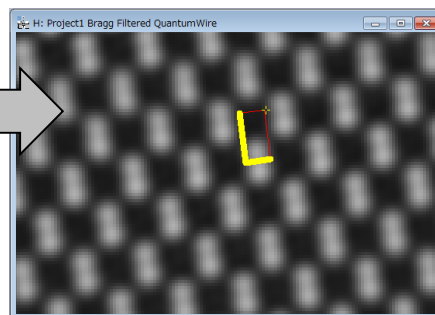
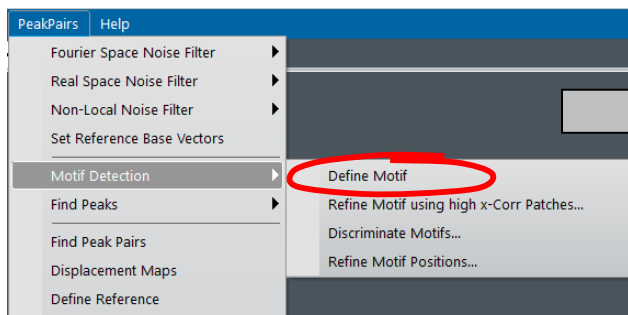
Motif Detection (for a complex structure)

In cases where the repeating unit in the image is more complex than a single column (dot), such as a *GaAs* dumbbell, the peak (and thus the peak-pair) will be obtained for each unique column. Thus, an alternative, more complex way to determine the lattice may be useful. Thus, the **Motif Detection** has been implemented. Here, we explain the Motif detection using the image *QuantumWire.dm3*.

First, a rectangle should be placed using the **Rectangle ROI** tool to defines the basic pattern that will be searched across the whole image using normalized cross-correlation. For example, in this image, a cation location (an upper part of a dumbbell) may be a good choice. Rectangle size and location is a critical decision in the accuracy of strain results. Let us zoom in the substrate, and select a rectangle area around a cation.

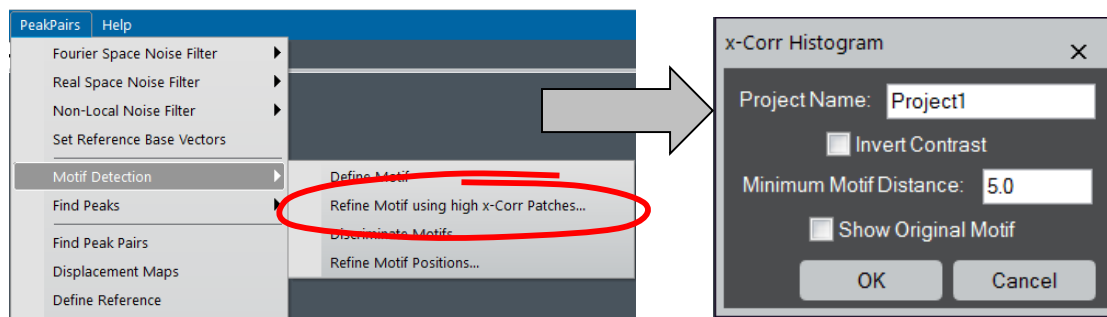


Once the rectangle ROI has been placed, select **Motif Detection...Define Motif** to determine the Motif. Then, using the handles of the ROI, you can change the size of the Motif ROI, and rotate the Motif ROI, if you want.

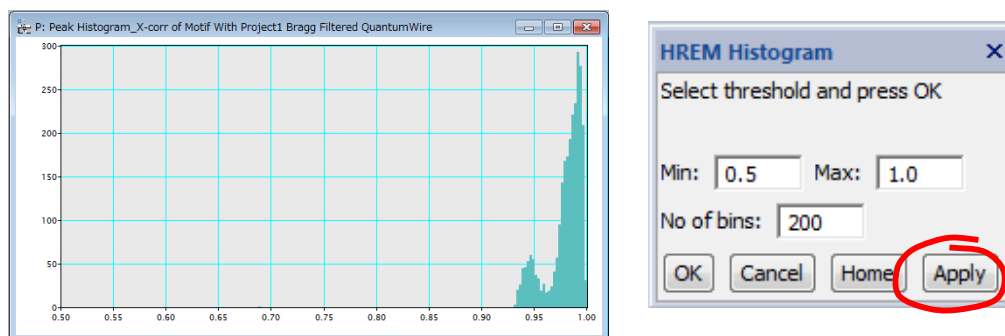


TIPS: You can *rotate* the ROI by dragging the yellow cross (+). You can adjust one of the edge lengths by selecting the yellow edge and dragging the handle. You can adjust both edge lengths while maintaining their ratio when dragging the yellow cross with the SHIFT key down.

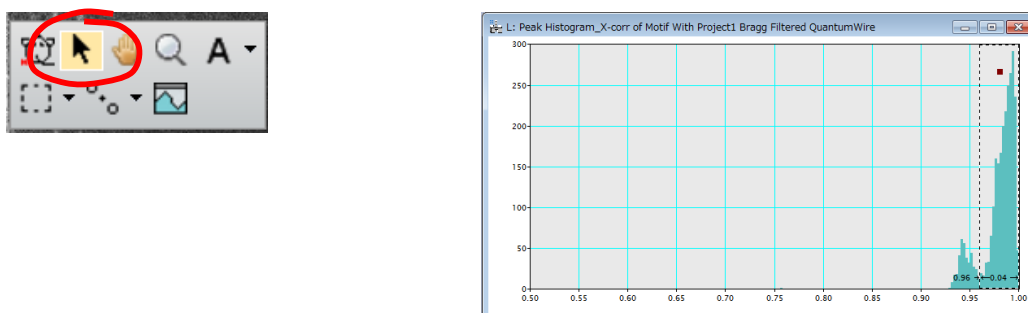
Once the Motif has been defined, select **Motif Detection...Refine Motif using high x-Corr Patches**. Here, **x-Corr** means Cross-Correlation. This command will refine motif using a high score cross-correlation patches with the original motif. When you select this command, a dialog shown below will open:



After clicking OK, a new window will appear showing the histogram of all maxima found in the Cross-Correlation map, obtained using the *User-Selected* motif and the whole image. At the same time, the **HREM Histogram** tool will appear as shown below.

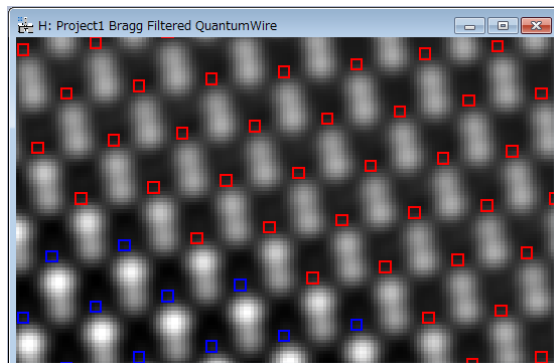


In this case, we may observe two peaks in the histogram, corresponding to *Ga* and *In* cations across the image. Once the histogram is shown, you should select the intensity threshold for identifying which peaks will be used in further analysis. To do so, choose the **Select** tool and click the mouse on the histogram. Then, move the left edge of the selection to define the lower threshold.

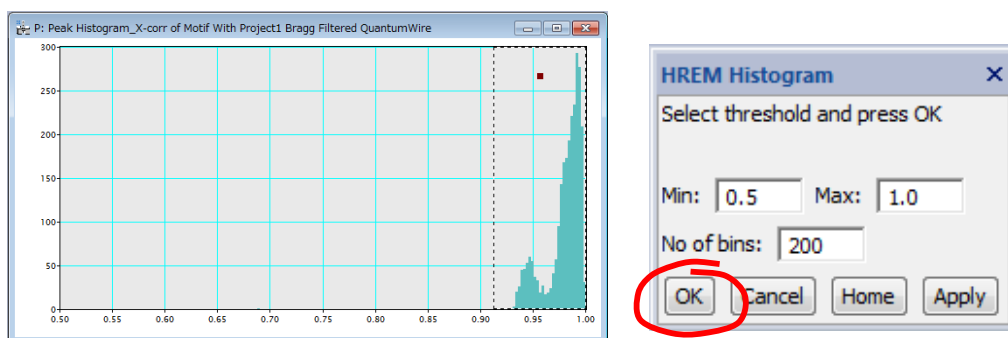


The default range of the histogram is set to 0.5 to 1.0. If you want, you can change the histogram range (**Min** and **Max**) as well as the number of bins (**No of bins**). When you change these values, push the **Apply** button.

The discovered motifs will be classified to red or blue depending on their cross-correlation values: red indicate the motif, whose cross-correlation value is higher than the selected threshold, while blue indicate the motif equal to or lower than the threshold. The peak color will be dynamically revised by changing the threshold.

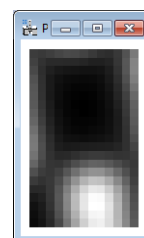


Given that we are interested in the detection of both cations, we will select a threshold lower than 0.9 to take all peaks into consideration.

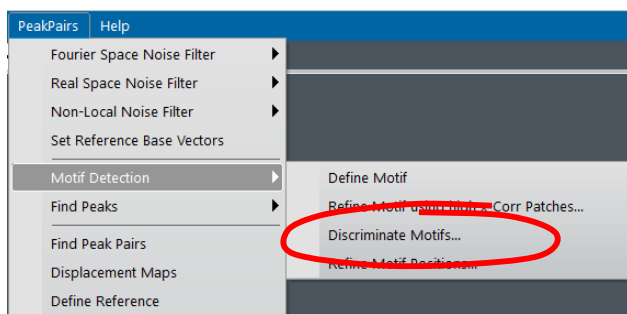


When you satisfy the threshold by looking the motif markers (red or blue), push the **OK** button of the Histogram tool, or the **Cancel** button to stop the process.

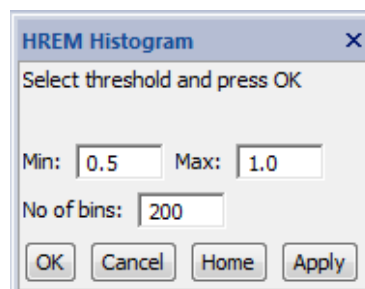
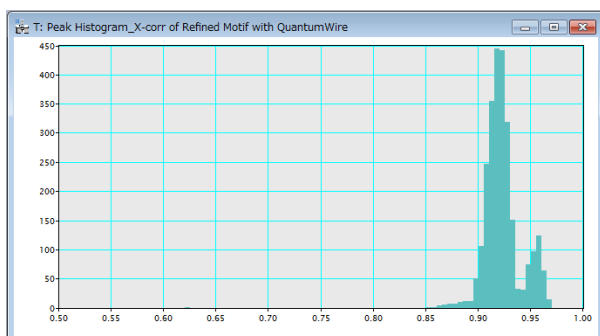
If you push the **OK** button, the first refined motif is calculated by averaging all patterns associated to each point in the histogram above the chosen threshold (0.91 in the figure). The averaged motif is automatically shown:



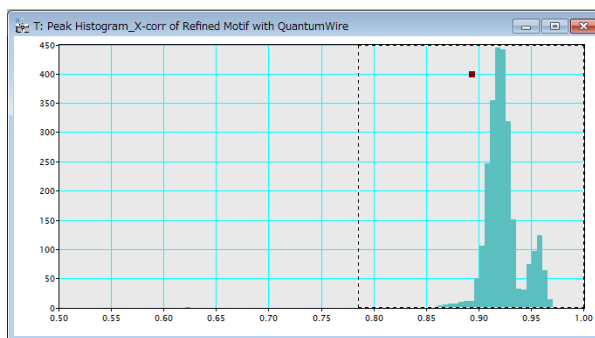
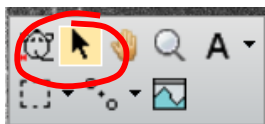
The third step of the Motif detection is calculating the cross-coefficients using the refined motif. To do so, select **Motif Detection...Discriminate Motifs** command.



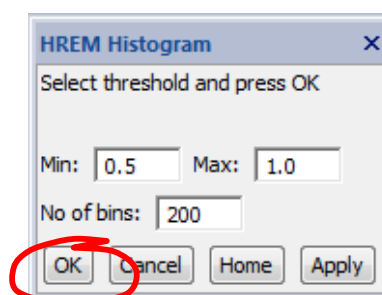
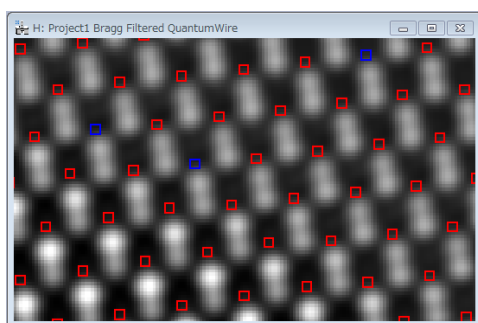
Then, the histogram of the cross-correlation between the refined Motif and the whole image will be shown. This step is especially useful in the presence of noise.



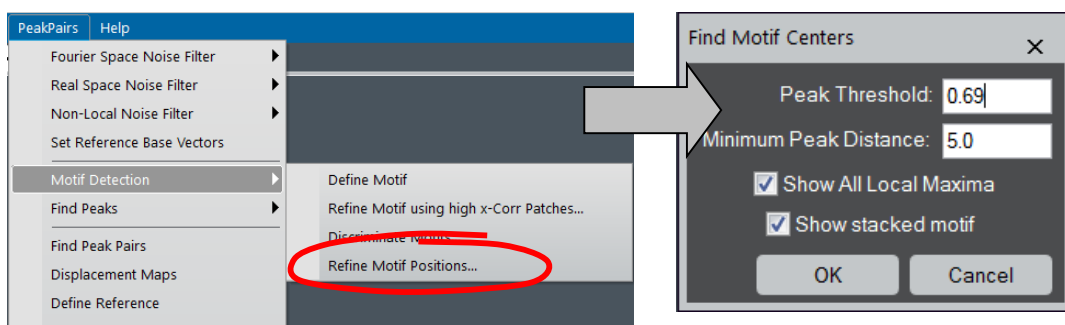
Once the refined histogram is shown, the user should select the intensity threshold on the refined histogram as before.



The discovered motifs will be classified to red or blue as before. The peak color will be dynamically revised by changing the threshold. When you satisfy the threshold by looking the motif markers (red or blue), push the **OK** button of the Histogram tool.

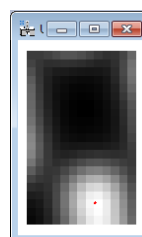
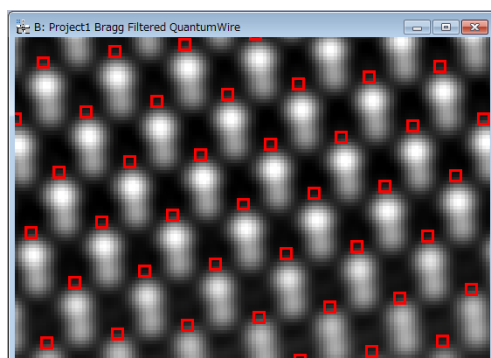


The final step of the Motif detection is finding the refined motif centers (positions) by using quadratic fitting to the cross-correlation peaks. To do so, select **Motif Detection...Refine Motif Positions**, which opens the dialog as shown below.



If the motif peaks within the minimum motif distance are found, these peaks will be merged into a single peak position.

Then, the refined motif positions (the centers of the motif boxes) are marked by the small *red* boxes, and the second refined motif will be displayed. When **Show All Local Maxima** is checked, all the peaks below the threshold are also displayed in *blue*. (Here, no blue boxes are shown.)

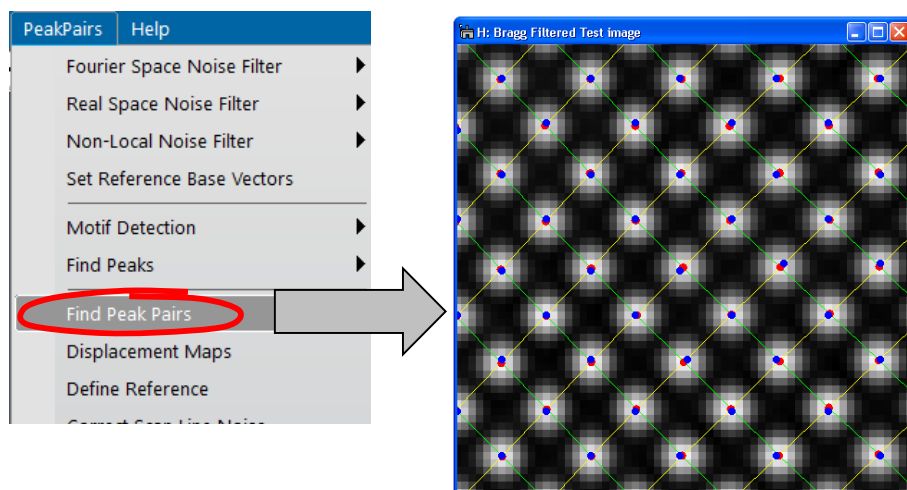


Refined
motif

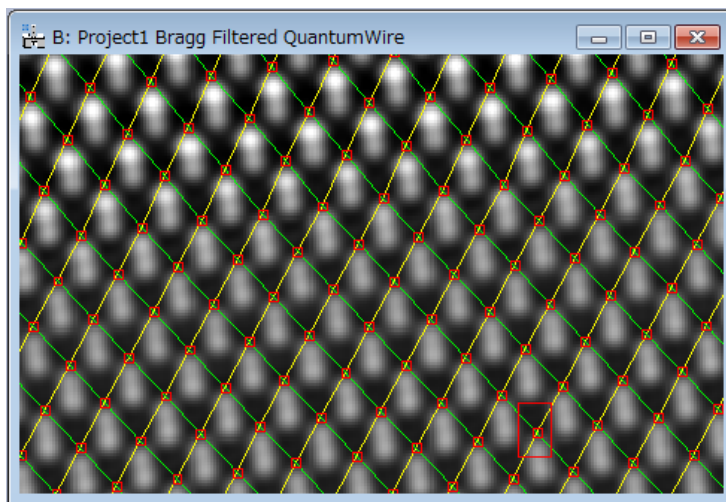
Peak Pairs Determination

IMPORTANT: Peak Pairs are calculated using two basis vectors. The Bragg filter defines the two base vectors automatically. However, when the two base vectors are not defined yet, they should be defined manually using the **Set Reference Base Vectors** command.

Once all peaks or motif centers have been selected, Peak Pairs should be calculated using the **Find Peak Pairs** command. This process will find all pairs of peaks along the predefined two basis vectors.



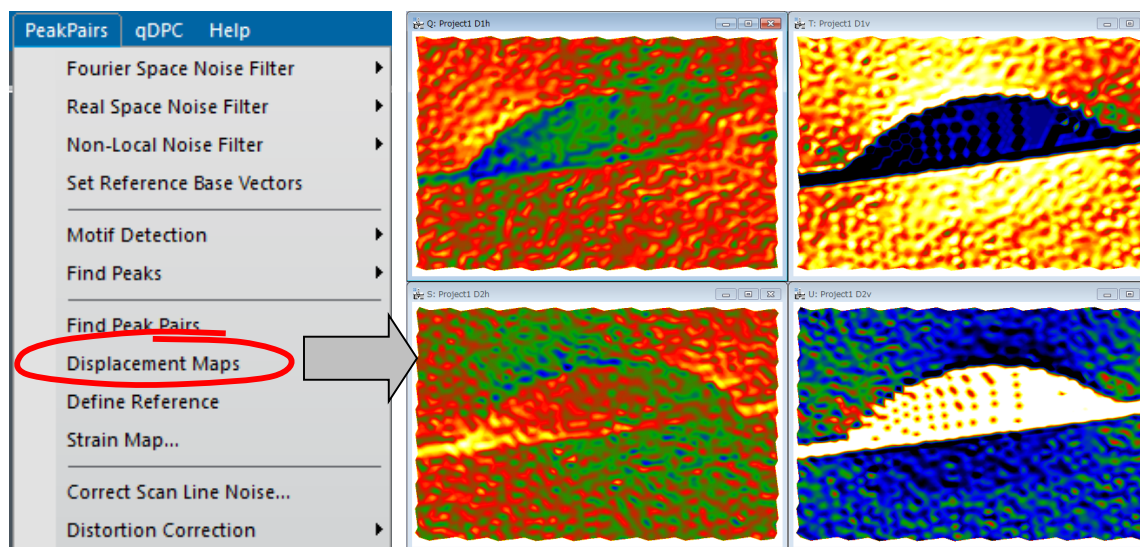
Peak Detection (simple structure)



Motif Detection (complex structure)

Displacement and Strain Maps calculation

Once all Peak Pairs have been determined, we can proceed to the calculation of displacement maps using the Displacement Maps command. This command generates horizontal and vertical displacements (D1h, D1v, D2h and D2v) for the two base vectors.



Technical note:

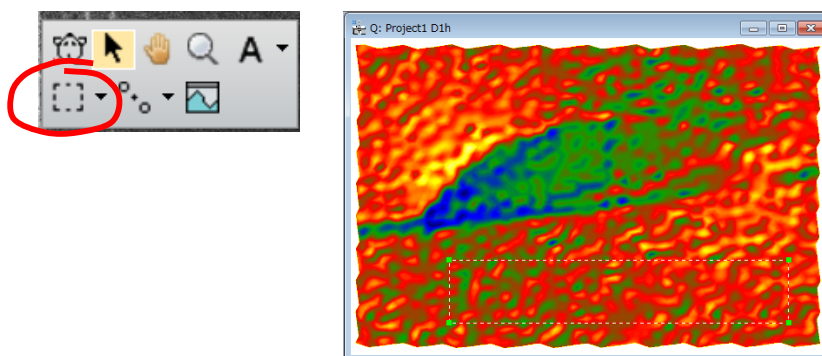
PPA uses an automatic selection of contrast and the temperature color scale for displaying image values. Default color range is ± 1 pixel.

If you prefer a grey scale or a different contrast limit, press the right button on the image, and modify **Image Display** options properly (consult the DigitalMicrograph manual).

