

# **The Scanning Probe Image Processor**

## **SPIP™**

### **User's and Reference Guide**

#### **Version 4.2**

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# User's Guide



## Introduction



Thank you for choosing the Scanning Probe Image Processor, SPIP™!

SPIP™ offers an unmatched level of image processing facilities designed with uncompromising attention to accuracy, efficiency, and data presentation excellence. To get a kick start we recommend spending a few minutes on the tutorial found in the first section. Although the tutorial by no means cover all the facilities in SPIP™ you will learn that even the most challenging image processing problems may be solved by a few mouse clicks. SPIP™ is a comprehensive product containing many generic analytical and visualization tools that can be applied on various types of images and curve data, for example images from electron-, interference-, and optical microscopes. In particular SPIP™ has specialized tools for correcting and analyzing Scanning Probe Microscope (SPM) data including force curve analysis and Continuous Imaging Tunneling Spectroscopy (CITS).

In addition to detailed surface characterization, SPIP™ is the most powerful tool for characterizing scanning probe instruments and diagnosing environmental noise and vibration problems. SPIP™ is therefore a valuable data analysis program for a wide range of applications and means higher quality and added value for instrument designers as well for end-users within industry and research institutes.

We are convinced that SPIP™ will work to your full satisfaction and we are committed to continue the innovative development of SPIP in close contact with our customers. Should you therefore have additional requirements or ideas for improvements, you are most welcome to contact us.

Jan F. Jørgensen  
CEO  
Image Metrology A/S



# Tutorial

To learn how to use SPIP efficiently we recommend that you run the following tutorial, which will guide you through the most important analytical procedures. The first part of the tutorial should give you a quick introduction while the second part will demonstrate some of the more advanced functions.

If you need help press **F1** at any time, or select **Help→Help Topics** from the menu bar.

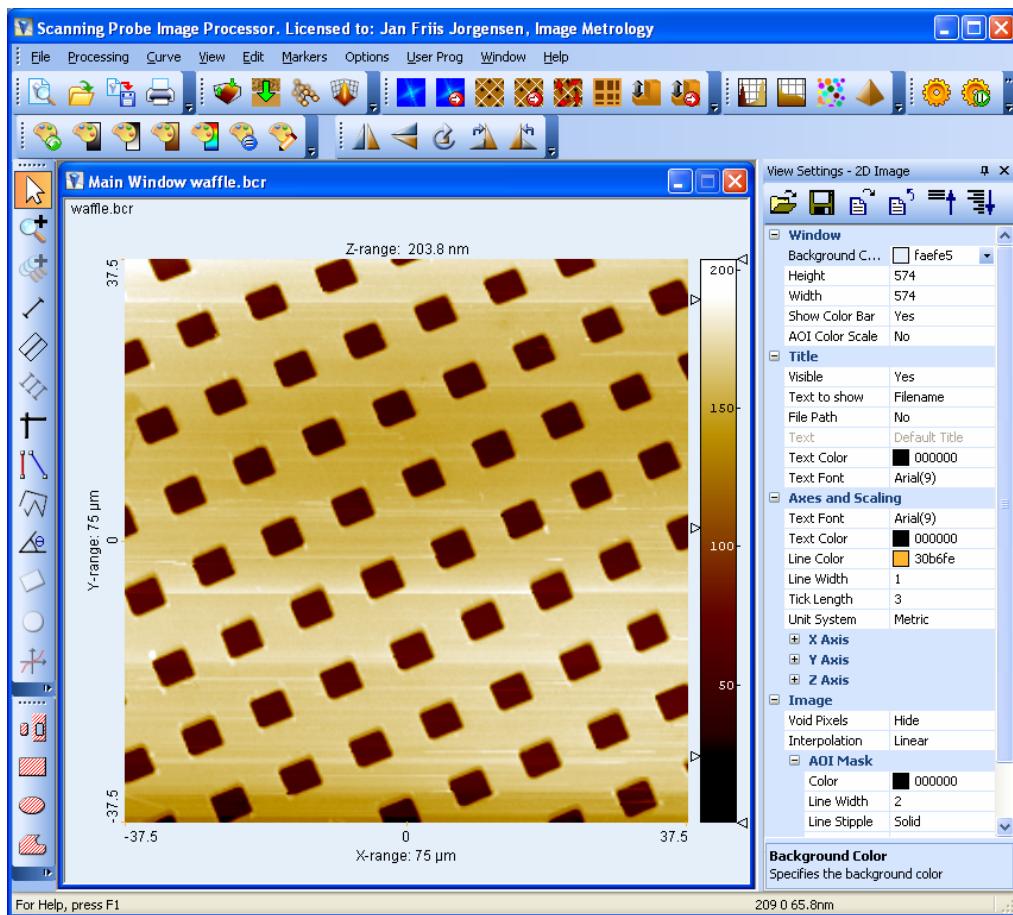
 There is context-sensitive help for all dialogue, just click on the question mark found in the upper right corner of the menu and drag it to the field or button of interest.

## Quick Introduction Tour

The following will give you a quick overview of the features included in SPIP.

 Start the **Open** file dialogue by the associated tool key. If you have ImageMet Explorer installed you will be able to browse for the files in thumbnail view. Now locate the Waffle.bcr image file, which is located in the same directory as the SPIP program and open it by a double click.

The result should be a screen similar to the one below:

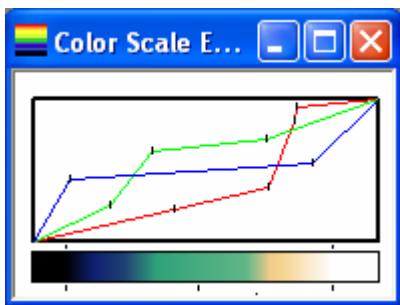


The image contains a waffle pattern with a repeat distance of 10  $\mu\text{m}$  and step-heights of 100 nm. It is suitable for demonstration of X, Y and Z calibration.

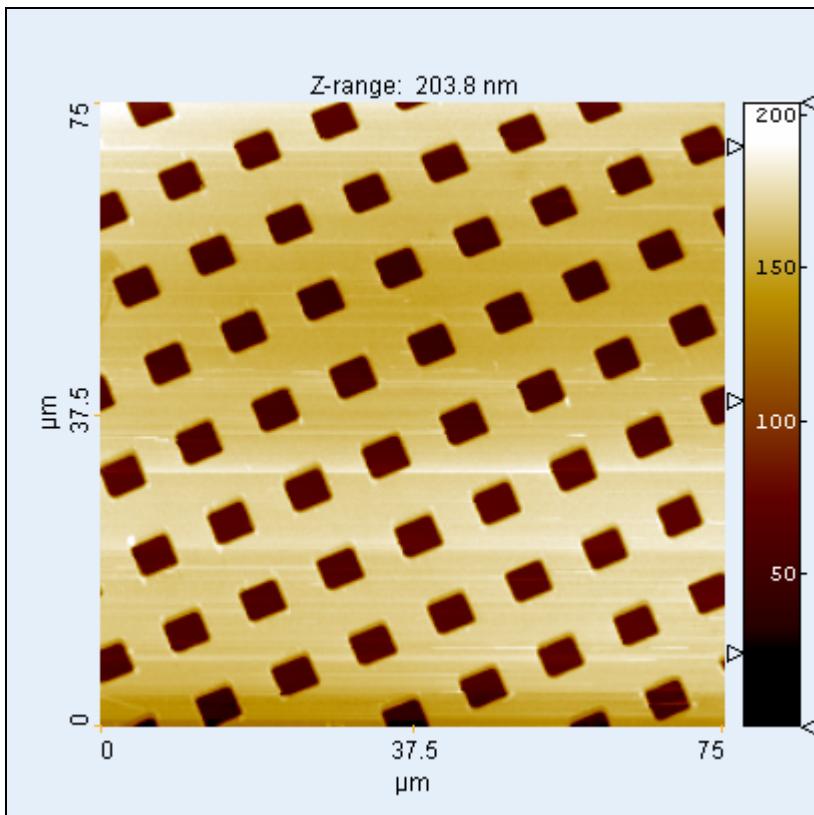
The View Settings Pane to the right allows you to modify the appearance of the image window, such as colors and fonts.



Try to change the colors with the color tool keys: or edit the color lines in the **Color Scale Editor**. Try also to place the mouse in the color bar of the image or the Color Scale Editor and change the contrast by moving or stretching color bar. The left set of markers on the color bar is used for contrast enhancement while the right marker set is used for defining threshold values without altering the contrast. You may also get quick impression of the finer details by pressing **Q** for color equalizing the color scaling. Pressing **Q** once more will produce a linear scale again.



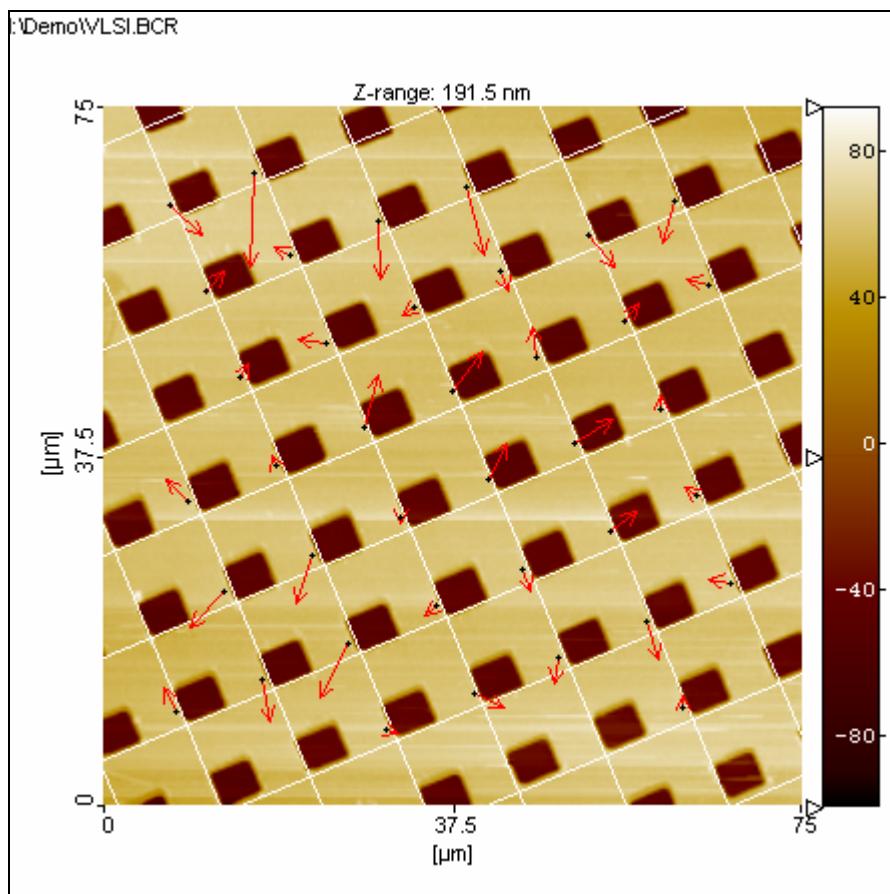
▣ Get a calculation of the unit cell (pitch). This will provide a Fourier image and the *Unit Cell and Calibration Results* dialogue where all results are shown. To get the proper correction parameters enter 1000 nm as the Reference Pitch value and press **Apply**. Note, that the unit cell is drawn on the image and that you can move it using the mouse or arrow keys. Convince yourself about its correctness and investigate the image uniformity.



 Click the Oblique maker tool once for seeing just one unit cell and twice for turning off the lattice indication.

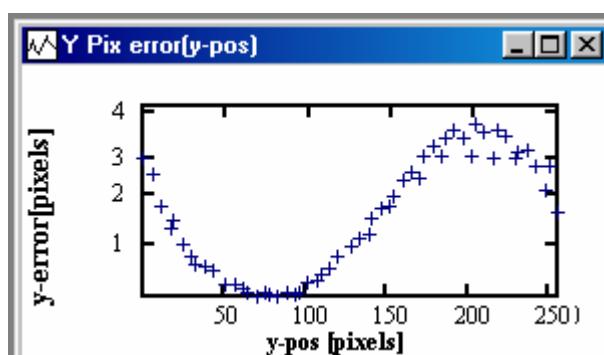
 Click the key associated with the Fine Linearity Analysis. If you have created a zoom image by the rectangle marker tool this image will be used as a template for finding similar structures in the image. Otherwise, SPIP automatically selects a template based on the calculated unit cell.

You should now see that the image has got an overlay of the calculated lattice and some small red arrows indicating the error vectors in relative size.



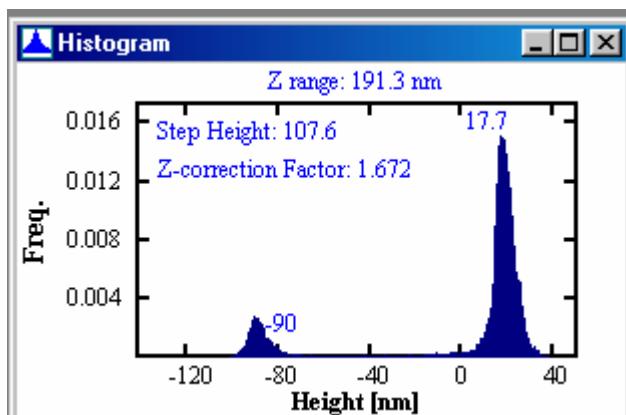
You can turn off the lattice and error indication by the oblique marker tool.

The absolute size of the errors is seen in the *Linearity Correction Dialog* and in the two scatter diagrams visualizing the linearity error for the X and Y directions:



The results are quantified and reported in the **Linearity Correction** window and in the **Unit Cell and Calibration Results** window. It is possible to correct this or other images by the correction parameters. A new estimation of the correction parameters should then result in neutral values, indicating that no further correction is needed.

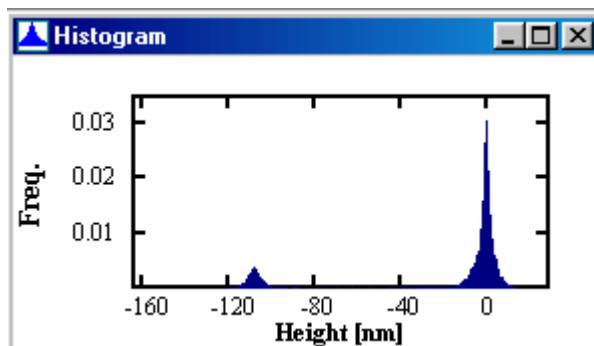
- Click on the toolbar button associated with the fast step-height calibration and a histogram showing peaks corresponding to the two dominant height levels appear:



The histogram also reports the detected step-height and the Z-calibration factor. To get the proper Z-Correction factor the reference step-height for the surface needs to be entered, - this can be done in the Z-calibration Dialog, which is activated by its toolbar button . Try to set the reference value to, for example, 100 nm and press **Calibrate**, you should then see that the correction factor is changed accordingly.

The image you are viewing was already plane corrected when it was loaded by a default third-order polynomial. It is possible to improve this image further by the Plane Correction Dialog.

- Activate the Plane Correction Dialog and observe the instant improvement of the histogram when setting **Histogram Alignment** on.



The different plane correction methods can be combined to obtain images with minimum distortion, assuring the most accurate Z-calibration.

- Click on the roughness key to calculate the bearing curve and a set of roughness parameters.

This was the quick tour introducing you to some of the important features. Before continuing with the advanced tour it is a good idea to close the windows, which are not needed any more, this can easily be done by the **Window→Close All**.

## Advanced Tour

To have an image to work with click on File in the menu bar and select, for example, the **Waffle.bcr** file, which can be found in the most recent files list in the File Menu.

### Coloring

You can change the coloring and visualization by the menu items in the View pull-down menu or the corresponding icons in the tool bar. Note that you can stretch all image- and curve windows to the size you want. However, the image windows will follow the aspect ratio of the raw image and the width of the images will be calculated based on the height of the window and the ratio between the x and y pixels. The image can also be shown without the color-bar and text: press the right mouse button and select **Color Bar On/Off** (or **CTRL+V**) Try changing the colors by the color toolbar buttons:



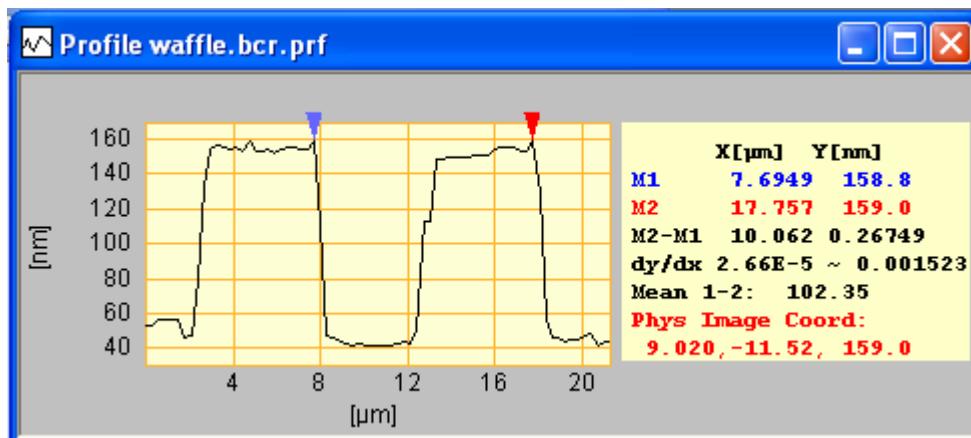
Alternatively, design your own color table by clicking on one of the red green or blue curves in the Color Scale Editor. When doing so a *nail* that can be moved by the mouse is created. The color curve will follow the defined nails. You can store the color bar by clicking with the right mouse button and selecting the **Store Color Scale** command and retrieve other color scales by selecting the **Recall Color Scale** command.

You can also re-scale the image colors by clicking on the color bar below the curves. By doing so, you can define the height values associated with the upper and lower color limits. Let us inspect the image using some of the basic functions:

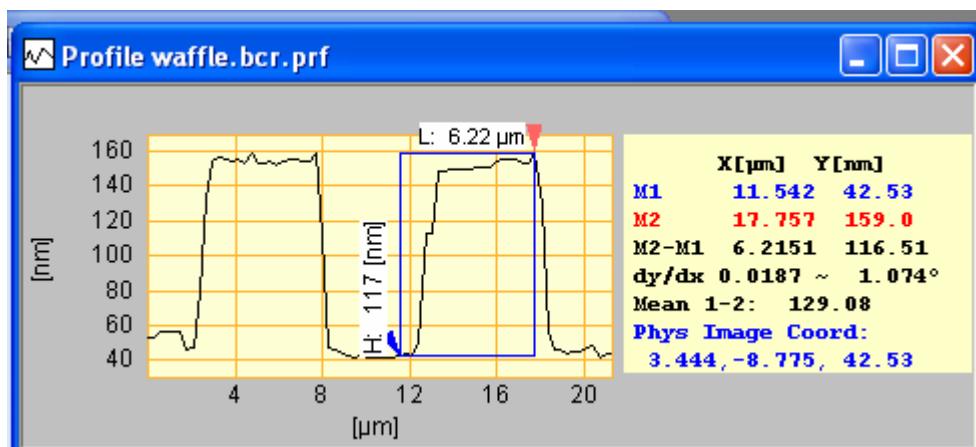
### Profiling

Create a profile by selecting the Line Drawing toolbar button and draw a line on the image. You will then see the corresponding profile. Change the size of the line by clicking the mouse close to one of the ends. Move the line by selecting a point close to the middle part of the curve. Try to make a diagonal line from one corner of the image to the other. Try also to move the line with the keyboard arrow keys.

Select the profile window and use the right mouse key or '**C**' on the keyboard to activate the cursors, press **C** twice and you will get two cursor pairs, move the cursors by the mouse or keyboard arrow keys to measure distance and height values. Notice, that the Up/Down arrow keys will locate the locale minimum and maximum positions and the angle of the markers will reflect the slope of the curve.



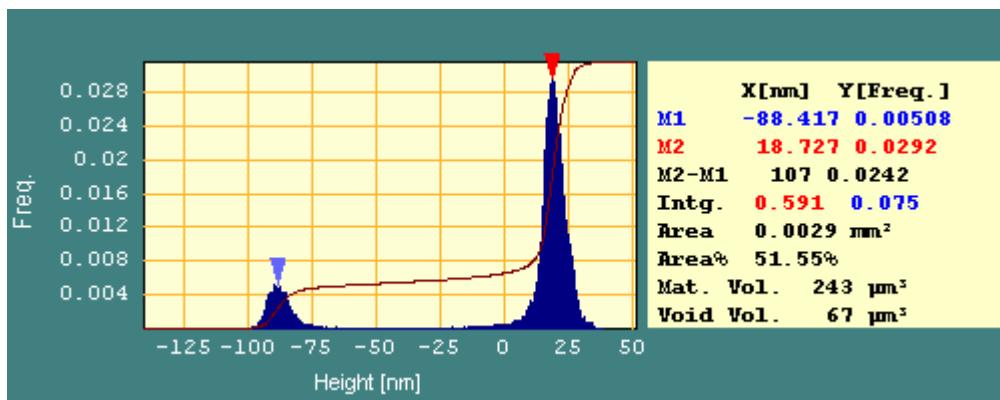
For easy reading of height and length you may also set the **Dimension Readout** by the right mouse:



To learn more about the profiling tools see Profile and Advanced Profiling and Fourier sections.

### Histogram

Take a look at the histogram with the two peaks representing the two characteristic height levels of the surface. To measure the height differences manually activate the cursors by the right mouse key. Here it is very convenient to use the key board Up Arrow key to locate the maximums of the histogram.



You should find that the step-height is about 107 nm.

To learn more about the histogram tools see the Histogram section

### Plane Correction

Now let us try to improve the image by plane correction (also called flattening) such that image bow distortions will be removed. For this purpose we apply the Plane Correction Dialog :



To plane correct the image you only need to click the Apply button.

When the "Quality Priority" mode is selected SPIP will combine a number of algorithms to get the best possible correction by detecting and handling steps, which may otherwise create undesired results.

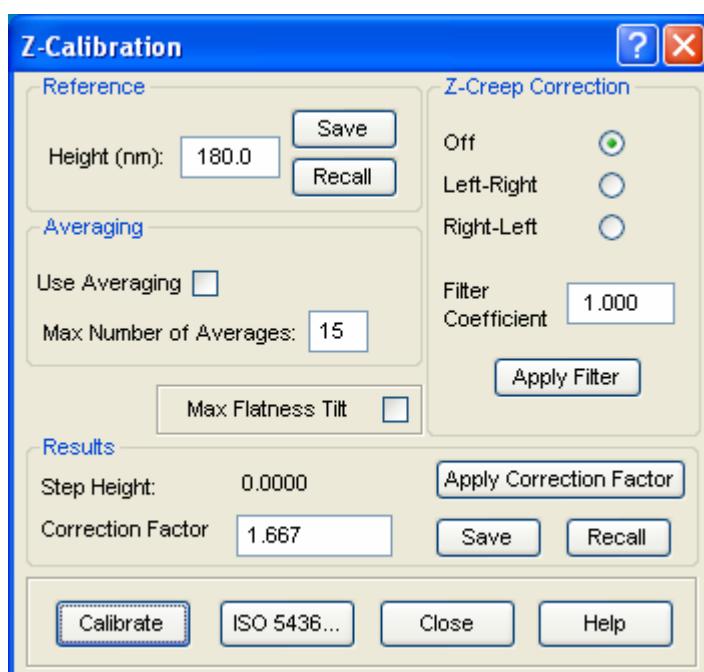
Notice, how the image changes and how the changes are reflected immediately in the histogram and the profile.

If you want to have more control of the correction procedure you may click the "More >>" button and set the correction settings as desired. You may for example set **Show Difference** on so that difference images will be created for each correction. You can try out the different methods and observe how it affects the image, the profile and the histogram.

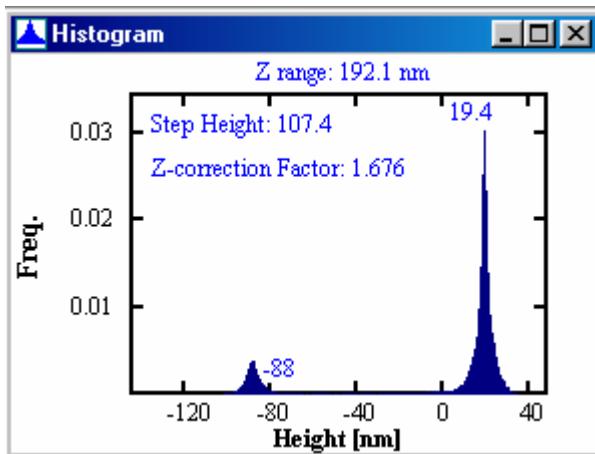
Learn more about the Plane Correction tools in Plane Correction Dialog

### Z-Calibration

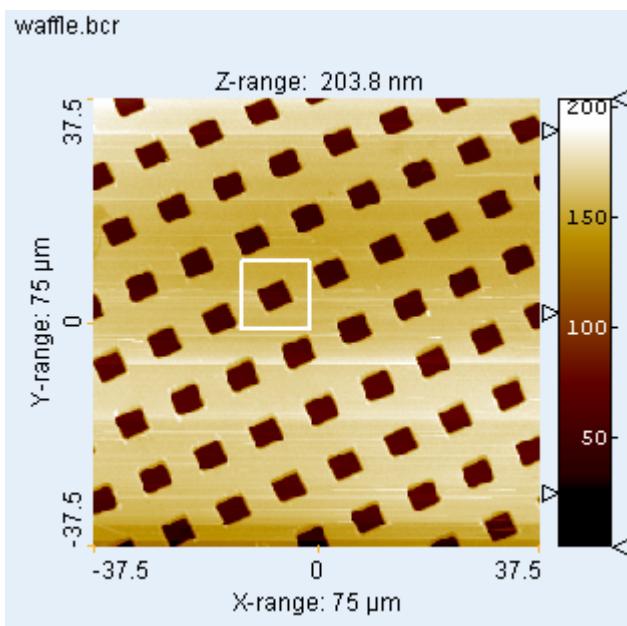
Let us continue with the Z-calibration Dialog:



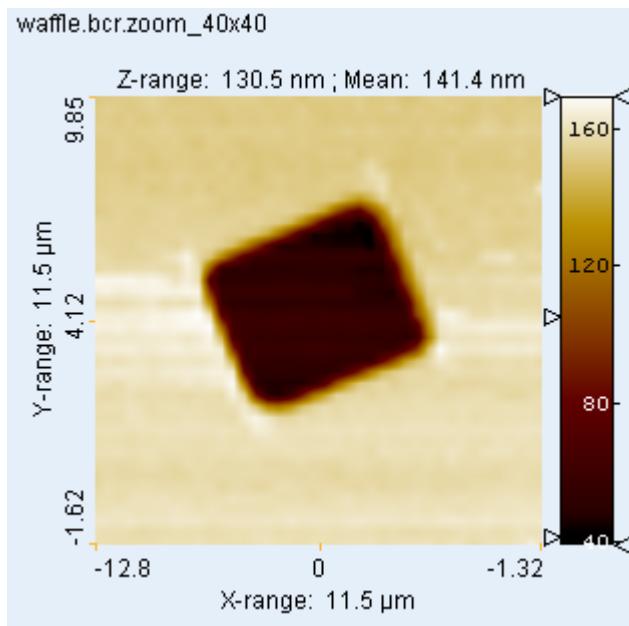
In the Z-calibration Dialog, you can enter the reference-height for the sample, which in this case should be 180 nm. To obtain a step-height estimate and a Z-correction factor click on the Calibrate button. You will see the results in the histogram window.