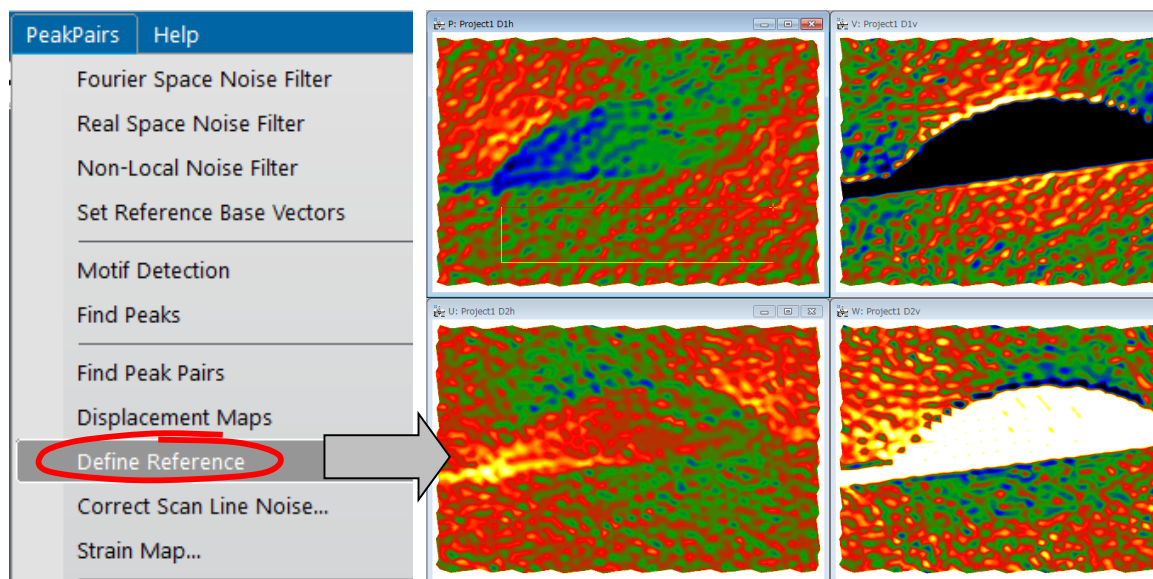
Changing this option will not change the actual values, only its appearance.

An essential step of strain determination is to define the Reference Area, the area that is considered to correspond to the reference lattice, where we refine the base vectors. It is important to note that the Peak-Pairs Analysis requires roughly determined base vectors to find the peak-pairs and to calculate the displacement maps.

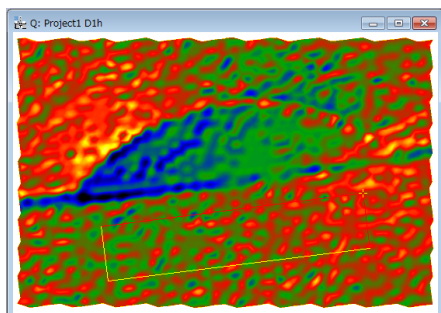
All displacements and strain values will be referred to this area. Use the **Rectangle ROI** tool, select an area on any one of the Displacement images (D1h, D1v, D2h or D2v):



Once the Rectangle ROI has been placed, the user should select the **Define Reference** command. This will change the displacement values, so as to obtain a uniform displacement in the chosen reference area. In some case, the displacement maps do not change so much even when their values actually change, since the color maps range is automatically adjusted.



The **Define Reference** command makes the Rectangle ROI rotatable. You can change the size and angle as shown below, if you want:

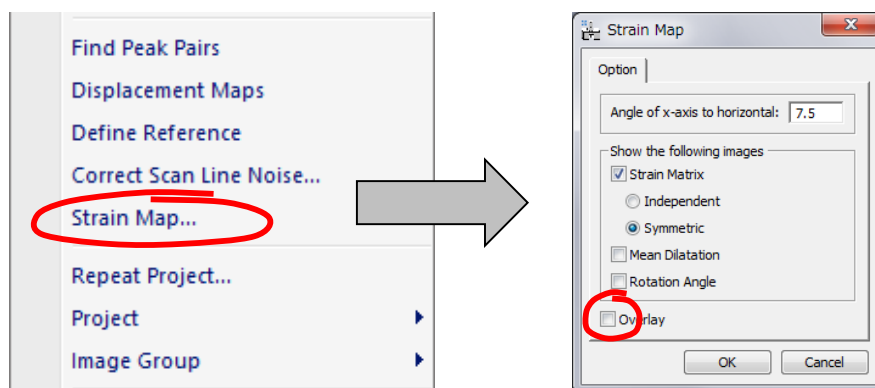


You can adjust the edge length by selecting the yellow edge and dragging the handle, and rotate the ROI by dragging the yellow cross (+).

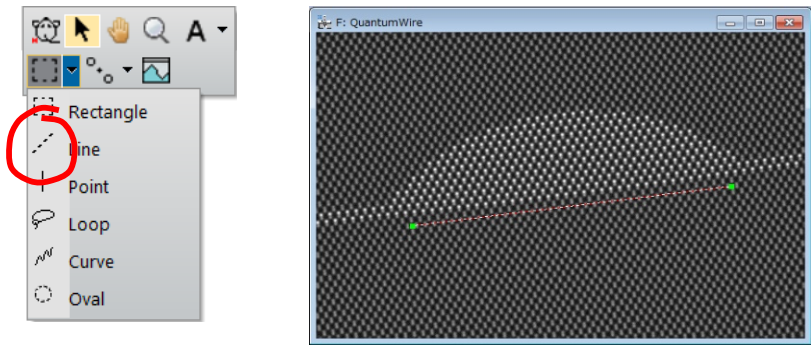
You can adjust the both edge lengths by dragging the yellow cross when pressing the SHIFT key.

When you change the ROI shape or displace the ROI, the average displacement within the ROI will be automatically set to zero.

The final step is to calculate *strain maps* (e_{xx} , e_{yy} , e_{xy} and e_{yx}) at the desired *angle*. When the **Strain Map** command is selected, the dialog below appears. Here, you can determine the direction of the x-axes to display the strain maps using **Angle of x-axis to horizontal**. If the angle is set equal to 0, horizontal direction corresponds to the x-axes.



The angle of x-axis to horizontal may be determined graphically. To do so, just put a **Line ROI** on the original image along the desired direction of x-axis, and launch the **Strain Map** command.



Once the OK button is chosen, a set of 4 images corresponding to (e_{xx} , e_{yy} , e_{xy} and e_{yx}) will be displayed when **Independent** is elected. When **Symmetric** is selected, e_{xy} is an average of e_{xy} and e_{yx} of the independent expression. The mean dilatation is an average of e_{xx} and e_{yy} . and the rotation is given by $\frac{1}{2}(e_{yx}-e_{xy})$.

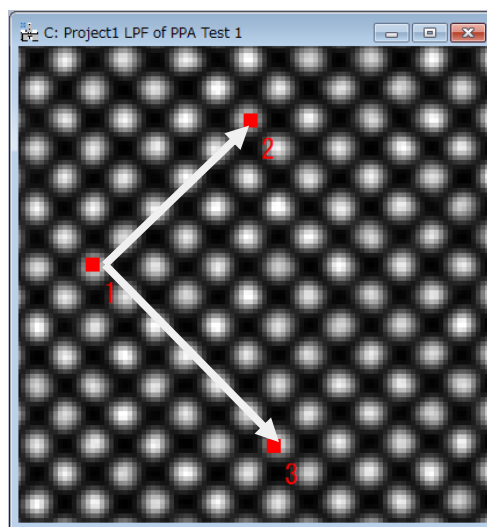
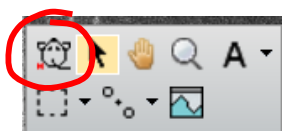
There is an option for strain representation (Overlay):

DESCRIPTION	Full image	Detail
<p>No overlay: Continuous strain maps are shown.</p> <p>Hint: If you prefer a grey scale or a different contrast limit, press the right button on the image, and modify ImageDisplay options properly.</p>		
<p>Overlay: Strain maps at each atomic column are shown with color dots over the original images.</p>		

Setting the Reference Base Vectors

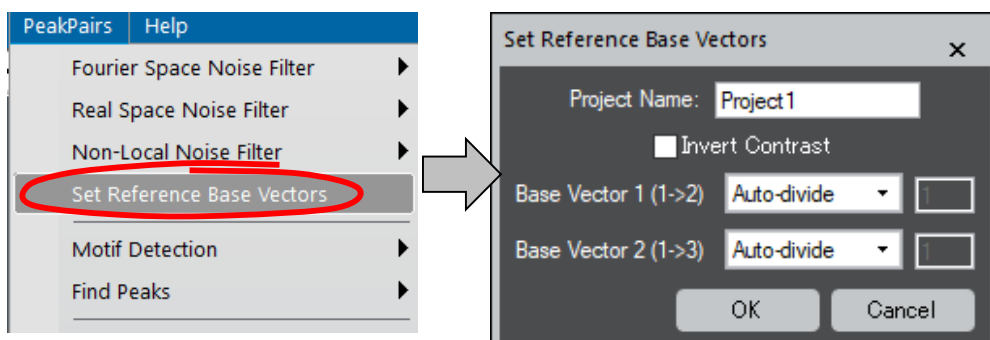
It is possible to manually set the reference base vectors.

To manually define the Reference Base vectors, use the **HREM Mouse Tool** to select 3 points in the order the origin of both vectors, terminal point of vector 1 and terminal point of vector 2, so that the *directions* of the desired reference base vectors are described by the directions of vectors 1->2 and 1->3.



Approximate directions
specified by the user

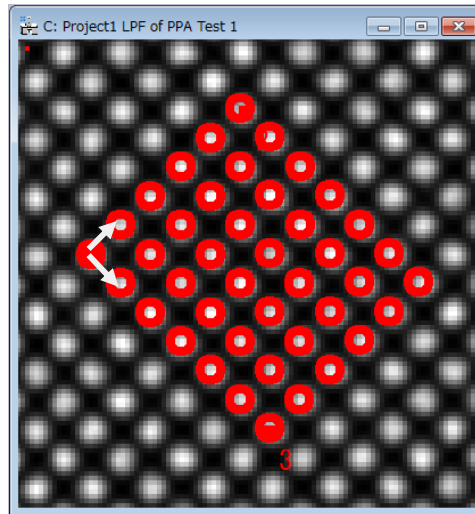
When applying the Set Reference Base Vectors command, the dialog shown below will open.



Normally, the reference base vectors along the user specified directions will be automatically estimated using **Auto-divide**. However, if the unit is not simple, the algorithm to determine a repeating unit will fail. In this case, you can specify the number of repeating units along two directions. In this case, 5 and 6 along the base vector directions 1 (1->2) and 2 (1->3), respectively.

NOTE: If you are interested in *black* spots, the **Invert Contrast** should be checked here.

The precise magnitude and direction of both reference base vectors are calculated using a least-squares fitting to all the peaks within the parallelogram defined by two vectors 1- \rightarrow 2 and 1- \rightarrow 3.



Other Noise Filters

Since the peak positions are often affected by noise, reducing the noise is very important for strain measurement by the PPA. Thus, we have used the Bragg filter in the Getting Started section. In this section, we will explain other noise filters available for the PPA plug-in, namely the Wiener filter in Fourier space, and real space noise filters including non-local noise filter.

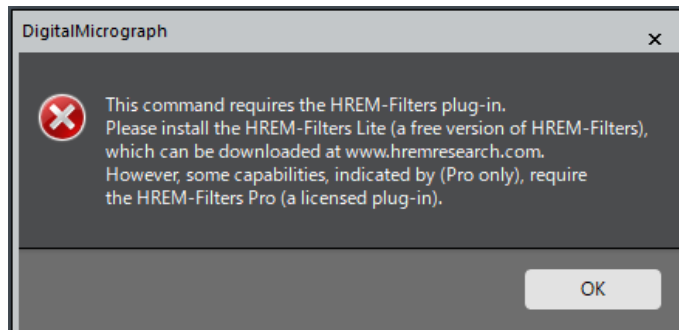
Fourier Space Noise Filters

Wiener Filter

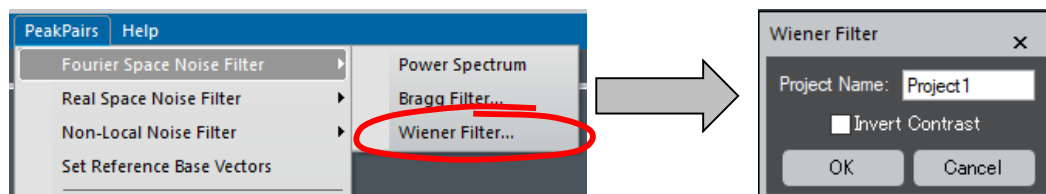
While the Bragg filter is very useful to reduce noise, all the spots that pass the filter should be selected manually to faithfully reproduce the original features. Furthermore, the noise inside of a filter mask will not be blocked and contribute to a filtered image.

The Wiener filter is widely used for image restoration and calculates the optimal filter for removing the noise. The Wiener filter selects significant spots (the peaks in Fourier space) over the noise power automatically. This means you don't need to select all the peaks to be included for filtering.

NOTE: The Wiener filter of the PPA is the Radial Wiener Filter, which means the noise power is estimated from rotational average of the power spectrum. This is the restricted version of Wiener filter implemented in the HREM-Filters plug-in. Thus, you have to install the HREM-Filters Lite (a freeware plug-in), or the HREM-Filters Pro (a commercial plug-in). When none of them is not installed, the warning message shown below will appear:



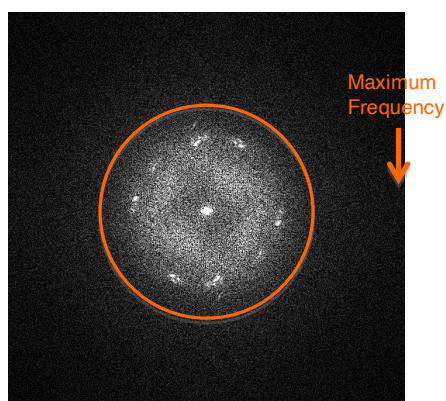
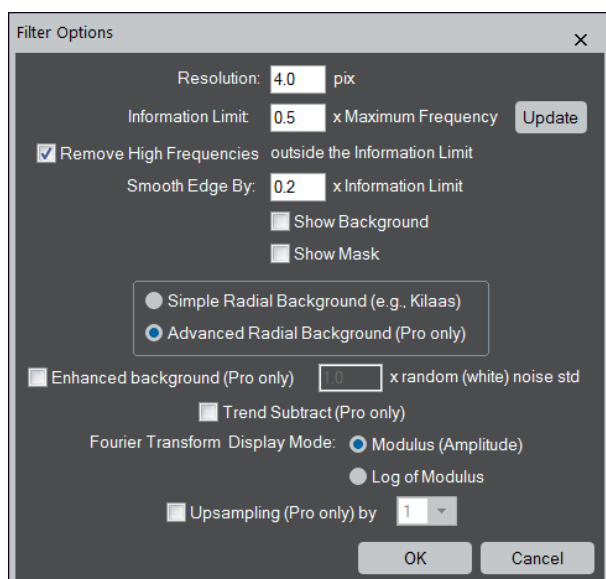
At first, calculate the Power Spectrum, and place two mouse points on it to define the base vectors in Fourier space. When the power spectrum is frontmost, select the **Wiener Filter** command. Then, the dialog to determine the project name will appear:



NOTE: If you image has hollows (dips), not peaks, the **Invert Contrast** will be checked here.

TIPS: The Wiener filter command can be used without using the power spectrum. In this case, however, the base vector in real space should be determined manually by using the **Set Reference Base Vectors** command.

When click **OK**, the dialog below will open, and a circle will be drawn on the Fourier transform as shown below left. If you want, you can change the **Display Mode** between Modulus (Amplitude) and Log of Modulus.



In the Filter Options dialog, some parameters with “(Pro only)” are applicable only when the HREM-Filters Pro (a commercial plug-in) has been installed.

The first four parameters determine how high frequency noise is eliminated. Using the circle on the Fourier transform you can tell the Wiener filter the highest frequency of the signal, namely the information limit. **Resolution** and **Information Limit** are inversely related. If you change one value, the other value will be changed. When the image is calibrated, you will see a physical unit for Resolution. If not, the unit of Resolution is pix (pixels). When you know the resolution of the micrograph in a physical unit or in pixels, you can directly input the value for **Resolution**. Alternatively, you can input the value for **Information Limit** in terms of the Maximum Frequency of the Fourier transform.

Resolution	When you know the resolution of the micrograph in a physical unit or in pixels, you can directly input the value here.
Information Limit:	The Information Limit given by a fraction of the Maximum Frequency of the image.
Update	By clicking the Update button, you can verify the Information Limit on the Fourier transform.
Remove High Frequencies	outside the Information Limit
Smooth Edge by	If checked, high frequencies will be smoothly attenuated over both sides of the Information Limit by the Smooth Edge by .
Radial Background type:	The choice of the type of Radial Background. <i>HREM-Filters Lite</i> can use <i>Simple Radial Background</i> obtained by rotational average of the intensity (e.g., Kilaas). <i>Advanced Radial Background</i> that is available for <i>Pro only</i> is superior to the Simple Radial Background.
Fourier Transform Display Mode	You can select the display mode of the Fourier transform between Modulus (Amplitude) and Log of Modulus.

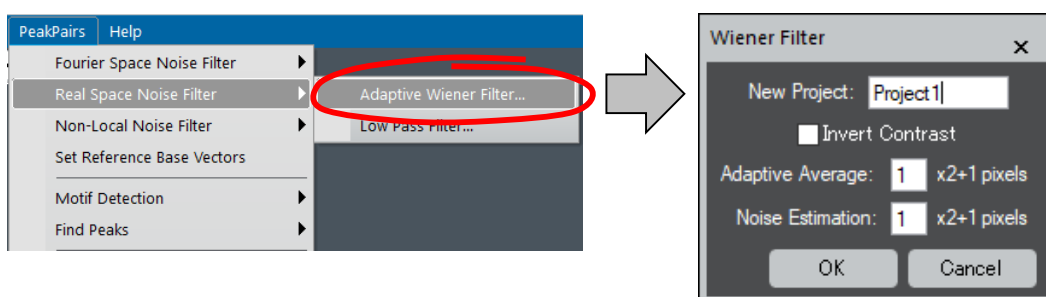
Real Space Noise Filters

While Bragg filtering is very useful to reduce noise, some researchers may prefer alternative noise filtering techniques in real space. There are two alternative noise filtering commands: Adaptive Wiener Filter and Low Pass Filter. Since the techniques have no way to determine automatically the *basis vectors*, they should be determined manually by using the Set Reference Base Vectors command

Adaptive Wiener Filter

The Wiener filter in real space assumes that if noise is present in the system, then it is considered to be additive white Gaussian noise.

When selecting the Adaptive Wiener Filter on the front image, the dialog below will open. In a typical Peak Pairs session, if Wiener filtering is desired, it is usually the first operation to be applied to the original image. Then, the project name should be given.

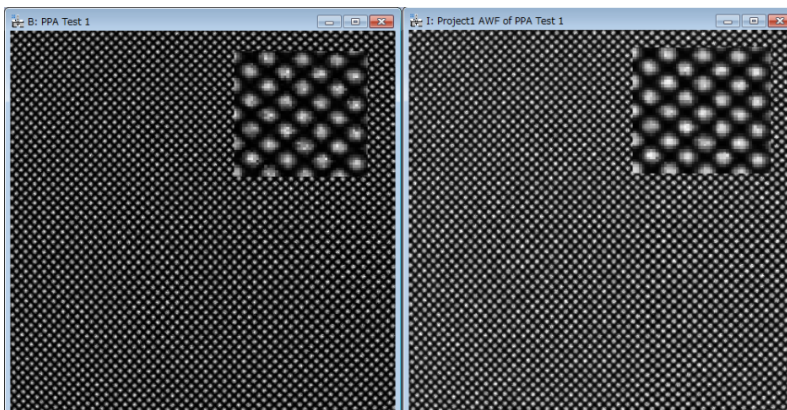


NOTE: If you peak is dark (black) over the background, the **Invert Contrast** will be checked here.

The user should decide the sizes of the windows used for calculating the **Adaptive Average** and the **Noise Estimation**.

If the standard deviation of the local area is small, then the pixel value will be replaced by a local average. On the other hand, if the standard deviation of the local area is large, then the pixel value will be retained. Thus, the pixel value of the filtered image will be between the original value and the local average according to the local standard deviation.

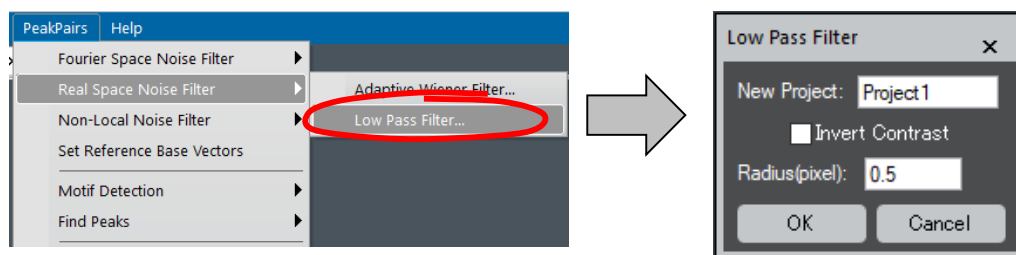
The result of the Wiener filtering applied to *Test image.dm3* is shown below. The insets show enlarged parts.