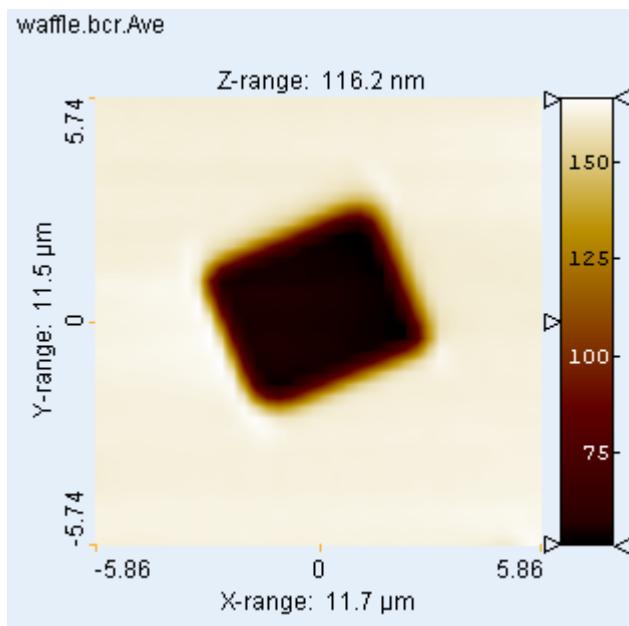
For images having step-heights that are small compared to the noise it will often be an advantage to apply the Correlation Averaging Technique. Pressing the associated tool key starts the correlation averaging. If the zoom image is active SPIP will use this image as the structure that has to be recognized and averaged, otherwise SPIP automatically determines a suitable template based on unit cell detection. You can define a template by the rectangle marker tool



The selected area will be shown immediately in the Zoom Window:

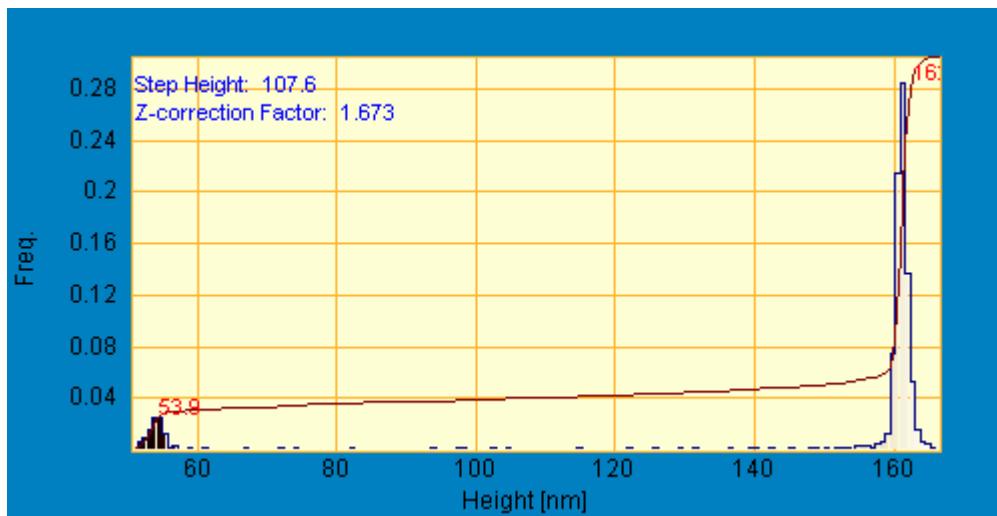


Press the **Calibrate** button to calculate the average image, which will be put into the Main Image Window:



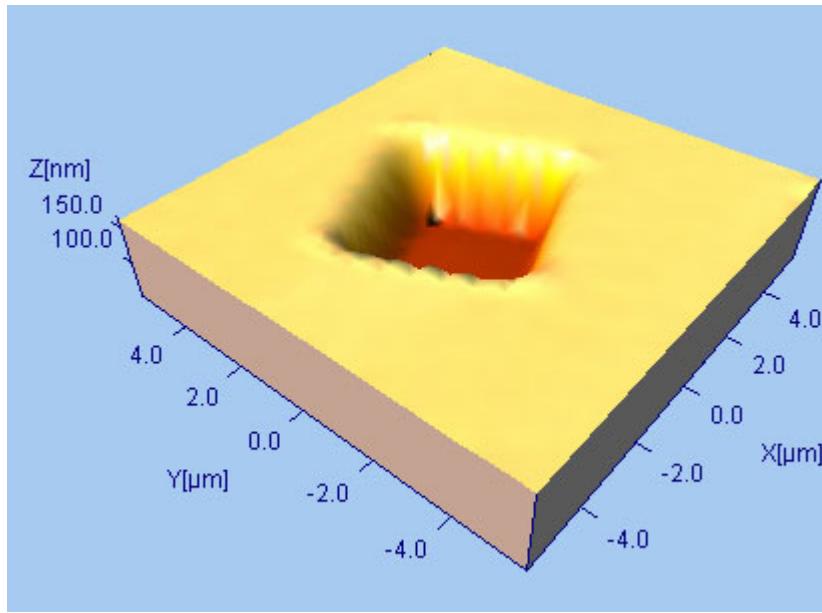
You will also see that a standard deviation image has been calculated and that the source image has been saved in another window from where it can be retrieved if desired.

The result is shown in the histogram and the Z-Calibration Dialog. Furthermore, the results can be saved in a text file called `waffle.bmp.zcal` that can be imported to spreadsheet programs; this requires only that you activate this option in the Options dialog.



The advantage of the averaging technique is that it improves the signal-to-noise-ratio by lowering the random noise. Therefore, the analysis will be more robust.

You can get a better impression of the finer structures in 3D view just click once in the average window and click the 3D-toolbar button



In the 3D window you can use the mouse to rotate, move, scale and dynamically change the color properties. With the mouse button down rotate axes the image around the X-and Y-axes by moving the mouse. Hold also down the SHIFT key and rotate around the Z-axis. To scale the image, move the mouse while keeping the CTRL key down. 8 light sources can be defined, and is activated by the numerical keys '1' to '8'. When combining the numerical keys with mouse movement light source positions can be set conveniently. By pressing 'A' or 'a' you can start the 3D animation that will display the image at different angles, positions and scaling. See section 3D Visualization Studio for further details on defining the 3D scene.

You can get a 3D view for the other images as well. Try to create a 3D view of the original template shown in the zoom image and compare with the average image.

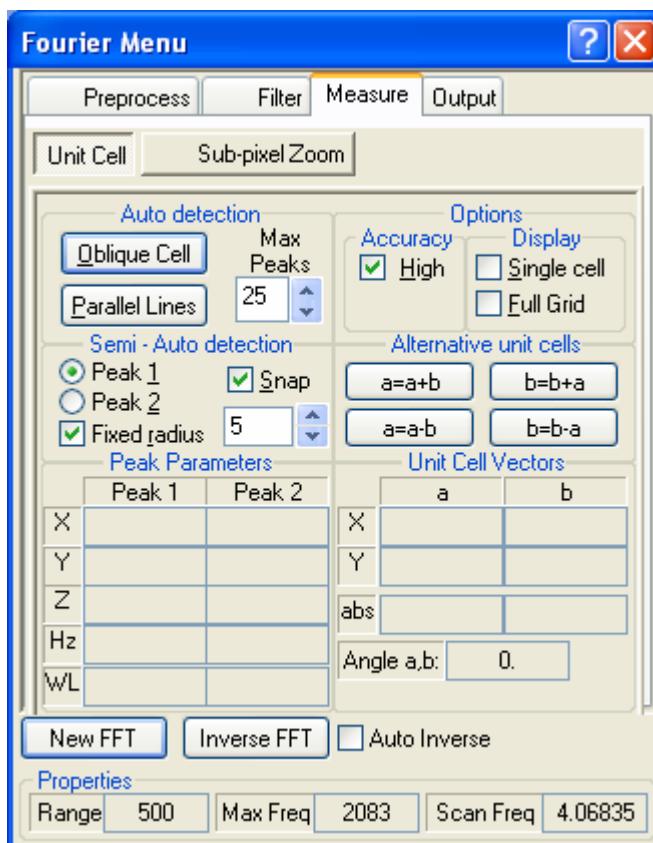
Notice also the Standard Deviation image, which reflects the uniformity (quality) of the structure. Naturally, the standard deviation is highest at the edges of the pit.

## Unit Cell Detection by Fourier Analysis

Before making an analysis of the lateral dimension it is a good idea to close all the windows in order to focus on the important windows you now are going to use.

Open the Waffle.bcr file once more.

Initiate the Fourier transform and the Fourier dialog and select the Measure tab.



Try to calculate the lateral unit cell by clicking on **Oblique Cell** as the target structure. The unit cell will be displayed in the main image and you can move it around. You will also get data for the unit cell in the Fourier Menu and in the Unit Cell and Calibration Results Window. The latter also calculates lateral correction parameters. To get the proper correction factors enter 10000 nm as the reference pitch and click on **Apply**. You can correct any image by this set of correction parameters. It is a good Idea to record the correction parameters for different measurement conditions and apply them when necessary.

The calculation is based on the Fourier peaks defining the reciprocal unit cell. When the **Fast Peak Detection** is disabled, you achieve the highest accuracy because the Fourier peaks are found at sub-pixel level by a sub-pixel Fourier algorithm. Otherwise, the peak positions are estimated by parabolic fits.

To analyze the Fourier image in detail it is an advantage to use high contrast colors, which is defined as the default colors for Fourier images. The contrast may also be changed by the **SquareRoot** or **Square** functions found in the Fourier Menu and in the Right Mouse Menu. Now, try to detect the unit cell semi-automatically: set the Circle Function in the Fourier Menu to **Defines Peak 1** and draw a circle around one of the innermost Fourier peaks associated with the reciprocal unit cell. Notice that the circle will snap its center to the highest point within the circle. Then set **Defines Peak 2** on and mark a circle around one of the other innermost peaks (this point should not be on the line with Peak 1 and the origin)

You have now defined two corners of a reciprocal unit cell and SPIP does the rest for you, it finds the spatial unit cell and the corresponding lateral correction parameters if a correct pitch reference value has been entered. The co-ordinates of the two peaks are given in the Fourier Menu together with their corresponding wavelengths and the frequency measured in Hz. The latter is very useful for diagnosing phenomena caused by noise.

Peak Parameters		
	Peak 1	Peak 2
X	2.3786	2.3786
Y	1.4175	1.4175
Z	0.03596	0.03596
Hz	4.7573	4.7573
WL	3.6114	3.6114

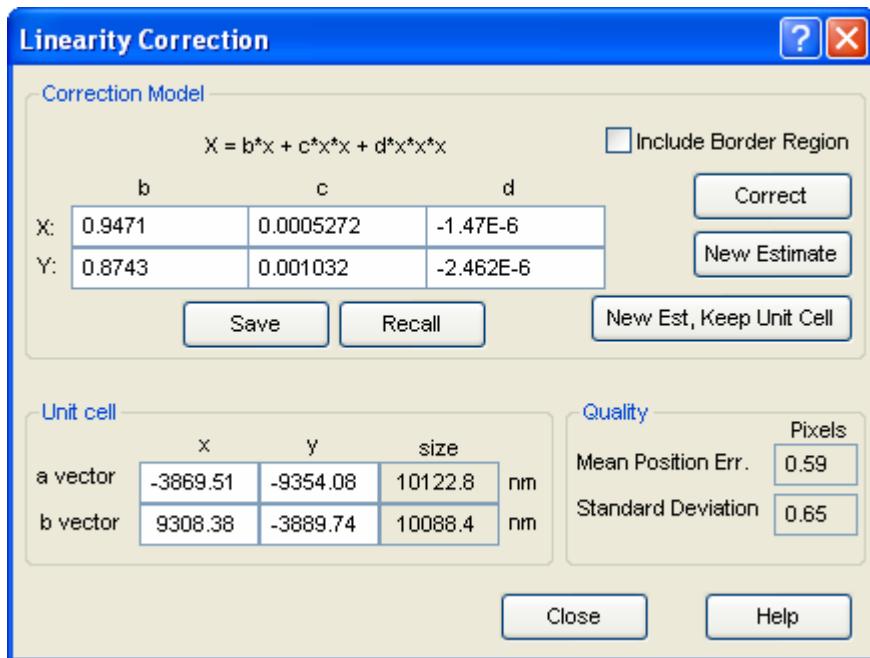
To learn more about the Fourier tools see Fourier Analysis and Filtering

## Linearity Analysis

The waffle.bcr image is also well suited for calibrating the linearity of your instrument:

 Click the rectangular marker tool and draw a rectangle about the size of the unit cell or smaller. The area should include a characteristic structure, for example, the corner of a pit. The zoom window will appear and display the selected area.

 Start the fine linearity analysis. From the cross correlation function SPIP will at sub-pixel level find the positions of all structures similar to the content of the zoom window. It will compare the positions with those predicted from the unit cell data. The differences are described as linearity errors, which are further minimized by tuning the unit cell (now in the spatial domain). The results are shown in the Linearity Correction Menu:



Consequently, we have not only quantified the non-linearity but also found the best-fit unit cell. Experiments have shown that this gives a better reproducibility than the faster Fourier method. However, the Fourier method is needed for getting a good initial estimation of the unit cell.

The overall linearity error Mean Position Error is also shown in Linearity Correction Menu and more detailed information can be retrieved from the waffle.bcr.linc file.

The correction parameters are based on a third-order polynomial model of the scanning system. You apply the correction parameters on the main image by clicking on **Correct**. Recheck the linearity by clicking on **New Estimate** and you should observe that the correction parameters become more neutral and that the errors in the scatter diagram reduce to the sub-pixel level, and that the Mean Position Error decreases.

 When calculating a new Fourier image you will also notice that the Fourier peaks have become sharper, especially the weaker peaks close to the border.

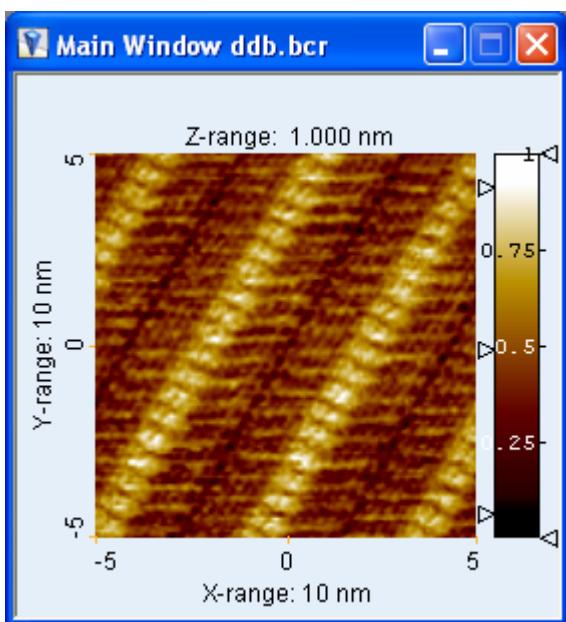
Try also to correct the physical scaling and orthogonality of the image using the **Unit Cell and Calibration Results** dialog. Enter 10 000 as the **Ref. Pitch La** reference pitch value and click on the **Apply** button and you will notice that the correction parameters changes accordingly. Then click the **Correct** button to get a corrected image.

## Analysis of Self-Assembled Molecules

Now let us try to analyze an image containing didodecylbenzene molecules self-assembled on a graphite substrate:

Check first the plane correction settings, disable **Line-wise leveling**, which will be applied when loading the file, close all windows (**Window→Close All**)

Open the *ddb.bcr* image file:



Get a calculation of the unit cell. You will notice that the calculated unit cell covers parts of more molecules and that a unit cell not necessarily equals the shape of the molecules. There are more alternative unit cells the default selected by SPIP is one having the angles closest to 90°.

To get a unit cell closer to the shape of the molecule activate the Fourier Menu and click on the  $\langle \mathbf{a} = \mathbf{a} + \mathbf{b} \rangle$  button four times. Try also the other arithmetic buttons.

Make a zoom image by the rectangle marker tool choose a representative area covering more molecules:

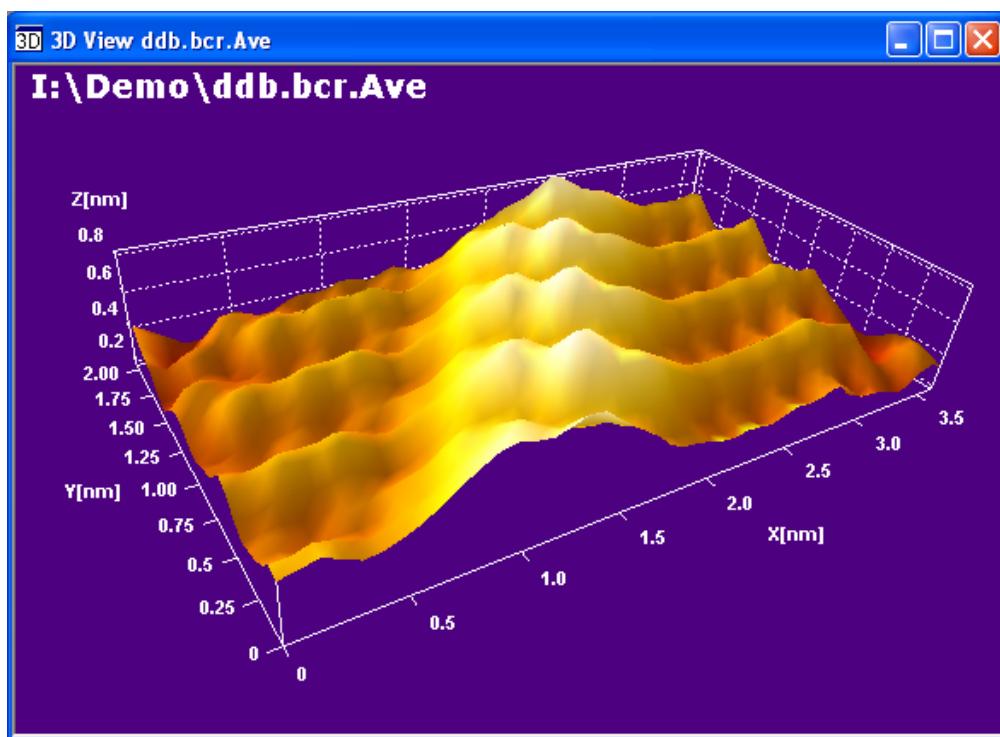


Calculate an average image by the **Processing→Average→Marked area**, which will result in an average image and its corresponding Standard Deviation image:

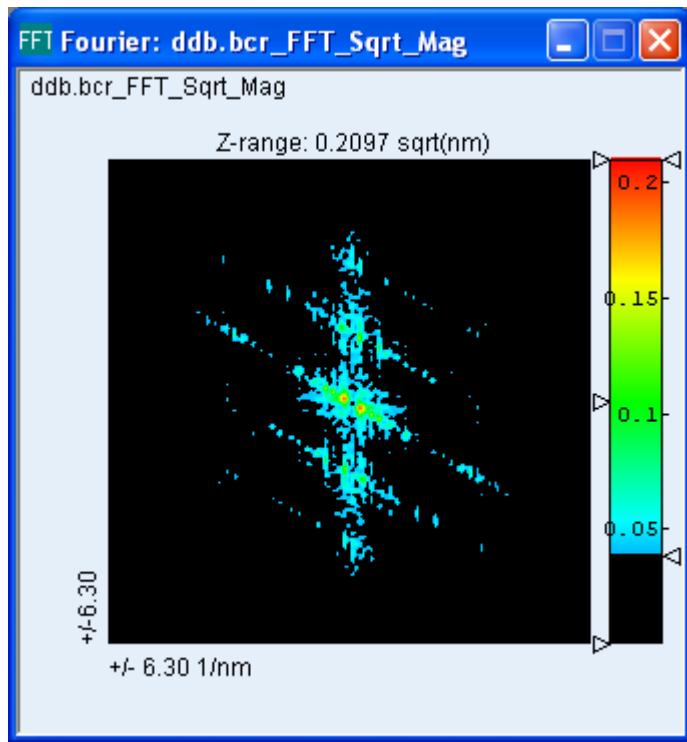


The average image has a much better signal-to-noise ratio and provides more detailed information about the inner molecular structure. The SD image provides important information about structural uniformity. Here, the low SD values at the right part of the benzene ring indicates that this part of the molecule is the part most fixed to the substrate.

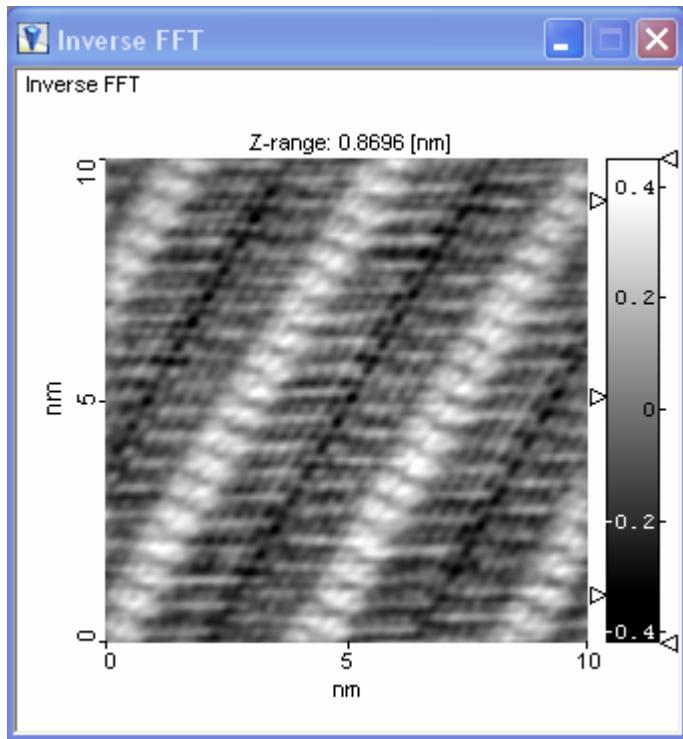
To create a nice presentation of the result you can show the average image in 3D; Click in the average image with the right mouse key and select **3D**:



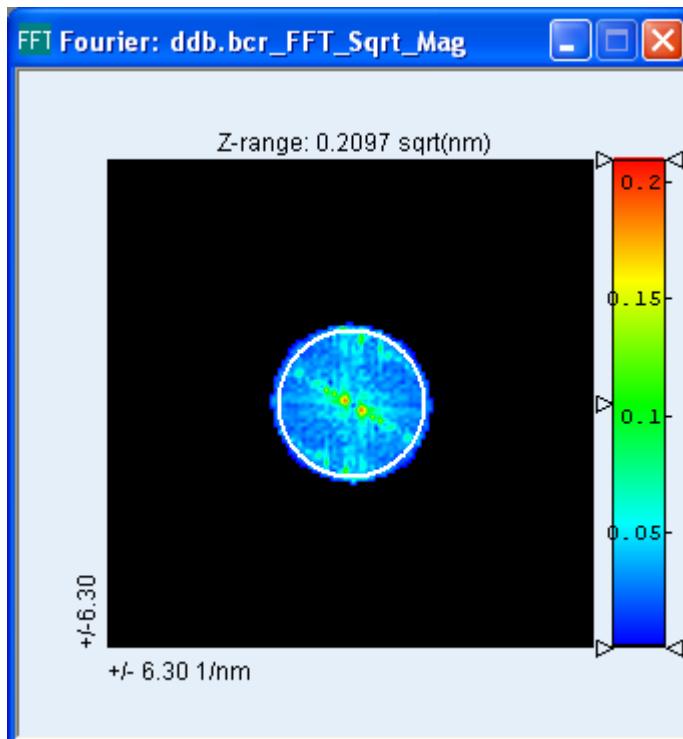
Another way to filter out unwanted noise without removing the specific Frequencies is to remove only the Fourier components having smaller amplitudes than a value you define by the color bar:



By moving the lower limit of the color bar you define all Fourier components shown as black to be removed when performing an inverse Fourier transformation. If the color bar is not shown in the Fourier window it can be clicked on by **CTRL+V** otherwise you can also change the limits for the Color Scale Editor. Click on the **Inverse** button in the Fourier menu and you should see an improved image with the contrast preserved (be careful no to filter too much):



You can also perform interactive filtering by excluding certain areas defined by the marker tools. To perform low-pass filtering enable **Center at Origin** in the Fourier Menu and mark a circle with the Circle marker tool. Note that the wavelength corresponding to the circle radius is written simultaneously in the lower right part of the SPIP program window. Click on **Include Only**:

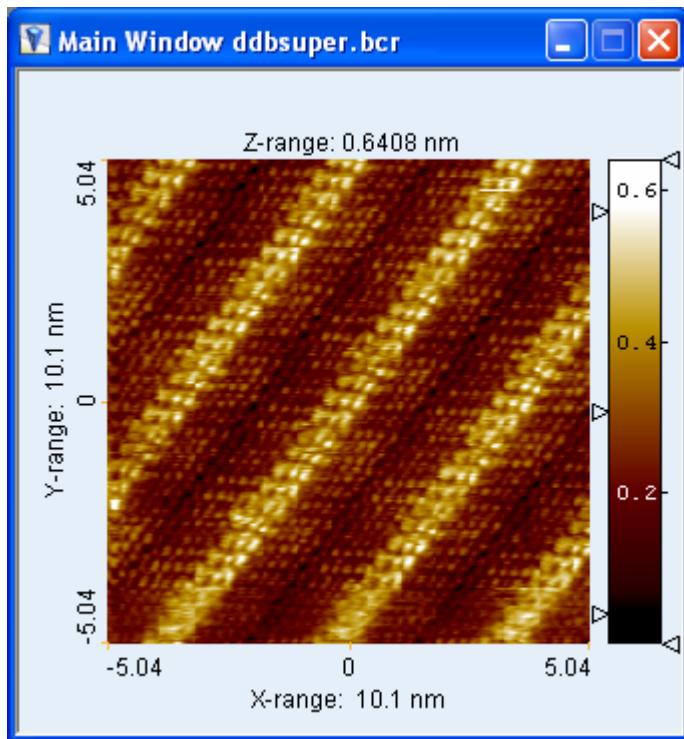


The filtering will first take place when you click in the **Inverse** button until then you can undo the exclusions by the **Undo** button. However, the current change in the Fourier image will

have effect on the unit cell detection algorithm, which will ignore the excluded areas. Therefore, you can also use this technique to force the program to find other structures than the unit cell, for example, super structures by ignoring the dominating waves as demonstrated below.

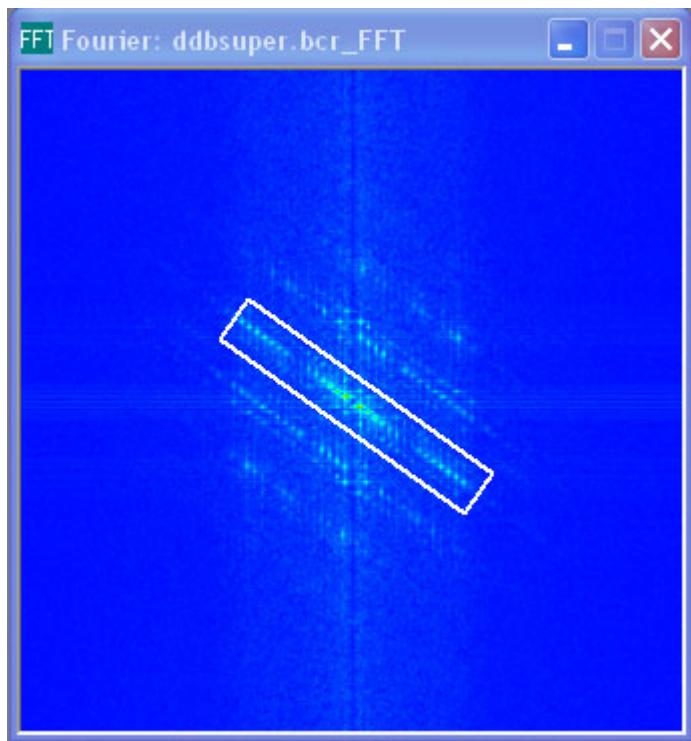
To perform band-pass filtering you can mark a new circle inside the previous marked circle and click on **Exclude AOI** (exclude Area of Interest, which is the opposite to of the **Include Only** function).

 Open the file *ddbsuper.bcr* to get a demonstration of a super structure analysis:

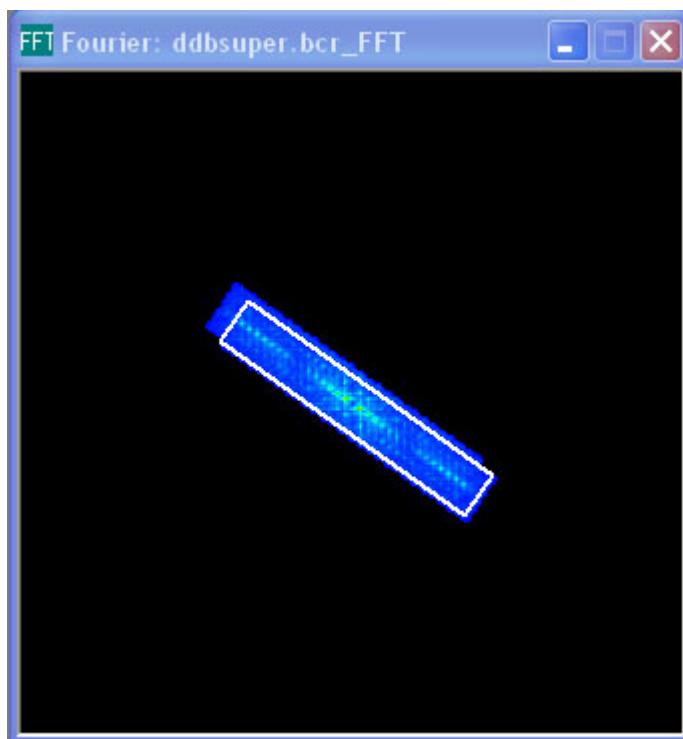


This is also an image of DDB self-assembled molecules, now with a more visible super structure.

-  Calculate a new Fourier image where you will see that main Fourier peaks have *satellites* associated with the super structure.
-  Make a fast calculation of the unit cell.
-  Activate the Oblique maker tool and draw a parallelogram around the inner peaks and their satellites:

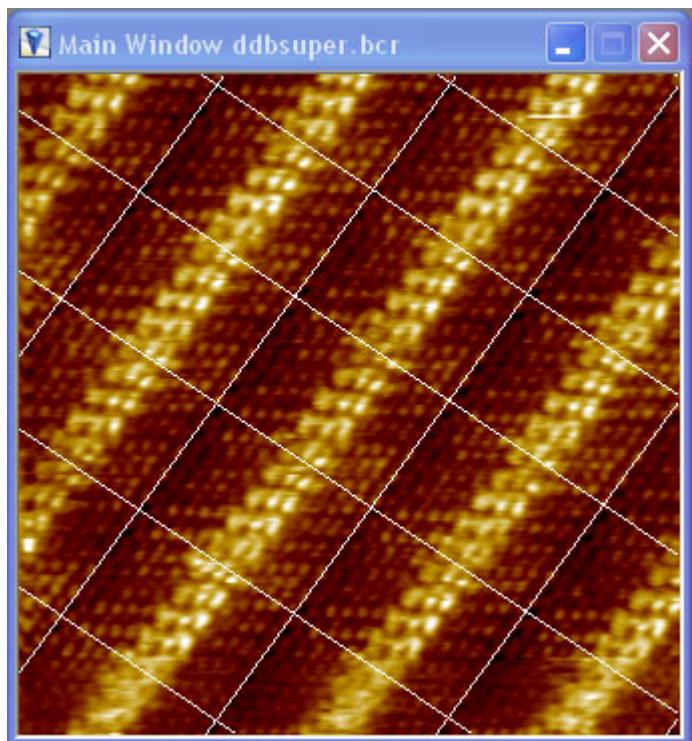


Click on **Include Only** to ignore all Fourier components outside the marked region.



▣ Make a calculation of the unit cell based on the current Fourier image and you will get the *super cell*:

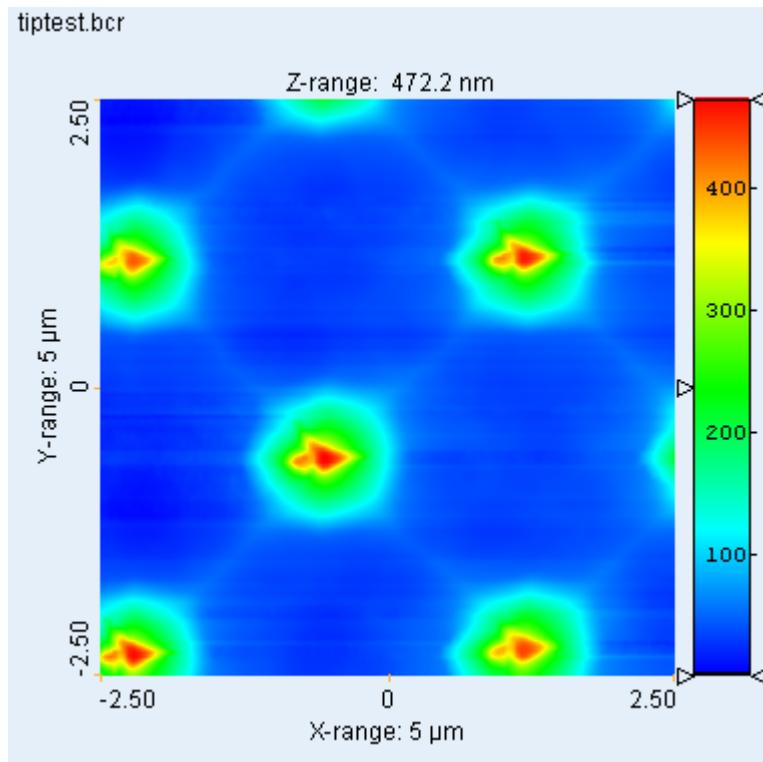
The Scanning Probe Image Processor, SPIP™ V. 4.2



## Tip Characterization and Deconvolution

The following will demonstrate a tip characterization based on a tip characterizer sample, it has only meaning for SPM and stylus instruments:

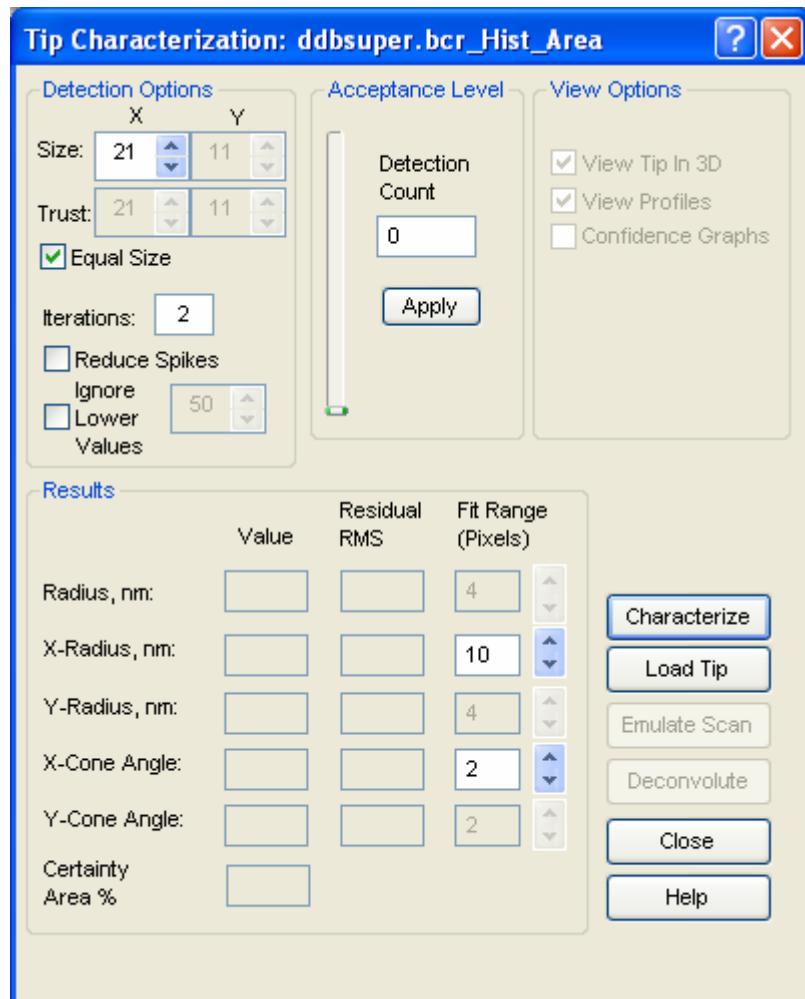
 Open the file *tiptest.bcr*:



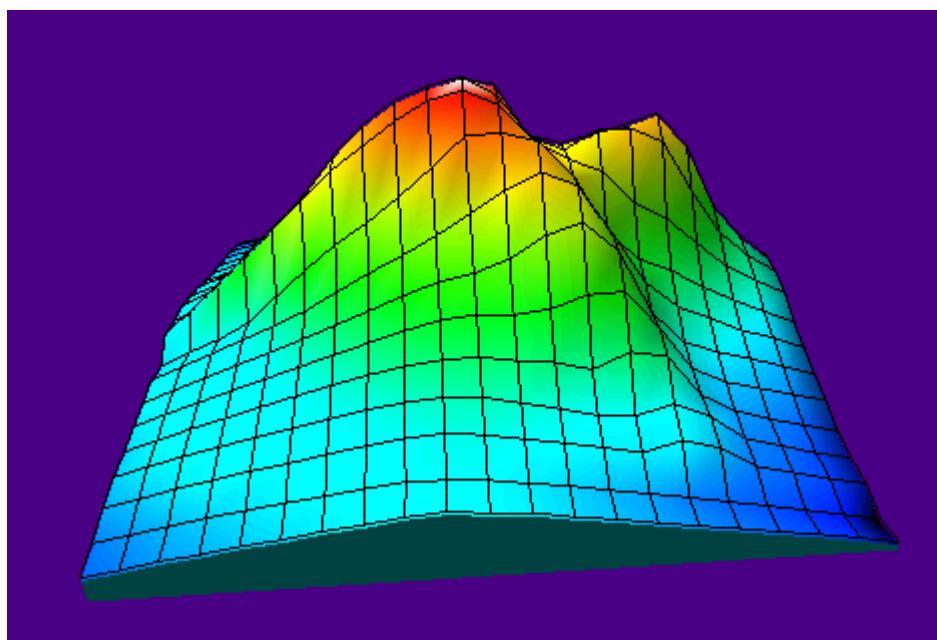
From other images is known that the surface only consist of single tips therefore the observed double peaks can only explained by a probe having a double tip.

 Click on the Tip Characterize tool key.

To define a suitable size of the tip area to be calculated set the size parameters to 21 x 21 pixels, this will cover the most interesting part of the tip. In this particular case it is important that it is large enough to cover the double tip pair:



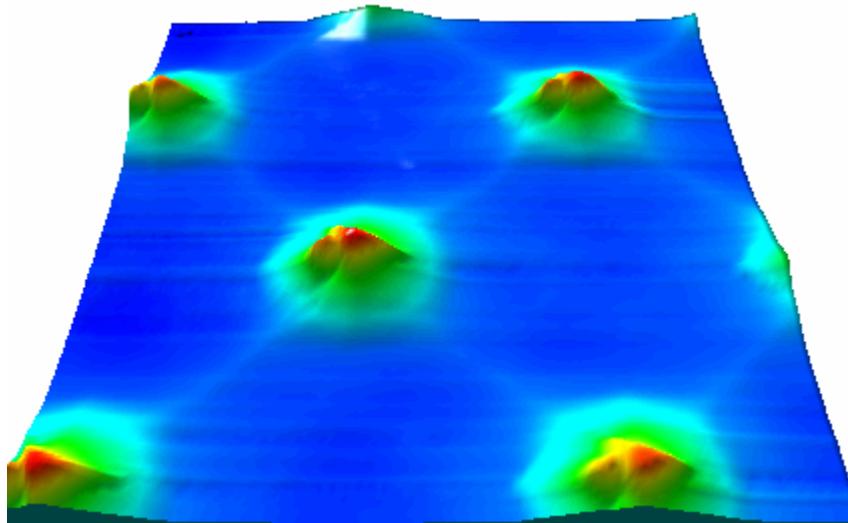
Click on **Characterize** to calculate the tip; this will cause several windows to appear, the most important one is the image of the estimated tip and by clicking the **View Tip in 3D** checkbox a 3D tip image will be created:



To get the best impression of the tip form it can be an advantage to use a combined wire-frame view as shown above; this is set in the 3D Visualization Settings dialog.

Note, that the relative flat outer part of the tip image not necessarily reflects the true shape of the tip. The problem is that the actual image does not possess enough information to extract a larger part of the tip. However, in most cases it is only an area within a radius of a few hundred nanometers that is important for the imaging process.

Now, that we have a good knowledge of the central part of the tip we can reconstruct the surface image; now press **Deconvolute**. The resulting image will be shown in the Main Image window while the original for convenience is stored in another window. It should now be observed that the double tip artifact now has disappeared. For comparison it is a good idea to view the original and the corrected image in 3D, just press '3' in the 2D image window you want to view in 3D:



Original Image

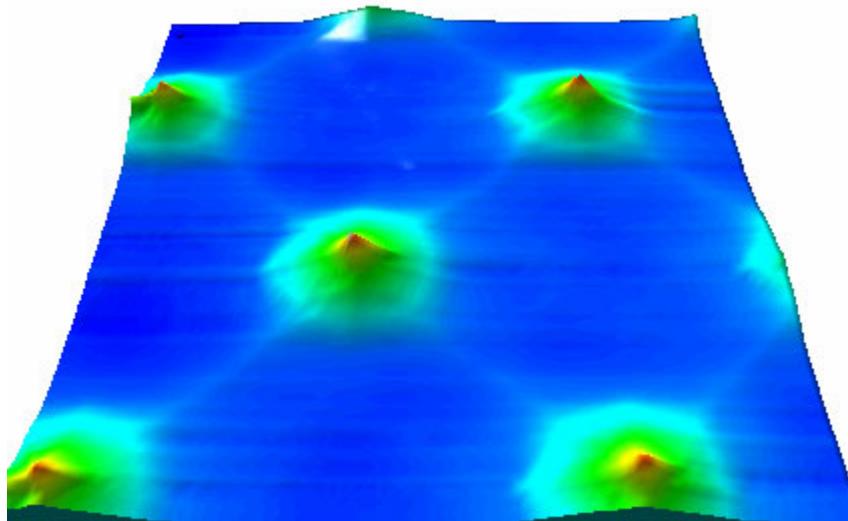


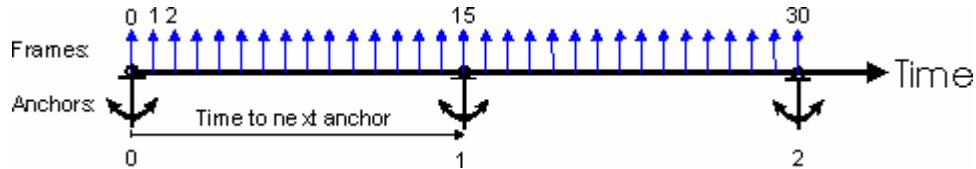
Image after Tip Correction

The demonstrated technique is not limited to the use of dedicated tip characterizers. What qualifies a good tip characterizer sample is that it possesses features in all directions having slopes larger than the tip; the structure does not need to be systematic or known in advance. Also, once knowing the tip shape it can be stored and used for deconvolution on other images.

## 3D Animation Tutorial

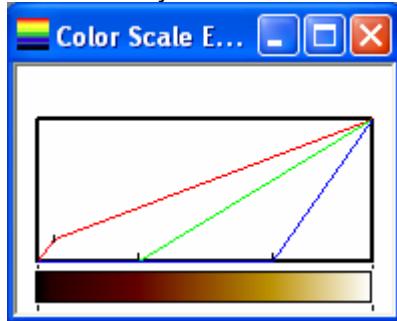
The following will show the few steps involved in creating an animation file. You can continue working with the current image in the 3D window or put one of the other windows into 3D just by pressing '3' in for the 2D window you want to see in 3D.

The principle in the 3D animation tool is to define a number of 3D scenes called anchor points. To each anchor point is related to a certain time in the movie to be generated. Between the anchor points SPIP will automatically calculate a number of frames that brings the 3D scene gradually from one anchor point to the other.

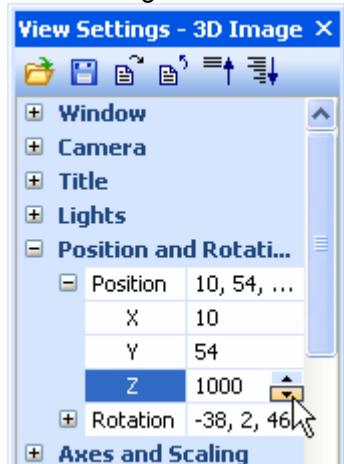


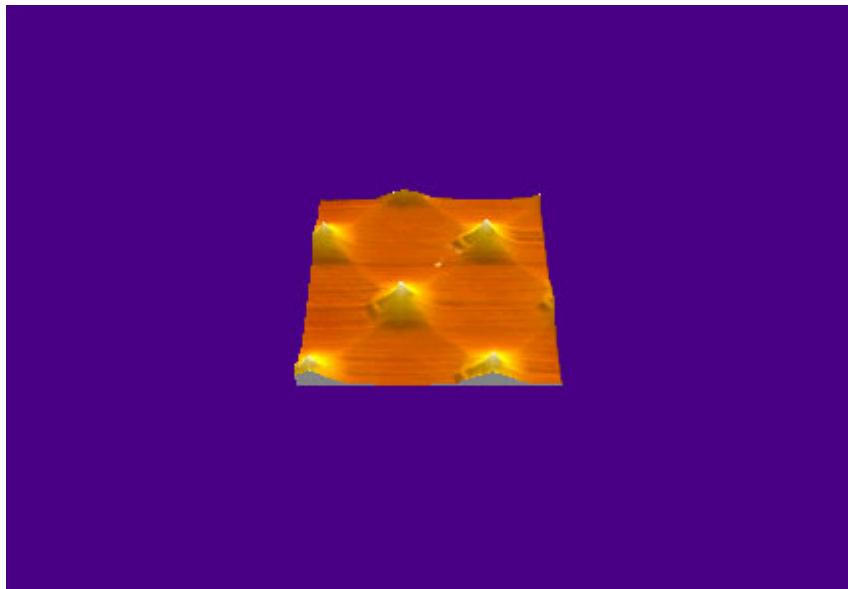
Let us try to make a simple approach and rotation animation by defining three anchor points:

- 1 Use the color bar to define a desirable color scheme; in 3D it is often best to avoid the darkest colors this is done by moving the right marker in the color bar further to the right so that it actually becomes outside the window area:

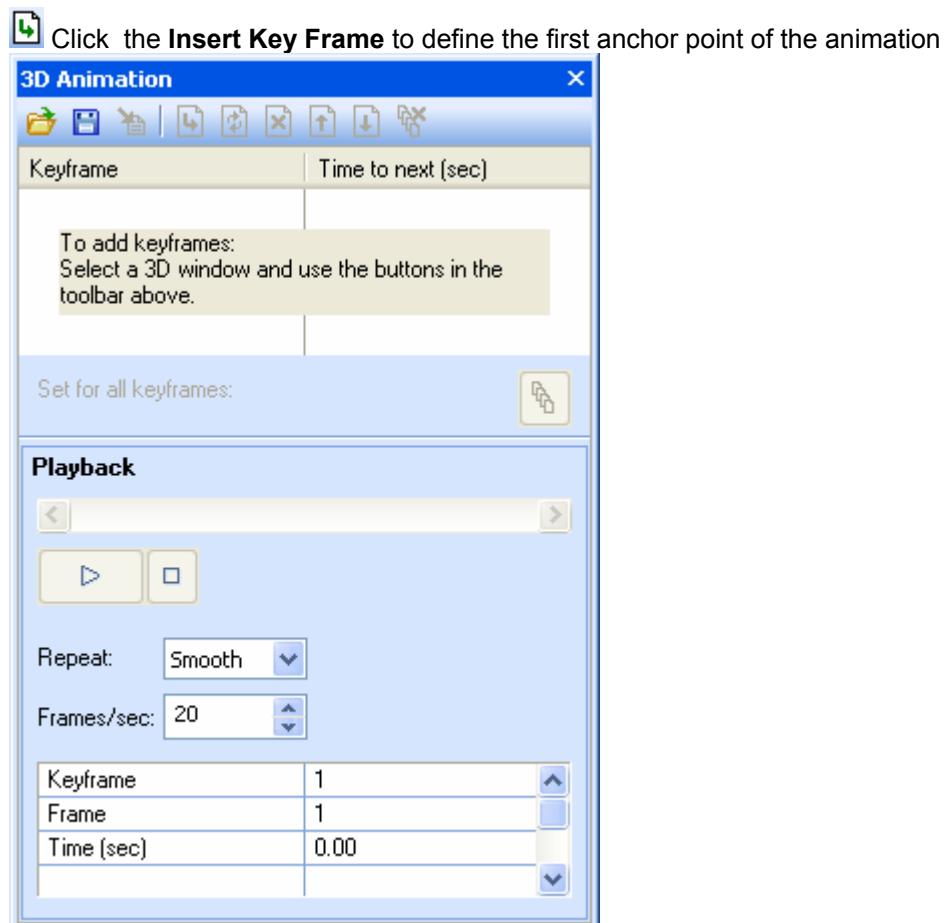


- 2 Put the image into a distant position this is done by the Z Position Parameter of the 3D View Settings Pane:



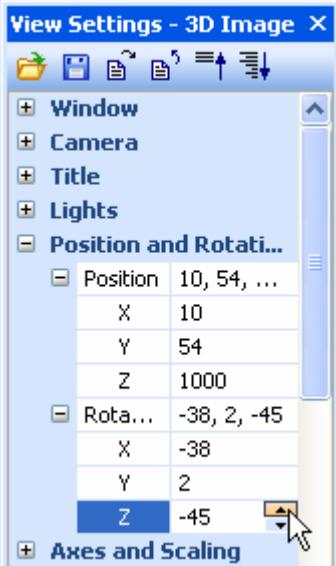


3 Activate the 3D Animation Pane, by right clicking in the 3D window on **3D Animation**.



4 Move the image closer by the Z Position Parameter as in 2) and press **Capture Anchor** to define the next anchor point.

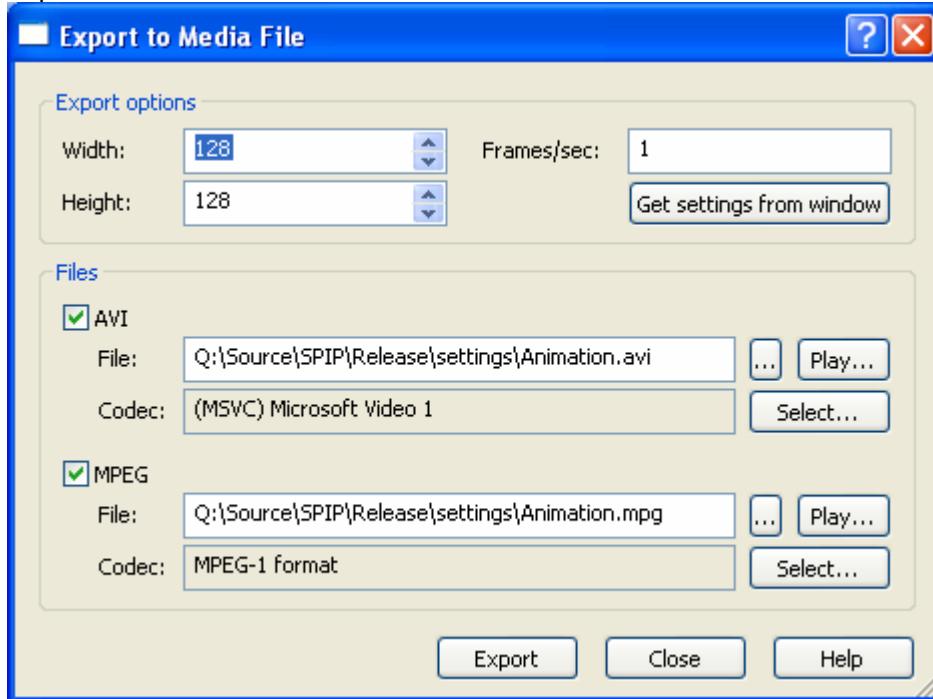
5 Now, perform a rotation by entering for example 360 in the Z-Rotation parameter field.



and press **Capture Anchor** to define the third anchor point. When asked where to put the anchor point select "End"

6 Now you have defined three anchor points and between these anchor points SPIP has automatically calculated frames that brings the 3D scene gradually from one anchor point to the other. You can use the slider at the bottom of the menu to view the individual frames.

7 To create an animation file that can be seen by third party movie players select File→Export 3D Animation



8 Select the output file as an AVI and/or MPEG file, enter proper file names and press **Export**

9 The selected AVI and/or MPEG files will be generated in some seconds and can afterwards be played by your default movie player by pressing one of the Play buttons.

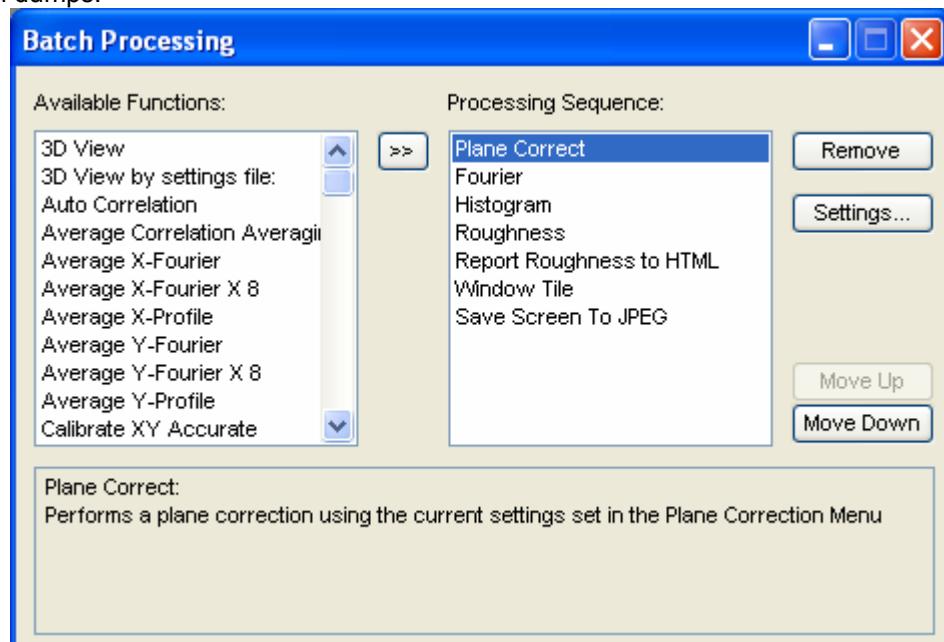
## Batch Processing

The Batch Processor enables you to perform the same processing steps on a large number of files and can save you a lot of time. Please follow the following steps to get a quick introduction to the Batch Processor.

Open the Batch Processor dialog with its associated tool key, the gear wheel 

Click the Load button to load one of the predefined batch sequences.

Select "roughness.batch" from the SPIP Settings folder. This will define a sequence where each image is plane corrected and the roughness calculated and reported to HTML including screen dumps.



Set the HTML Reporting Mode to "**Autogenerated filename**".

Now, select some files from the ImageMet Explorer or the Window Explorer and Drag-Drop them into the SPIP program. The batch sequence will be processed on each input file and a HTML file is generated.

In the HTML section click on the Open button to show the generated HTML file.

Please consult the Batch Processor section for more detailed information.

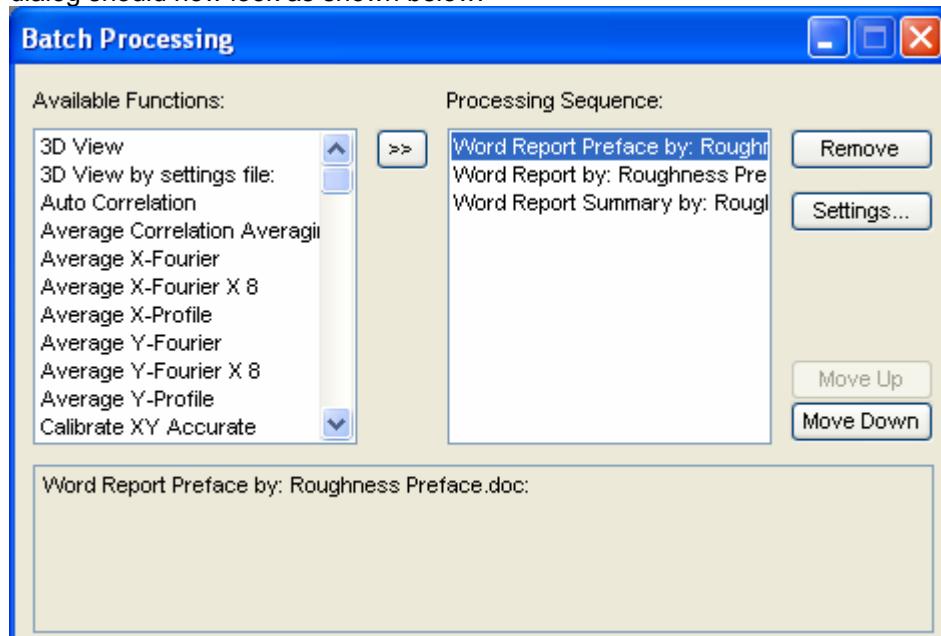
## ActiveReporter

The following steps will demonstrate the advantage of the ActiveReporter when combined with the Batch Processor. It will show how to generate customized reports automatically by use of MS Word templates.

Open the Batch Processor dialog once again.

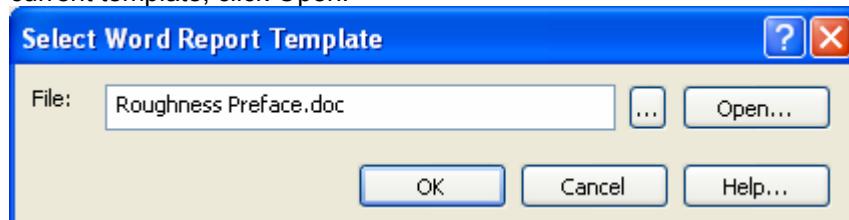
Click the Load button to load one of the predefined batch sequences.

Select "Roughness ActiveReport.batch" from the SPIP Settings folder. The upper part of the dialog should now look as shown below:



The batch sequence contains three items, each referring to a word template instructing SPIP how to generate the report. The first item is the preface containing the page layout information and the text you want to have at the very beginning of the report. The second item contains ActiveX controls specifying, which data you want to have reported for each data file. The third item defines the statistical summary number you want to have shown at the end of the report.