Left: Original; Right: Wiener (Adaptive Average: 3, Noise Estimation: 3)

Low Pass Filter

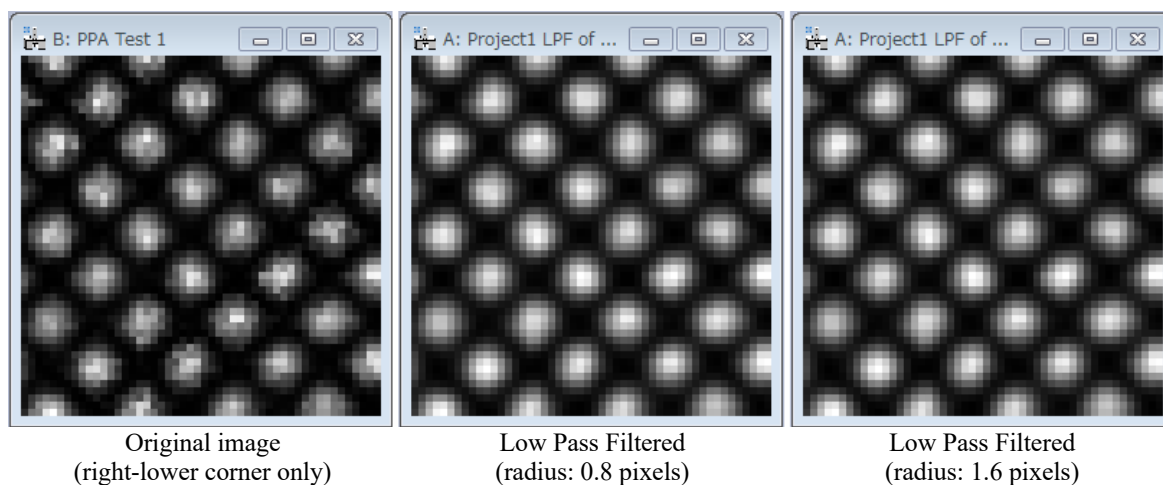
In order to generate a Low-Pass filtered image, use the **Low Pass Filter** command on the front image. Then, the dialog below will open. If the low-pass filtering is the first operation applied to the original image, the project name should be given.



NOTE: If you are interested in *black* spots, the **Invert Contrast** will be checked here.

The strength of the filter is defined by the **Radius** of the mask in pixels. The new pixel value will be a local average with a Gaussian weight (mask) of the defined radius. Thus, the larger the radius, the stronger the filter. You can specify a radius of less than one pixel.

In the figures blow, the resulting images after the application of a Low-Pass filter to the original image *Test image.dm3* (lower left) with different radius are shown:



Non-Local Noise Filter (from v5.0)

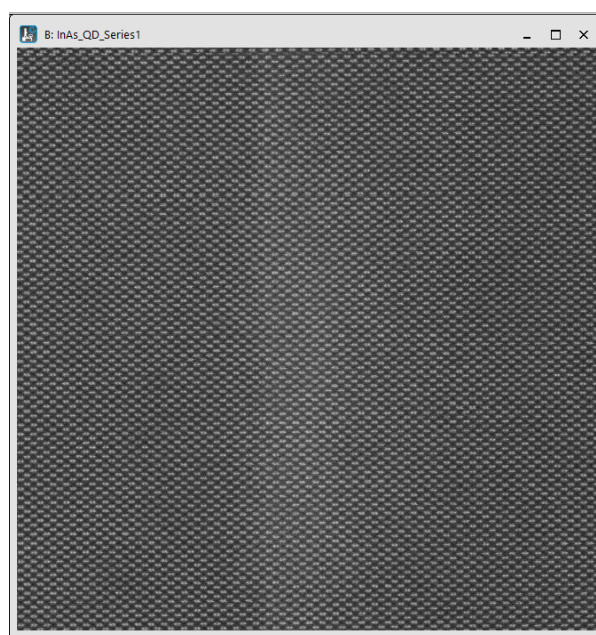
This filter allows the user to obtain a single image from a sequence of images of the same specimen, usually a time-series (TS), obtained by a scanning system such as Scanning Transmission Electron Microscopy (STEM). In order to make the scan distortion during the image acquisition negligible, an acquisition time of each scanning image should be small. Then, each image becomes noisy due to an avoidable quantum noise. Furthermore, the images obtained by a scanning system have some scanning noise, so called jitter. Therefore, a simple rigid alignment over the time series will make an atomic peak blurred, and degrade resolution.

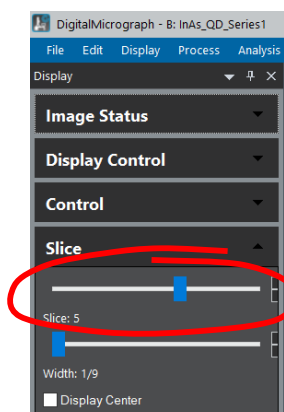
The non-local noise filter performs non-local averaging (NLA) over the time series based on a concept of non-local mean (NLM). Thus, the NLA over the time series is one of the *non-rigid alignments*. The resulting image obtained by NLA reduces the scan noise without degrading resolution and improves signal-to-noise (SNR) ratio (Barcena, 2016). This usually improves peak location, which results in improved strain mapping.

The non-local noise filter has two steps: (i) Rigid image alignment and (ii) Image reconstruction (non-rigid alignment).

- i. The **rigid image alignment** estimates an average displacement of each image using the cross-correlation between two images, and creates a new stacked image after correcting the estimated displacements. Here, there are two modes of estimating the image displacements: the image displacements between consecutive two neighbor images or between a fixed reference image and other image.
- ii. The **image reconstruction** performs non-local average over the rigid-aligned time-series image, and gives a non-rigid aligned single image. For medium/large size images, Non-Local-Average is very time consuming, and its calculation may take minutes or even hours in a standard workstation. For this reason, we provide the NLA mode to use a NVIDIA GPU for intensive calculation.

Here, we use the image series, *InAs_QD_Series1.dm3* (courtesy of Prof. David González, Universidad de Cádiz).





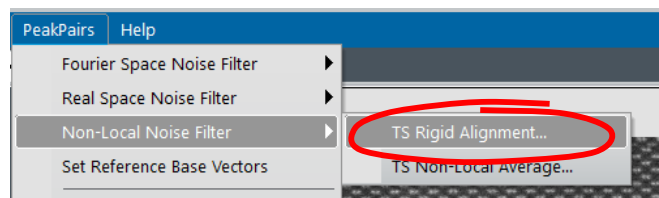
Once loaded, the user may navigate across different images of the time-series using the standard GMS tool called **Slice (Slice Player)** tool. Scrolling the cursor to the left allow the selection of the first images in the series, and scrolling it to the right, the last ones.

When scrolling this data, the user may observe the sample drift over the time series.

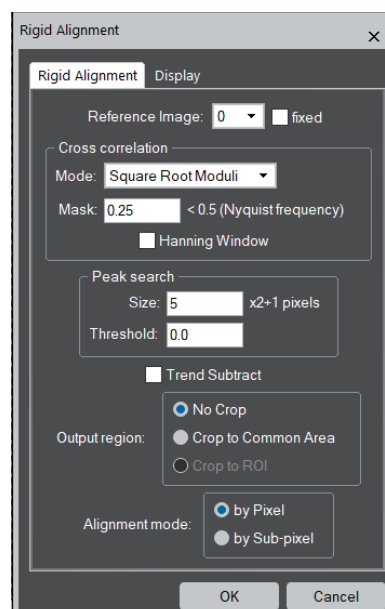
TIP: If the drift is not visible, zooming in the image to show a partial area may help.

TS (Time-Series) RIGID ALIGNMENT

The first step for applying the non-local noise filter is the rigid alignment. To do so, select the Non-Local Noise filter...TS Rigid Alignment, where TS means Time Series.



After selection, the dialog shown below appears, where the user can choose all the options available for Rigid Alignment:



Reference Image

This dropdown menu allows the user to choose the **Reference Image**. When the **fixed** checkbox is *not activated*, the image displacements between the *consecutive* two neighbor images will be estimated downward starting from the selected Reference Image, and then upward from the Reference Image. In this case, the

choice of the Reference Image is not so important, since only two image displacements depend on the selected the Reference.

However, when the **fixed** checkbox is *activated*, all the remaining images will be aligned to the selected Reference Image. In this case, the choice of the Reference Image is important, since all the image displacements depend on the selected Reference.

Cross correlation

Here, the user selects three important features that control the cross-correlation performance.

Mode: specifies the cross-correlation algorithm. There are three possible options:

Conventional: cross-correlation with normal amplitudes.

Square Root Moduli: cross-correlation with square root amplitudes

Phase Only: cross-correlation with unit amplitudes (only phase will be retained)

Mask: Specifies the radius of a low-pass filter in Fourier space (relative to the Nyquist frequency) to eliminate high-frequency noise. Its value should be between 0 to 0.5.

Hanning window: When checked, a Hanning Window will be applied before taking the cross-correlation to reduce the effect from intensity discontinuity at the image boundary.

Peak Search

Search conditions for the cross-correlation peak.

Size: Radius of the cross-correlation peak.

Threshold: Intensity below this level will be ignored when estimating a peak center.

Trend Subtract

If checked, a trend (slowly varying feature) is subtracted before alignment to enhance the image feature.

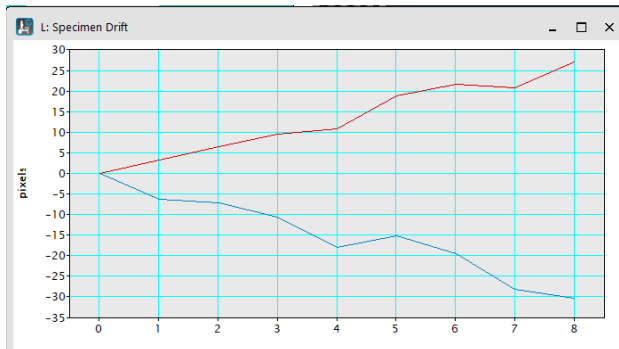
Output region

Output region of the aligned image will be specified here. If the ROI is not present, "Crop to ROI" is disabled.

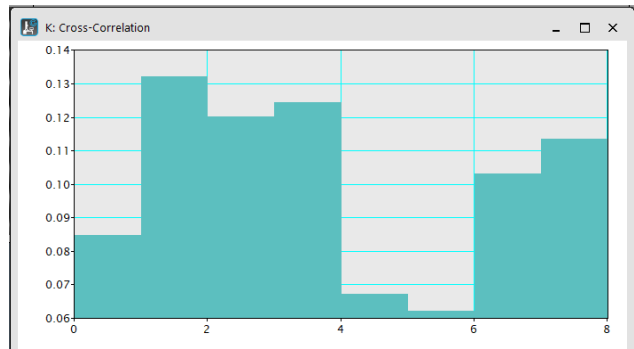
Alignment mode

Here, the user can choose the way to determine the image displacement from **by Pixel** and **by Sub-pixel**. When the alignment mode is **by Pixel**, the estimated displacement is rounded into an integer (pixels) and no interpolation of the intensity is performed. On the other hand, when the alignment mode is **by Sub-pixel**, the image is shifted by estimated amount using Fourier transform.

After choosing the options and pressing the **OK** button, two different windows are automatically created: one shows the estimated displacements and the other the cross-correlation values.



Specimen drift window

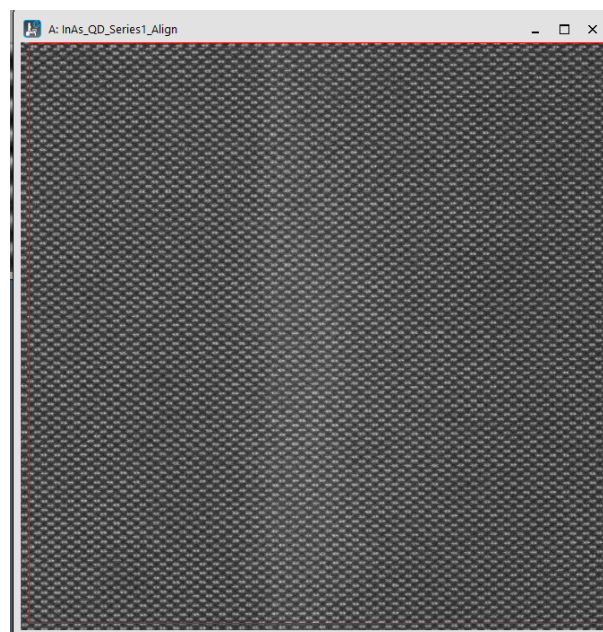


Cross-correlation window

Specimen drift window shows the estimated drift of each image in pixels with respect to the Reference Image. The blue and red lines correspond to drift in the horizontal and vertical directions, respectively. In this case the Reference Image is set to zero (0).

Cross-correlation window shows the cross-correlation values between two neighbor images or between a fixed Reference Image and other image.

When the image displacements are estimated, the aligned image will appear in a new window as shown below:



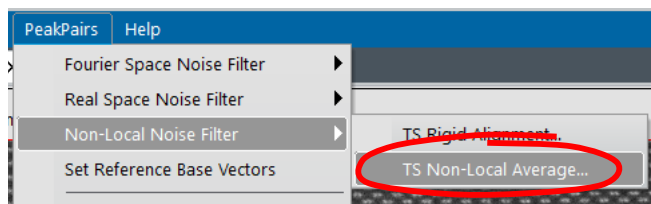
The aligned image consists on the images aligned with respect to the Reference Image. If the aligned image stack is scrolled using the **Slice Player**, it may be observed that the drift has been substantially reduced/removed from the series.

The red rectangle represents the common area where the series has valid values over all images. The greater the drift, the smaller the common area and vice versa.

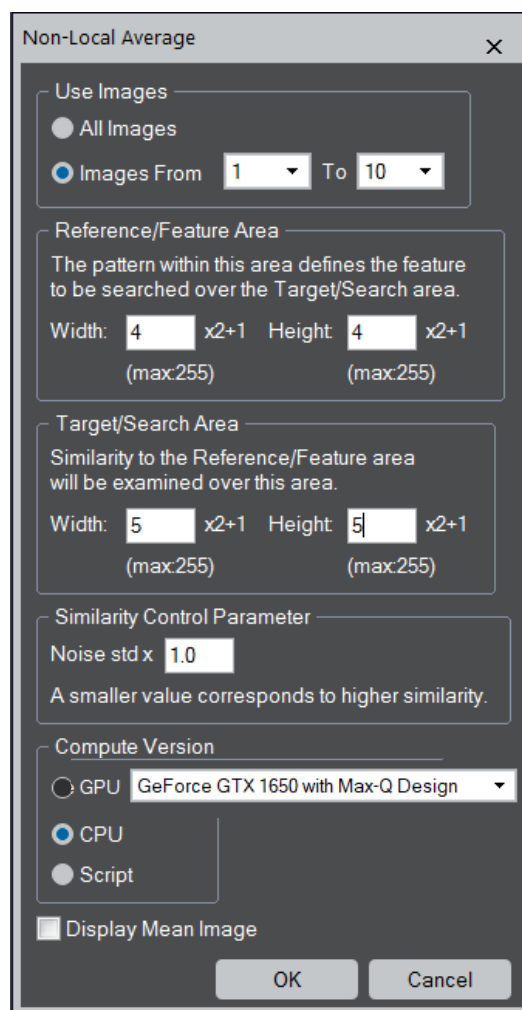
TS (Time-Series) NON-LOCAL AVERAGE

Non-Local Average (NLA) of the time-series is the additional module for the PPA, which requires a separate license. However, the script version that works without a license is provided to evaluate the functionality of the NLA module. Since the script version takes almost a few thousands of times of the GPU version of the NLA module, please use the script version only for a small image or a small area defined by a rectangular ROI.

The second step of the *non-local noise filter* is the *non-local average*. To do so, select the **Non-Local Noise Filter...TS Non-Local Average**, when the rigid aligned image is the front most.



After selection, the dialog shown below will appear, where the user can setup all the options available for Non-Local Average.



Use Images:

This option gives the user the possibility to select a range of images to be used for non-local averaging. This is useful when some first (or last) images of the time-series are anomalous (blurred or distorted), or the user want to test the parameters using the small number of images.

Reference/Feature Area:

The pattern within this area defines the feature to be searched over the Target/Search area. The Reference/Feature area is defined by the rectangle box. You may want to include a single peak of a few peaks in this box. If a larger area is used, the fidelity of the similarity will increase.

Target/Search Area:

The Target/Search area is defined by the rectangle box. The similarity to the Reference/Feature Area will be examined at each pixel over this area. The size of this box should cover the magnitude of the scan jitter to perform non-rigid alignment. Usually, the scan jitter is less than several pixels.

Similarity Control Parameter:

The similarity (S) between the Reference and Target areas is defined by the ratio of the sum of squared difference (SSD) of intensities between the two areas to the noise standard deviation (std), σ_{noise} , multiplied by this parameter:

$$S = SSD/2(\sigma_{noise} \times \text{this parameter})^2$$

The contribution of the target area to the non-local average is set proportional to e^{-S} . Thus, a smaller value of this parameter gives stronger contribution of the target area to the non-local average. Usually, the value of one (1) will work satisfactorily.

Compute version:

Here, you can choose the compute version from GPU, CPU and Script to be used for non-local averaging. The calculation time will be dramatically reduced by using the GPU, though it depends on the GPU characteristics (Core Count, Core Clock Speed, Memory Type, Memory Size, Memory Bandwidth, etc.). However, reductions times are usually in an order of (1/100) or even greater compared with the CPU. Thus, we strongly encourage using GPU for Non-Local-Average calculation.

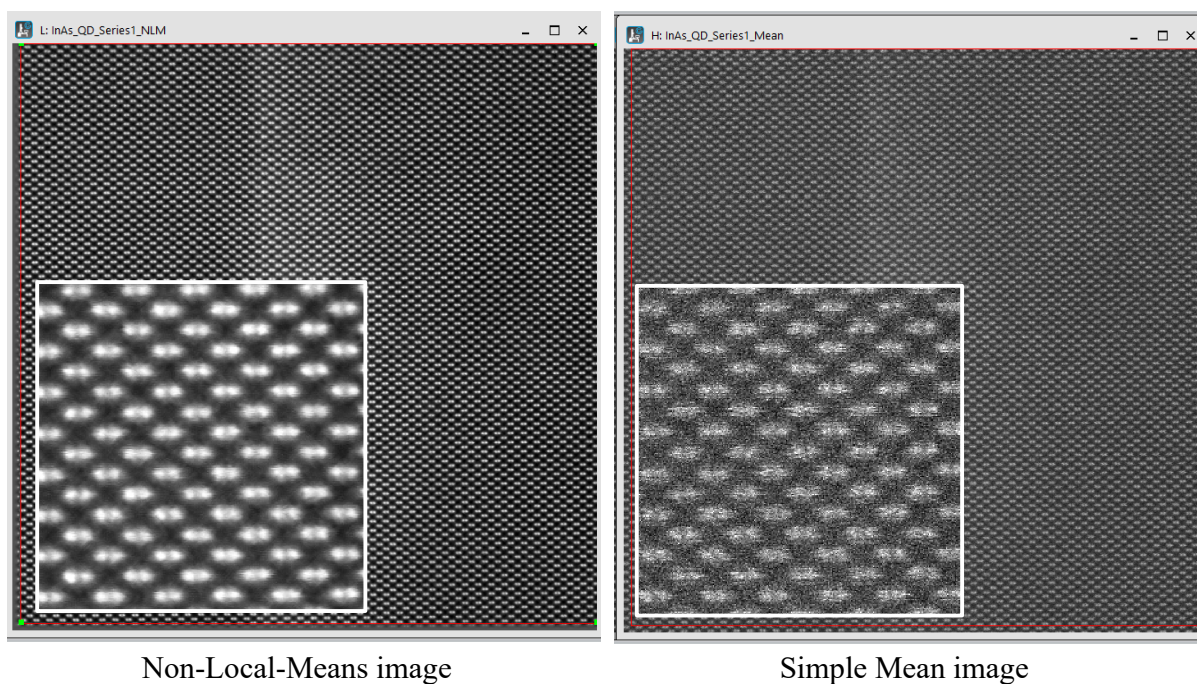
NOTE: The selection for GPU becomes active only when you have the license for the Non-Local Average module and the NVIDIA GPU is found on your PC.

NOTE: Even without the Non-Local Average license, you can still use Script version to evaluate the functionality of the NLA module. However, the script version takes almost a few thousands of times of the GPU version.

TIPS: You can stop the execution by pressing the SPACE bar at any time.

Display Mean Image:

Selecting this checkbox will display the average image, where each point in the result image is simply the mean of the values at that point of the rigid aligned image. This mean image is used as the reference image for the non-local averaging.



References

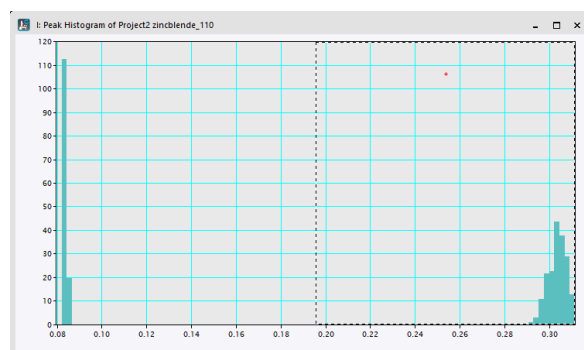
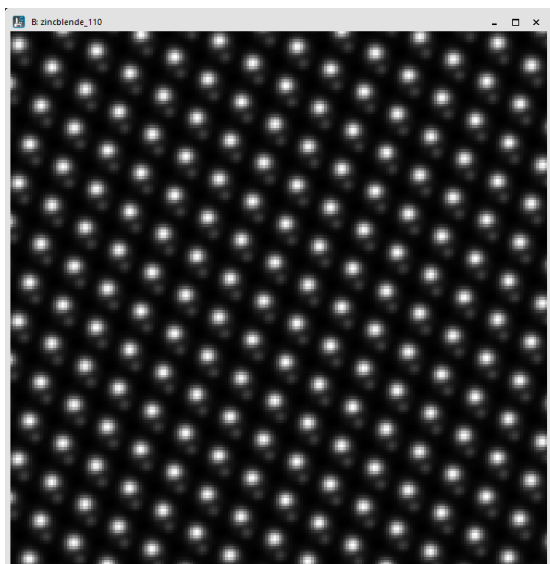
- G Bárcena-González, PL Galindo et Al. (2016) Strain mapping accuracy improvement using super-resolution techniques. *Journal of Microscopy*, vol. 262, pp. 50-58
- G Bárcena-González, PL Galindo et Al. (2017) Evaluation of high-quality image reconstruction techniques applied to high-resolution Z-contrast imaging. *Ultramicroscopy* vol. 182, pp. 283-291
- G Bárcena-González, PL Galindo et Al. (2019) HAADF-STEM Image Resolution Enhancement Using High-Quality Image Reconstruction Techniques: Case of the Fe₃O₄ (111) surface, *Microscopy and Microanalysis*, vol. 25(6), pp. 1297-1303

Advanced Topics

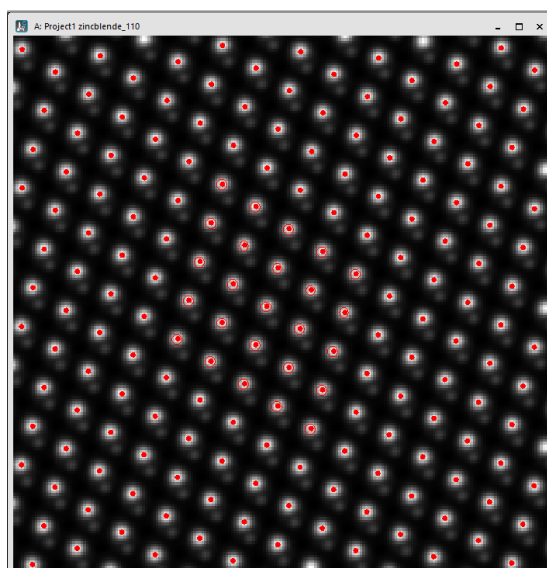
Find Weak Peaks (using Find Peaks)

Detecting weak peaks in the presence of the strong peaks is problematic. A STEM-HAADF image is such a case, since the image intensity is roughly proportional to the square of atomic number. If you set a threshold to a low value to detect weak peaks, some pixels around strong peaks may be erroneously assigned as peaks due to noise. This problem may be circumvented by repeating the Find Peaks to detect the peaks. This will be explained by using the simulated STEM-HAADF image of *InP* [110] (*zincblende.dm3*).

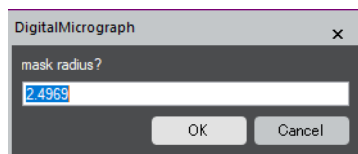
The first trial of Find Peaks...Discriminate Peaks on *zincblende.dm3* data (below left) gives the histogram (below right). You can see two distributions of strong and weak peaks corresponding to *In* and *P* columns, respectively.



Using the threshold shown in the histogram you can detect all strong peaks of *In* columns. When you perform Refine Peak Positions, you will get the image shown below.

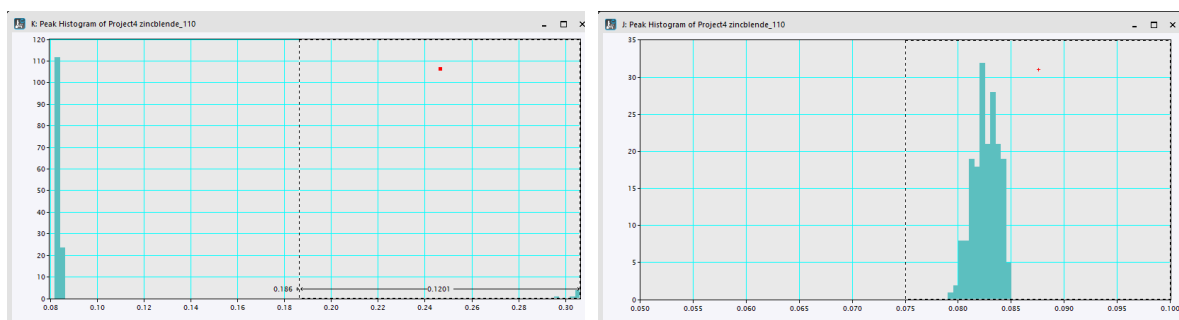


Then, you can try again **Find Peaks...Discriminate Peaks**. At that time, you will get the small dialog that requests you to input a radius of the circular mask in pixels:

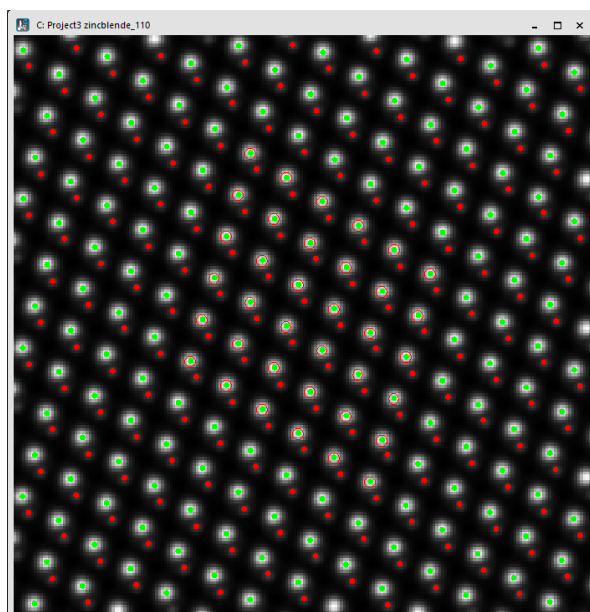


The pixels within the circular masks around the already found peaks will be excluded in this step. When the dialog is opened, the default value is shown, which is an average of the peak radius determined at the previous **Refine Peak Positions**. If you want, you can increase this number to exclude more pixels around the strong (already detected) peaks.

Using the default mask radius, a new histogram will be shown. When some high intensity pixels at image borders are not excluded by the mask, the **Max** value of the histogram tool will be high as shown by the left histogram. In such a case, you can change the **Max** value to see the peak shape of the histogram as shown below right. Then, a good threshold value can be easily determined.



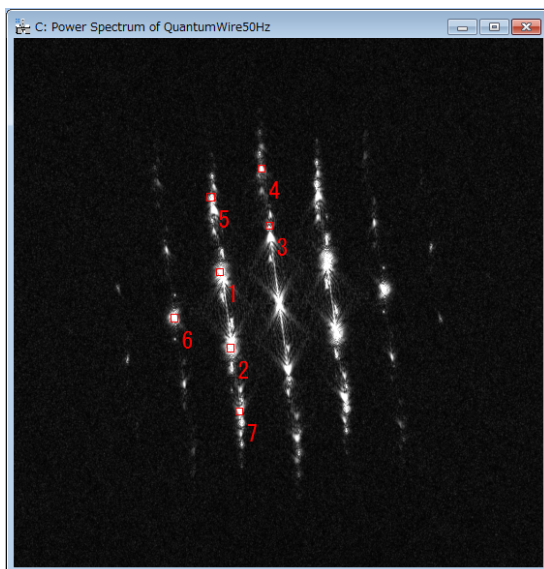
Using the shown threshold, all the weak peaks corresponding to P columns can be detected. After performing the second **Refine Peak Positions**, you will get the image shown below. Here, newly found peaks are marked in red, and previously detected peaks are shown in green.



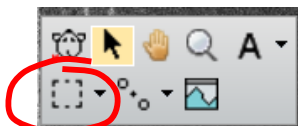
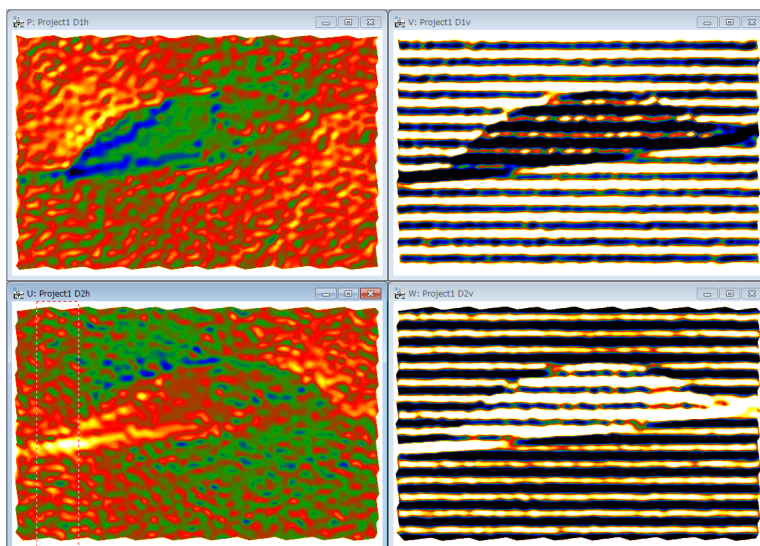
Correct Scan-Line Noise

There are situations in which the scanning electron microscopy image is altered by the presence of scanning errors, such as small beam deflections due to external electromagnetic fields, as well as hysteresis effects during the ‘fly back’ between scan lines, that may severely distort strain results from the STEM image. The presence of scanning errors may produce annoying stripes in the strain maps. In these cases, the option **Correct scan line noise** may be quite useful.

In order to show how to use this option, let us calculate strain maps from the image *QuantumWire50Hz.dm3* in the usual way, as we did with *QuantumWire.dm3* image in previous section. Then, we will get the Power spectrum as shown below:

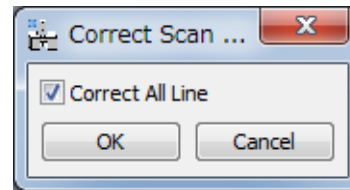
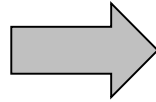
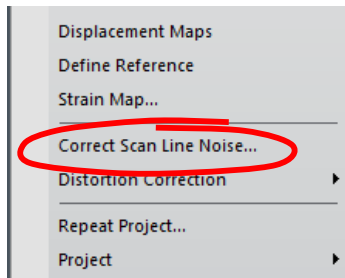


If we specify the lattice base vector (#1 and #2 as indicated), displacement maps shown below may be obtained. As we may observe, a set of stripes is shown in these maps:

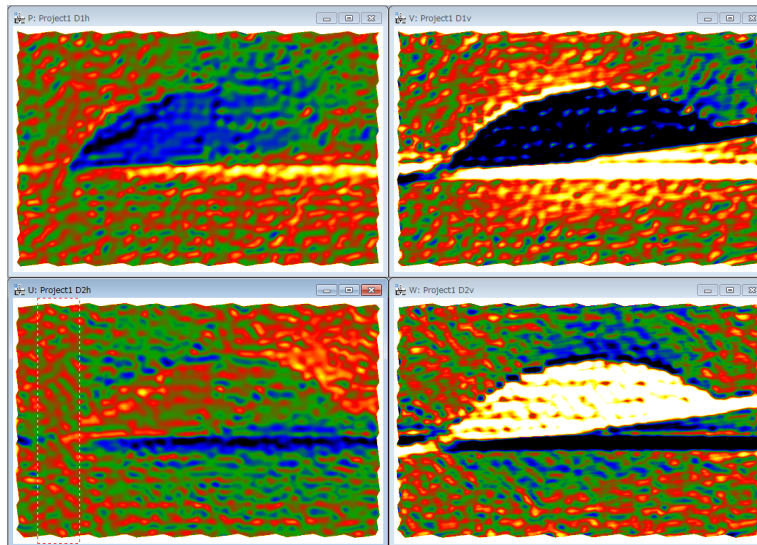


We can then add a Rectangle ROI in one of the Displacement maps (here, the image D2h, the bottom left image).

When pressing the **Correct Scan Line Noise** command to correct scan-line error, the dialog below will open.

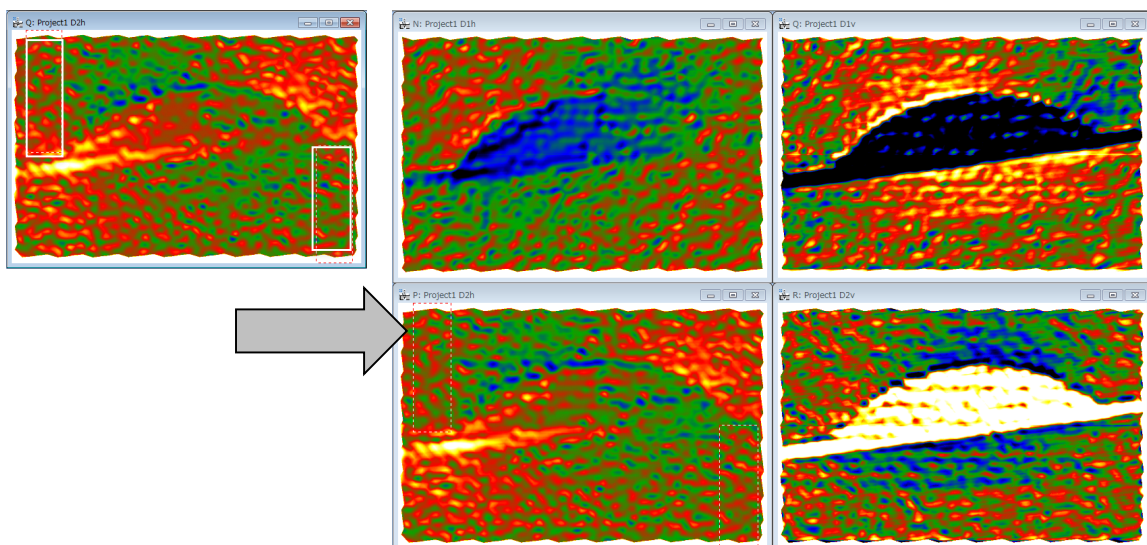


You can extend the reference area for the scan-line correction from the very top to bottom lines, when you check **Correct All Line** in the dialog.



Unfortunately, in this example there is no perfect reference area from the top to bottom of this image. Therefore, we have horizontal artefacts as clearly see in the images D1v and D2v.

The scan-line correction has a capability to merge multiple reference areas. Here, we use two reference areas at the top left and the bottom right. Then, we can better perform the scan-line correction as shown below. There is no appreciable artefact observed before.

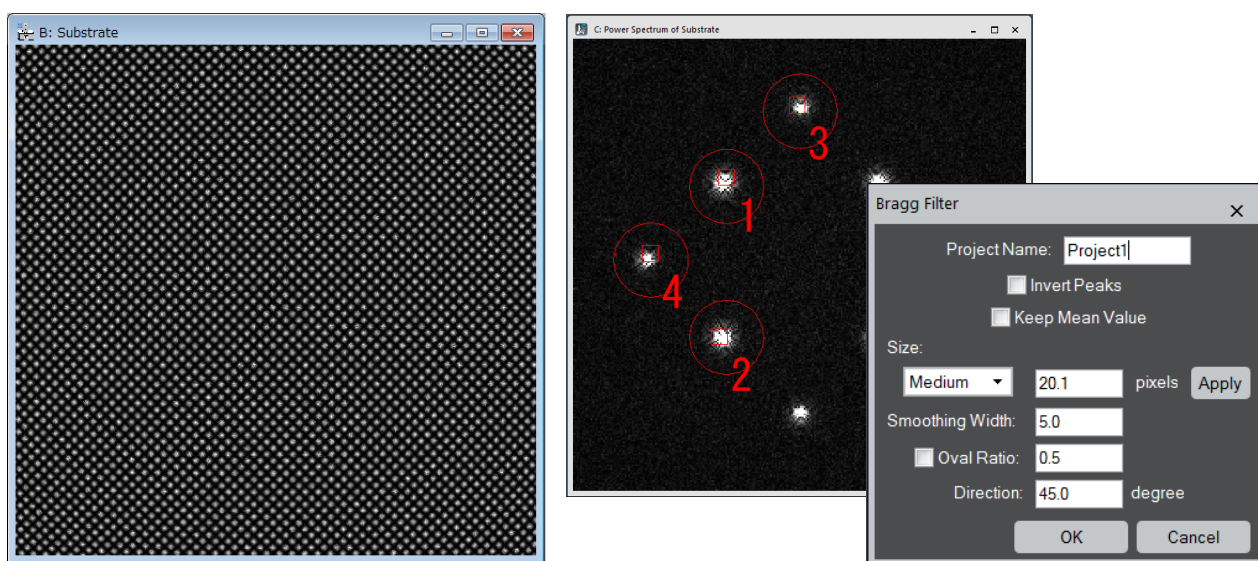


Geometric Distortion Correction

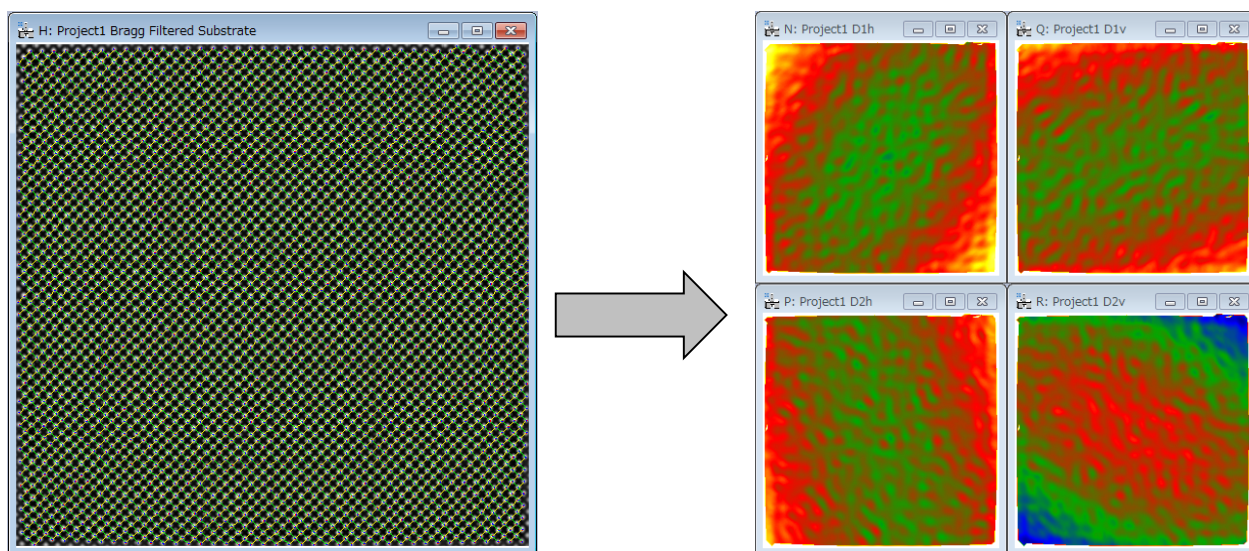
All optical systems and scanning systems distort the images they form. If these geometric distortions are reproducible, it is possible to eliminate them when the image taken from the perfect crystal is available. This is valid not only for projector lens distortions but also for any other systematic distortions present in the image.

In order to correct the distortions, at first, we have to measure the distortions using an image of a perfect crystal. We explain distortion correction here using a pair of images with the same distortion, *Test image.dm3* and *Substrate.dm3*, the latter of which corresponds to an image of a perfect crystal.

Open the image *Substrate.dm3*, execute the Power Spectrum, and then Bragg Filter in the usual way by selecting relevant spots in the Power Spectrum.

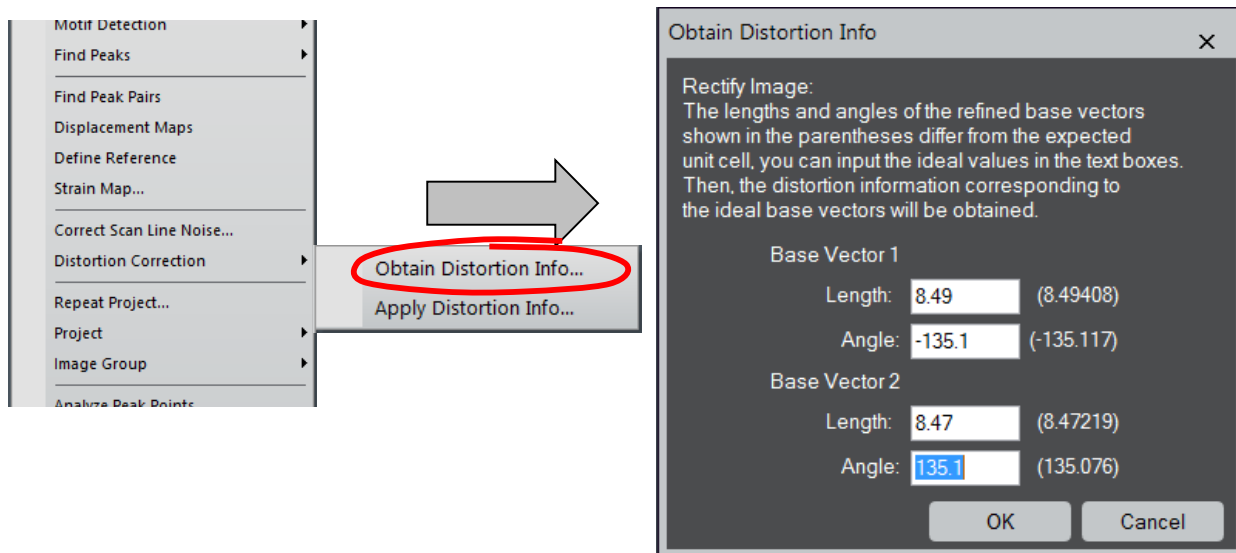


Then, calculate the *Peak Pairs* using the usual commands Find Peaks and Find Peak Pairs. If we analyze the displacements with the Displacement Maps command, we can observe that the image of a perfect crystal is distorted (they are not flat) as shown below right.



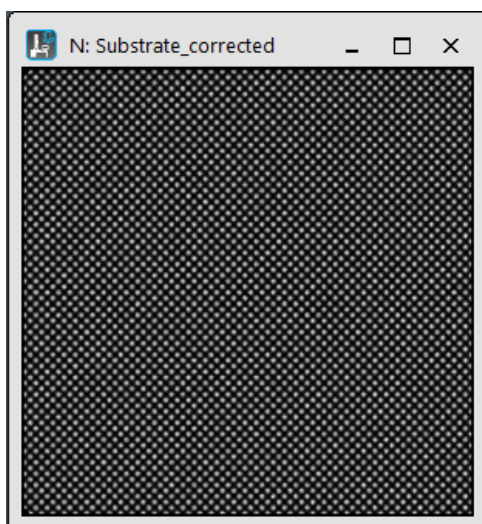
Measuring Distortion using the Image of a Perfect Crystal

The distortion information can be obtained from the perfect crystal image, which then can be used to correct distortions in any other image with the same image distortion. In order to obtain the distortion information, select the project image with *Peak Pairs* information, and apply the command **Obtain Distortion Info**. Then, dialog shown below will open. Here, you can simply press **OK** in the dialog.