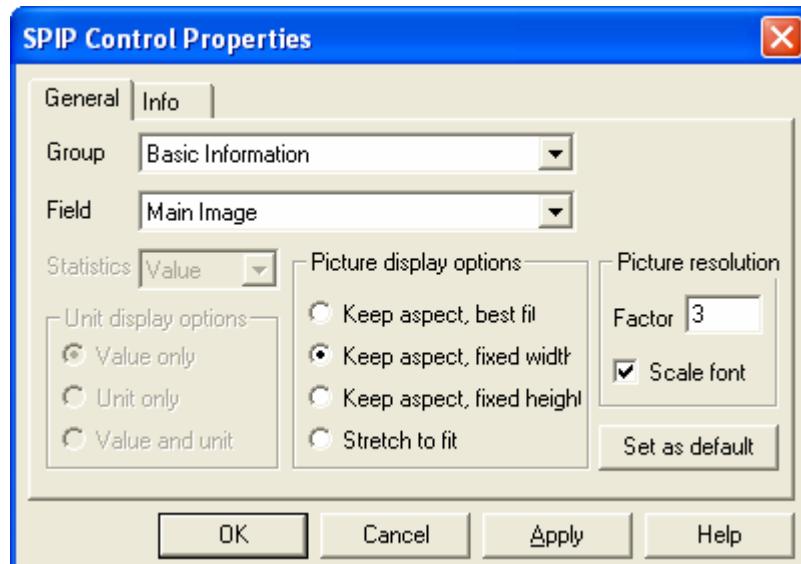
To view or modify the second template double click on it or select it and click the Settings button. This will give you the possibility to select another predefined template or to open the current template, click Open.



To modify the ActiveX controls defining the numbers and graphs to be included in the report make sure the Microsoft Word is in design mode. To enter the design mode you can do the following in the Word program:

Click Tools→Customize... and check the Control Toolbox on. In the Control Toolbox you will then be able to enter the design mode by clicking the Design Mode button.

You can now modify the ActiveX Controls by right clicking on "SPIP Control Object"→ Properties

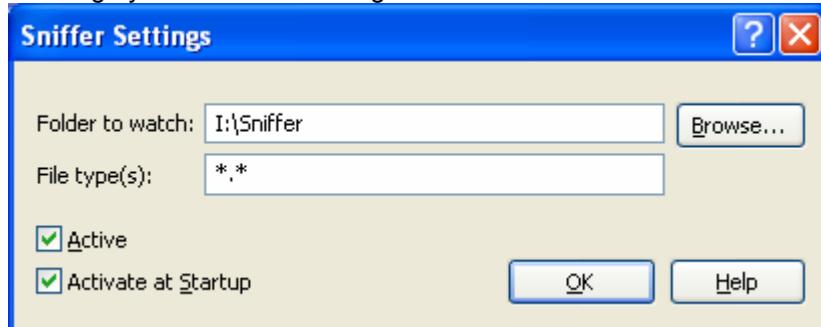


you will see that you can choose fields from the logically separated groups.  
You may also insert new SPIP controls by clicking on Insert→Object→SPIP Control.  
Remember to save the template before running the Batch Process.  
Set the Word ActiveReporter Mode to "Autogenerated filename".  
Now, select some files from the ImageMet Explorer or the Window Explorer and Drag-Drop them into the SPIP program. The batch sequence will be processed on each input file according to the description in the Word templates.  
To see the results click on the Open button in the word section.

## The Sniffer

The Sniffer is part of the Basic Module but gets most powerful when combined with the Batch Processor and the ActiveReporter. You can set the Sniffer up to open all new files put into a defined Sniffer Folder and if the Batch Processing dialog is open also to run the defined batch sequence.

Open the Sniffer Dialog by File→Sniffer Settings



Select the folder that you want SPIP to watch.

Click Active On.

Close the dialog.

Find some of your own images or those demo images delivered together with SPIP and copy them to the folder you just defined as being the Sniffer Folder.

You will now see the images appearing in SPIP and if you have the Batch Processor dialog open you will also see the images being processed.

If you have an instrument that can create image files on a network folder, which can be accessed by SPIP, try to define such a folder as the Sniffer Folder and let your instrument produce images to this folder. You are now able to monitor the data produced by the instrument remotely by SPIP and to process them automatically.

## **End of tour**

This was the end of the tour. There are still a lot of other advanced features to explore and we hope that you now feel inspired and encouraged to use SPIP on your own images!

## Data Windows

Different types of data windows may be created during a SPIP session:

- The Main Image window,
- 3D Image Window
- Fourier Image Window
- Zoom Image Window
- CITS Image Window
- Single Profile Window
- Multi Profile Window,
- IV-Curve Window
- Force Curve Window
- 1D Fourier Window,
- Histogram Window,
- Bearing curve (Abbott),
- Polar Plot Window,
- Grain detection window,
- Linearity Scatter Diagram Window
- Color Scale Editor

Except for the Color Scale Editor, all windows depend on real data. Some functions can only be calculated based on the main image, for example, Fourier transform, slope correction, lateral and vertical calibration, roughness calculation, and histogram calculation and averaging. For the other image windows, the functionality is limited to the zoom function, profiling and a few other operations. However, it is possible to transfer any image to the main image window by use of the right mouse key and utilize all the functionality of the main window.

The Fourier window has a lot of additional functionality that can be activated by use of the Fourier Menu.

### Windows pull-down menu

The Windows pull-down menu can control the organization of the windows:



#### Tile Automatically

The menu contains the option to auto tile the data windows whenever a new window is created so that all windows are visible and not overlapping.

#### Tiling Modes

The windows can be tile by the **Tile Best Fit** Method where SPIP tries to figure out how to use the space best as possible or in 1, 2, 3 or 4 columns. Or the number of columns can be fixed to 1, 2, 3 or four by the associated keys.

#### Closing Windows

When working with more images and performing different types of analysis the number of windows can grow so high that it can be difficult to navigate and find the specific windows, therefore SPIP has included convenient functions for closing specific groups of windows. For example **Close All Except Main** will close all SPIP client windows except the Main Window.

#### Windows Appearance

All windows can be resized simply by dragging a corner or border with the mouse. Image windows will be adjusted so that the x-y aspect ratio equals the aspect ratio of the physical dimensions for curve window the aspect ratio can be defined differently.

Note to achieve the best accuracy the raw image data is saved in floating point and the graphical output is calculated by interpolation and transferring raw image data into colors. Thus, the raw data is not affected by changing the window size or coloring.

#### Window Size Dialog

More precise control of the window size be controlled by the Window size dialog, which is activated from the Window pul down menu, **Window→Set Window Size...**



### Size

The size values reflect the size of the data window, excluding the borders and are identical to the size of the image which will be generated when copying to the clipboard or saving to bitmap formats. For images where the aspect ratio is given by the geometrical dimension the y-size parameter will be locked to the x-size parameter.

### Favorite Size

It is possible to define the entered size as the "Favorite size" for the given windows type by clicking the **Save** button. The favorite size may be used when tiling windows or can be activated by the **Recall** button or the **Window→Favorite Size** menu item.

It is possible to define independent favorite sizes for 1D, 2D and 3D data Windows.

### Apply when Tiling

When setting "Apply when Tiling" is set the windows will be tiled such that their size will match the defined favorite sizes. In case of many windows it might be necessary to find the windows by use of the scroll bar. When this option is not set the windows tiling function will try to adjust the size of the individual windows such that all windows can be seen at the same time.

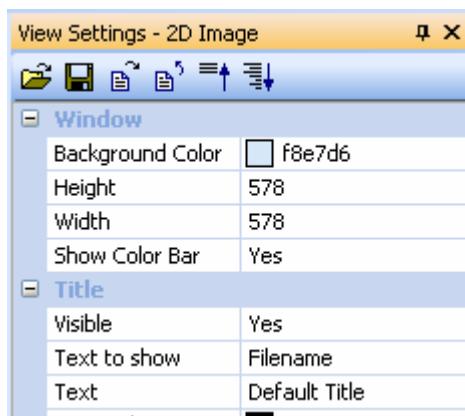
### Tile Now

To see the result of changed favorite settings click the "Tile Now" button.

## View Settings Pane

All data windows, except the color bar window, are sharing the View Settings Pane, which allow you to modify the appearance of the windows.

The content of the pane will always reflect the active data window and when altering the changes will be reflected in the data window simultaneously. By default the view pane will be shown "docked" to the right SPIP frame, but it can also be shown "floating" or docked to the left SPIP frame.



The View Settings Pane can be activated from the right click menu of the data windows or from the View pull down menu.

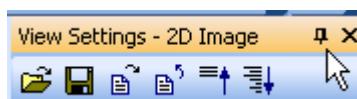
### Changing the size and position of the View Settings Pane.

To move a docked pane into a "floating" window put the cursor in the caption area and drag it to the desired position. This window is fully resizable

To dock a floating pane, move its window to the left or right frame of SPIP, such that the mouse cursor is on the SPIP frame. The width of docked panes is resizable.

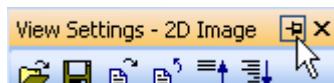
### Auto Hiding Panes

All window panes can be auto hidden by left-clicking on the push-pin button in the upper right hand corner of the pane:



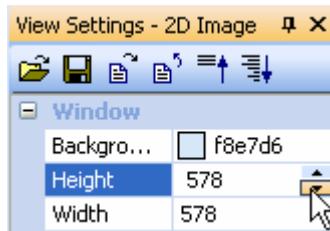
When auto hided, the pane will appear again just by moving the mouse into the edge where the pane is hidden.

To turn off the auto hiding mode click on the horizontal push-pin button



### Modifying settings parameters

To modify a parameter, select the parameter of interest and enter a new value. You may also use the arrow buttons which appears automatically when applicable. Likewise toggle fields can be changed by pressing the space bar or the up down arrow keys on the keyboard.



### Saving and loading Settings

To load and save settings click the associated load and save buttons:



To recall default settings, which are applied when a new data window is created, click the "Reset to Default" button: .

To define the current settings as default click the "Set as Default" button: .

The saved settings will only define the settings for the active windows type, such that settings for profile windows are independent from, e.g., image windows.

### Collapsing and Expanding Settings Groups

The setting parameters are grouped into logical groups, which can be individually collapsed or expanded by clicking on the associated buttons.

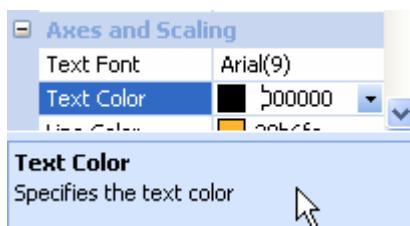


To collapse or expand all groups click on the association tool keys in top of the pane:



### Help Field

At the bottom of the pane there is a Help Field explaining the function of the selected parameter. The help section is resizable.



## Toolbars and Menus Customization

You may take advantage of the menu customization tool to improve your productivity and convenience by putting your most frequently used commands into toolbars and defining shortcut keys.

The layout and content of the menus and toolbars depends on which modules that are covered by your license and how you may have customized it.

Below is an example on how the menu bar with toolbars may appear:



The tool buttons are grouped logically into toolbars, which can be repositioned or docked to the four borders of the program window or shown floating in their own window. You may add or remove other menu items to the toolbars.

Below are the possible toolbars shown as they may appear as floating toolbars.

File Toolbar



Color Toolbar



Markers Toolbar



Transformation Toolbar



Correction Toolbar



Calibration and Enhancement Toolbar



Analysis Toolbar

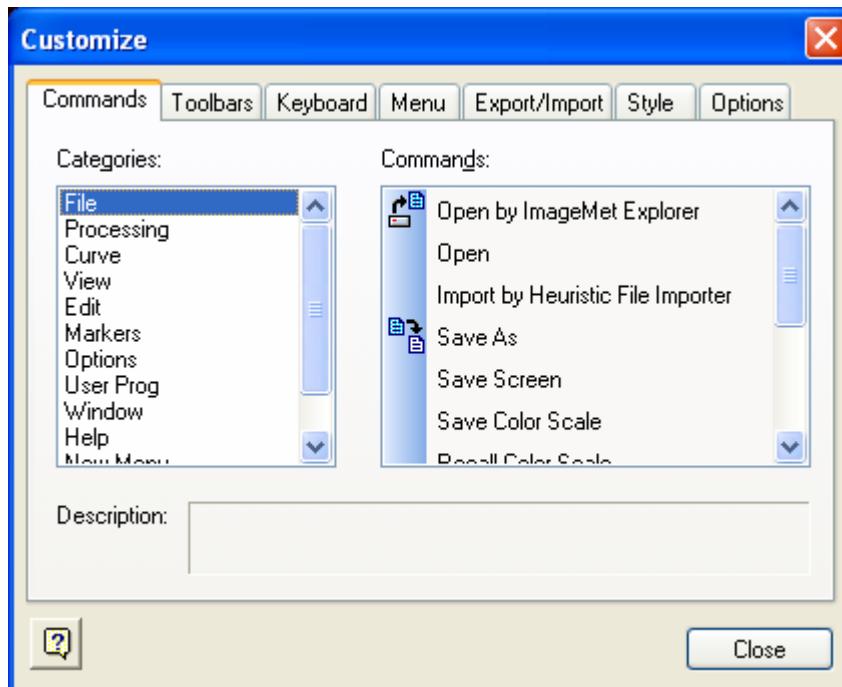




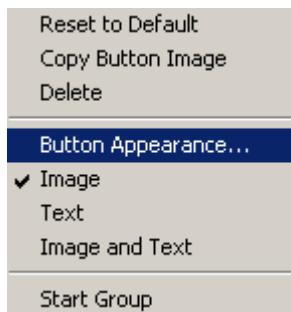
By right clicking on one of the tool bars you can turn the individual toolbars on/off:



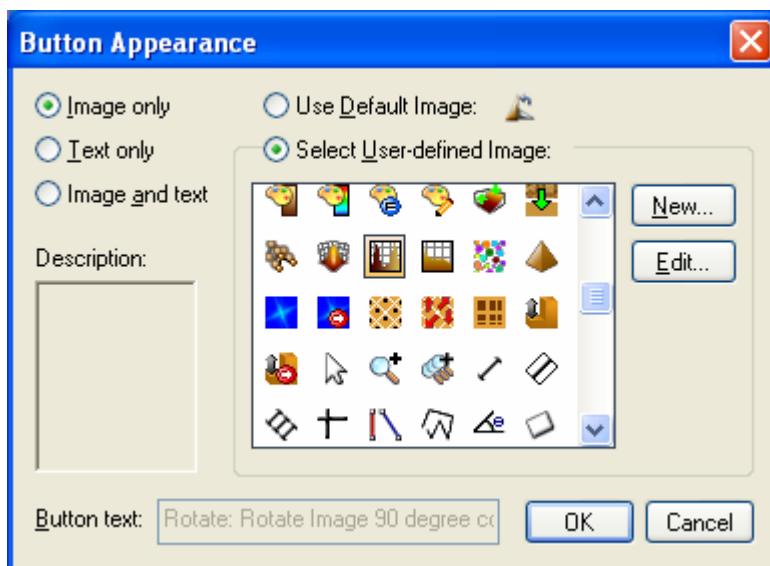
The toolbars and menus can be customized further by clicking on the **Options→ Customize...** command, or the right clicking on the menu bar and selecting **Customize..** :



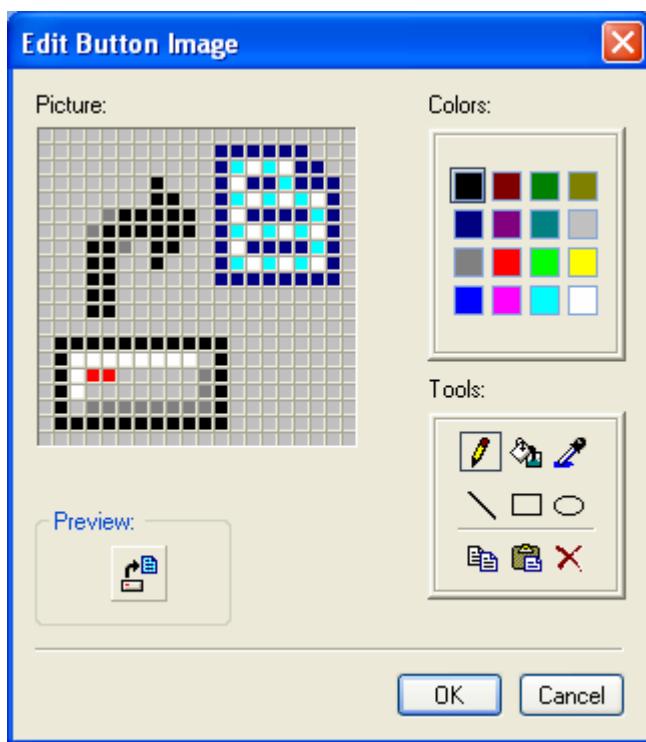
While the Customize dialog is active you are in a mode where you can modify the menus and tool bars. To organize one of the categories in the main menu bar select the category and the menu item you want to reorganize then drag-drop it into the desired location. You may also modify the appearance of any menu item by right clicking on it in the main window:



Clicking on the "Button Appearance" will activate the Appearance dialog from which you can define the text and/or the image by which the menu item will appear.



You can design or modify an existing button image by selecting "Image Only" or "Image and text" and click on the **New...** or the **Edit...** buttons, which will activate the Edit Button Image dialog:



**Example 1: Creating a tool button for the Print Screen:**

Suppose you are using the **Print Screen** command frequently. Then it will be convenient to have the command to appear in the **File** tool bar always at hand.

Right click on the menu bar and select "**Customize...**"

In the Customize dialog select "**File**" as Category in the left pane, then select "**Print Screen**" in the right pane

Drag-drop the "**Print Screen**" command into the File toolbar.

If this is the first time you define an image for the Print Screen command the "Button Appearance" dialog will be launched automatically otherwise to modify the appearance of the command and assign a button image, right click on the new "Print Screen" toolbar button and select "**Button Appearance...**".

In the Button Appearance dialog select **Image only** or **Image and text**.

To have a starting image to work on select the Printer image and press the **Edit**.

In the **Edit Button Image** dialog click on the "**Copy**" button to bring the image to the clipboard and click the Cancel button. Alternatively the buttons can be copied by right clicking on a button and selecting "**Copy Button Image**" before step 4. above.

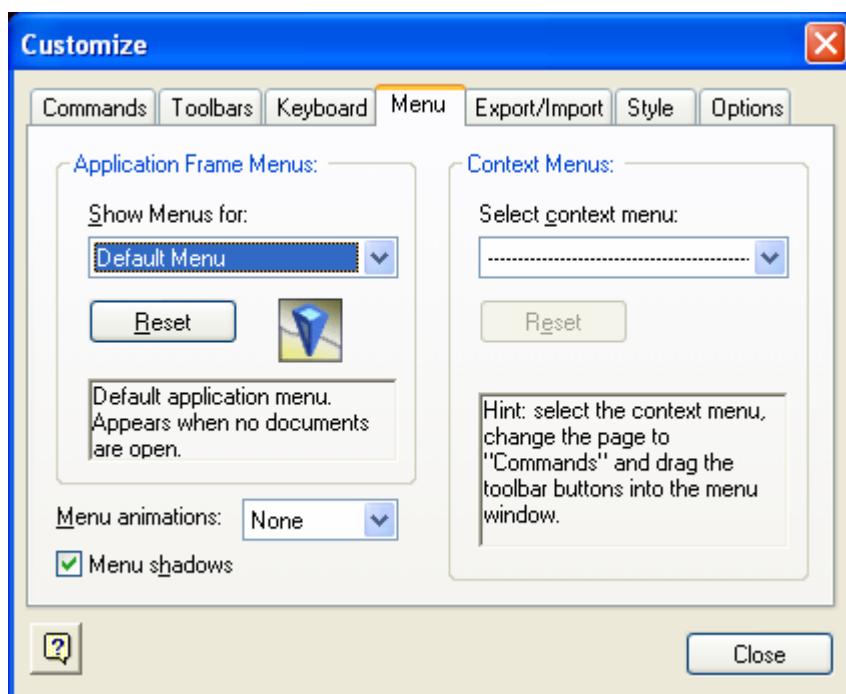
Click **Cancel**

Click the **New...** button in the **Button Appearance...** dialog.

Click the **Paste** button

You may now modify the image by the drawing tools and click the **OK** button when finished

The context menus (i.e. the menus which appear when right clicking in the data windows) and their items can be organized similar to the main menu. First select the **Menu** tab of the Customize dialog:



To organize a specific context menu first select the context menu. This will create a new window with the context menu and you will be able to reposition the menu items or bring the menu items into one of the toolbars by drag-dropping.

It is also possible to copy menu items from the main menu bar by activating the **Commands** tab, selecting one of the Categories and drag-dropping commands or tool button to the context menu window. To copy context menu items to the main menu activate the desired category in the menu bar and drag-drop the menu item into place.

**Example 2: Creating a tool button for the Curve Aspect Ratio commands:**

Suppose you are frequently switching the aspect ratio of curves between the **1:1** aspect ratio and the "**Match Window**" mode. Then it will be convenient to have these commands always at hand in one of the toolbars, which can be achieved by the following procedure:

Right click on the menu bar and select "**Customize...**"

In the Customize dialog select the **Menu** tab

Select the Curve context menu

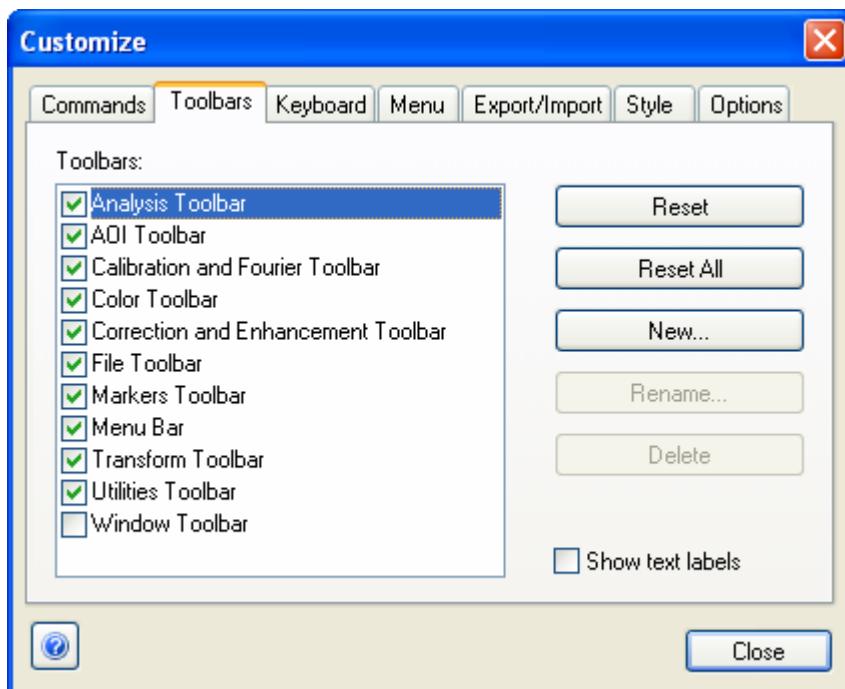
In the Curve context menu window select Aspect Ratio→1:1

Drag-drop it into the desired toolbar.

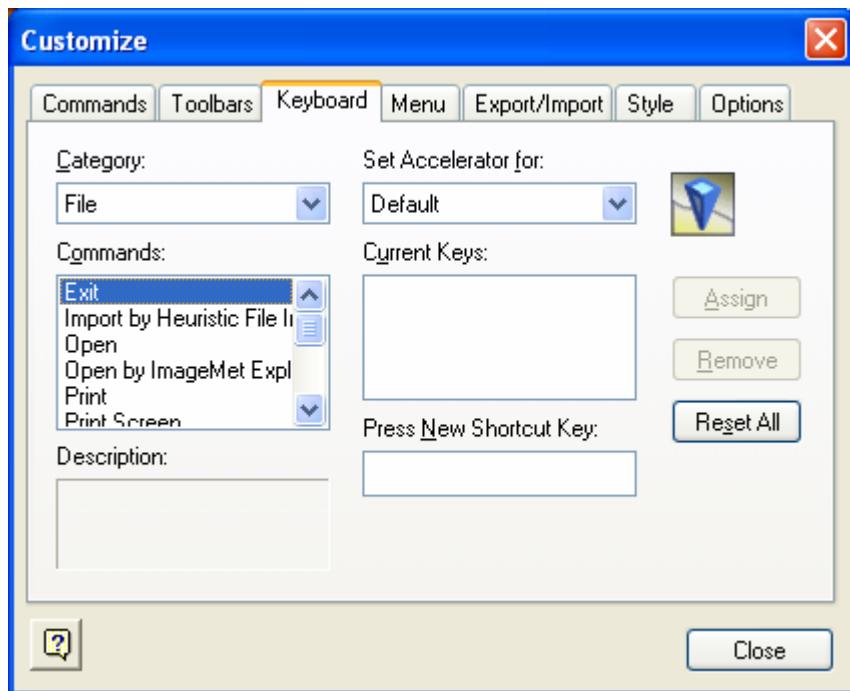
Repeat step 4 and 5 for the **Aspect Ratio→Match Window** command

To modify the appearance of the new toolbar items right click on the items and select **Button Appearance** and proceed as described in Example 1, step 5-10

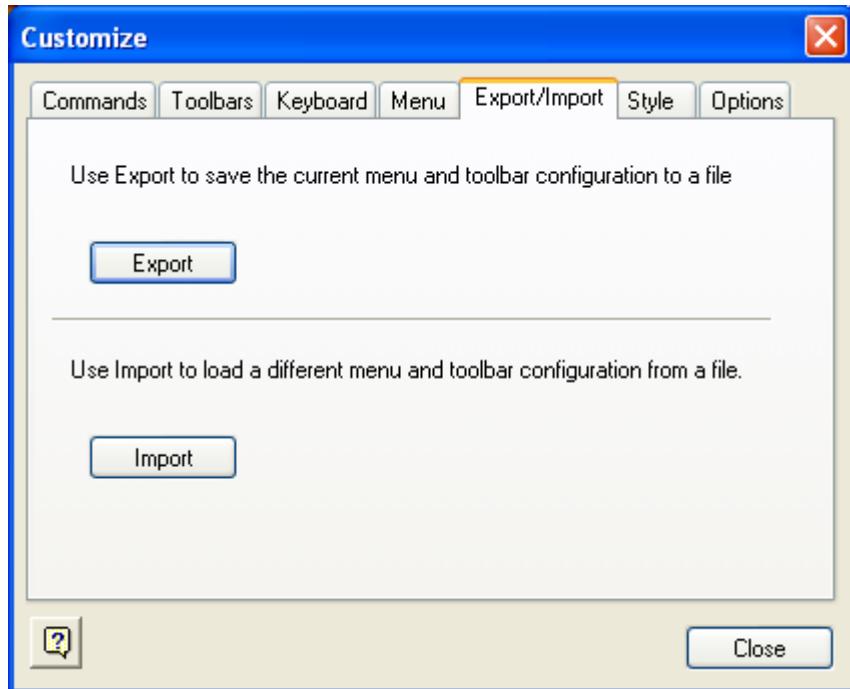
In the **Toolbars** tab you have the possibility to create new tool bars, rename the existing and turn the individual toolbars on/off. Here you can also define that you want the name of the tool buttons shown together with their icon, by clicking on the "**Show text labels**" check box.



In the **Keyboard** tab Shortcut keys can be assigned to the individual commands.



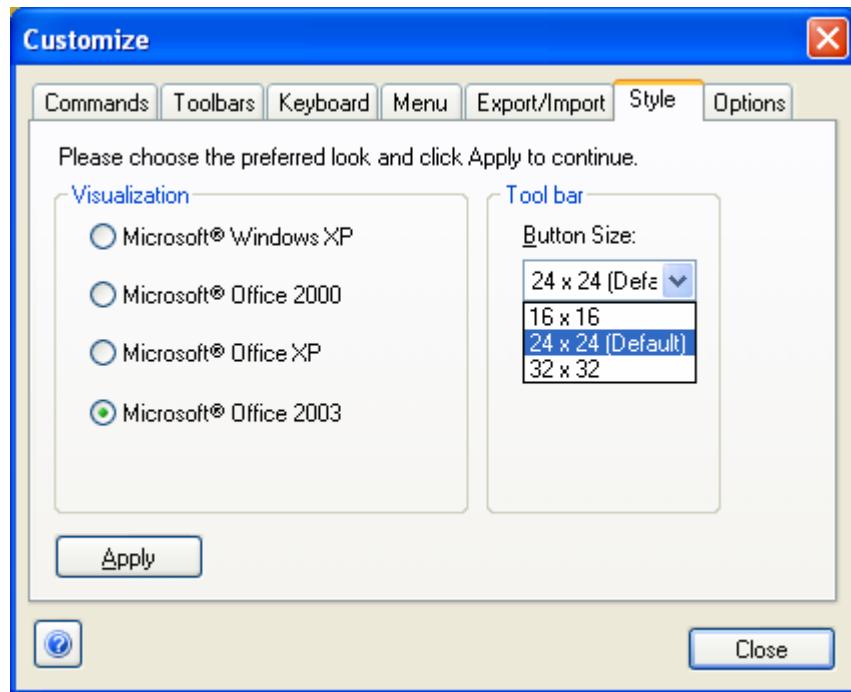
From the **Export/Import** tab you can export the current toolbar and menu configuration to file and import previously exported configurations. You may use these function as a backup tool or storing configuration adapted to specific applications. If you are setting are managing more systems these function will make it easy for you to have all systems to appear in the same way.



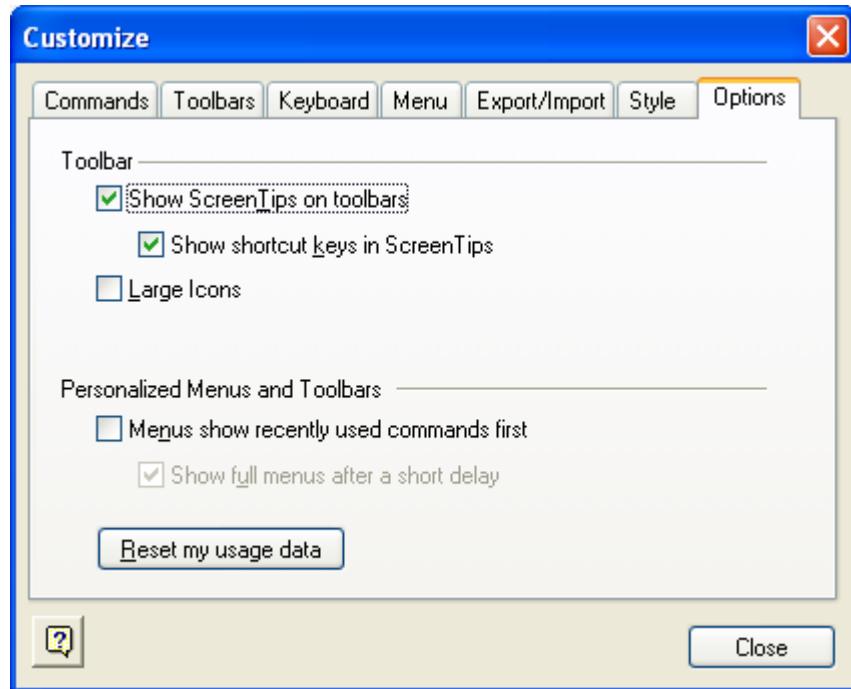
The **Style** tab enables you to choose between three different appearance styles:

- Microsoft® Windows XP
- Microsoft® Office 2000
- Microsoft® Office XP

- Microsoft® Office 2003



In the **Options** tab you can select a number of appearance options:



**Show Tool Tips on toolbars:** When set you will see tool tips for while the mouse is positioned over a tool button.

**Show shortcut keys together with tool tips.** This is a good idea if you want to learn the shortcut keys.

**Large Icons.** This will increase the size of the icons.

**Menus show recently used commands first.** When set it will be easier to find the commands you are using most frequently.

**Show full menus after a short delay.**

Clicking on the "**Reset my usage date**" will reset the history recording determining the menu appearance when "**Menus show recently used commands first**" is set.

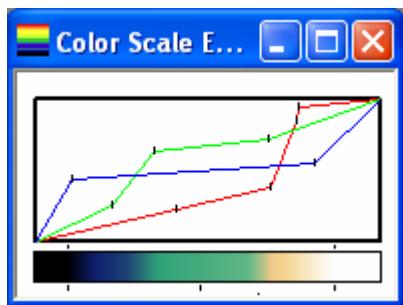
## Colors

SPIP contains tools for designing your own color scales select among predefined color scales that determines how the image data are visualized.

The tool bar contains color tools keys associated with specific color scaled the first refers to a user definable default scale while the next four refers to SPIP defined color scales. The last button is used for color equalization using all colors equally and thereby providing a better contrast for the weaker image details, see color equalization example below

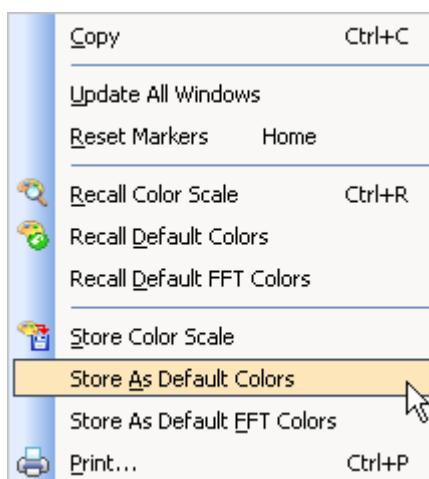


You can edit the color scale easily by the Color Editor window. The window contains three curves: red, green and blue. The colors of the color bar in the lower part of the window are determined by the y-values of the red, green and blue curves. The resulting colors will be a mixture of the relative RGB values.



The curves contain *nails*, which the curves are forced to follow. The mouse can move the nails and new nails can be defined. Between the nails, the curves are linear. On a mouse click, the curve closest to the click point will get a new nail at the click point.

You can store the color scale by clicking with the right mouse button and selecting the **Store Color Scale** command and retrieve other color scales by selecting the **Recall Color Scale** command.



 It is possible to define a default startup color scale by storing the color scale into the **Default.col** file associated with the first color bar tool key. Likewise it is possible to store a default color bar for the Fourier images in the **DefaultFFT.col** file.

When no *Default.col* file exists the Brown Color scale is applied at startup and for Fourier images the High Contrast scale will be used.

By default each image has its own color scale that can be changed independently from the open image windows. You may for example want to use high contrast colors for the Fourier image and the more smooth brown color scale for normal images. However, all images can be set to share the same color bar by right clicking on "**Update All Windows**". The default color scale for the Fourier image window can be stored in the **DefaultFFT.col** file.

### Contrast Enhancement by Colorbar Markers

The color bar at the bottom works together with the color bars of the images. It is possible to move the lower left marker of the color bar to the right and thereby turn all the lower colors to the minimum color (usually black). This will give a higher contrast for the middle height values. Likewise, the right end of the color bar can be moved to the left, when clicking on the right side of the color bar. Positioning the mouse pointer in the middle part of the bar can move the entire color bar.

The same procedure can also be performed on the color bars of the images where the mouse sensitive parts of the color bar are indicated by triangles. The left set of markers on the color bar is used for contrast enhancement while the right marker set is used for defining threshold values without altering the contrast. The threshold setting is used in connection with more tools e.g. Grain Analysis, Fourier Filtering and Spike Removal.

Because the modification of the color bar is reflected simultaneously in the Main Image and the Fourier image you can use the color bar as a WYSIWYG interface to the definition of threshold values for Grain analysis, Fourier filtering and Outlier Filtering. By setting the **Update All Windows** in the right mouse menu the other 2D Windows will adapt the changes as well.

For the 3D visualization studio the colors will follow the Color Editor for the default settings.

### Automated Contrast Enhancement by Quantiles

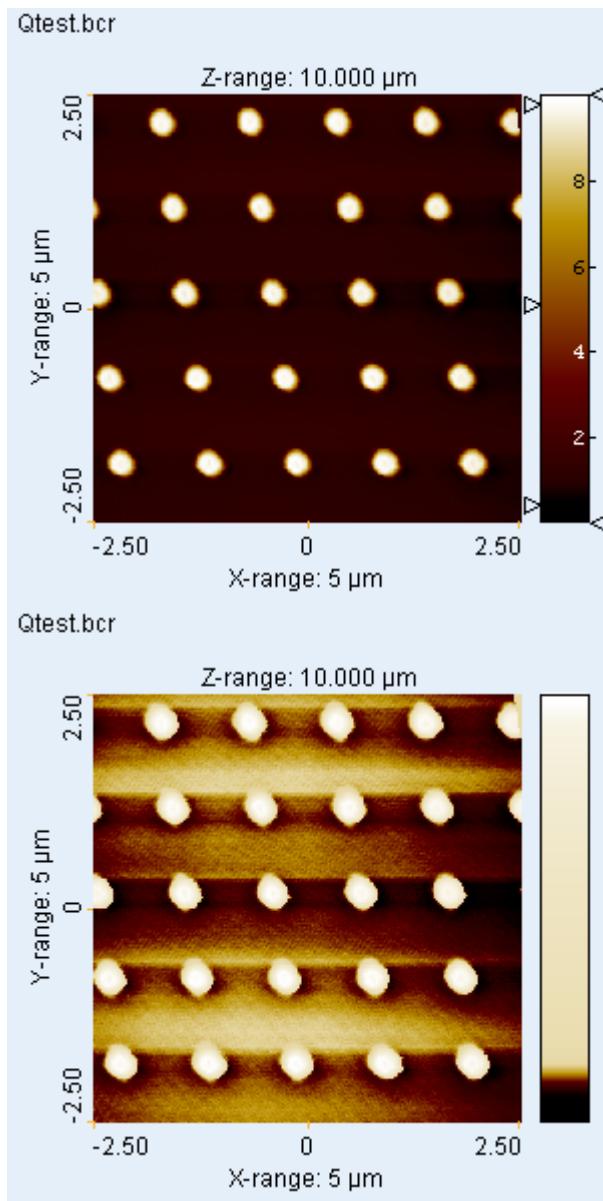
The colors of an image can be scaled automatically by defining upper and lower quantiles for the associated height range; this is done in the Image Property Dialog. By defining the lower quantile to e.g. 1.0% the lowest 1% of the pixels will determine the position of the lower left color marker in the color bar of the image. Likewise by defining an upper quantile of e.g. 98% the upper left color marker will be set to the 98% quantile so that the highest 2% of the pixels will not influence the contrast.

Color scaling by quantiles is a strong technique for achieving a good contrast in images having relative few pixels with extreme values, e.g. noise or contamination on a flat substrate.

### Color Equalization

The Color Equalization mode of an image is toggled by the corresponding tool button, right-clicking **Color Equalize** in the image window or just by pressing **Q**.

Because the color bar by default covers all the height valued of and image the contrast can be weakened by and outlier values causing small features to be invisible. In such cases it can be very useful to apply *Color Equalization*, which will cause all the different colors to be distributed equally. This will have the effect that the contrast of the small corrugations will improve dramatically, see example below:



It is also a strong tool for evaluation of small plane distortions and plane correction. The disadvantage is that the transformation is highly nonlinear and does not provide the correct feeling for the height differences.

## Markers

SPIP has different marker shapes that can be used for marking specific areas of interest in the images and there are specific functions associated with the markers. The markers can be selected from the markers menu or the toolbar marker buttons:



The **Line Marker** can be applied to all 2D image windows and will generate a profile curve of the corresponding cross section. On a mouse click, the line end closest to the click point will be move to the click point. However, if the click point is closer to the center of the line it follows the mouse pointer while keeping its length and orientation.

In some situations it can be convenient the move the line 1 pixel at a time by the arrow keys. The corresponding profile window will be updated simultaneously when changing the cross section line. To make straight horizontal or vertical line you can conveniently combine the mouse movement with the 'X' or 'Y' keys.

The Average Profile marker enables you to average parallel profiles with in the marked oblique. Thus, it is useful for reducing noise and obtaining more accurate measurements

When Synchronized Multi Profiling in the markers pull-down menu is set it is possible to create a profile for each image window having images of identical size and update them dynamically while moving or resizing the Line Marker in one of the image windows.

You can obtain a cross-section profile along a poly line by use of the Poly-line marker tool; see Advanced Profiling for more information.

By use of the Cross Hair marker you can obtain horizontal and vertical cross-section profiles simultaneously.

The **Zoom Box** also called the **Rectangle Marker** is used for marking zoom areas and activation of the zoom function. Furthermore, in the Fourier image the rectangle will mark an *Area of Interest*, which can be modified by the Fourier tools in the Fourier Menu. The rectangle has nine reference points that can be changed by the mouse: The four corners, the center of the four sides, and the center of the rectangle. On a mouse click, the reference point closest to click point will be activated. If the center point is activated the rectangle will be moved while keeping its size.

You can also move the box by the arrow keys while monitoring the zoom window. By use of the arrow keys, it is often easier to control the exact position of the zoom box.

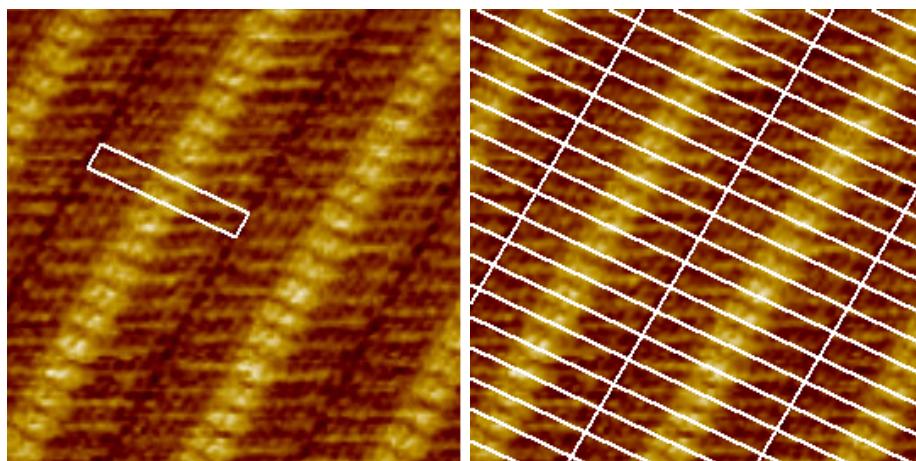
### Synchronized Multi Zoom

When dealing with image for the same physical area but showing different properties, for example height, friction, cantilever amplitude, phase, capacitance, magnetic force, etc. it can be very practical to display zoom ins of the different images at the exact same area. This can be achieved enabling Synchronized Multi Zoom in the Markers pull-down menu. When active, a zoom image for each image window having images of identical size is dynamically updated while moving or resizing the Rectangle Marker in one of the image windows.

The **Oblique Marker** is used to indicate the calculated lattice from unit cell detection and is default activated after unit cell detection. It has three modes, which is changed by the oblique marker tool:

- **Off**,
- **Single Unit Cell** mode where only a single unit cell is shown as seen below, -

- **Full Grid** with the entire lattice is indicated together and if calculated also together with the linearity dislocation arrows.

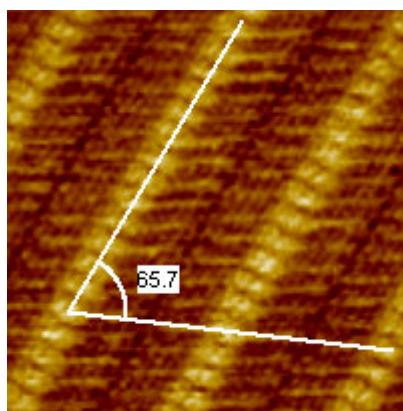


The mouse or the arrow keys can move the shape so that it can be compared with the image structure. Alternative unit cells can be defined by the Advanced Fourier Menu.

When the **oblique marker** is active in the **Fourier** image it is used for marking areas of interest (AOI), - typically an array of Fourier peaks, not parallel to the horizontal or vertical axes. The corners of the parallelogram are defined by mouse clicks: The first mouse click defines the first corner, the following mouse release determines the second corner and on the second mouse click/release the third and fourth corner are defined.

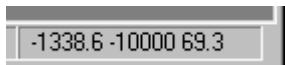
The **Circle Marker** is also dedicated to the Fourier window and additionally to the marking of AOI-s it can initiate the detection of a Fourier peak in the marked circle. In the Fourier Menu you can set the circle function to define **Peak 1** or **Peak 2** or **None**. For at defined peak the corresponding x, y and z co-ordinates will be written as well as the corresponding wavelength in nanometer and time frequency in Hz. The latter is useful for detecting electrical noise or environmental vibration. When both peaks are defined they will together with the origin, be regarded as corners in the reciprocal unit cell and the corresponding spatial unit cell will be calculated and displayed in the Fourier Menu.

The **Angle Measurement Tool Marker** is used for measuring angles. The shape and thereby the angle can be changed with the mouse by moving the end positions of the tool marker. The corresponding angle will be written on the screen simultaneously:



#### Mouse Position Indicator

When the Mouse Pointer is in a 2D spatial image window, the physical X, Y, Z co-ordinates of that point will be shown in the lower right corner of the SPIP program window:



The unit of the co-ordinates will be the same as for the Actual image. Note that the X, Y co-ordinates may be negative because they are reflecting the physical co-ordinate system of the image generator. For image files not containing information about the physical co-ordinate system the center of the image is set to (X=0, Y=0)

For the Fourier image, the Mouse Pointer will cause the lower right status field to show the wavelength and the amplitude/magnitude of the Fourier component pointed to by the Mouse Pointer:



This indication is useful for wavelength estimation associated with certain Fourier components. In combination with the Circle marker the cutoff frequency for low-pass, high-pass and band-pass filters can be defined. For more advanced Fourier filtering see Advanced Fourier Filtering

## Area of Interest Tools

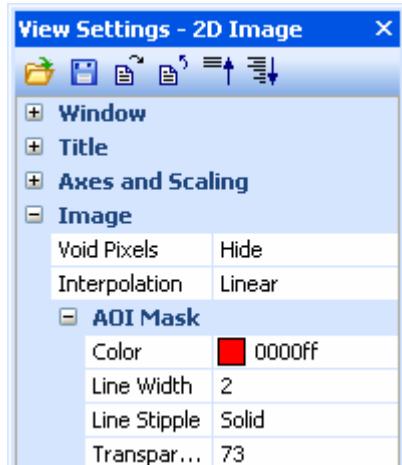
### Area of Interest Marking Tools

The Area of Interest (AOI) drawing tools are used for including or excluding certain areas from analysis and modification, or to define pixels as void pixels. The AOI Toolbar is shown below:

- ▣ This tool key toggles between include and exclude mode. In the include mode the area inside the drawn shapes are included while the exterior is excluded. The excluded area will be shown in a slightly modified colors defined by the AOI View Settings. Selected AOI shapes can be toggled between include and exclude mode by clicking this tool key.
  - ▣ The Rectangular AOI tool key is used for drawing rectangular shapes. To create at quadratic shapes keep the Shift key down while drawing.
  - ▣ The Elliptical AOI tool key is used for drawing elliptical shapes. To create circular shapes keep the Shift key down while drawing.
  - ▣ The Polygon AOI tool key is used for drawing any shape in free hand. The drawing is performed by clicking the mouse at desired points or just by moving the mouse while keeping the left mouse key down. The drawing will finish when clicking the right mouse button.
  - ☒ You can use the Clear All AOIs button to clear all defined AOI shapes at once or delete individual AOI shapes using the Delete key.
- ☞ To select a drawn AOI shape click the Selection tool key and the click on the desired AOI shape. To select close together or overlapping AOI shapes it may be practical to use the Tab button to select the individual shapes

### AOI View Settings

You can modify the appearance of the AOI and the excluded region from the view settings connected to the image window. The settings are seen in the Image section:



You may modify the color, line width, Line style and transparency of the excluded area and define your own default style.

### AOI Context Menu

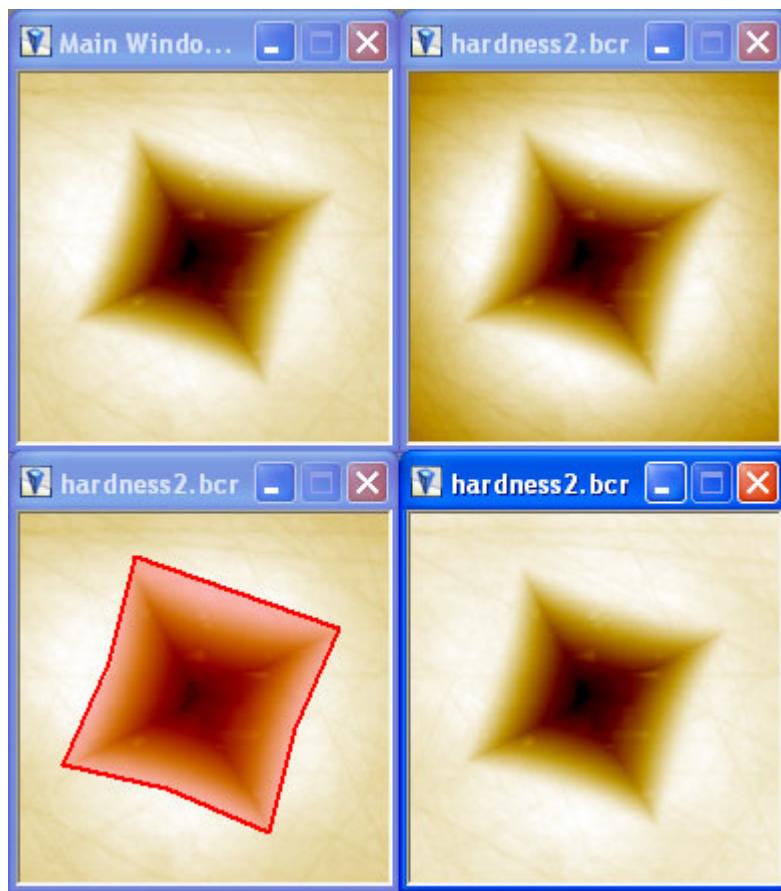
The context menu of AOI shapes can in addition to the previously described functions be used for defining AOI's as being Void Pixels in such case these pixels will not be included in roughness analysis or plane correction even when the AOI shapes has been removed. Likewise void pixels may be set to appear invisible in 2D and 3D images.

## AOI Application Examples

In the following are a number of examples on how the AOI facilities can be applied it does not cover all possibilities but the intention is to give inspiration to the use of the AOI facilities.

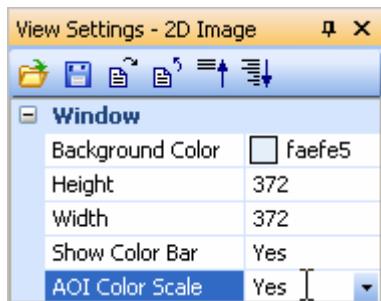
### Plane Correction

When performing plane correction you might want to eliminate certain areas from influencing the result. This may for example be the case for surfaces dominated by indentations or particles. The following case demonstrates how the plane correction can be improved by rejecting an indentation area from the AOI. Top left is seen the original image and to the right is show the plane corrected image performed by subtracting a 3<sup>rd</sup> order polynomial fit the entire image. It is seen that the plane correction has created an undesired bow at the top surface because the algorithm tries to fit a function that applies also to the indentation. Below is seen the result when excluding the indentation from the AOI and it is seen that the top layer now is much flatter. Note, that when using the Quality Optimized option in the Plane Correction dialog SPIP™ will automatically exclude the indentation area when fitting a surface function.

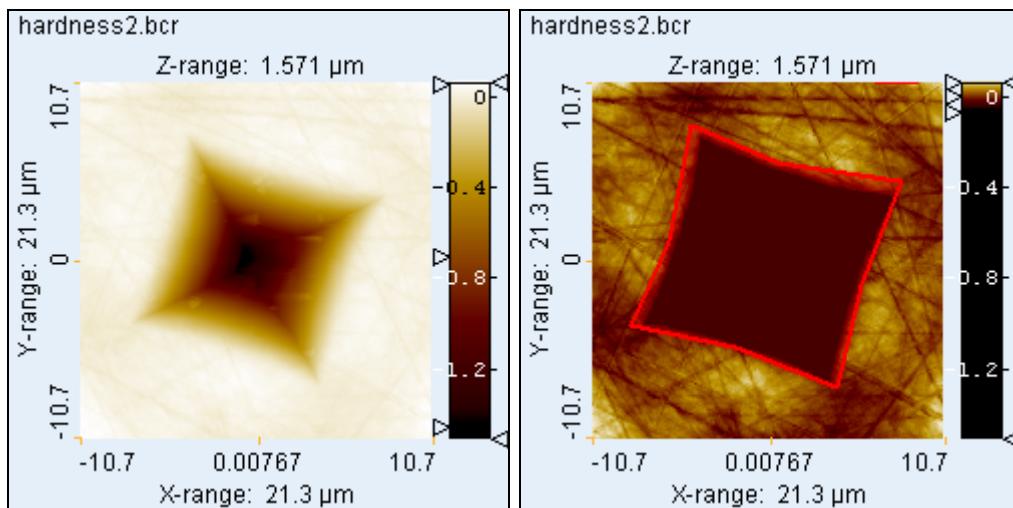


### AOI Color Adaptation

To achieve the best color contrast with a certain area of an image you can set the "AOI Color Scale" setting on in the view setting. When changing the AOI the colors will automatically adopt the new area. You may move the AOI with the mouse or arrow keys and this way find it as useful inspection tool.



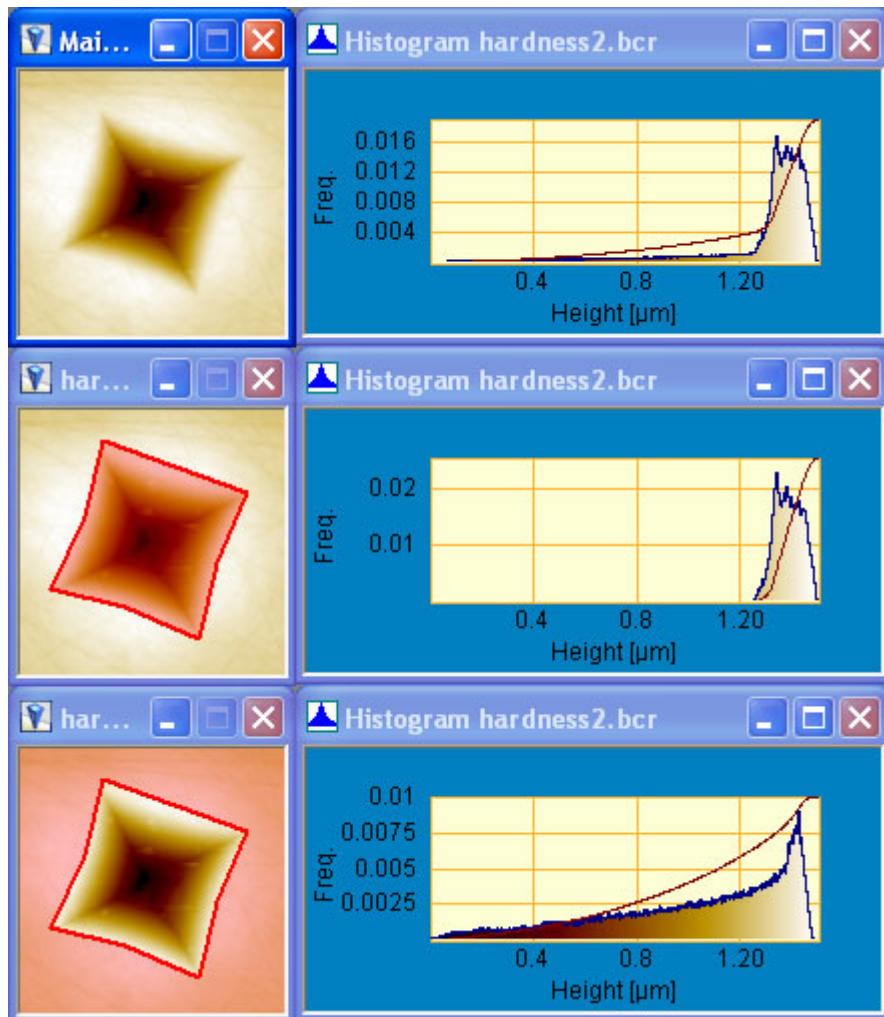
Below is seen the same image shown without and with AOI color adaptation. In the right image the indentation area is excluded from the AOI so that the color range matches to top level.



#### Histogram Analysis inside AOI

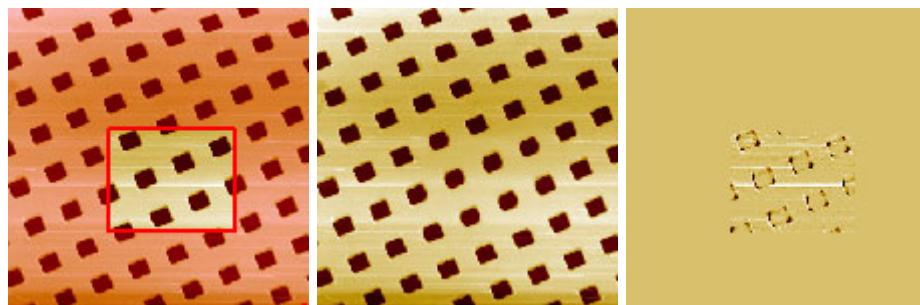
The height distribution may be very different within different area of an image and you can use the AOI tool to investigate the local height distribution. You only need to activate the histogram window and the histogram will always reflect the defined AOI.

The three pair of images below illustrates how the histogram reflects the defined AOI.