NOTE: Using this command, any distortion of an image obtained from a *perfect crystal* can be corrected, when you input the expected lattice information here (see *Image Rectification* section below).

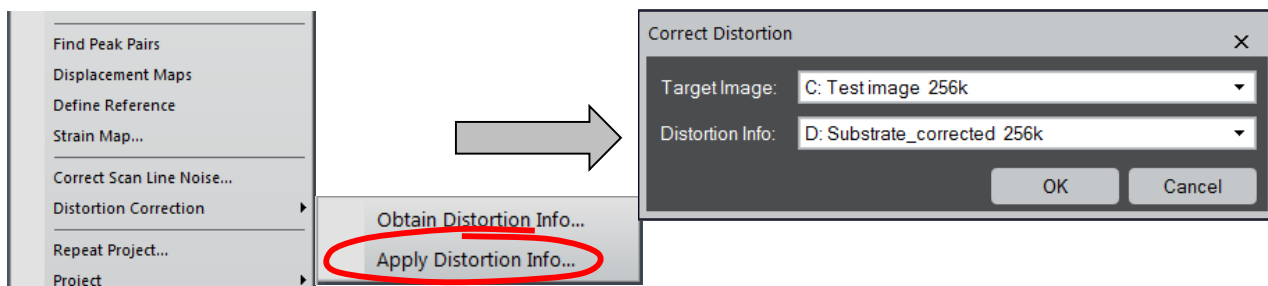
Then, the distortion corrected image, named "<image name>_corrected", will be displayed in a new window as shown below.



This *Substrate_corrected* image has distortion information inside, and can be used in later analysis of the image affected by the same distortion. Therefore, you may want to save this image to a disk with a distinct name (e.g., *Distortion Info of Substrate*) using **Save As** command.

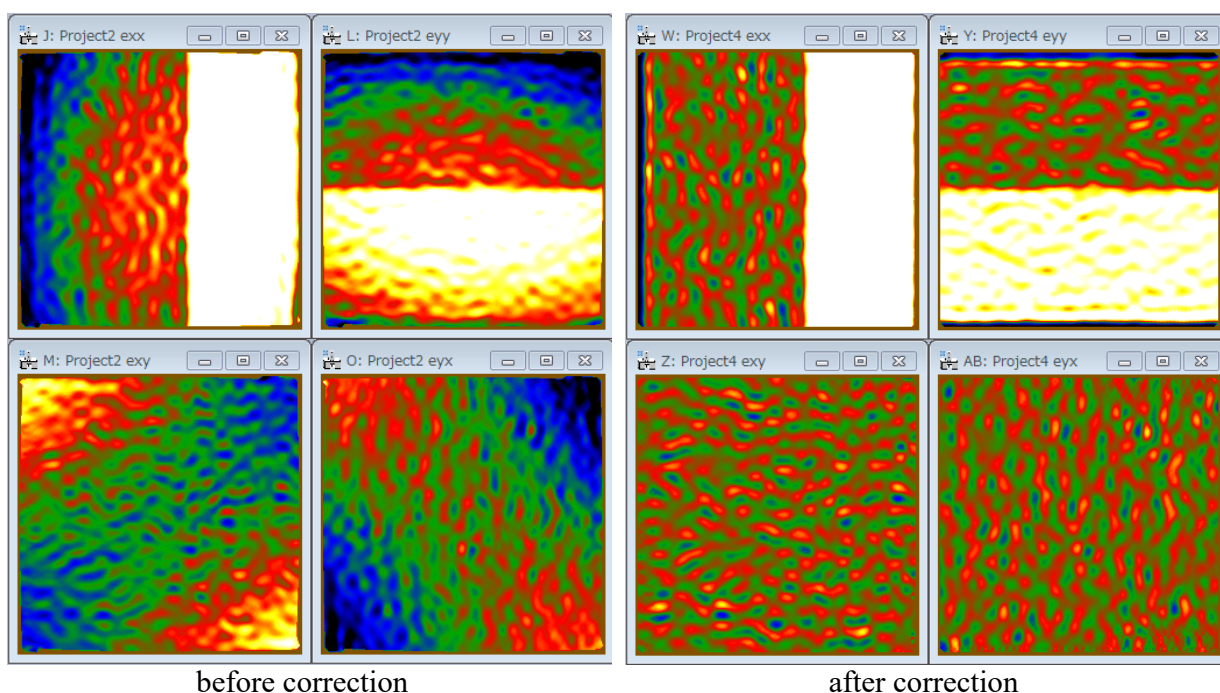
Correcting Distortion using the Distortion Information

In order to correct another image with the same distortion using the distortion information, just apply the Apply Distortion info. Then, the diagram shown below will open;



Here, the **Target Image** is the image to be corrected, while the **Distortion Info** is the image created by the Obtain Distortion Info command. In this case, we use 'Test image.dm3' as **Target Image** and 'Substrate_corrected.dm3' obtained from Substrate.dm3 as **Distortion Info** image. By pressing **OK**, the new image (<image name>_corrected) will be created, where all the distortions estimated from the perfect crystal image have been eliminated.

We can now proceed to analyze the distortion corrected image in the usual way to get the final strains. The strain maps before and after distortion correction are shown below left and right, respectively. The expected strains are reproduced by correcting the distortion.



If we plot a horizontal profile across exx and a vertical one across eyy, we get the expected results ($exx=0.1$ and $eyy=0.05$), which become flat after distortion correction.

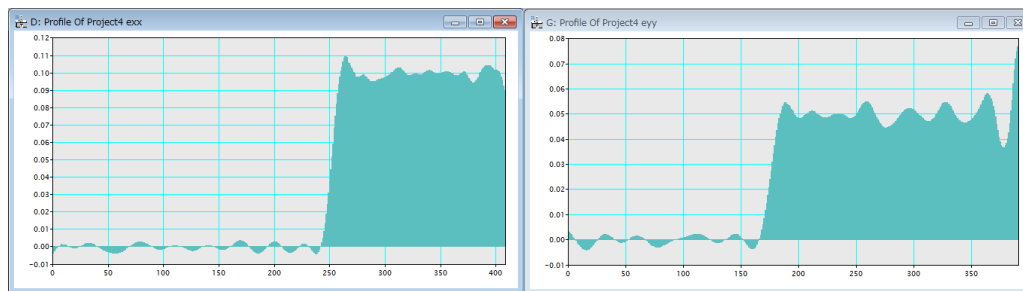


Image Rectification

When we know that the image is taken from a perfect crystal, we can get a rectified image using the peak-pairs information and the information of the sample. To do so, we can use the dialog that appears when Obtain Distortion Info command is launched.

Obtain Distortion Info

Rectify Image:
The lengths and angles of the refined base vectors shown in the parentheses differ from the expected unit cell, you can input the ideal values in the text boxes. Then, the distortion information corresponding to the ideal base vectors will be obtained.

Base Vector 1

Length: (8.49408)

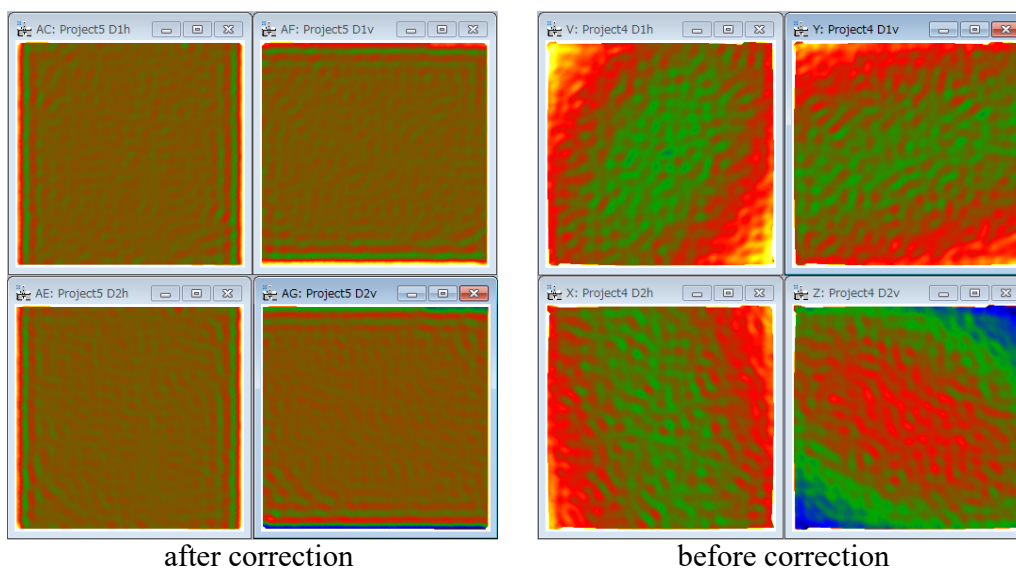
Angle: (-135.117)

Base Vector 2

Length: (8.47219)

Angle: (135.076)

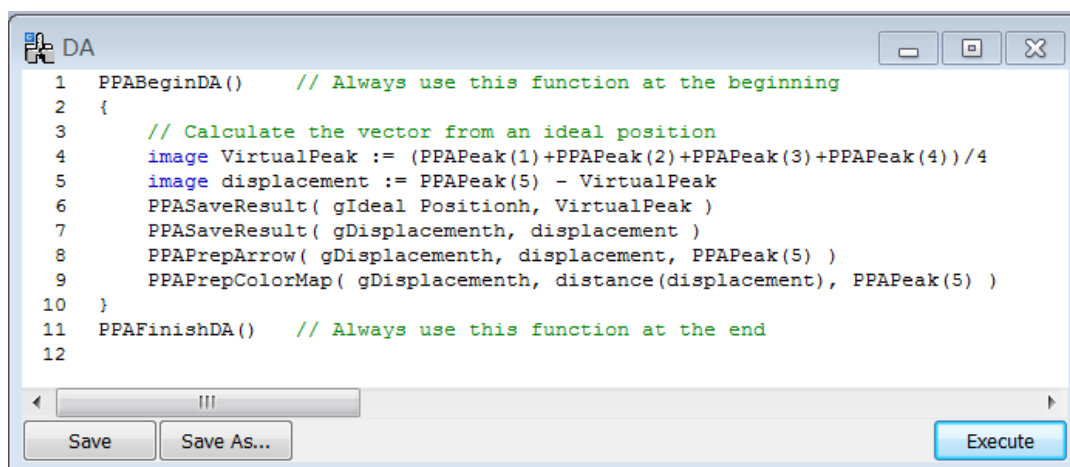
Here, the lengths and angles of the base vectors used to calculate the displacement maps will be shown in parentheses. If the values in the parentheses differ from the values expected from an ideal unit cell, you can change the values accordingly. Then, by pressing **OK**, the distorted image is rectified using the local distortions at each point of the image. We can verify this, by calculating the displacement maps from the rectified image. Then, we observe that distortions have been corrected as shown below left:



Distortion Analysis (from v4.0)

From information on the peak positions of a complex structure, you can analyze a peak distance and angle (a length and angle of the peak-pair vector). Furthermore, in principle, you can calculate a rotation of a structural unit (e.g. tetrahedron or octahedron), or even a distance from the ideal/virtual position to the observed peak. However, such an advanced analysis requires some skill in programming. The Distortion Analysis of the PPA will provide an easy way to perform such an analysis using the DM script.

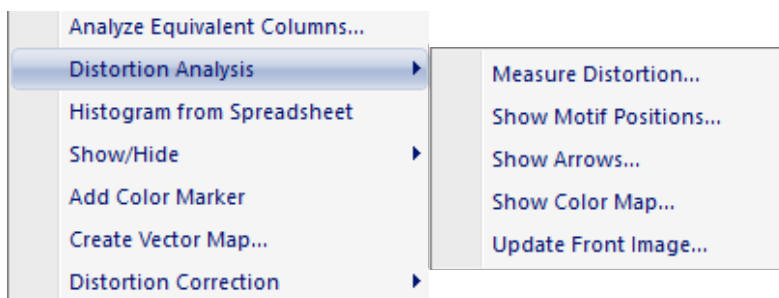
For the Distortion Analysis, firstly perform Motif detection, and Find Peak Pairs. On the other hand, write a script to measure distortions in the script window as shown below:



NOTE: This script will measure a distance from the virtual position (the center of the four peaks from peak #1 to peak #4) to the observed peak #5, and save some information for a later use. Here, the functions with the prefix of PPA are provided with the PPA plug-in v4.0 or later and explained at the end of this section.

TIPS: If you have no error messages, you may want to save the script for a future use by clicking **Save As...** button. As you see the example script, you have to respectively use PPABeginDA() and PPAFinishDA() at the beginning and the end of the script in addition to your analyzing code.

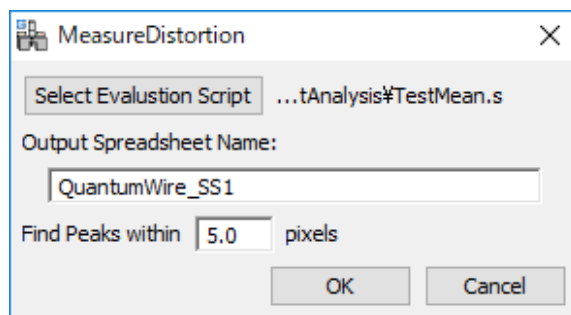
The following shows the submenu for the Distortion Analysis.



Measure Distortion

The first step of the Distortion Analysis is to measure distortions using a script tailored to your purpose. To do so, firstly, place a rectangle ROI to define the area to be analyzed on the original image, and select the peaks to be used in the analysis using the HREM mouse on the original image, the project image or the refined second Motif. Then, put the project image at the front most, and run the script written in the script window. or launch the command **Measure Distortion** to run the saved script.

When you launch the **Measure Distortion** command, the dialog shown below will open:

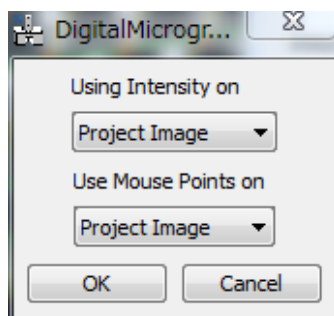


Here, you can select one saved script file to evaluate distortions, and specify the output spreadsheet name.

NOTE: When you directly execute the script, you will have a dialog without the script file selection.

Each peak of the motif will be searched within the circle with the radius defined by the value in the **Find Peaks within** box. If the peak is not found within the specified region, you will find NaN (not-a-number) in the spreadsheet.

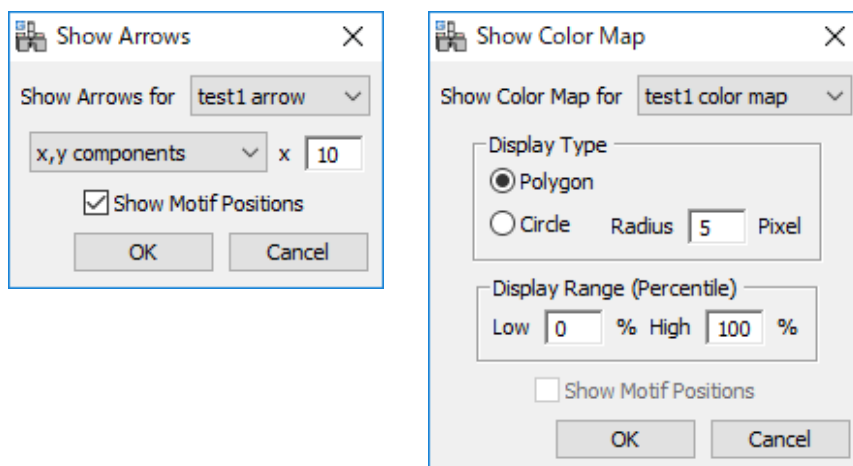
When pressing OK on the **Measure Distortion** dialog, the dialog shown below will open, where you can choose the image intensity to be used to find the peak positions from the Original and Project Images, and you can select the image with the HREM Mouse points from the Original, Project and the (refined second) Motif images.



When pressing OK on this dialog, the distortion analysis script will run, and the spreadsheet will appear with the information saved by PPASaveResult() as well as the information of the peaks corresponding to the mouse points.

Show Arrows or Show Color Map

When the distortion information is saved as a vector or a scalar value using `PPAPrepArrow()` and `PPAPrepColorMap()`, the measured distortion can be visualized using the commands **Show Arrows** or **Show Color Map**. Launching one of the two commands on the spreadsheet will open the corresponding dialog below, where you can select the column to be displayed and setup other display conditions.



NOTE: When you select these commands on the project image, at first, the dialog to select a spreadsheet will open, and then the dialog shown above will appear.

TIPS: You can modify the appearance of the map using the **Update Front Image...** command, if the front-most image is an arrow or color map.

TIPS: You can check the positions of the approximate motif centers on the original image using the **Show Motif Positions** command.

Description of the functions

PPABeginDA()

should be called at the beginning of the script

PPAFinishDA()

should be called at the end of the script

image PPAPeak(number n)

generates a list of column positions for the peak #n.

image PPALength(image vector)

calculates the vector length.

image PPALength(image point1, image point2)

calculates the length of the vector (point1 to point2).

image PPAngle(image vector)

calculates the vector angle, anticlockwise from the horizontal axis.

image PPAngle(image point1, image point2)

calculates the angle of the vector (point1 to point2), anticlockwise from the horizontal axis.

image PPAngle(image point1, image point2, image point3)

calculates the angle between two vectors (point1 to point2, and point1 to point3), anticlockwise measured from point2 to point3.

void PPASaveResult(string "name", image result_data)

saves result_data with an identifier “name” to the spreadsheet.
 if result_data is vector, its coordinates (x, y), length and angle (measured anticlockwise from the horizontal axis) will be saved to the spreadsheet.

```
void PPAPrepArrow( string “name”, image vector_data, image start_point)
  saves the vector_data and the start point to the spreadsheet for an arrow map.
void PPAPrepArrow( string “name”, image angle, image start_point)
  saves the unit vector with the specified angle and the start point to the spreadsheet for an
  arrow map.
void PPAPrepColorMap( string “name”, image scalar_data, image display_point)
  saves the scalar data and the display point to the spreadsheet for a color map.
```

Sample code

```
PPABeginDA()
// calculate the vector from an ideal position
image VirtualPeak := (PPAPeak(1)+PPAPeak(2)+PPAPeak(3)+PPAPeak(4))/4
// Here, we define the image “VirtualPeak” to which the center of the four peaks saved.
image displacement := PPAPeak(5) - VirtualPeak
PPASaveResult( “Ideal Position”, VirtualPeak )
PPASaveResult( “Displacement”, displacement )
PPAPrepArrow( “Displacement”, displacement, PPAPeak(5) )

//calculate angle between two vectors Peak(5) to Peak(2), and Peak(5) to Peak(1)
image angle := PPAAngle( PPAPeak(5), PPAPeak(2), PPAPeak(1) )
PPASaveResult( “Angle”, angle )
PPAPrepColorMap( “Angle”, angle, PPAPeak(5) )
PPAFinishDA()
```

Another sample code

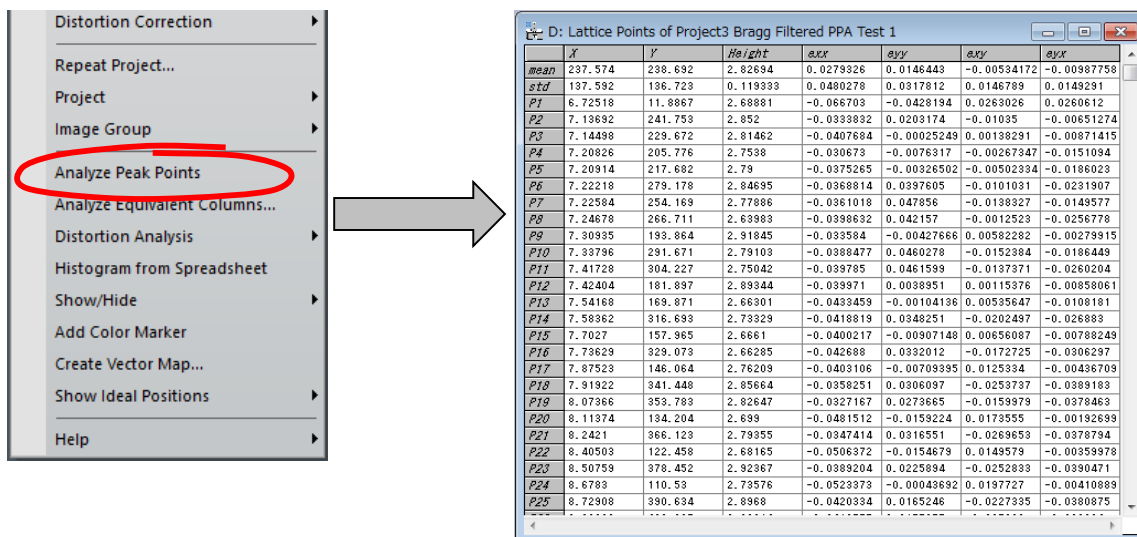
```
PPABeginDA()
// Here, we define the image “peakn” to which the coordinates of the peak #n is saved.
image peak1 := PPAPeak(1)
image peak2 := PPAPeak(2)
image peak3 := PPAPeak(3)
image peak4 := PPAPeak(4)
image peak5 := PPAPeak(5)
// calculate the vector from an ideal position
image VirtualPeak := (peak1+peak2+peak3+peak4)/4
// Here, we define the image “VirtualPeak” to which the center of the four peaks saved.
image displacement := peak5 - VirtualPeak
PPASaveResult( “Ideal Position”, VirtualPeak )
PPASaveResult( “Displacement”, displacement )
PPAPrepArrow( “Displacement”, displacement, peak5 )

//calculate angle between two vectors Peak(5) to Peak(2), and Peak(5) to Peak(1)
image angle := PPAAngle( peak5, peak2, peak1 )
PPASaveResult( “Angle”, angle )
PPAPrepColorMap( “Angle”, angle, peak5 )
PPAFinishDA()
```

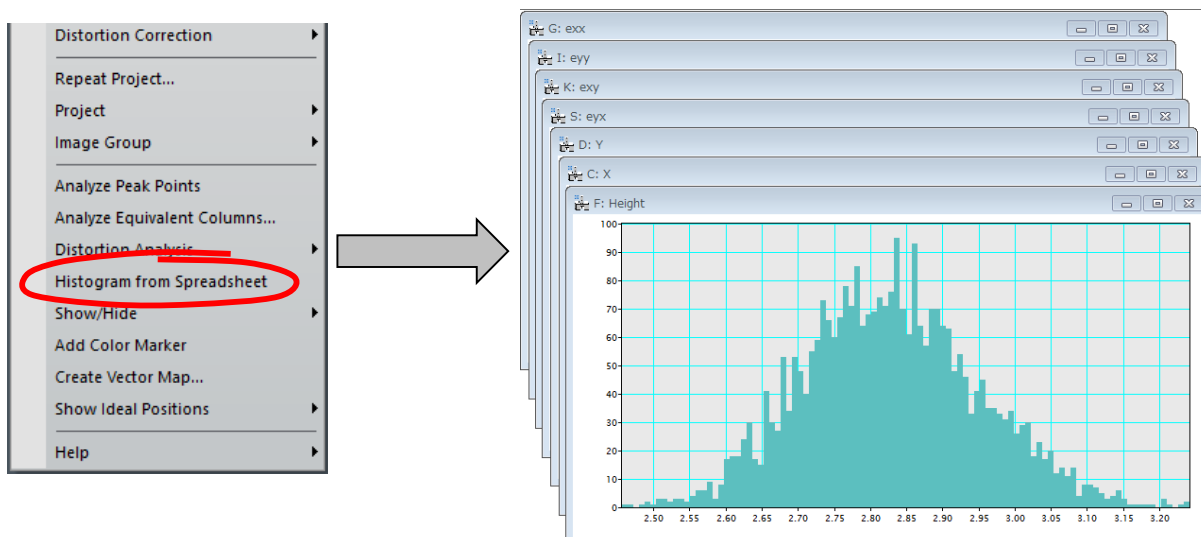
Analyze Peak Points

The Analyze Peak Points command applied on the project image, such as Bragg filtered image, will generate an output in spreadsheet including the following information (one row for each lattice peak) that are already evaluated:

- Peak position at sub-pixel resolution (x,y coordinates)
- Peak intensity
- Strain tensor at each peak points (exx,eyy,exy and eyx): only after **Strain Analysis**.



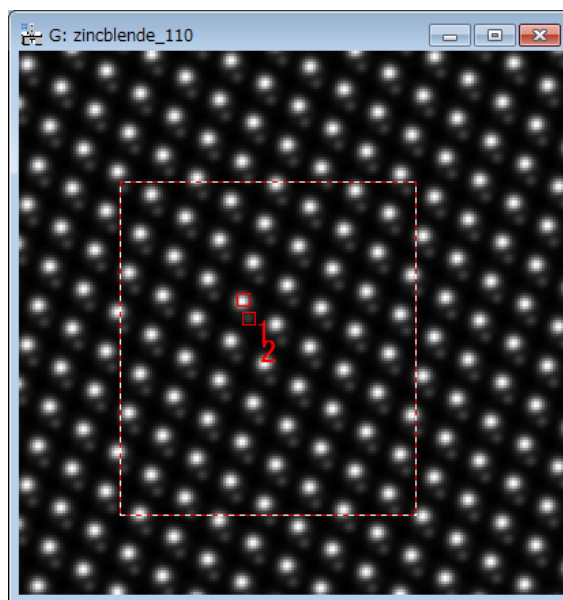
If you want to see visually the distribution of, say, the peak height, you can use the Histogram from Spreadsheet command. When you select the command, a dialog will open, where you can select the data to be displayed.



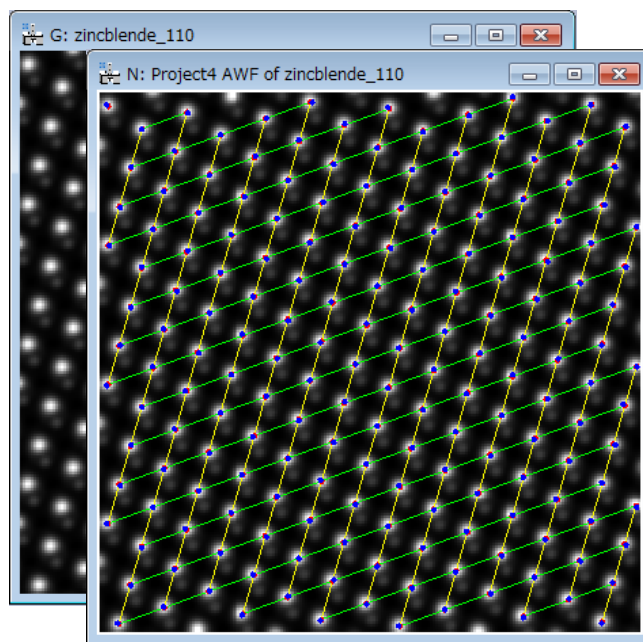
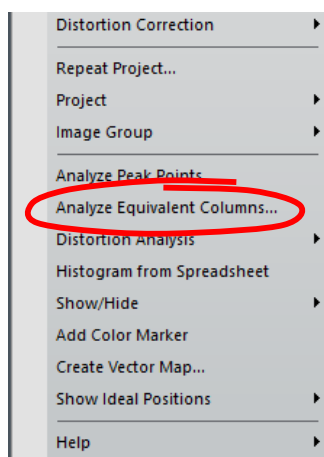
Analyze Equivalent Columns

Once Peak Pairs have been located, it is possible to analyze atomic column positions. This is very useful when there is more than one atomic column within a unit cell. For example, in the case of [110] projection of *InP* (the zincblende type materials), we can evaluate cation and/or anion atomic columns. In order to do so, go through the following steps (on *zincblende.dm3*):

- Calculate Peak Pairs in the usual way
- Bring the original raw image to frontmost.
- Choose the area of interest on the original image using the Rectangle ROI tool.
- Select atomic column(s) to be analyzed using the **HREM mouse** tool. (Here, we select a set of cation and anion columns)

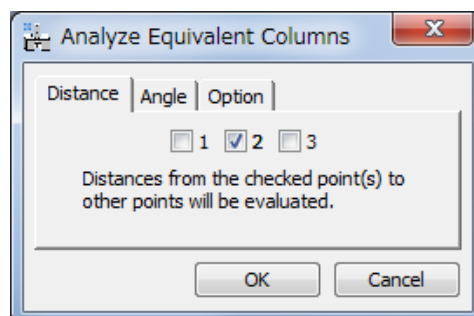


- Bring the project image with Peak Pairs information to frontmost.
- Apply the Analyze Equivalent Columns command

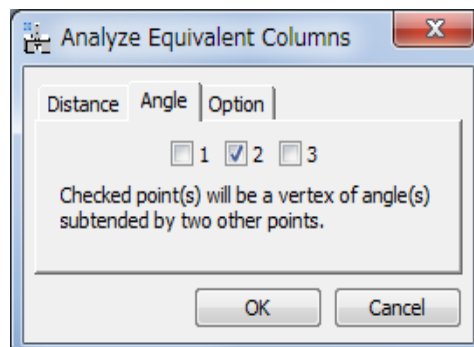


Then, the dialog **Analyze Equivalent Columns** will open.

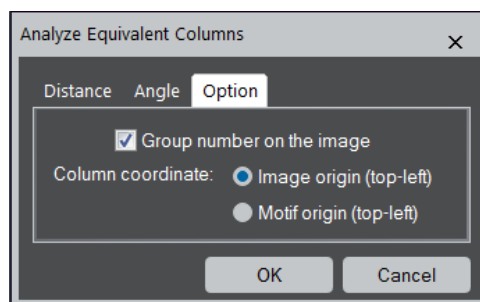
In the **Distance** tab, the user will have the option to select the column(s), from which the distance(s) to other column(s) will be evaluated.



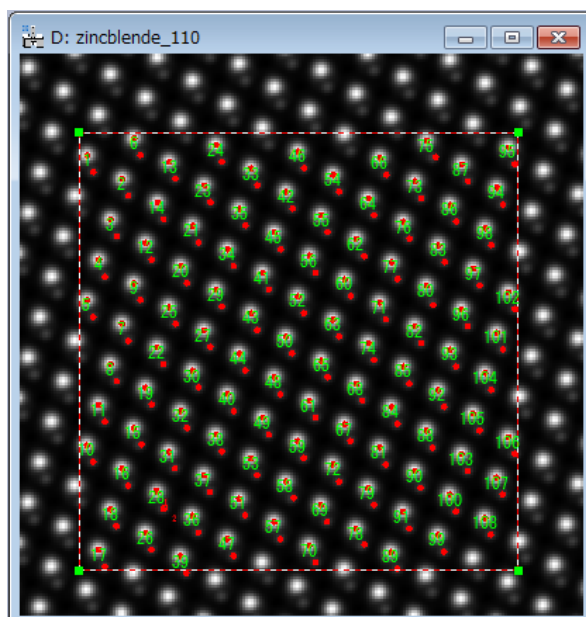
In the **Angle** tab, if there are more than three columns, the user will have the option to select the column(s), from which the angle(s) subtended by two neighbor columns will be evaluated.



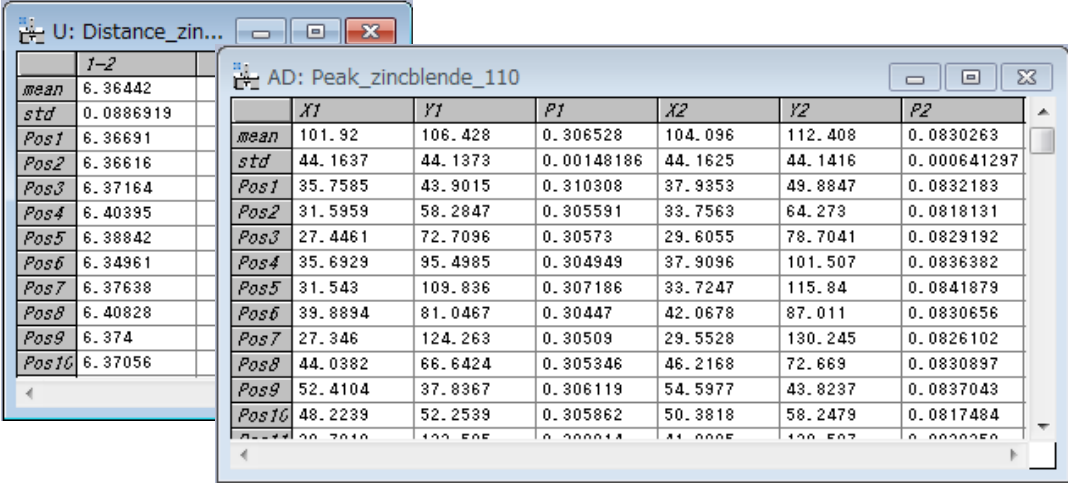
In the **Option** tab, you can set two options: 1) the group number on the original image, 2) the coordinate system of the column positions.



When the **OK** button is pressed, all the columns in the selected area will be located in the image as shown below. The group number will be added on the image according to the setting in the **Option** tab.



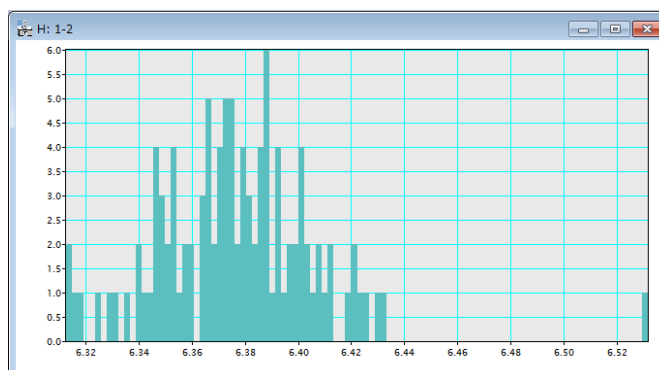
Furthermore, the position and intensity of each column as well as the distances and/or angles will be stored in a spreadsheet.



	I-2
mean	6.36442
std	0.0886919
Pos1	6.36691
Pos2	6.36616
Pos3	6.37164
Pos4	6.40395
Pos5	6.38842
Pos6	6.34961
Pos7	6.37638
Pos8	6.40828
Pos9	6.374
Pos10	6.37056

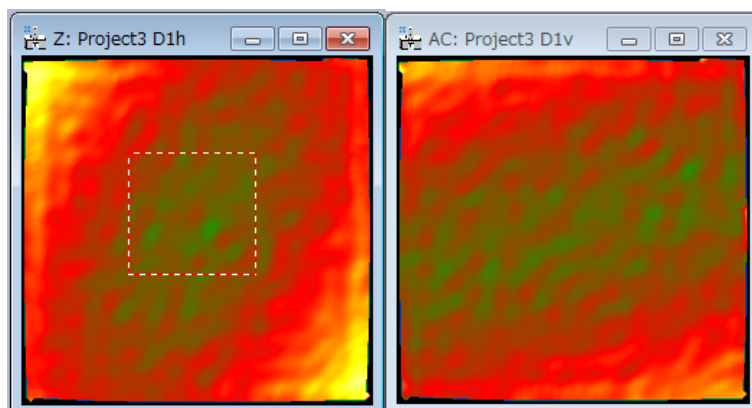
	X1	Y1	P1	X2	Y2	P2
mean	101.92	106.428	0.306528	104.096	112.408	0.0830263
std	44.1637	44.1373	0.00148186	44.1625	44.1416	0.000641297
Pos1	35.7585	43.9015	0.310308	37.9353	49.8847	0.0832183
Pos2	31.5959	58.2847	0.305591	33.7563	64.273	0.0818131
Pos3	27.4461	72.7096	0.30573	29.6055	78.7041	0.0829192
Pos4	35.6929	95.4985	0.304949	37.9096	101.507	0.0836382
Pos5	31.543	109.836	0.307186	33.7247	115.84	0.0841879
Pos6	39.8894	81.0467	0.30447	42.0678	87.011	0.0830656
Pos7	27.346	124.263	0.30509	29.5528	130.245	0.0826102
Pos8	44.0382	66.6424	0.305346	46.2168	72.669	0.0830897
Pos9	52.4104	37.8367	0.306119	54.5977	43.8237	0.0837043
Pos10	48.2239	52.2539	0.305862	50.3818	58.2479	0.0817484

If you want to see visually the distributions of quantities stored in the spreadsheet, you can use the Histogram from Spreadsheet command. When you select the command, a dialog will open, where you can select the data to be displayed. The histogram below shows the distribution of distances:

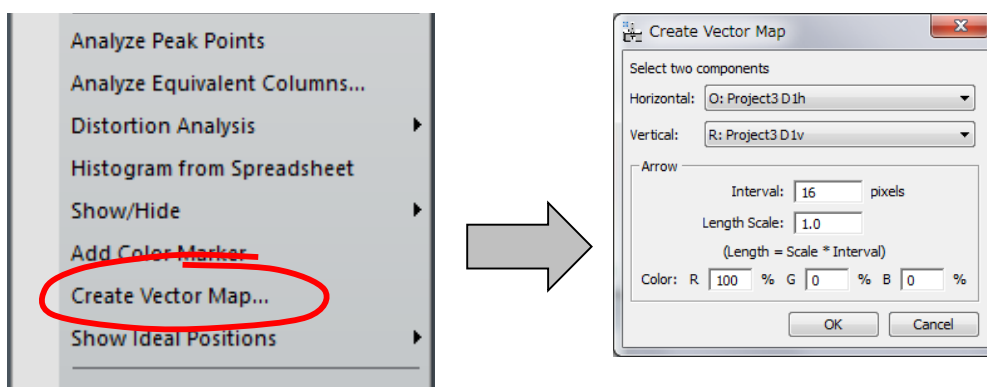


Create Vector Maps

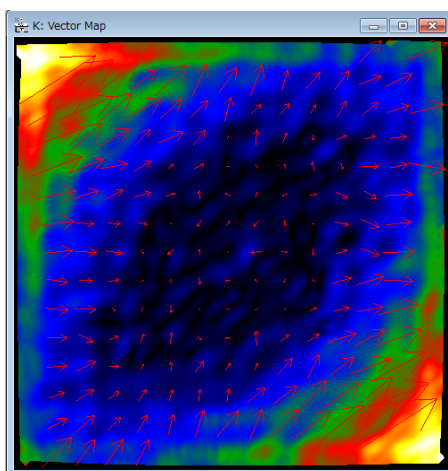
It is possible to create a vector map from *two vector components*, such as D1h and D1v. We explain here the Create Vector Maps command using the displacement maps calculated from *Substrate.dm3*, as shown below:



After launching the Create Vector Map command, select these two vector component images of the associated vector map, say D1h and D1v, and press **OK**.



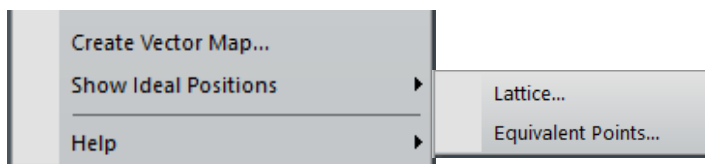
Then, you will get a color map corresponding to the vector magnitude, where the arrows show the directions and magnitudes of the vectors as shown below:



The vector map here is a complex DM image, whose real and imaginary parts correspond respectively to the Horizontal and Vertical images selected in the dialog.

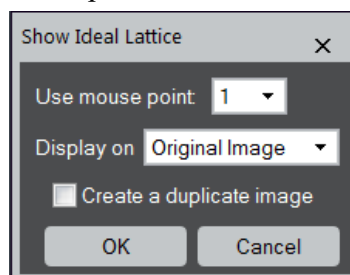
Show Ideal Positions

Using the base vectors refined for the reference area, the ideal lattice or the ideal equivalent positions can be drawn on the original image or the project image. To do so, two submenu commands shown below are provided. These commands require a rectangular ROI, within which the ideal positions will be displayed.



Show Ideal Positions...Lattice

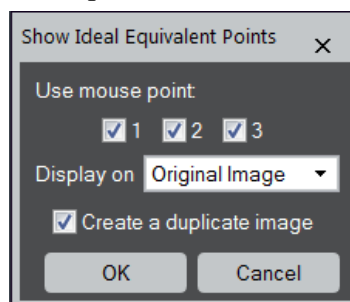
When selecting this command, the dialog shown below will open:



This command requires a mouse point to specify the unit cell corner. When there is more than one mouse points, you can select one mouse point from the pull-down list. Furthermore, the image, where the lattice is drawn, can be selected from the original image or the project image. If you want, the lattice is drawn on a duplicate image of the selected image.

Show Ideal Positions...Equivalent Points

When selecting this command, the dialog shown below will open:



This command requires the mouse points to define the equivalent points. You can select the equivalent points to be drawn by selecting the corresponding check boxes. Furthermore, the image, where the equivalent ideal points are drawn, can be selected from the original image or the project image. If you want, the equivalent ideal points are drawn on a duplicate image of the selected image.

NOTE: This command will draw the equivalent points using the refined base vectors. Therefore, these points may differ from the points determined by Find Peaks command.

Appendix

Technical Note:

The results of the PPA package is the complete strain tensor defined as follows:

Strain values

$$e_{xx} = \frac{\partial u_x}{\partial x}, e_{yy} = \frac{\partial u_y}{\partial y}, e_{xy} = \frac{\partial u_x}{\partial y}, e_{yx} = \frac{\partial u_y}{\partial x}$$

Strain tensor:

$$\varepsilon_{ij} = \frac{1}{2} \left(\frac{\partial u_i}{\partial x_j} + \frac{\partial u_j}{\partial x_i} \right) \text{ i.e. } \varepsilon_{xx} = \frac{\partial u_x}{\partial x}, \varepsilon_{yy} = \frac{\partial u_y}{\partial y}, \varepsilon_{xy} = \frac{1}{2} \left(\frac{\partial u_x}{\partial y} + \frac{\partial u_y}{\partial x} \right)$$

Mean dilatation :

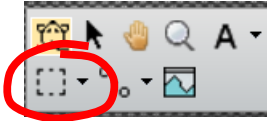
$$\Delta_{ij} = \frac{1}{2} \left(\frac{\partial u_i}{\partial x_i} + \frac{\partial u_j}{\partial x_j} \right) \text{ i.e. } \Delta_{xy} = \frac{1}{2} (\varepsilon_{xx} + \varepsilon_{yy})$$

Rotation (in radians and anti-clockwise positive):

$$\omega_{ij} = \frac{1}{2} \left(\frac{\partial u_j}{\partial x_i} - \frac{\partial u_i}{\partial x_j} \right) \text{ i.e. } \omega_{xy} = \frac{1}{2} \left(\frac{\partial u_y}{\partial x} - \frac{\partial u_x}{\partial y} \right)$$

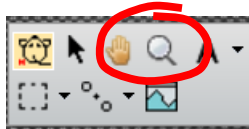
Some useful DM tricks

DM ROI tool:



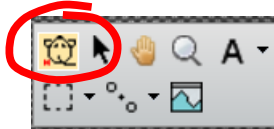
Hint: to select a square area, hold down SHIFT. To select powers of two, hold down SHIFT-ALT.

DM Zoom tool:

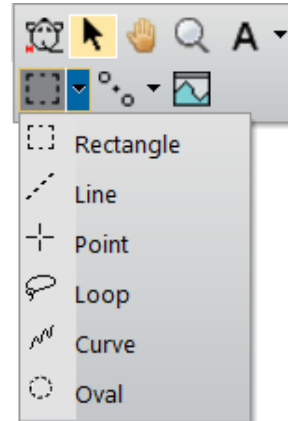


Hint: to demagnify, press ALT.