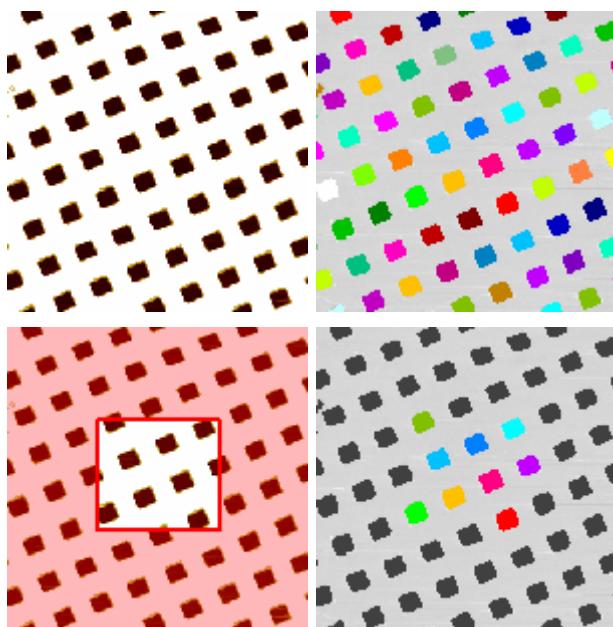
### Spatial Filtering inside AOI

If you want restrict filtering to a specific area you can do this by defining an AOI. The below example shows the result (middle image) of a median filter performed only within the AOI. The most right image is the difference image between the original and the filter result image.



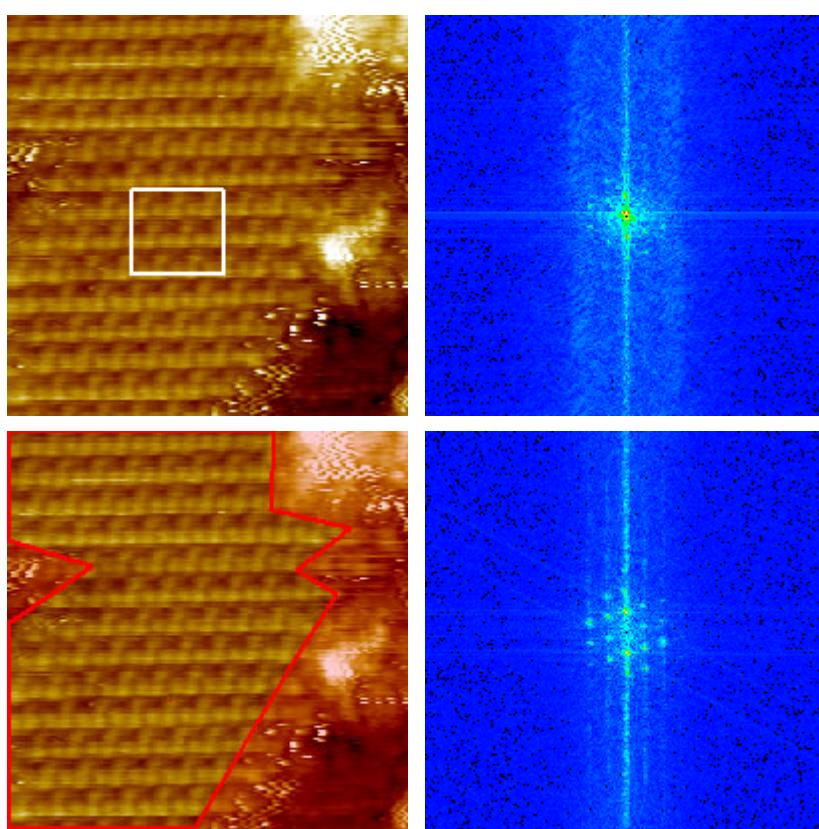
### Grain Analysis inside AOI

Grain Analysis can also be restricted to a defined AOI as shown below, where the top image pair shows the result without use of AOI and the bottom pair the results with a defined AOI.



#### Fourier Analysis inside AOI

Sometime distortions or contamination in an image may complicate Fourier analysis and make it difficult to find and characterize the Fourier peaks associated with at lattice structure. The below example shows how the Fourier peaks are much more apparent when eliminating the distorted area from the Fourier analysis by excluding it outside the AOI.



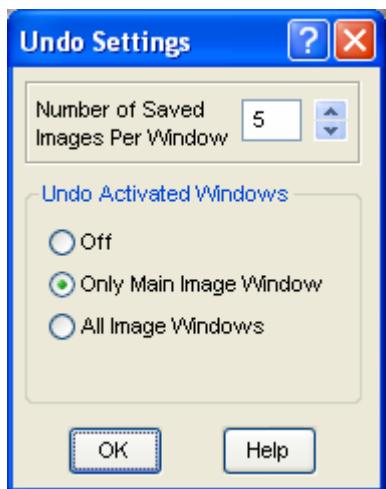
### **AOI in General**

In addition to the above examples you may use it in most analysis and correction function such as:

- Linearity Analysis
- Cross Correlation
- Correlation Averaging
- Auto Correlation
- Image Alignment
- Fourier Filtering
- Roughness Analysis

## Undo

Each of the image windows can remember up to 9 of the previous images, so than undoing undesired processes is possible. To define the Undo settings click on **Undo Settings** of the **Edit** pull-down menu:



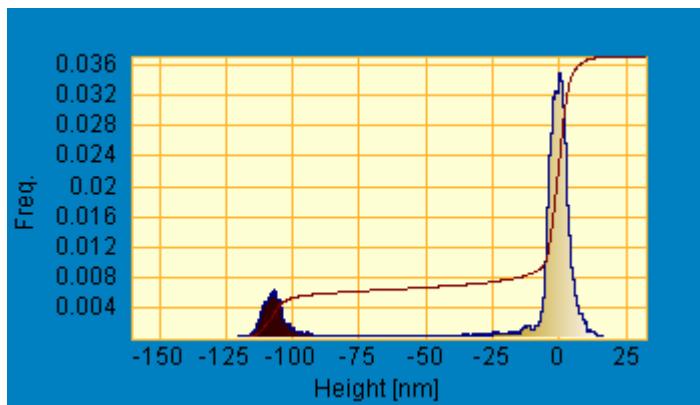
By selecting the number of images to be saved per image you can find the right compromise between memory consumption and the ability to go many steps back.

The Radio buttons determine if the Undo function should be Off, Only active for the Main Image Window or all images.

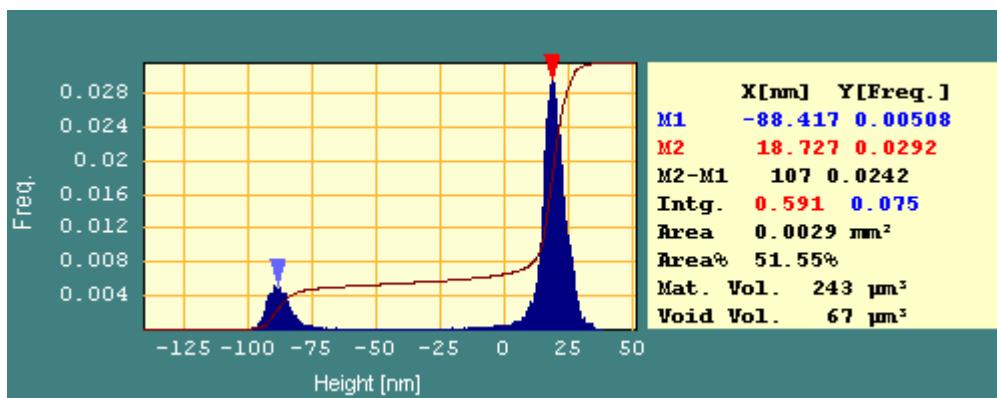
When active, functions can be undone by **Edit**→**Undo** or **Ctrl+Z** and redone again by **Edit**→**Redo** or **Ctrl+Y**.

## Histogram

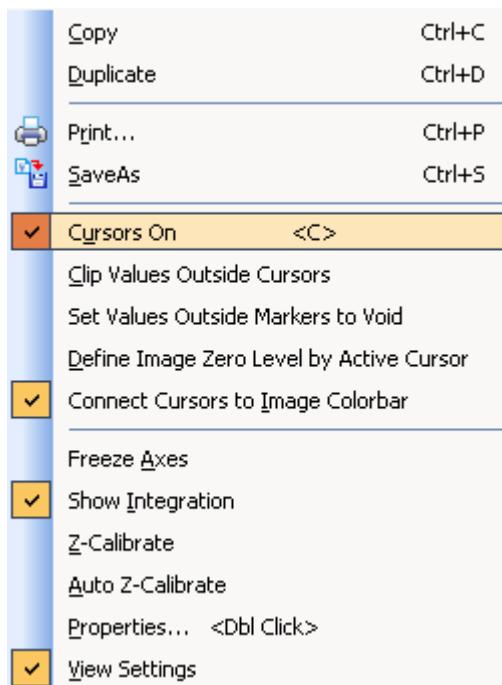
 The height distribution histogram window is activated by the histogram tool button or from the **Processing→Histogram** menu item.



The histogram is an important analytical tool that provides important information about the height distribution and serves as an important tool for the Z-calibration algorithm. It is a good idea to monitor the histogram while performing slope correction because the histogram is the best indicator for the flatness of the surface. Plane surfaces are characterized by high and narrow histogram peaks.



The context menu (right click) contains more functions dedicated to histogram analysis:



### Cursors On

To activate the cursors right click on **Cursors On**, use the View Pane, or just press "C" on the keyboard. When pressed repeatable the number of cursor pairs will shift between 0, 1, and 2.

The cursors can be moved by mouse and for precise positioning by the arrow keys. The Up/Down arrow keys will move the cursor in the direction of a local summit, which is useful for finding local minimum or maximum points. When a cursor is positioned on a slope, it will be indicated by a tilt of the cursor. Summits are indicated by the cursors pointing straight downwards.

Based on the cursor positions you can also determine the area and volume for the range between the markers. There are provided two volume numbers Material Volume (**Mat. Vol.**) and Void Volume (**Void Vol.**). All height values below the surface is considered as material while height values above the surface are considered as void. Thus it is possible to calculate the volumes between the height values given by the markers.

### Clip Values Outside Markers

It is possible to use the blue and red markers for defining the lower and upper clipping values of the image. To perform the clipping right click and select **Clip Values Outside Markers**.

### Set Values Outside Markers to Void

To define the pixel values outside the z-range given by the markers as void pixels click on **Set Values Outside Markers to Void**. This function will also define pixels inside the z-range if they are located on a slope between the two z-values and has shown to be useful in grain analysis for separating particles at different levels.

### Define Image Zero Level by Active Cursor

This function will level the entire image so that height value given by the active cursor will be set to zero. In combination with grain analysis where it is desirable to report z-values relative to a certain surface height you may take advantage of this function, because you may then use the absolute values directly.

### Freeze Axes

Right click on **Freeze Axes** to keep the X and Y scaling fixed. This is very practical when comparing histograms from different images on the same scale. You might for comparison purposes also want to save a duplicate by pressing **Ctrl+D**.

To define the scaling more specifically enter the property menu, by right clicking on **Properties** or double clicking

#### **Show Integration**

Right click on Show Integration so display the Integration curve of the histogram. The difference between the integration values at the cursor positions reflect the relative surface area having height values between those marked with the cursor pair and will be indicated in the **Area%** numerical field.

#### **Z-Calibrate** (Requires the Calibration Module to be included in the license)

Right click on **Z-Calibrate** to perform a step height measurement and calibration, see Z-calibration for further details.

#### **Auto Z-Calibrate**

Right click on **Auto Z-Calibrate** to automate Z-Calibration measurements whenever the histogram is changed. This is for example practical when the histogram is linked to a profile of an image, in which case both the profile, the histogram and the Z-Calibration result is updated when moving the cross section line in the image.

#### **Save As**

The histogram data can be saved into an ASCII file or the STM-BCR file format or as graphical bitmap, jpeg or tiff file. The ASCII file contains the floating point x, y co-ordinate and can be imported by, *for example*, spreadsheet programs and the STM-BCR file can be read by SPIP.

#### **Copy**

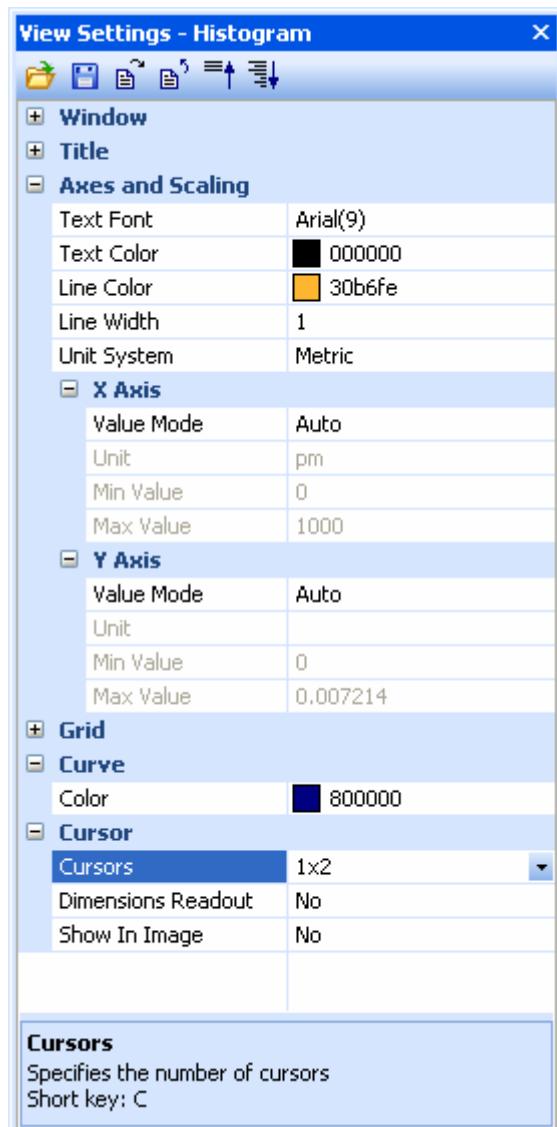
The window can be copied to the clipboard by pressing **CTRL+C** and pasted into third party programs by pressing **CTRL+V**.

#### **Duplicate**

A duplicate of the window can be create by pressing **CTRL+D** or right clicking on **Duplicate**

#### **View Settings and Properties**

Different view options can be defined in the View Settings Pane belonging to the histogram. From the Property dialog it is possible to change the number of bins if the origin of the histogram is from an image or curve. The Property dialog is activated by a double click. For histograms produced by grain analysis the number of bins is defined in the Grain Analysis dialog.



## Profiling

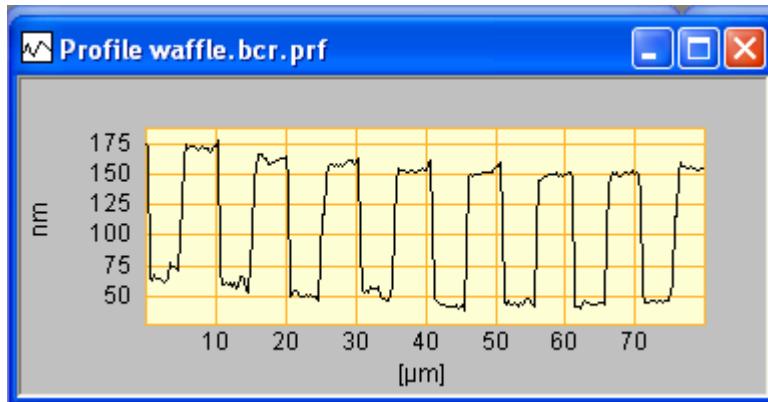
SPIP offers more options for cross-section profiling:

- Single Line Profiling (Cross-section profiling by single line)
- Multi Line Profiling (Cross-section profiling by multiple lines)
- Crosshair Profiling (Create horizontal and vertical cross-sections simultaneously)
- Poly-line Profiling (Create a cross-section along a poly-line)
- Average Profiling (Average parallel cross-sections)

### Single Line Profiling



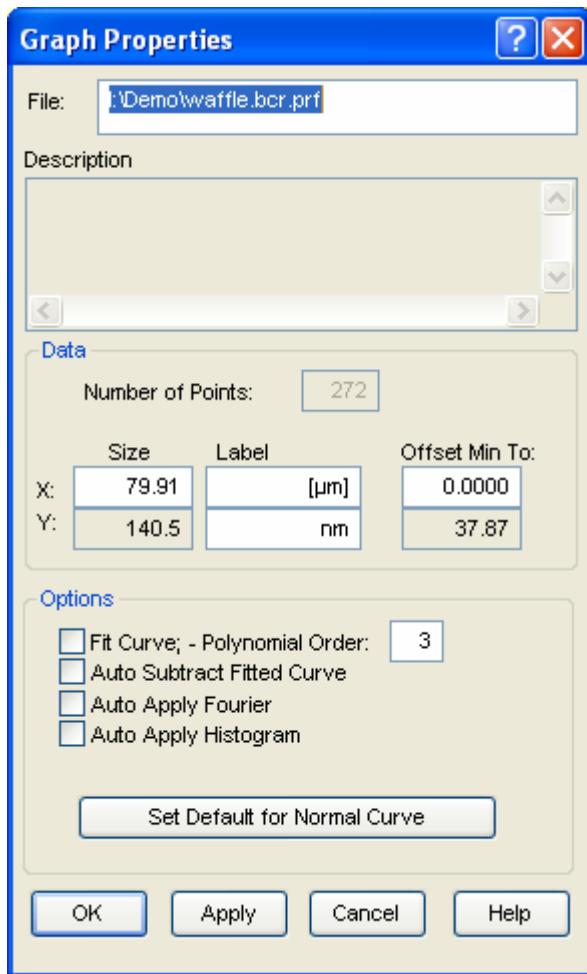
The profile curve window is activated by the Line Marker tool key and is updated simultaneously with movements of the line markers.



#### Profile Properties

The SPIP default view is as shown above, but coloring and other options can be defined and set as new default parameters in the **Graph Properties Dialog**, which is activated by a double click.

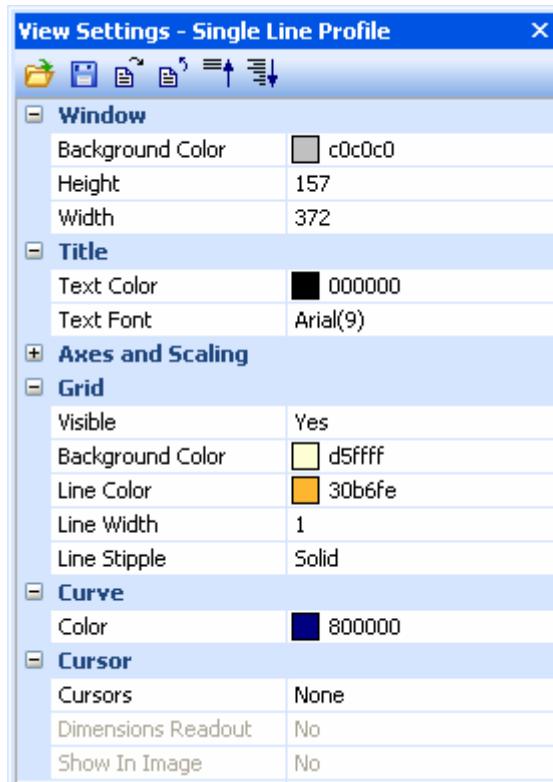
The Property menu provides more detailed control of the functionality of the graphs.



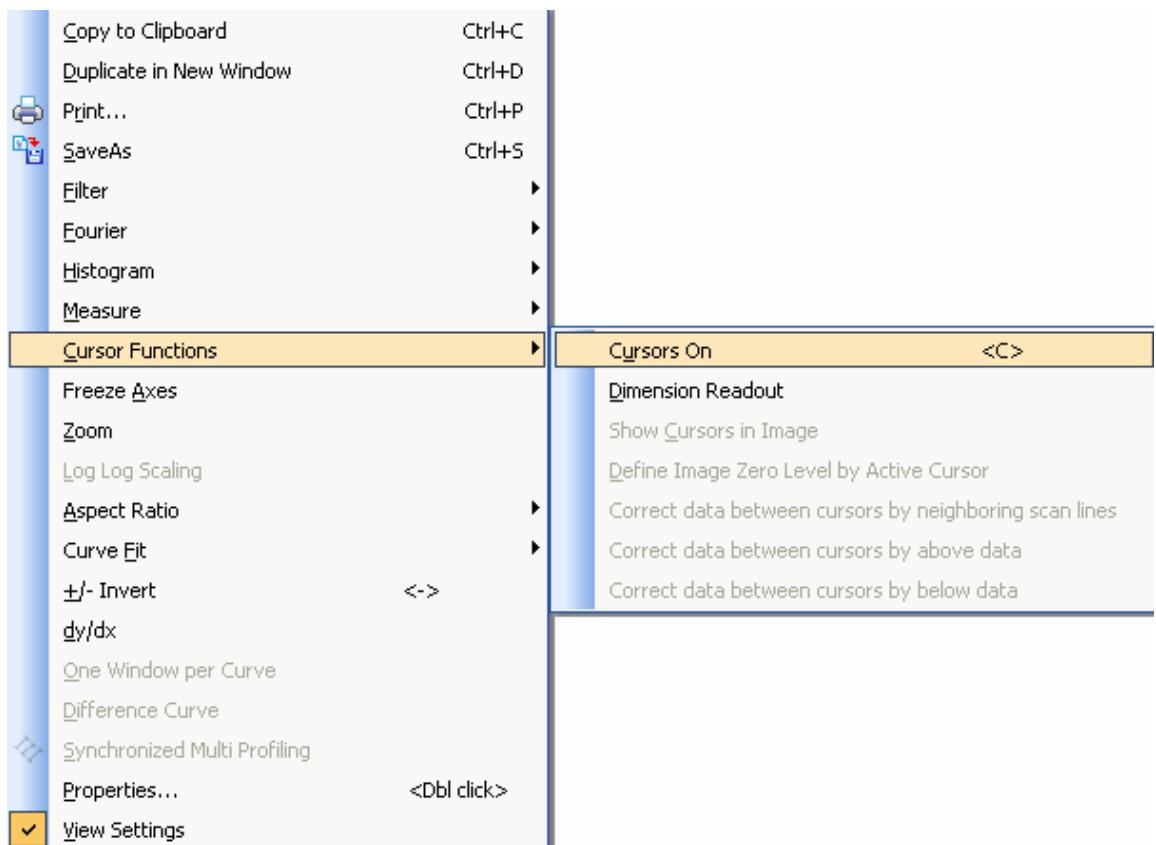
The default parameters will be stored along with their associated curve types, such that the default settings for, e.g., Fourier graphs are independent from the other curve classes.

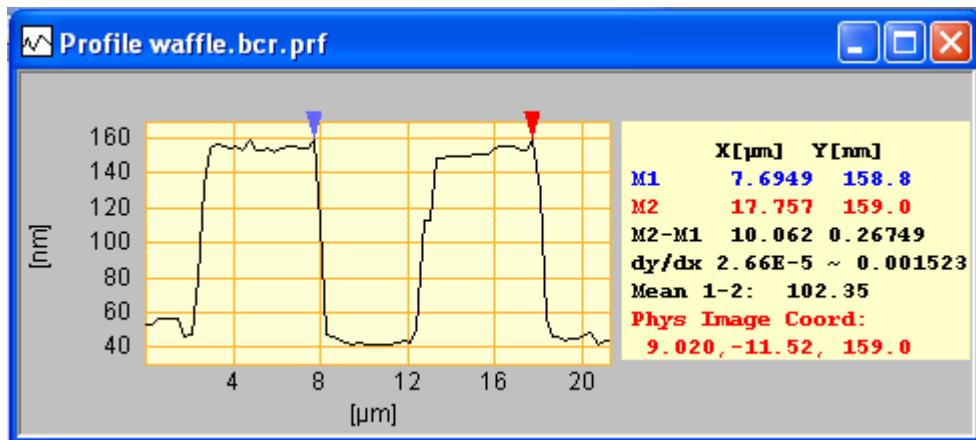
#### Profile View Settings

From the Cross-section View Settings the appearance of the profile window can be controlled.



Cursors can be activated to make interactive measurements from the View Settings Pane or by clicking on the right mouse key and selecting the **Cursors On** or just by pressing 'C' on the keyboard:





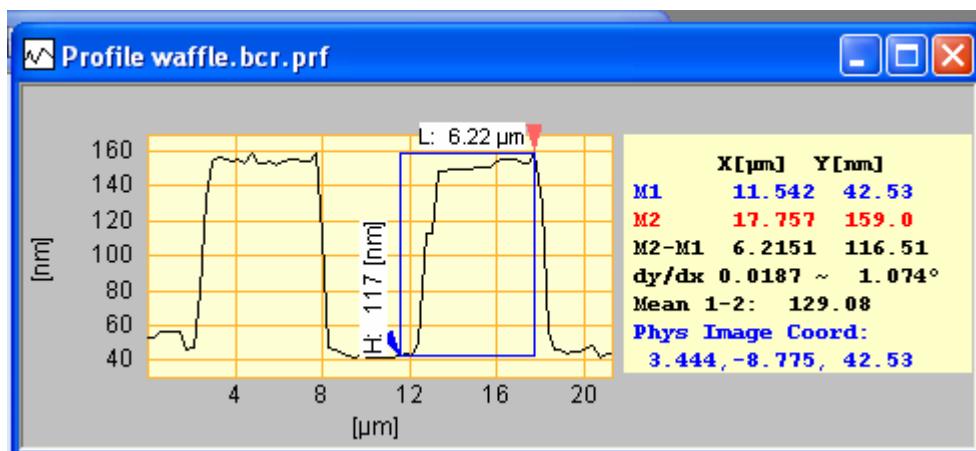
By hitting the 'C' key twice an extra pair of cursors will be activated.

In this mode, it is possible interactively to move the blue and red cursor and get the associated distance and height values written in the yellow box to the right. The red line indicates the most right marker M1 for which the x and y co-ordinate is written. Likewise, values for the lower blue cursor are written. The length and height differences are given in the **M2-M1** fields and the effective slope in the **dy/dx** field in ratio numbers and degrees. Similar readings are seen for the **M3** and **M4** marker pairs

The cursors can be moved by mouse and for precise positioning by arrow keys. The Up/Down arrow keys will move the cursor in the direction of a local summit, which is useful for finding local minimum or maximum points. When a cursor is positioned on a slope, it will be indicated by a tilt of the cursor. Summits will be indicated by cursors pointing straight downwards.

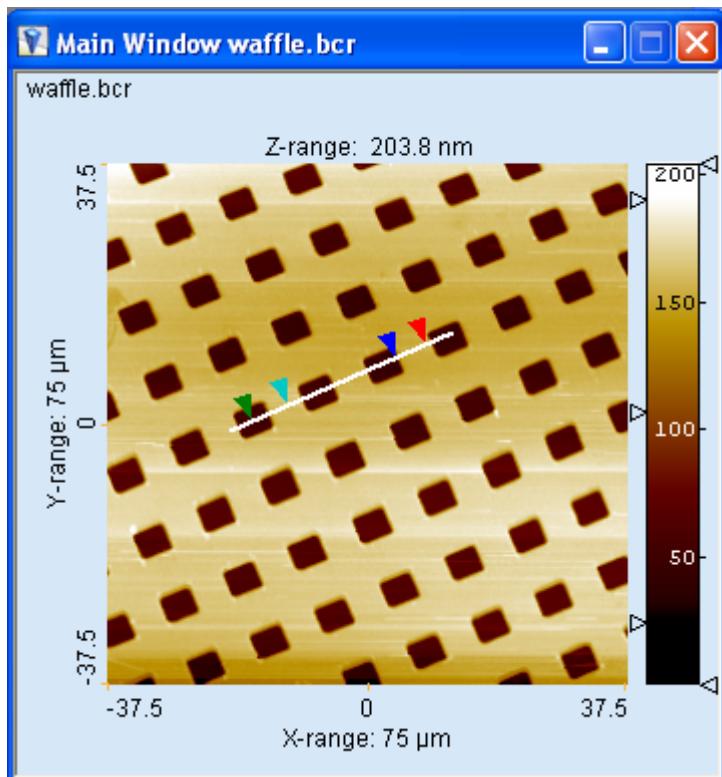
#### Dimension Readout

By activating **Dimension Readout** from the right mouse **Cursor Function** sub menu or the **Properties** menu, height and distance values will be written between the markers in the profile window:



#### Show Cursors in Image

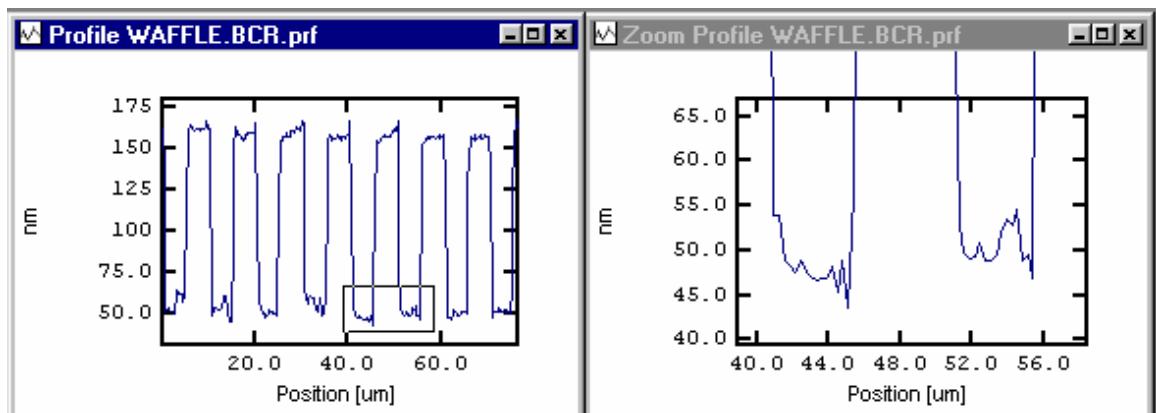
To view the cursor positions in the source image right click on **Cursor Functions→Show Cursors in Image** while inside the profile window:



**Define Image Zero Level by Active Cursor;** when pressed the source image will be leveled so that the height at the pixel corresponding to the active cursor becomes zero. This can be practical for setting a reference plane and making it easier to make direct comparisons of multiple images.

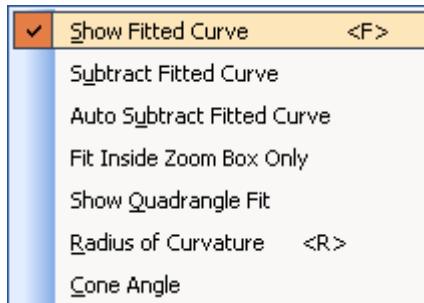
**Freeze Axes;** when set on the scaling of the x- and y-axes will keep their current form even when the newer profiles are exceeding the limits. Otherwise the axes will automatically be adjusted to the current profile. The scaling can also be defined numerically in the Curve Properties menu.

**Curve zoom** is done easily by a zoom box that is handled similar to the zoom box of an image window. Just press 'Z' and move and resize the zoom box while the zoomed area is updated simultaneously in the corresponding zoom window.



**Curve fitting** is default performed automatically by a third order polynomial but can be toggled On/Off by the 'F' key or the right mouse key menu. Like wise it is possible

automatically to subtract the estimated fit from the input curve by clicking **Subtract Fitted Curve** on. The polynomial order can be defined in the Properties menu activated by a double click.



#### **Radius of Curvature**

When Radius of Curvature is selected it will be estimated based on the regions between the markers. The curvature is based on a 2<sup>nd</sup> order polynomial fit, which will be displayed in the graph.

#### **Cone Angle**

You can estimate the cone angle of a positive or negative peak of a curve profile by turning the markers on and right click on **Curve Fit→Cone Angle**. The cone angle will be base on two fitted lines between the most extreme value and the cursor positions.

**Quadrangle Fit;** Set this option on for fitting a quadrangle to the actual curve. The fit will automatically be updated when the curve changes, see Quadrangle Analysis for further details.

**Curve filtering** can be activated by the **Filter** tool key or from the right mouse menu, this will define the actual window as the Filter Source Window. Any changes in the Filter Dialog will apply to the curve window until filtering of another curve or image window is selected as the Filter Source Window.

**Filter Auto Apply;** When set on this option will cause the selected filter to be performed whenever the profile data changes. This may for example be practical when moving the cross section line in the source image.

**Histogram;** Press **Histogram** to create a height distribution histogram of the profile, see further details in the Histogram section.

**Histogram Auto Apply;** When set on the connected histogram window will be updated whenever there is a change in the profile data.

**Curve Roughness;** a subset of the roughness parameters defined for images can be calculated for curves by right clicking on **Roughness**. The resulting roughness parameters will be entered to a text file and will use the pre letter 'R' instead of 'S'. For example, the Roughness Average is denoted Ra for profiles and Sa for images.

#### **Saving Curve Data**

By use of the right mouse popup menu or **CTRL+C** is possible to copy the window content to the Clipboard of the operating system from where it can be pasted into, for example, word processors. It is also possible to print the window or save it to an ASCII file or the STM-BCR file format or save the graphics in a bitmap file.

The ASCII file contains the floating point x, y co-ordinate and can be imported by, for example, spreadsheet programs and the STM-BCR file can be read by SPIP.

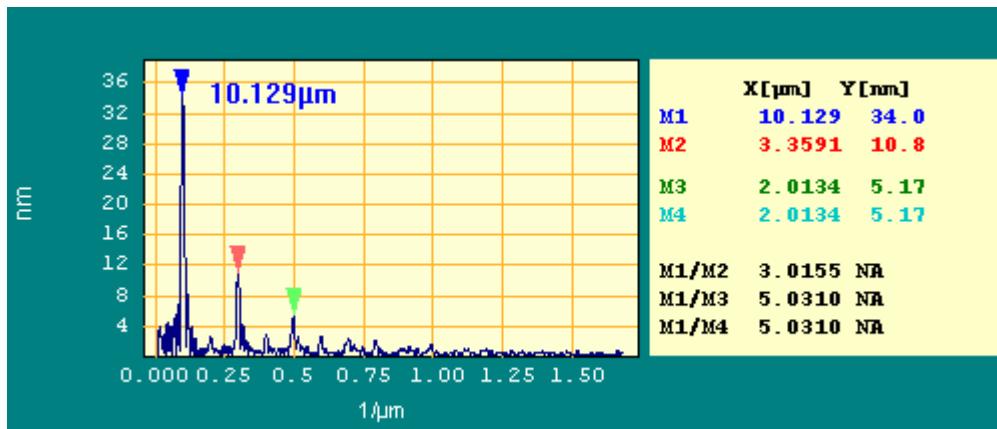
When more profiles are desired for comparison it is possible to keep a copy of any profile by the **Duplicate** menu item.

### Fourier from Profile

It is possible to calculate a Fourier analysis on any size profile and it is even possible to increase the resolution of the Fourier transform by a factor eight.

Perform a Fourier transform by selecting **Fourier**, **Fourier X 8** or **Fourier X 16** (Requires the Calibration Module) in the context menu. **Fourier x 8** will create a profile with 8 times the normal resolution and **Fourier X 16** will provide 16 times higher resolution than the normal. This is performed by padding zeros to the curve data until it contains 8 or 16 times more data.

Below is seen an example of a Fourier result:



**Fourier Auto Apply;** Click this option on and the connected Fourier window will be updated automatically when the curve changes.

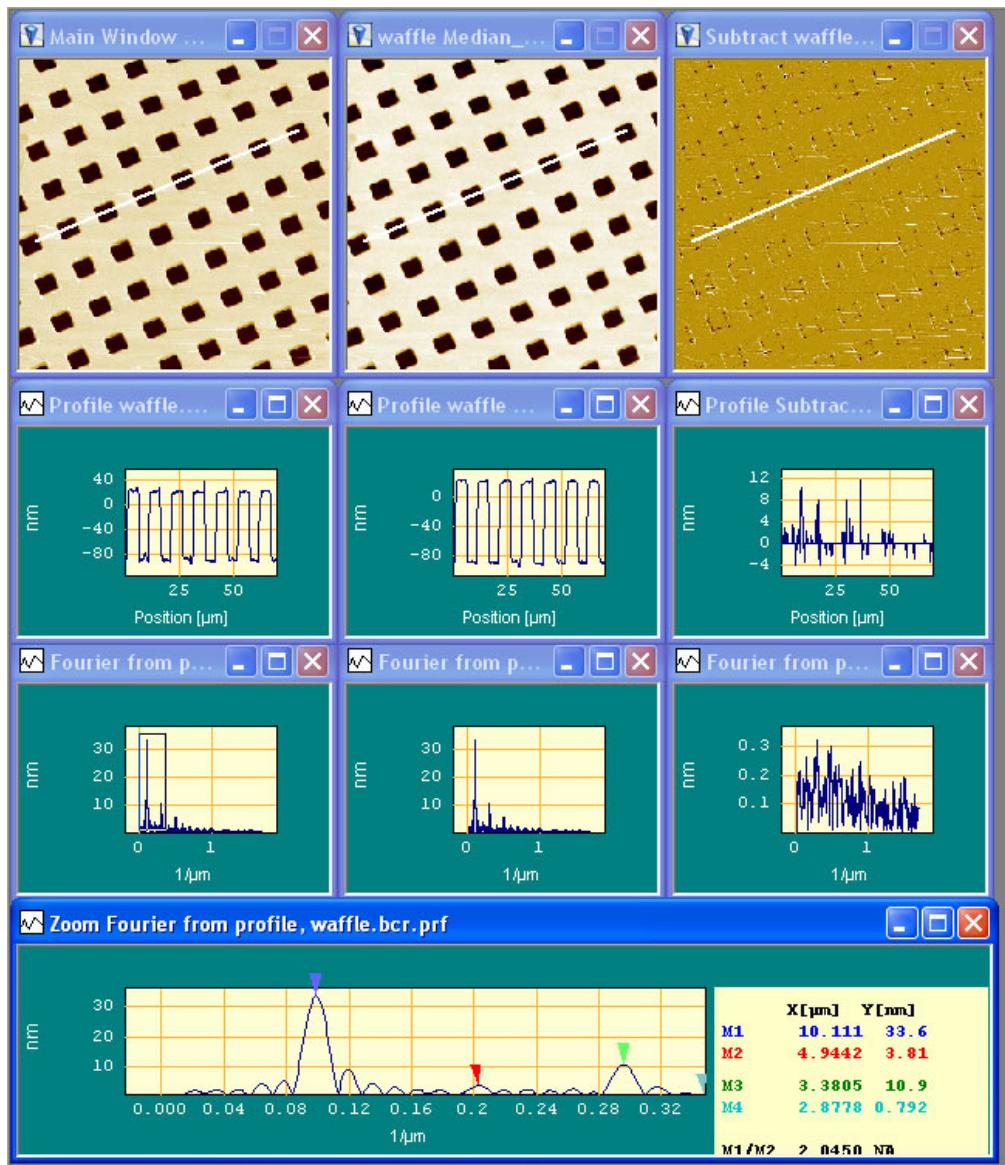
See 1D Fourier Analysis for more information on how to analyze the Fourier spectrum.

### ❖ Synchronized Multi Profiling

When dealing with image for the same physical area but showing different properties, for example height, friction, cantilever amplitude, phase, capacitance, magnetic force, etc. it can be very practical to display profiles of the different images at the exact same cross-sections. This can be achieved by enabling **Synchronized Multi Profiling** in the Right Mouse menu of the curve window or the Markers pull-down menu. When active a profile for each image window having images of identical size is dynamically updated while moving or resizing the Line Marker in one of the image windows.

Below is seen an example on how it can be applied for comparison of a filtered image with the original and the difference image. Note, also that all the 1D Fourier transforms and 1D zooms can be set to be updated simultaneously.

## The Scanning Probe Image Processor, SPIP™ V. 4.2



### Profile Correlation Averaging

To perform Correlation averaging of profiles from selected regions see section Average Profiles.

## Multi Line Profiling

The Multi Line Profiling allows you to show more cross-section profiles in the same window and to manually align them so that they can be conveniently compared.

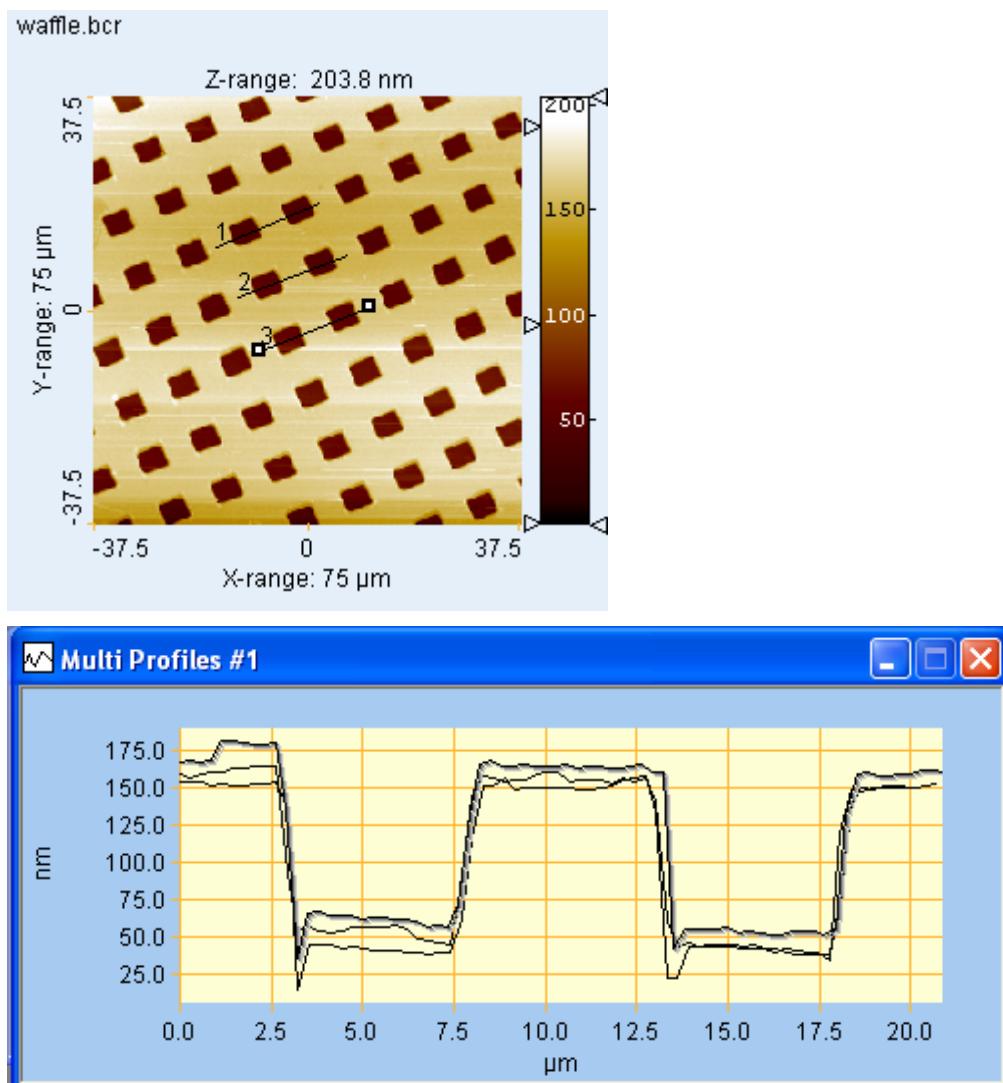
You can also examine differences between images in small detail, by the Synchronized Profiling, which displays cross-section profiles from the same positions into the same Multi Profile window.

In addition it is also possible to calculate average and standard deviation curves.



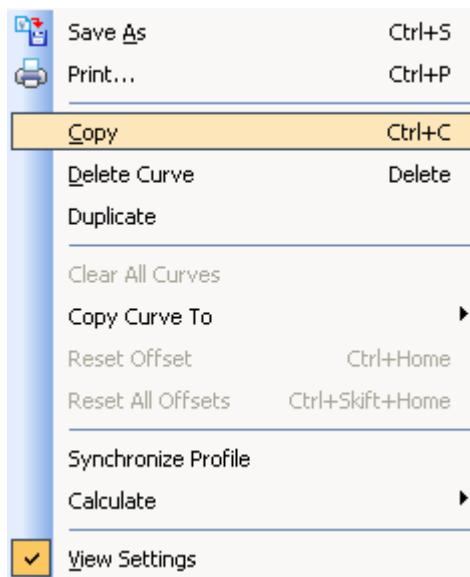
The Multi Profiling tool is activated by its associated tool key.

From the image you can then define one or more cross-section lines, which are automatically put into the Multi Profiling window as shown below:



Once a multi profile line has been defined, it can be dragged, resized or deleted.

While having selected at multi profiling line the context menu of the profile can be activated by a right mouse click in the image window or in the multi profile window



The Save As, Print, Copy, Duplicate, and View Settings menu items works on the window it self while the remaining are dedicated to the multi curve data as explained below.

**Delete Curve:**

Removes the selected line profile

**Clear All Curves:**

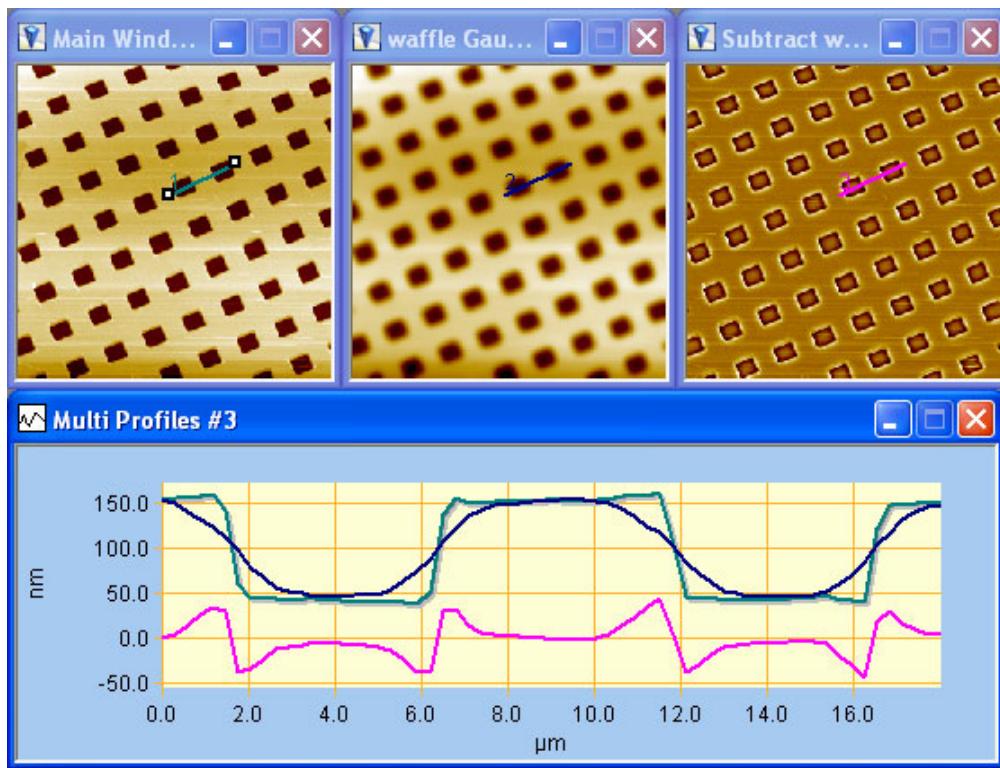
Removes all select line profiles

**Copy Curve To → Single Curve Window**

Copy the selected curve a new single curve window. This can be advantageous if you want to use the specialized measurement tool of the Single Curve Window.

**Synchronize Profile**

When the Synchronize Profile is selected then all image windows containing images of the same pixel size will get a cross section line, which will be synchronized to each other. This means that when moving a line in one window the others will follow to the same position and all cross sections will be shown together in the multi profile window. This is illustrated in the example below where a raw image is shown together with the results from smoothening and sharpening filters.



#### **Calculate→Mean Curve**

Calculates the mean curve of all curves shown in the multi profiling window

#### **Calculate→Standard Deviation**

Calculates the standard deviation curve of all curves shown in the multi profiling window

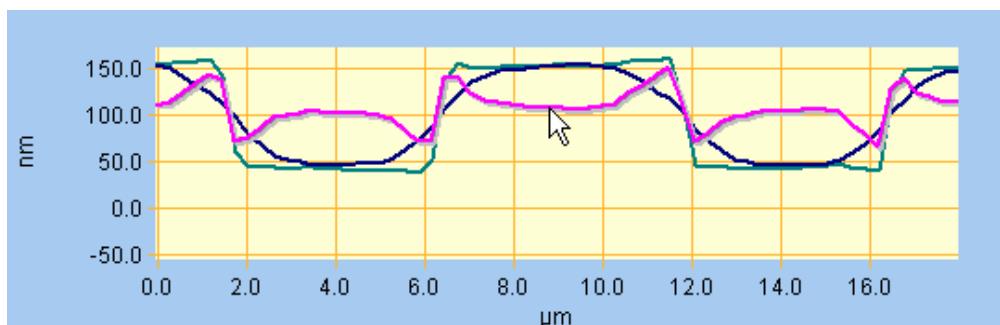
#### **View Settings**

From the View Settings dialog it is possible to define the color

#### **Offsetting and aligning Curves**

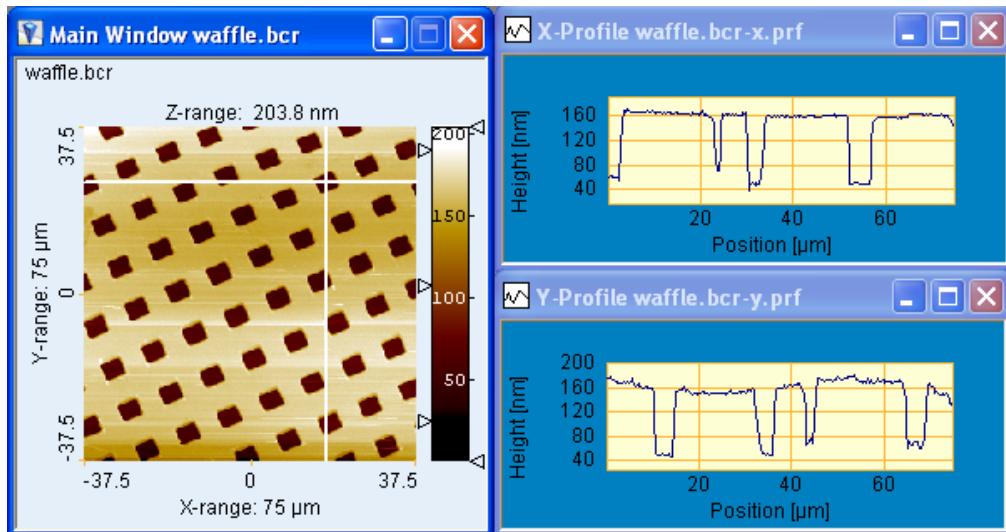
In the Multi Profiling window the individual curves can be put to a new position without moving the cross section line. This makes it easy to align features of interest and study their similarities in detail.

The image below show how the pink colored curve also shown in the previous image is being moved upwards by use of the mouse:



## Cross Hair Profiling

 The Cross Hair profiling tool will provide two simultaneous cross section profiles one in the vertical direction and one in the horizontal direction, which will be shown in two single profile windows. The crossing point of the lines are determined by the mouse, see example below:



## Poly-line Profiling

 **Profiling by poly lines is activated by selecting the **Markers→Poly Line marker tool**.**  
**This tool facilitates mainly three functions:**

Drawing tool used for highlighting certain features in the image.

Profiling through image objects, which are not aligned on the same line.

Extraction of height profiles from Scanning Electron Microscope (SEM) Images.

When the Poly Line marker tool is activated each Left Mouse click will define a new point in the poly line. The Right Mouse button or the **ESC** key deactivates the drawing. When the **Show Z(Dist)** is active the profile through the defined line segments is calculated and shown as a graph. A new Left Mouse click will activate the drawing again and extend the current poly line.

To clear the poly line, press the **CTRL+Delete** or click **Markers→ClearPoly Line**.

To delete a point in the poly line put the mouse close the point and press the Delete key.

To change the position of a point, press the Shift key simultaneously with the left mouse key.

A scatter diagram showing the path of the poly line can be created by the **Markers→Show XY-Scatter** function and the graph can be used for performing different types of measurements.

New points between the interactively defined poly line points can automatically be calculated by

**Markers→Extend Poly Lines.** This function will try best as possible to define new points by following the highest values between the poly points. In combination with the **Markers→Show XY-Scatter** function this is particularly useful for detailed analysis of SEM images showing surfaces structures in side view, i.e., the y-axis is associated with height.

## Average Profiling and Fourier

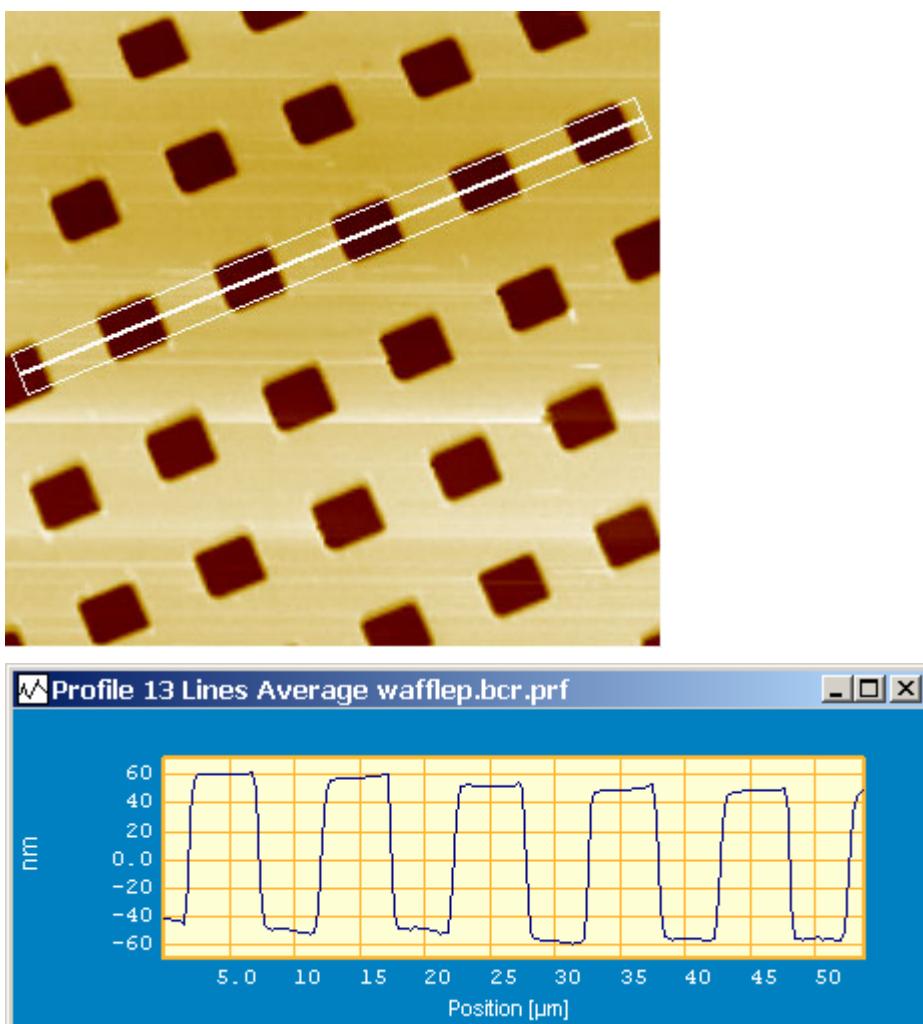
To limit the influence from noise or smooth the profiles SPIP offers three ways for calculating average profiles:

- from a region of lines parallel to the line marker
- from the entire image
- from a region selected by the zoom box.

Furthermore, it is possible to calculate the average Fourier amplitude spectra of profiles within a selected area.

### Profile Averaging of Lines Parallel to the Line Marker:

Activate the Average Parallel Lines marker by its tool key , or **Markers→Average Parallel Lines**. A region around the Line marker is now marked and the corresponding average profile is calculated and shown. To change the size of the average region keep the 'A' key and the left mouse button pressed while moving the mouse. The number of averaged lines is written in the caption of the profile window.

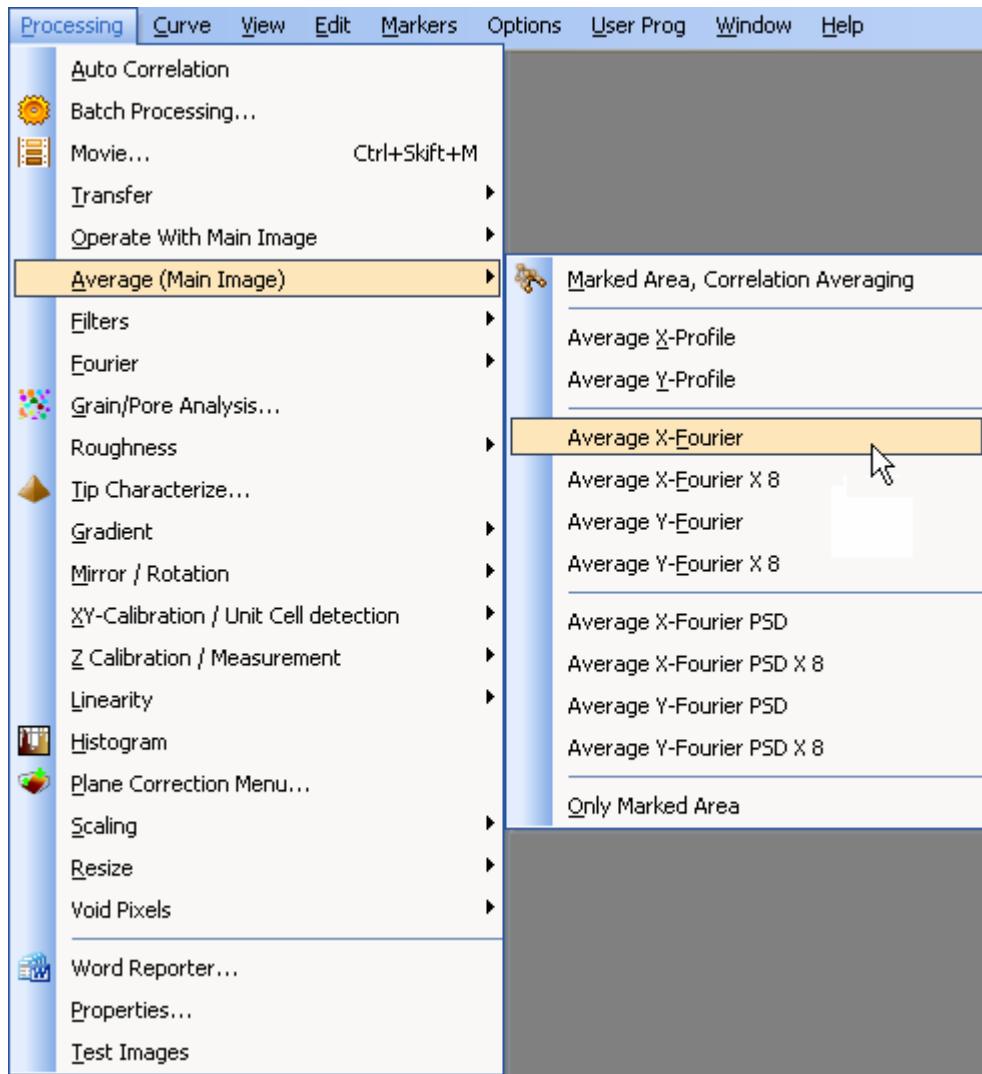


To turn off the averaging press the 'L' key or **Markers→Line Average Parallel Lines** once more. You can conveniently toggle between the average mode and the normal profile mode and observe the difference between the plain profile and the average profiles by pressing the 'A' and 'L' key. As for other profiles there are several options for further analysis available on the right-mouse key menu and you can for example activate the **Fourier Auto Apply** to get

the Fourier spectrum calculated automatically while changing the size and orientation of the line marker.