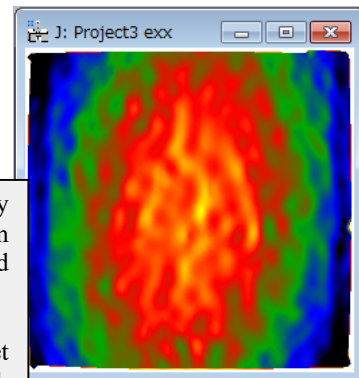
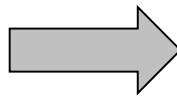
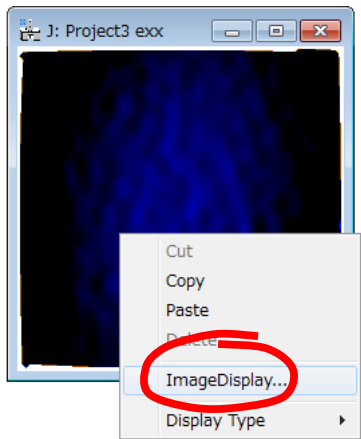
HREM Mouse tool



Hint: to delete any spot, just click on the mouse mark with the SHIFT key down.



DM Image Display Command

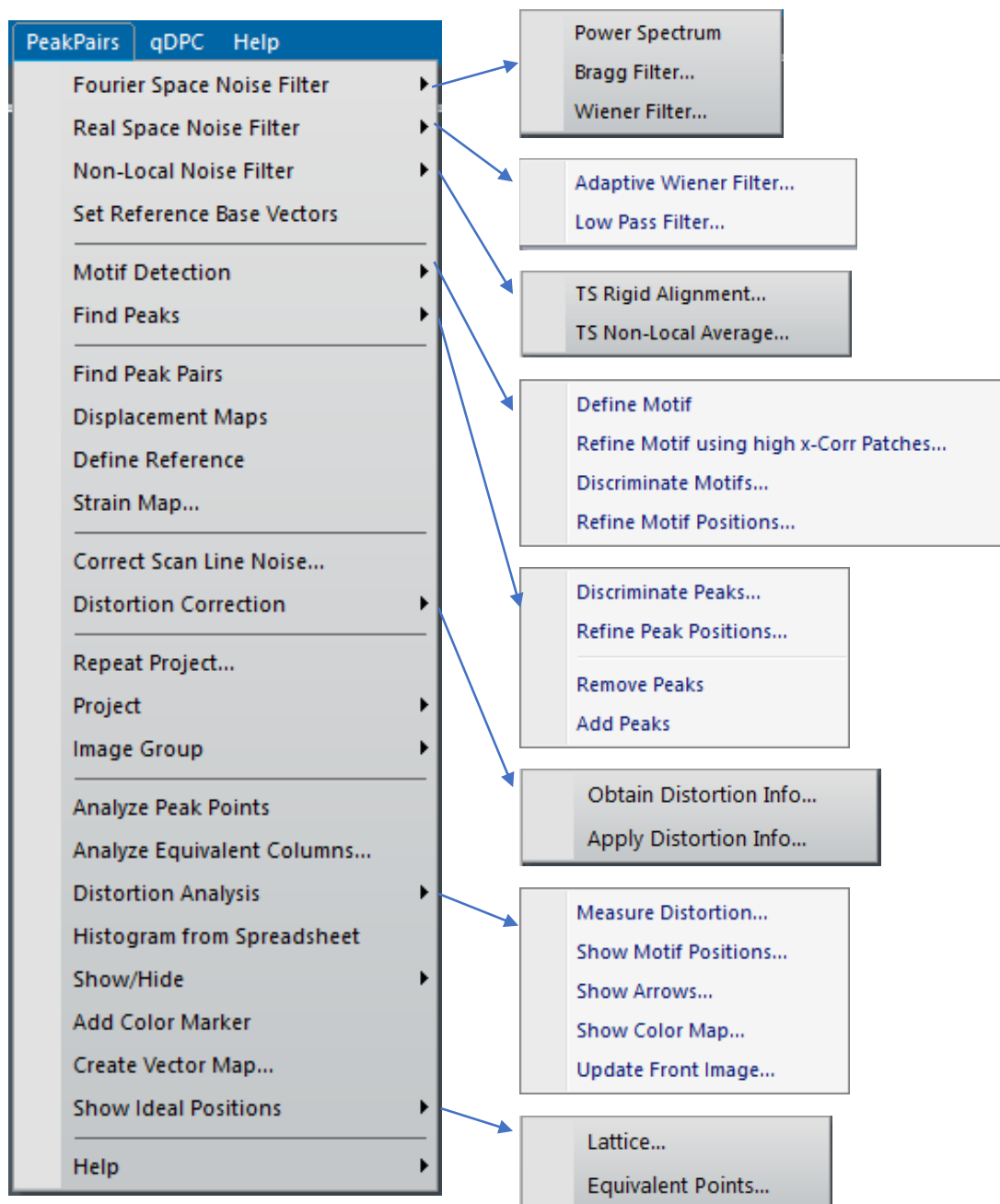


Hint: to change the color map of any image, press the right mouse button on it, select ImageDisplay, and modify the options as desired.

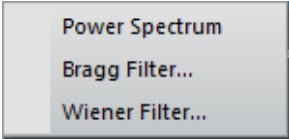

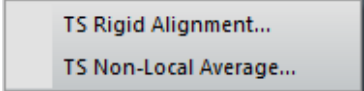

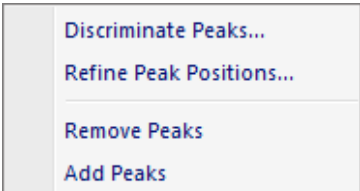
For example, it is useful to set manually the color range of each map to be the same, so as to be able to compare each other.

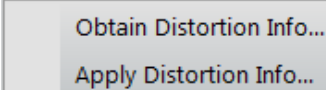
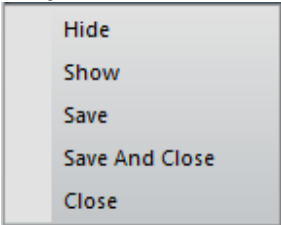


Quick Reference Guide

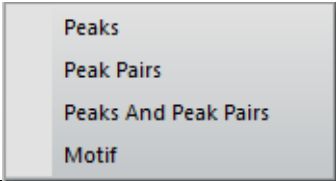
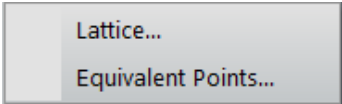
The PPA Main Menu



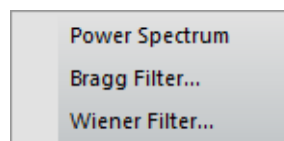
The commands in the PPA menu are described below.

Command	Description
Fourier Space Noise Filter 	Reduces noise using Fourier space filter. The power spectrum will be used to define the base vectors in Fourier space (reciprocal space), and to select the spots for the Bragg Filter. The Fourier space base vectors will be converted to the base vectors in real space
Real Space Noise Filter 	Reduces noise using Real Space Filter.
Non-Local Noise Filter 	Reduces noise using Non-Local Averaging over a time-series (TS) data. This performs rigid and non-rigid alignment.
Set Reference Base Vectors (see Dialog)	Sets the reference base vectors manually on an original image or a noise-filtered image. Note: Bragg filter sets the reference base vectors automatically.
Motif Detection 	Detects positions of the repeating units (motif: a group of peaks). This is useful for a complex structure. Note: Reference base vectors should be defined beforehand.
Find Peaks 	Locates peak positions in an image. The peak position is determined by fitting the intensity to a quadratic function. Note: Reference base vectors should be defined beforehand.
Find Peak Pairs	Calculates pairs of peaks along two base vectors automatically.
Displacement Maps	Generates a set of horizontal and vertical displacements for each base vector.
Define Reference	Changes the displacement values, so as to obtain a uniform displacement in the chosen area. Note: The area should be selected using the ROI tool on any one of the displacement maps.
Strain Map... (see Dialog)	Calculates strain maps (e_{xx} , e_{yy} , e_{xy} and e_{yx}) at any desired angle.

Correct Scan Line Noise... (see Dialog)	Corrects imperfect scan-line control (scan-line noise) of the STEM scanning system using a perfect area in the image. Note: The area(s) should be selected using the ROI tool on any one of the displacement maps.
Distortion Correction 	Eliminates systematic distortions present in the image based on the measurement of an ideal distortion-free image.
Repeat Project... (see Dialog)	Generates strain maps and other outputs for the front most image by performing the same process(es) of a selected project.
Project 	Menu to manage all the images corresponding to a particular project.
Image Group 	Menu to close or save the images of a same group of a particular project, such as the displacement maps, strain maps, etc..
Analyze Peak Points	Generates a spreadsheet of data (peak position, peak intensities, strain values) for each peak
Analyze Equivalent Columns... (see Dialog)	Analyzes equivalent column positions, as well as the distances and angles between specified columns. The independent column(s) will be specified using the HREM Mouse tool.
Distortion Analysis 	Analyzes peak distances or angles of the peak-pairs, or rotation angles of structural units (e.g. tetrahedron or octahedron). The advanced analysis can be performed using the DM script that simply calls the functions provided by the PPA.
Histogram from Spreadsheet	Calculates a different histogram for each selected column in the spreadsheet

Show/Hide 	Shows/hides a selected annotation on the image. This command is useful when the image display becomes crowded.
Add Color Marker	Adds a color bar with the low and high display ranges. You can move the whole color marker or change its size. You can move and edit them as you like. The color marker can be moved outside of the image display. You can rotate and flip using Edit commands. (The ratio of the color bar is fixed.)
Create Vector Map... (see Dialog)	Create a vector map from two component images selected in the dialog.
Show Ideal Positions 	Shows the lattice or equivalent points based on the refined base vectors.

Fourier Space Noise Filter Submenu

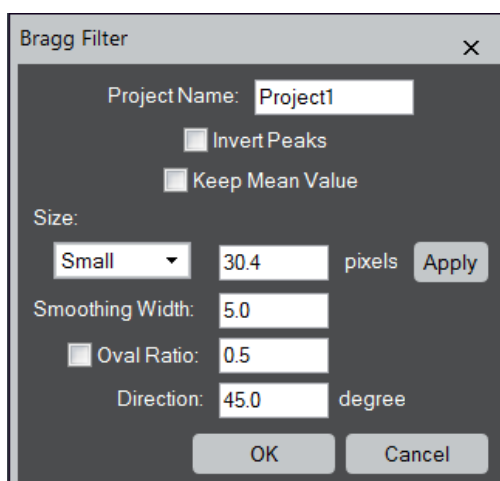


Component	Description
Power Spectrum	Calculates the Fourier transform of the front most image, and displays the power at each frequency (commonly called the Power Spectrum).
Bragg Filter... (see Dialog)	Calculates the noise filtered image using the spots selected on the Power Spectrum. The shape and size of the mask can be defined by the user in the dialog. Note: Spots should be selected beforehand on the Power Spectrum using the Mouse Tool. Note: The first and second spots defined the base vectors in Fourier (reciprocal) space, that are converted to the base vectors in real space,.
Wiener Filter... (see Dialog)	Calculates the noise filtered image using the Wiener filter, where the background is estimated by the radial average of the power spectrum. NOTE: The base vector can be defined by the two mouse points on the Power spectrum. NOTE: This command requires the HREM-Filter Lite (free plug-in) or the HREM-Filters Pro.

Bragg Filter Dialog

The components of the dialog are described below.

Dialog



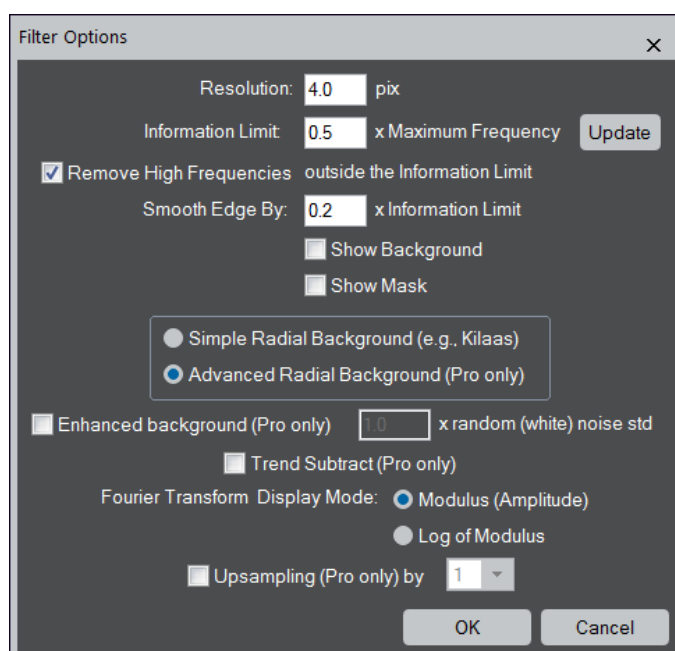
Component	Description
Project Name	Name given to the group of images and results

Invert Contrast	If you want to analyze the hollows (dips), not peaks, you should check this item.
Keep Mean Value	If checked, the mean value of the original image will be kept. Otherwise, the mean value will become zero.
Size	Defines mask radius in pixels.
Smoothing Width	Specifies mask smoothing width in pixels
Oval Ratio	Defines the shape of the oval, as major to minor axis ratio
Direction	Sets the direction of the major axis of the oval in degrees

Wiener Filter Dialog

The components of the dialog are described below.

Dialog



Component	Description
Resolution	Put the resolution of the micrograph in a physical unit or in pixels. Since the resolution may not depend on the magnification, it is convenient to use this when the image is calibrated.
Information Limit:	Set the Information Limit given by a fraction of the Maximum Frequency of the image.
Update	By clicking the Update button, you can verify the Information Limit on the Fourier transform.

	When you change the value of the resolution or information limit, click this button to check the size of the circle on the power spectrum.
Remove High Frequencies outside the Information Limit	
Smooth Edge by	If checked, high frequencies will be smoothly attenuated over both sides of the Information Limit by the Smooth Edge by .
Show Background:	If checked, the background of the Wiener filter will be displayed.
Show Mask:	If checked, the Wiener/Difference filter mask will be displayed.
Radial Background type:	The choice of the type of Radial Background. The <i>HREM-Filters Lite</i> can use <i>Simple Radial Background</i> obtained by rotational average of the intensity (e.g., Kilaas). <i>Advanced Radial Background</i> that is available for <i>Pro</i> only is a smooth version of the Simple Radial Background. Usually, this advanced background is <i>far superior to</i> the Simple Radial Background.
Enhanced background (Pro only)	If checked, the background is increased by the factor multiplied by the std of the random noise.
Trend Subtract (Pro Only):	If checked, the trend of the original image is subtracted before Wiener filtering, and put back afterward.
Fourier Transform Display Mode	You can select the display mode of Fourier transform between Modulus (Amplitude) and Log of Modulus.
Upsampling (Pro only)	If checked, the filtered image will be up-sampled by the selected factor.

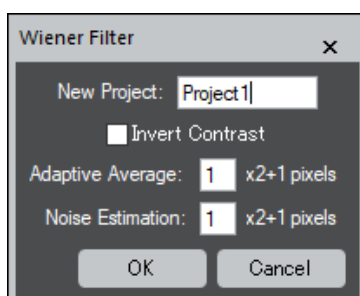
Real Space Noise Filter Submenu

Adaptive Wiener Filter...
Low Pass Filter...

Component	Description
Adaptive Wiener Filter... (see Dialog)	Removes noise from the image using an adaptive Wiener filter in real-space based on a local variance.
Low Pass Filter... (see Dialog)	Applies a Low Pass filter in real-space to the image, which is a weighted local average of the image.

Adaptive Wiener Filter Dialog

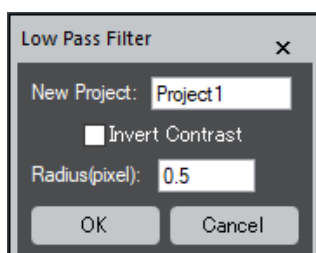
Dialog



Component	Description
New Project	Name given to the group of images and results.
Invert Contrast	If you want to analyze the hollows (dips), not peaks, you should check this item.
Adaptive Average	Defines a square area to be used to calculate a local average.
Noise Estimation	Defines a square area to be used to estimate a local noise power.

Low Pass Filter Dialog

Dialog



Component	Description
New Project	Name given to the group of images and results.
Invert Contrast	If you want to analyze the hollows (dips), not peaks, you should check this item.
Radius (pixel)	The radius of the mask in pixels

Non-Local Noise Filter Submenu

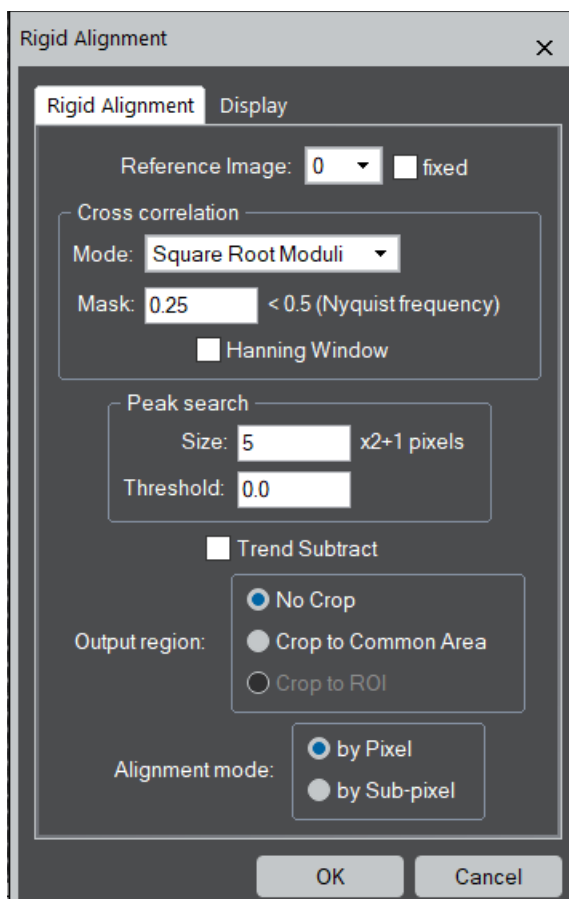
TS Rigid Alignment...
TS Non-Local Average...

Component	Description
TS Rigid Alignment... (see Dialog)	Estimates an average displacement of each image using the cross-correlation between two images, and creates a new stacked image after correcting the estimated displacements.
TS Non-Local Average... (see Dialog)	Performs non-local average over the rigid-aligned time-series image, and gives a non-rigid aligned single image.

TS Rigid Alignment Dialog

The components of the dialog are described below.

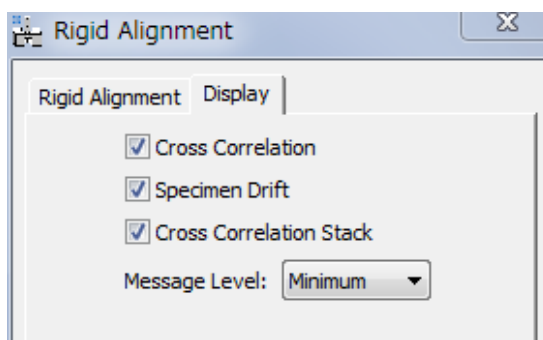
Dialog /Alignment Tab



Component	Description
Reference Image	Select a slice number of a good image to start alignment. The cross-correlation will be evaluated between two consecutive images downward starting with the reference image, and then upward.

	If “fixed” is selected, however, all the cross-correlation will be evaluated with the selected image.
Cross Correlation	
Mode	Cross-correlation mode will be selected from: <i>Conventional</i> : normal cross-correlation using Fourier transform coefficient. <i>Square Root Moduli</i> : cross-correlation using square-root of the amplitudes and the phase of the Fourier transform. <i>Phase Only</i> : cross-correlation using only phase of the Fourier transform (amplitude is set to unit). <i>None</i> : no alignment will be done.
Mask	Specifies the radius of a low-pass filter in Fourier space (relative to the Nyquist frequency) to reduce high-frequency noise.
Hanning Window	When checked, a Hanning Window will be applied to the image before Fourier transform.
Peak Search	Search conditions for the cross-correlation peak.
Size	Radius of the cross-correlation peak.
Threshold	Intensity below this level will be ignored when estimating a peak center.
Trend Subtract	If checked, a trend (slowly varying feature) is subtracted before alignment to enhance the image feature.
Output region	Output region will be specified here. If you want, you can crop the result to the Common Area or to the ROI. When the ROI is not present, “Crop to ROI” is disabled.
Alignment mode	<i>By Pixel</i> : the estimated image shift will be rounded, and no interpolation is performed. <i>By Sub-pixel</i> : the image will be shifted by the estimated image shift using the Fourier transform.

Display Tab



Component	Description
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Cross Correlation	Displays cross correlation values between adjacent images, or the fixed image.
Specimen Drift	Displays specimen drift values relative to the reference image.
Cross Correlation Stack	Displays 2D cross correlation maps.
Message level	Controls the amount of output messaging to the Results Window. (Minimum/Normal/Detail)

TS Non-Local Average Dialog

The components of the dialog are described below.

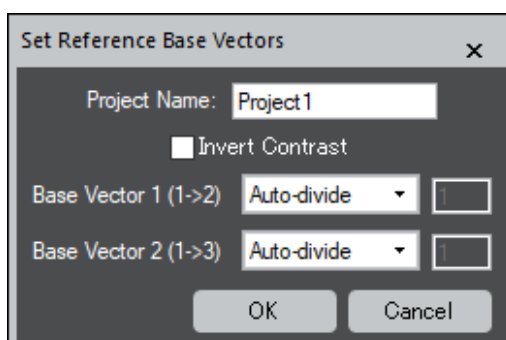
Dialog

Component	Description
Use Images	The images to be averaged will be specified here.
Reference/Feature Area	The size of the feature (reference) area will be specified here in pixels.
Target/Search Area	The size of the search (target) area will be specified.

Similarity Control Parameter	The similarity (SSD: sum of squared difference) between the Reference and Target area is evaluated by dividing the standard deviation (std) of the noise distribution multiplied by this parameter.
Compute Version	<p>The compute version can be selected here. If the user has the NLA (non-Local Average) module license and any NVIDIA GPU is found on your PC, the GPU becomes active. In this case, you can select the GPU from the pull-down list.</p> <p>If the user has the NLA module license, the CPU becomes active.</p> <p>Even when the user does not have the NLA module license, the Script can be selected.</p>
Display Mean Image	If checked, a simple mean image over the aligned stack will be displayed.

Set Reference Base Vectors Dialog

Dialog



Component	Description
Project Name	Name given to the group of images and results
Invert Contrast	If you want to analyze the hollows (dips), not peaks, you should check this item.
Base Vector 1 and 2	You can select Auto-divide or specify the number of repeating units along two directions.

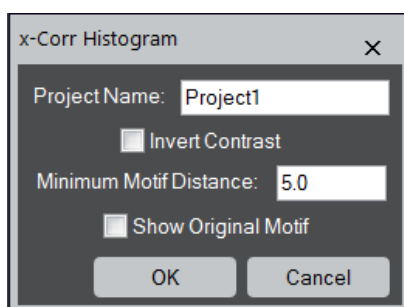
Motif Detection Submenu

Define Motif
 Refine Motif using high x-Corr Patches...
 Discriminate Motifs...
 Refine Motif Positions...

Component	Description
Define Motif	Defines a Rectangle ROI as a Motif, and make it rotatable.
Refine Motif using high x-Corr Patches... (see Dialog)	Calculates Cross-Correlation Histogram between the selected reference region (motif) and the original image, and obtains a refined motif using high-scored patches above the threshold. Note: The left edge of the selection in the histogram defines the threshold.
Discriminate Motifs	Calculates Cross-Correlation Histogram between the refined motif and the original image, where you can set the threshold for the good motif. Note: The left edge of the selection in the histogram defines the threshold.
Refine Motif Positions... (see Dialog)	Refines Motif positions by fitting a quadratic function to cross-correlation peaks.

Refine Motif using high x-Corr Patches Dialog

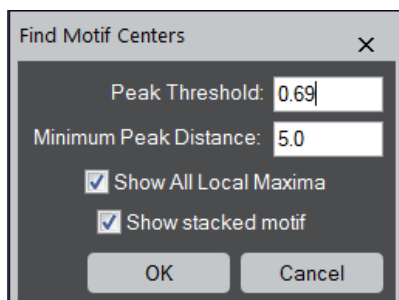
Dialog



Component	Description
Project Name	Name given to the group of images and results
Invert Contrast	If you want to analyze the hollows (dips), not peaks, you should check this item.
Minimum Motif Distance	Specifies a minimum distance between allowed motifs. This parameter can be changed at Refine Motif Positions .
Show Original Motif	If checked, the original motif will be displayed.

Refine Motif Positions Dialog

Dialog



Component	Description
Peak Threshold	Specifies the minimum value for the cross-correlation peak. The default value is the threshold obtained at Discriminate Motifs .
Minimum Motif Distance	Specifies a minimum distance between allowed motifs. The default value is carried from Refine Motif using high x-Corr Patches .
Show All Local Maxima	If checked, the Motif centers rejected by the Peak Threshold and/or the Minimum Motif Distance will be shown in blue. (Namely, all the motif centers are displayed in red or blue color.)
Show stacked motif	If checked, a stacked image of the good motifs will be created.

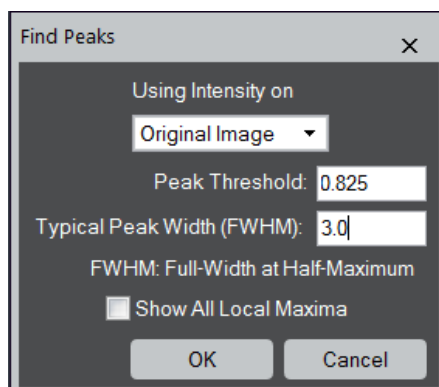
Find Peaks Submenu



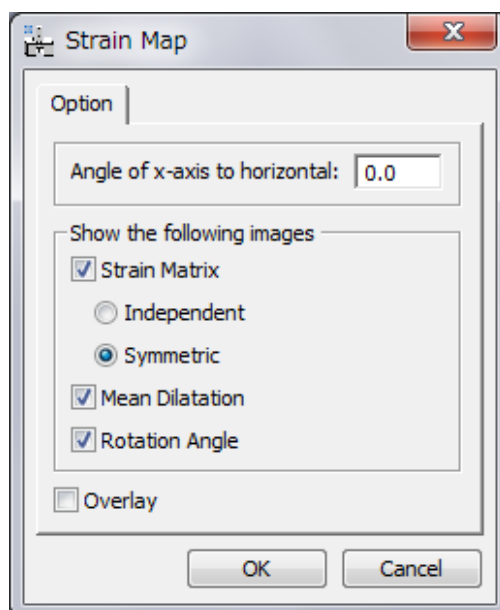
Component	Description
Discriminate Peaks	Shows a histogram of peaks intensities, helping the user to determine the threshold for peak intensity. Note: The left edge of the selection in the histogram is used as a threshold for good peaks.
Refine Peak Positions... (see Dialog)	Refines peak positions by fitting a quadratic function to intensity around the peaks. The peaks within a minimum distance will be merged.
Remove Peaks	Remove the peaks, which are selected by using HREM Mouse .
Add Peaks	Refine and add the peaks, which are selected by using HREM Mouse .

Refine Peak Positions Dialog

Dialog



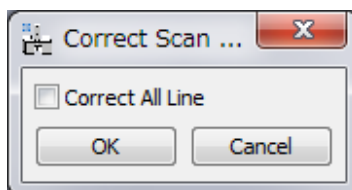
Component	Description
Using Intensity on	Select the project or original image where the peaks to be searched.
Peak Threshold	Specifies a minimum for the intensity of allowed peaks. The default value is the threshold obtained at Discriminate Peaks .
Typical Peak Width (FWHM)	Specifies a typical peak width (FWHM in pixels). This value will be used to merge the peaks.
Show All Local Maxima	Shows local maxima (of 8-neighbourhood) as blue points.

Strain Map Dialog**Dialog**

Option	Description
Angle of x-axis to horizontal	Specifies the angle of the direction to be considered as x-axis. You can specify the orientation of the x-axis by placing a Line ROI on the HREM image. In this case, the angle of the Line ROI appears here automatically. Note: If angle is set equal to 0, the x coordinate axis is assumed to be horizontal.
Strain Matrix	Specifies the images to be shown
Independent	Images of du/dx , du/dy , dv/dx , dv/dy will be displayed
Symmetric	Images of ϵ_{xx} , ϵ_{yy} and ϵ_{xy} will be displayed.
Mean Dilatation	Image of δ_{xy} will be displayed (average of ϵ_{xx} and ϵ_{yy}).
Rotation Angle	Image of ω_{xy} will be displayed. Values in degrees and anticlockwise positive.
Overlay	Shows the strain at each atomic column, and displayed as colored dots over the original image

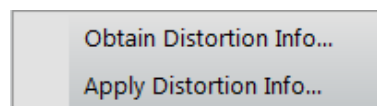
Correct Scan Line Noise Dialog

Dialog

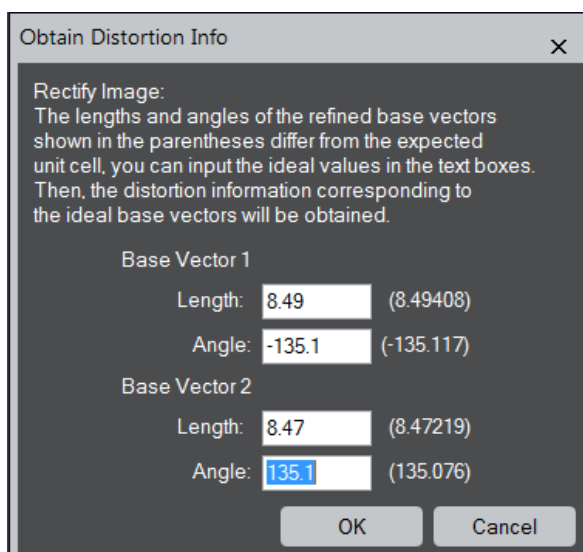


Component	Description
Correct All Line	When checked, all the scan lines, below and above the ROI, will be corrected.

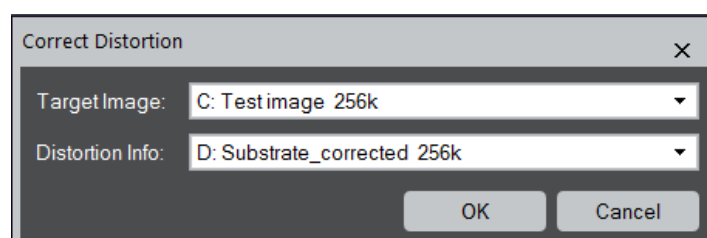
Distortion Correction Submenu



Command	Description
Obtain Distortion Info... (see Dialog)	Extracts distortion information from the image of an undistorted crystal using the knowledge of peak-pairs. This information will be used by the "Apply Distortion Info" command. NOTE: Using this command, you can rectify any image distortions appeared at the image of an undistorted sample.
Apply Distortion Info... (see Dialog)	Corrects a distorted image using the distortion information obtained from the image of an undistorted sample.

Obtain Distortion Info Dialog**Dialog**

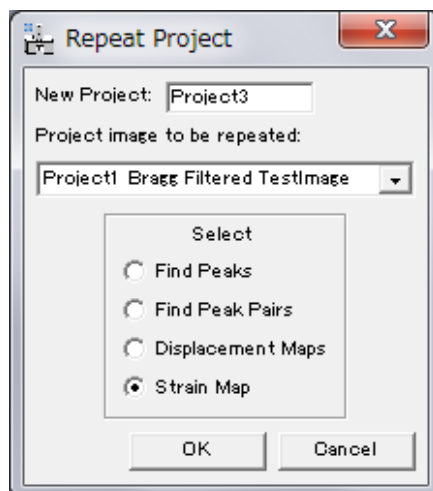
Component	Description
Base Vector 1 and Base Vector 2	
	The values in the parentheses correspond to the refined base vectors. You can modify them by typing the values in the boxes.
Length	Length of base vector considered for image rectification, measured in pixels.
Angle	Angle of base vector considered for image rectification, measured in degrees from the horizontal axis.

Apply Distortion Info Dialog**Dialog**

Component	Description
Target Image	Length of base vector considered for image rectification, measured in pixels
Distortion Info	Length of base vector considered for image rectification, measured in pixels

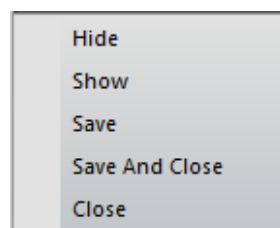
Repeat Project Dialog

Dialog



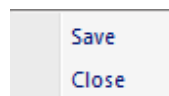
Component	Description
New Project	Defines the name of the new project.
Project image to be repeated	Selects an open project to be used to generate strain maps and other outputs for the front most image. Note: If you want to use the project created during the previous session, you may want to open it again.
Find Peaks	Repeats Find Peaks Operation.
Find Peak Pairs	Repeats Find Peak Pairs Operation.
Displacement Maps	Repeats Displacement Maps Operation.
Strain Map	Repeats Strain Map Operation.

Project Submenu



Component	Description
Hide	Hides all the images belong to a project.
Show	Shows all the images belong to a hidden project.
Save	Saves all the images belong to a project (with save dialog window).
Save And Close	Closes all the images belong to a project after saving them.
Close	Closes all the images belong to a project without saving.

Image Group Sub-Menu

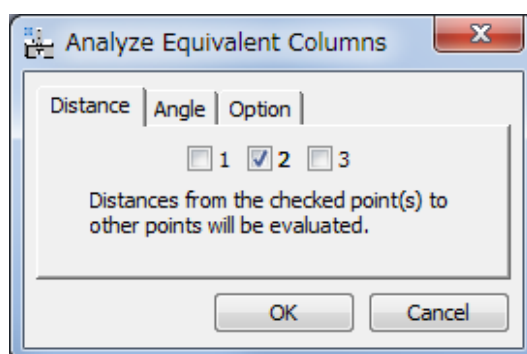


Component	Description
Save	Saves all images of the same type belong to a project (e.g. strain map images).
Close	Closes without saving all images of the same type belong to a project.

Analyze Equivalent Columns Dialog

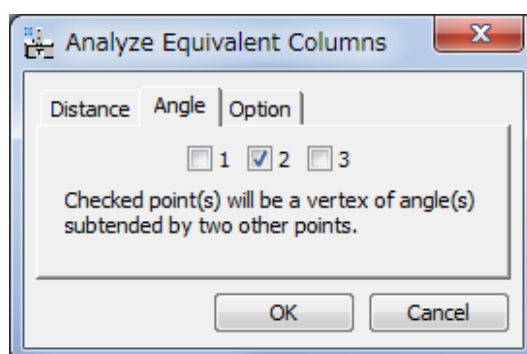
The user will have the option to output the distances and/or angles by placing the check(s) on the box(es).

Distance Tab



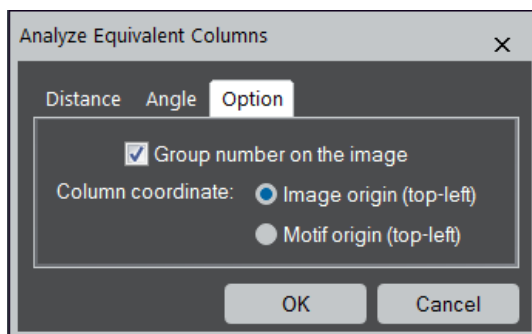
The number of each check box corresponds to the assigned number to the mouse click. All the distance(s) from the checked point to other points will be calculated.

Angle Tab



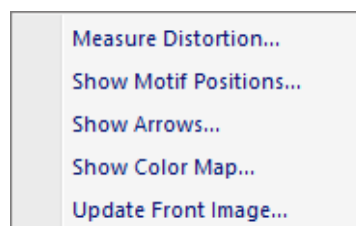
The number of each check box corresponds to the assigned number to the mouse click. All the angles at the checked point subtended by two other points will be calculated.

Option Tab

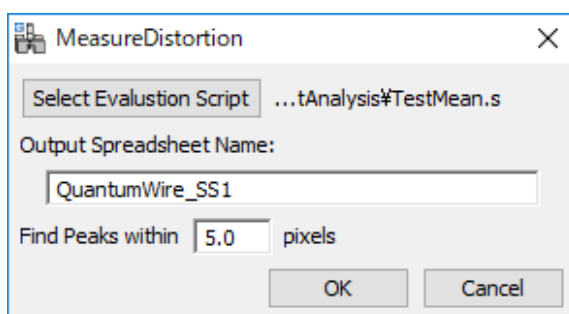


Component	Description
Group number on the image	Display the group number (corresponds to the left column of the spread sheet) on original image.
Column coordinate	In the case of Motif Detection , you can select the coordinates of column positions from Image or Motif origin.

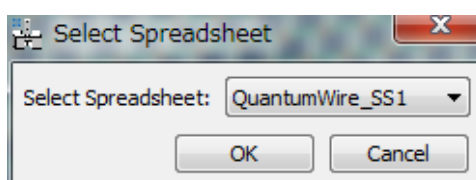
Distortion Analysis Submenu



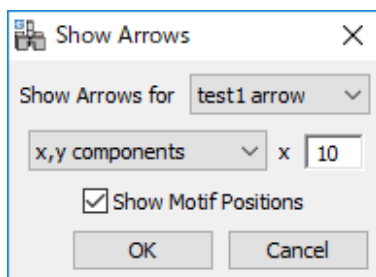
Command	Description
Measure Distortion... (see Dialog)	At first, distortion values will be measured by running the saved script. This command will open the dialog to select the script. NOTE: Alternatively, the distortions will be directly measured by executing the script from the script window.
Show Motif Positions... (see Dialog)	Displays the motif positions on the original image.
Show Arrows... (see Dialog)	Displays the distortions measured by using <i>PPAPrepArrow</i> in an arrow map.
Show Color Map... (see Dialog)	Displays the distortions measured by using <i>PPAPrepColorMap</i> in a color map.
Update Front Image...	The dialog for the Show Arrows or Show Color Map will open according to the type of the front image. Using the dialog, you can change the appearance of the arrows or color map.

Measure Distortion Dialog**Dialog**

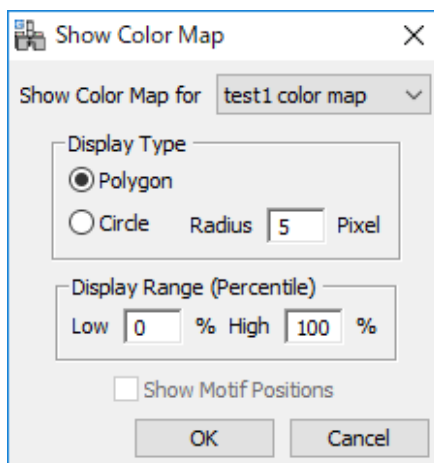
Component	Description
Select Evaluation Script	Clicking on this button will open the file browser to select the saved script. NOTE: If you directly execute the script from the script window, you will have a dialog without the file selection capability.
Output Spreadsheet Name	Specify an output spreadsheet name. The measured distortion values will be saved as a spreadsheet.
Find Peaks within	Peaks will be searched in the specified area in pixel from the corresponding points in the Motif.

Show Motif Positions Dialog**Dialog**

Component	Description
Select Spreadsheet	Select the spreadsheet corresponding to the ROI and mouse points.

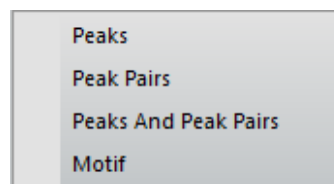
Show Arrows Dialog**Dialog**

Component	Description
Show Arrows for	Select the column in the spreadsheet corresponding to the arrows to be drawn.
Output value selector	Select the value(s) to be drawn and input the scale.
Show Motif Positions	Shows the potions of the approximate motif centers.

Show Color Map Dialog**Dialog**

Component	Description
Show Color map for	Select the column in the spreadsheet corresponding to the measured values to be drawn as a color map.
Display Type	Select the display type from Polygon and Circle . In the case of the circle, the radius of the circle can be specified in pixels.
Display Range	The display ranges will be specified in percentiles.
Show Motif Positions	If the display type is Circle , the potions of the approximate motif centers can be drawn.

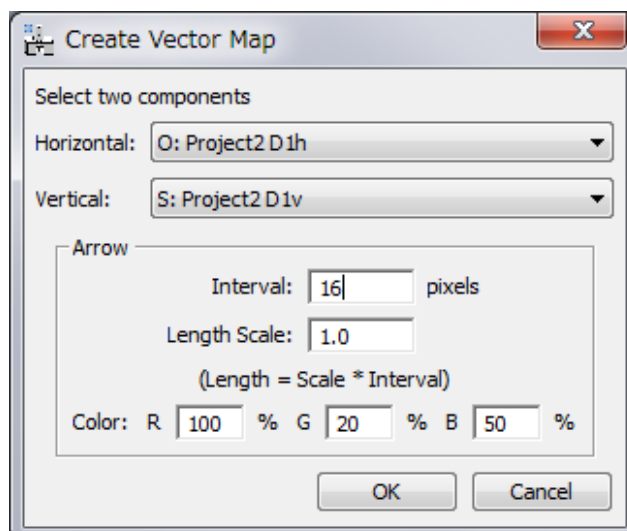
Show/Hide Submenu



Command	Description
Peaks	Hides the circles at the peak positions, or shows again when the peaks are in a hidden state.
Peak Pairs	Hides the lines connecting the peak-pairs, or shows again when the peak-pair lines are in a hidden state.
Peaks And Peak Pairs	Hides the circles at the peak positions and/or the lines connecting the peak-pairs, or shows again when the circles and/or lines are in a hidden state.
Motif	Shows the refined Motif of the project, when it has been closed. This is useful to check the motif of the project.

Create Vector Map Dialog

Dialog



Component	Description
Horizontal	Select an image corresponding to the horizontal component.
Vertical	Select an image corresponding to the vertical component.
Interval	Specifies a distance between the arrows (in pixel)
Length Scale	Specifies an arrow length. An actual length is Interval * this Scale (in pixel)
Color	Specifies an arrow color in RGB.

Show Ideal Positions Submenu

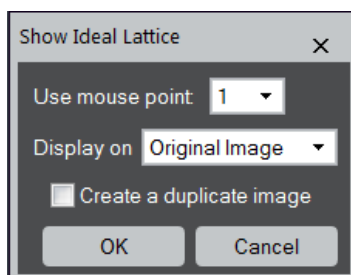
Obtain Distortion Info...

Apply Distortion Info...

Command	Description
Lattice... (see Dialog)	Using the reference base vectors, the ideal lattice is drawn on the original image or the project image. The ideal lattice can be shifted using the arrow keys.
Equivalent Points... (see Dialog)	Using the reference base vectors, the ideal equivalent positions are drawn on the original image or the project image. All the ideal points can be shifted using the arrow keys.

Show Ideal Lattice Dialog

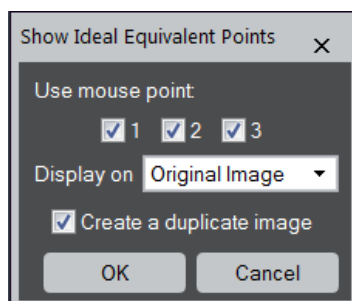
Dialog



Component	Description
Use mouse point	Select one mouse point from the list to be used for drawing the lattice.
Display on	Select the image where the lattice is displayed.
Create a duplicate image	When checked, the lattice is displayed after duplicating the selected image.

Show Ideal Equivalent Positions Dialog

Dialog



Component	Description
Use mouse points	Select the mouse points to be displayed by checking the boxes.

Display on	Select the image where the equivalent points are displayed.
Create a duplicate image	When checked, the equivalent points are displayed after duplicating the selected image.