### Profile Averaging from Entire Image:

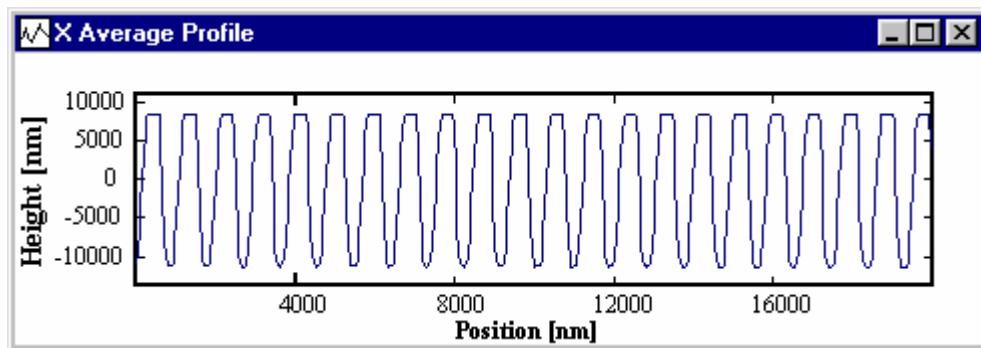
From the **Processing→Average** popup menu it is possible to calculate average profiles and average Fourier on profiles:



#### Average X- and Y-Profiles:

It is possible to obtain the average X-profile  $z_{ax}$  and the average Y-profile  $z_{ay}$  calculated as:

$$z_{ax}[x] = \sum_{y=0}^{N_y} z[x][y] \quad z_{ay}[x] = \sum_{x=0}^{N_x} z[x][y]$$



This function is especially powerful when analyzing line profiles aligned parallel to the scan directions.

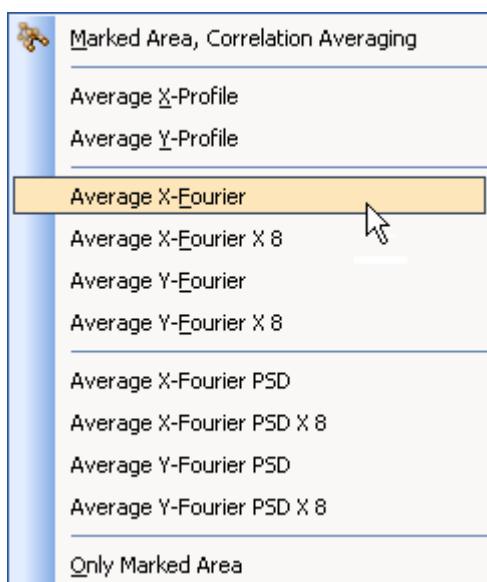
The functions are activated from the menu item **Processing→Average→Average X\_Profile** or item **Processing→Average→Average Y\_Profile**.

#### Profile Averaging of Area Defined by Zoom Box:

By setting **Processing→Average→Only Marked Area** the calculation will be limited to the pixels inside the rectangle drawn by the rectangle marker tool. Note, that this setting can be used for the Average Fourier transforms as well.

#### Average Fourier and Power Spectrum Density (PSD)

By clicking **Processing→Average (Main Image)** you will see a number of menu items for creating average Fourier transforms and Power Spectrum Density



#### Average X- and Y-Fourier:

To get a smooth 1D Fourier it can be an advantage to calculate the average Fourier amplitude  $F_{au}$  and  $F_{av}$  of the individual profiles:

$$F_{au}[u] = \sum_{y=0}^{N_y} F_y[u] \quad F_{av}[v] = \sum_{x=0}^{N_x} F_x[v],$$

where  $F_y$  is the Fourier transform of the profile having the row number equal to  $y$  and  $F_x$  is the Fourier transform of the profile having the column number equal to  $x$ .

**Average X-Fourier x 8 and Y-Fourier x 8**

Same as above but with 8 times higher resolution, which gives higher accuracy when measuring wavelength associated with Fourier peaks.

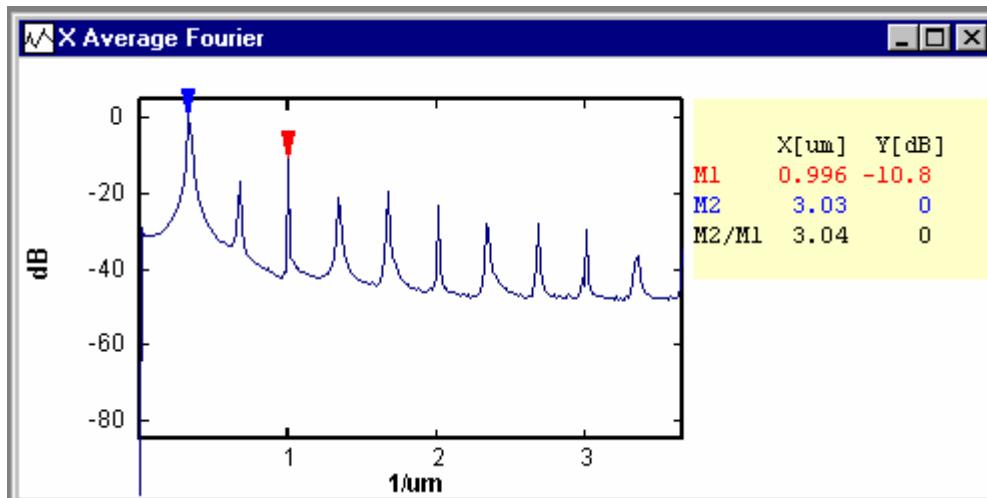
**Average X-Fourier PSD and Y-Fourier PSD**

Same as X-Fourier but with calculation of the power spectrum for each scan line instead of the amplitude spectrum. The power spectrum equals the amplitude spectrum squared. The resulting spectrum is called Power Spectrum Density (PSD). The spectrum is normalized by the number of pixels such that the result is relatively insensitive to the pixel resolution.

**Average X-Fourier PSD x 8 and Y-Fourier PSD x 8**

Same as above but with 8 times higher resolution.

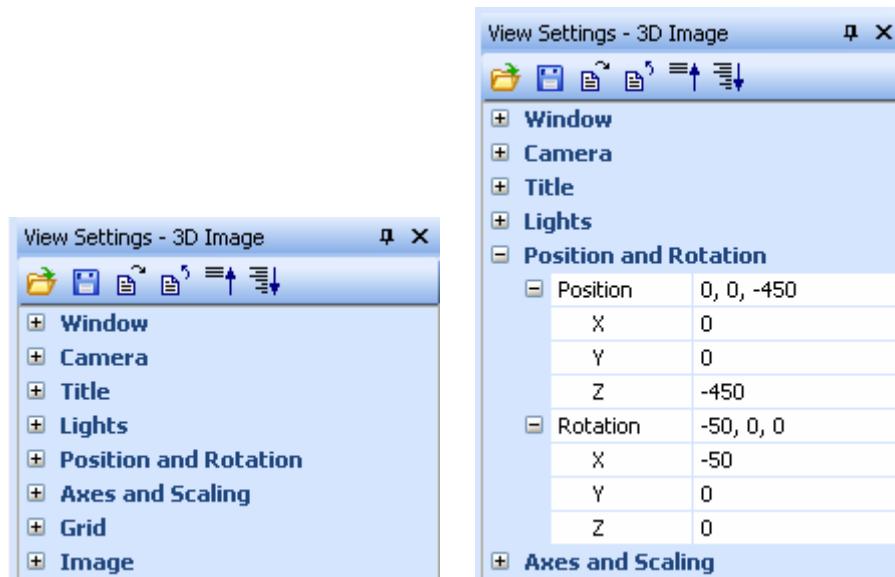
Below is seen how an average Fourier transform may look when displayed on a dB scale. The cursors indicate the first and third harmonic components. Note also that the corresponding wavelengths are written in  $\mu\text{m}$ . It is therefore possible to estimate the pitch by positioning a cursor on the first harmonic. For accurate estimation of the pitch, a statistical mean value can be calculated based on the other harmonic components. However, if the profile is based on an image, you will find the pitch more easily and accurately by the unit cell detection algorithm.



To learn more about 1D Fourier analysis, please consult section 1D Fourier Analysis.

## 3D Visualization Studio

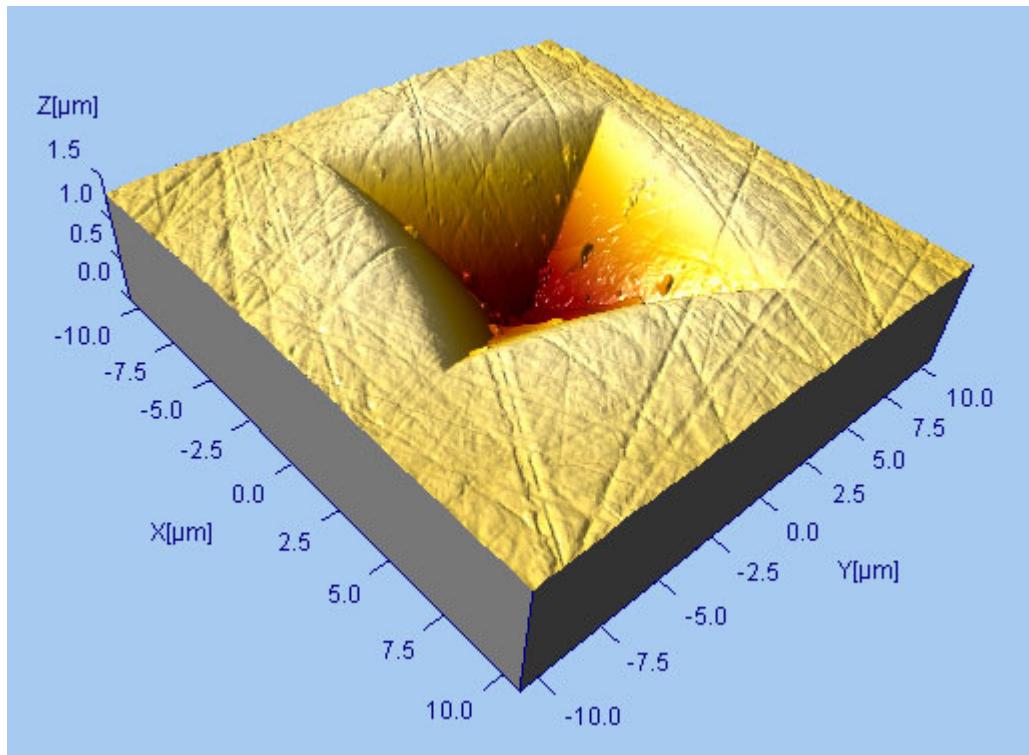
 All SPIP 2D images can be visualized in 3D by clicking on the 3D-tool key or just the numerical '3' on the key board. This will create the 3D Window showing the image in 3D perspective and the 3D Visualization menu by which you can control the display parameters. The menu contains a number of submenus, which can be opened or closed by clicking on the associated buttons. Below is seen the menu in its most compact form to the left and with the Position submenu opened to the right:



As seen above the 3D Menu contains 5 submenus, which controls the following functions:

Window	Defines the background color and the window size
Camera	Defines the View Angle
Title	Defines the Title appearance
Lights	Controls emulated light sources illuminating the surface
Position and Rotation	Controls the position, and rotation angle of the surface
Axes and Scaling	Defines the appearance of axes and scaling of the surface image
Grid	Defines the appearance of outer grid
Image	Defines coloring of the surface, handling of void pixels, block mode
Wire frame	Defines optional wire frame settings,

Below is seen a visualization example of a an indented surface



## 3D Surface Positioning

By use of the Position section and the Axes and Scaling section of the View Settings Pane it is possible to control the position, scaling and rotation angles of the surface.

Axes and Scaling	
Visible	Yes
Text Font	Arial(9)
Text Color	<span style="color: #800000;">█</span>
Line Color	<span style="color: #800000;">█</span>
Line Width	1
Tick Length	10
Unit System	Metric
Origin	Use Image Values
Scale Mode	Auto
Scale	1, 1, 2.5
X	1
Y	1
Z	2.5

Position and Rotation	
Position	10, 54, -518.3...
X	10
Y	54
Z	-518.350504
Rotation	-47, 4, -47
X	-47
Y	4
Z	-47

X Axis	
Decimals	1
Value Mode	Auto
Unit	nm
Min Value	-5
Max Value	5

Y Axis	
--------	--

The surface image can also be rotated, scaled dynamically with the mouse and the keyboard. The following will describe the different parameters and how they can be controlled.

#### X,Y,Z -Rotation angles:

These angles describes the rotation around the x,y and z axes they can be changed by the menu using its sliders or arrow buttons. Alternatively the parameters can be modified from the 3D window itself by mouse or arrow keys:

↑ ↓ UP ARROW and DOWN ARROW change the X-rotation angle.

← → LEFT ARROW and RIGHT ARROW change the Y-rotation angle.

SHIFT+ combined with LEFT ARROW or RIGHT ARROW changes the Z-rotation angle.

When the left mouse-key button is down the mouse position controls the X and Y rotation angles and when combined with the SHIFT key the Z-rotation angle is determined by the Y-coordinate of the mouse.

#### Surface Position

The XY-position of the image can be controlled horizontally by ALT + Mouse Movement and ALT+ARROW keys

The Z-position is controlled by ALT+CONTROL+Mouse Y-Movement and **ALT+CTRL+UP/DOWN ARROW**. The Z-position should be negative and may range from -10000 to -1.

#### Scale Factors

The XYZ Scale factors determine the geometric shape of the surface.

The most important is the Z-scale factor, which scales the height values of the image and can be controlled by: **CTRL+ Mouse Y-movement and the PAGE UP/ DOWN**

#### 3D Comparison at same scale

For surface structures with large corrugations it can be an advantage to show the image in the 1:1 Aspect ratio as this gives the best geometrical feeling. This is especially true for images used for tip characterization.

For direct comparison of images it might be useful to define fixed min and max values for the Z axis.

#### View Angle

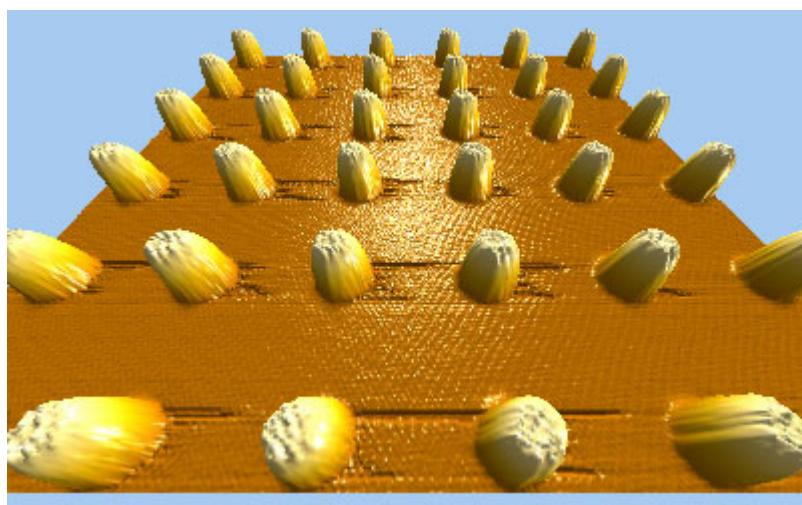
The view angle takes care of the current angle by which the object is viewed and corresponds to changing the lens of a camera. The View angle is found in the Camera section of the View Settings Pane:



The default View Angle is 40 degrees as shown in the example below:



Enlarging the view angle corresponds to changing the lens of a camera to a wide angle lens. It will appear as if the surface is further away and you might want to bring it closer again by changing the Z-position coordinate. The net result will show the individual features with a larger perspective distortion, below is used a view angle of 80 degrees:



### Axes

The X-Y-Z axes can be displayed with a user defined font and with Tick marks of an optional length.

## 3D Color Properties and Decoration

### Image Properties

The Image section of the View Settings Pane defines how the image is drawn

<b>Image</b>	
Void Pixels	Hide
Show Block	Yes
Block Color	<input type="color" value="#646464"/> 646464
Preview Resol...	Auto
Final Resolution	1:1

#### Void Pixels

Void pixels can be shown or hidden, which means that they are transparent.

#### Show Block

To give the surface the appearance as if it was cut out of a block you can turn show block on.

#### Resolution

During interactive rotation and scaling of the image it is often necessary to lower the "preview resolution" in order get a feeling of real-time updates, this is by default done automatically. Likewise, it might be desirable to lower the "Final Resolution" which is applied after when the interactive modification of the 3D scene has finished.

By the altering the resolution parameters you have the possibility to define how much you want to lower the resolution and adapt it to the performance of your computer.

### Surface Properties

It is possible to attribute a single color to the surface or let the colors depend on the height values of the 3d image or some other image of same size. Below is seen the Surface section of the View Settings Pane

<b>Surface</b>	
Mode	Color bar
Color	<input type="color" value="ffffff"/> ffffff
Window	Default pattern
Limit Palette Range	Yes
Palette Limits Unit	nm
Low Palette Limit	-0.439261
High Palette Limit	1.051763

When **Mode** is set to **Color Bar** the surface color property is determined by the height values of the surface. Combined with light sources it can create the illusion of a surface consisting of different materials. The height values will by default be scaled linearly between the min and max height values range of the image. This is the default mode and when using a color bar with low contrast the best results are usually obtained.

However, by setting **Limit Palette Range** on it is possible to have the colors scaled differently.

#### Material Color

When Mode is set to Material the surface color can be defined by a fixed color.

Note, that the observed colors are determined by the light sources in combination with the surface color. Shining a white surface with a blue color will create a blue image.

When no light sources are present the surface colors will be determined by the height values just as for the 2D images.

### Texture

Some times it can be useful to combine the topographic information from one image with colors from another image expressing some other surface properties, for example a combination of an AFM height image with a phase image acquired simultaneously. To do this just set Mode to Texture and select the window in the Window parameter field.

### **Background Color**

The default background color is white but you can select any color with the associated color button..

### **Grid**

When clicking the Grid option on a grid will be drawn behind the 3D image. The spacing of the pattern will be the same as the Axes tick marks.

### **Title**

To identify the image a title can be written with an optional font style. The title text can adopt the filename of the images or be to an entered text.

By Checking **In Front** the title will always be shown in front of the image.

### **Wire frame**

<b>Wireframe</b>	
Mode	With image
Elevation	1
Color	<input type="color" value="#800000"/> 800000
X/Y lines indepen...	Yes
Lines	29, 25
X	29
Y	25

A wire frame can be shown combined with or instead of the rendered image. The number of lines in the wire frame can be set individually for the x and y directions.

To assure that all parts of the wire frame are visible when combined with a solid image it can be elevated or lowered relative to the rendered image.

The wire frame colors can be set to adopt the current color bar (Var color) otherwise a fixed color can be defined.

## 3D Light Sources

<b>Lights</b>	
Lighting Enabled	Yes
Ambient Color	<input type="color" value="#808080"/>
<b>Light 1 (On)</b>	
Enabled	Yes
Diffuse Color	<input type="color" value="#ffffff"/>
Specular Color	<input type="color" value="#ffffff"/>
Position -261.864, -400, 333...	
X	-261.864
Y	-400
Z	333.522
<b>Light 2 (Off)</b>	
<b>Light 3 (Off)</b>	

Up to eight light sources can be defined by position and color. The light source number will determine which light source parameter is displayed.

Each of the light sources can easily be turned on and off by the numeric keys '1' to '8'. The '0' key will turn all lights off and bring the window in to a normal color mode where the Color Scale Editor defines the colors.

### Light Position

The light position co-ordinates can be defined within a range of +/- 1000 this should be compared with the view port of the window, which corresponds to 400 x 400 and a typical viewer distance from the surface of 400.

When the left mouse-key button is down and combined with one of the numerical keys the mouse position will determine the X and Y position of the active light source and when also combined with the SHIFT key the Z-position is defined instead of the Y-position.

### Diffuse Color

Diffuse light comes from a particular direction but is reflected evenly off the surface. Even though the light is reflected evenly, the object is brighter if the light is pointed directly at the surface than if the light grazes the surface from an angle.

### Specular Color

Specular light is also directional, but is reflected sharply and in a particular direction. Highly Specular lights tend to cause bright reflective spots on the surface.

### Ambient Color

The ambient light is light that doesn't come from any particular direction. A surface illuminated by ambient light is evenly lit on the entire surface in all directions.

The individual Red, Green and Blue values can be set between 0 and 1 or selected from Color Select dialogue.

A neutral ambient light would consist of an average value of all three basic colors, resulting in a gray color.

## 3D Trouble Shooting

3D rendering is extremely dependent on display hardware and drivers, so in case of problems the first thing to try is to make sure that the display driver is up to date by downloading the newest version from the manufacturer's website (e.g. [www.ati.com](http://www.ati.com) for ATI cards, [www.nvidia.com](http://www.nvidia.com) for GeForce cards).

Some users with ATI Radeon Mobility have resolved issues by using drivers from [www.omegadrivers.net](http://www.omegadrivers.net), which offer 3rd party ATI Radeon and GeForce drivers.

If this doesn't solve the problem, it should be possible to work around the problem by limiting the amount of hardware acceleration, at the cost of slower 3D rendering. There are two ways of doing this:

1. Try out the different "Acceleration Modes" in SPIP (in the menu of the 3D settings dialog). The "Safe" mode should work on all systems.
2. Try lowering the acceleration for Windows as a whole. This is done by the following procedure:
  - 2.1 Close SPIP.
  - 2.2 Right-click the desktop and select "Properties".
  - 2.3 Go to the "Settings" tab and click the "Advanced" button.
  - 2.4 Go to the "Troubleshoot" tab and move the slider all the way to the left.
  - 2.5 Restart SPIP.

Some users have reported that changing the "Color Quality" setting of Windows can help work around 3D problems without resorting to lowering the acceleration setting. The "Color Quality" is found on the "Settings" tab mentioned in item 2.2 above.

Please contact [support@imagemet.com](mailto:support@imagemet.com) if you continue to experience problems. In your problem report, please state the make and model of your graphics card, and what version of Windows you are using.

### 3D Acceleration Mode

The acceleration mode controls to what extent SPIP uses the available hardware acceleration to speed up 3D drawing. It can thus be used for dealing with display driver related problems, or for optimizing performance at the possible cost of display quality. The acceleration mode is selected from the Options→3D Acceleration Modes menu.

#### **The available 3D acceleration modes are:**

**High:** Uses all available accelerations to draw to screen and bitmap as fast as possible. If the 3D window is obscured by a dialog or protrudes outside the screen area, then the obscured area will most likely appear garbled if it is revealed. "Save As" may also result in garbled images.

**Normal:** Uses all available accelerations for screen drawing only. Bitmap drawing may be accelerated if this can be done safely. Thus, "Save As" will always produce correct images. This is the default mode.

**Low:** Uses all available accelerations for screen drawing of previews only. Full resolution drawing and bitmap drawing may be accelerated if this can be done safely. Thus, images will never appear garbled. Please note that with newer display drivers this mode will often be as fast as High acceleration.

**Safe:** All acceleration disabled. This gives the best chance of producing correct images, at a performance penalty. It should only be used in case of display driver related problems. Please note that SPIP is subject to the Windows Display Troubleshooting Settings, and thus cannot take advantage of hardware acceleration if it is disabled by Windows.

## 3D Keyboard and Mouse Interface

It is possible to control most of the scene parameters directly from the 3D image window by use of the key combinations listed below.

Summary of keyboard / mouse interface:

Scene Parameter	Control Keys
X-rotation angle	UP/DOWN ARROW Mouse X-Movement
Y-rotation angle	LEFT/RIGHT ARROW Mouse Y-Movement
Z-rotation angle	SHIFT+LEFT/RIGHT ARROW SHIFT+Mouse X-Movement
Surface X-position	ALT+LEFT/RIGHT ARROW, ALT+Mouse X-Movement
Surface Y-position	ALT+UP/DOWN ARROW ALT+Mouse Y-Movement
Surface Z-position	SHIFT+ UP/DOWN ARROW ALT+CTRL+Mouse Y-Movement
Z-Scale	PAGE UP / PAGE DOWN CTRL+ Mouse Y-Movement
Surface XY-Scale	SHIFT+UP/DOWN ARROW
Light Source X-Position	1...8+Mouse X-Movement (and 1...8+SHIFT+Mouse X-Movem.)
Light Source Y-Position	1...8+Mouse Y-Movement
Light Source Z-Position	1...8+SHIFT+Mouse Y-Movement
Individual Lights On/Off	1...8 numerical keys turns the associated lights On/Off
Light Mode On/Off	0, numerical key '0' turns all light sources off
Adopt Color Bar	9, numerical key '9' toggles the Adopt Color Bar setting

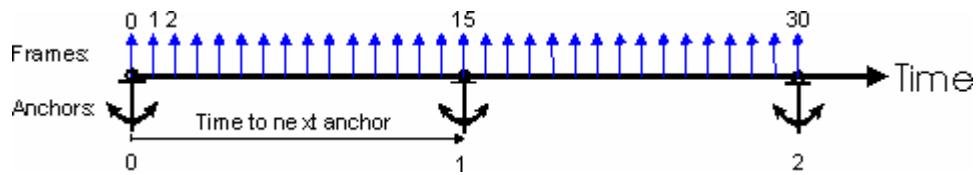
## 3D Animation

The 3D Animation utilities are used for creating 3D animations files such as AVI or MPEG. The generated movie files can for example be included in Power Point presentations or web pages. It might also serve as a good tool for inspecting a surface from different angles and with different light settings.

### Introduction

An animation sequence is simply defined by two or more **key frames**, where the key frame contains all the 3D parameters defining a 3D scene plus a time difference to the next anchor. For each key frame you can define specific position, color, light and wire frame parameters. You can define a given 3D scene as a key frame just by pressing the Capture button. Between the key frame SPIP can automatically calculate key frame, which are 3D images where the viewing parameters are defined by interpolation of the two neighboring key frame. This way you can create a smooth animation that brings you from one key frame to the next by key frame changing in smaller steps.

Below is seen the relation between key frame shown as anchors and frames and how they can be arranged on the time axis.



When having defined one or more key frame you can preview the animations by the preview buttons or export it to AVI or MPEG files, which can then be shown by third party movie players.

The 3D animation pane is activated from right click menu of the 3D image or from the View pull down menu in the SPIP menu bar.



To add a new key frame setup the 3D image as desired and click the Insert Key Frame button: . When having more key frame the new key frame will after the select key frame. It is also possible to overwrite a key frame using the overwrite button: . For each of the defined key frame the time to next key frame can be set

#### Key frame/Second

The number of key frame per second defines how fast the animation will be shown by movie players and influences the duration and quality of the animation. Few key frame per second will increase the duration but might cause the animation to appear less smooth.

#### Repeat Mode:

When setting the repeat mode to smooth extra key frame will be calculated for animating the image smoothly from the last frame to the first.

**Hint:** If you want your third party movie player to show the animation in a repeatable mode it is a good idea to let the last anchor be identical to the first. This is simply done by selecting the first anchor pressing the Capture Anchor button and choosing End as the anchor position.

#### Navigating

You can select the individual frames and key frame by the associated arrow keys and the preview slider. The 3D image will automatically reflect the parameters of the selected frame.

#### Preview

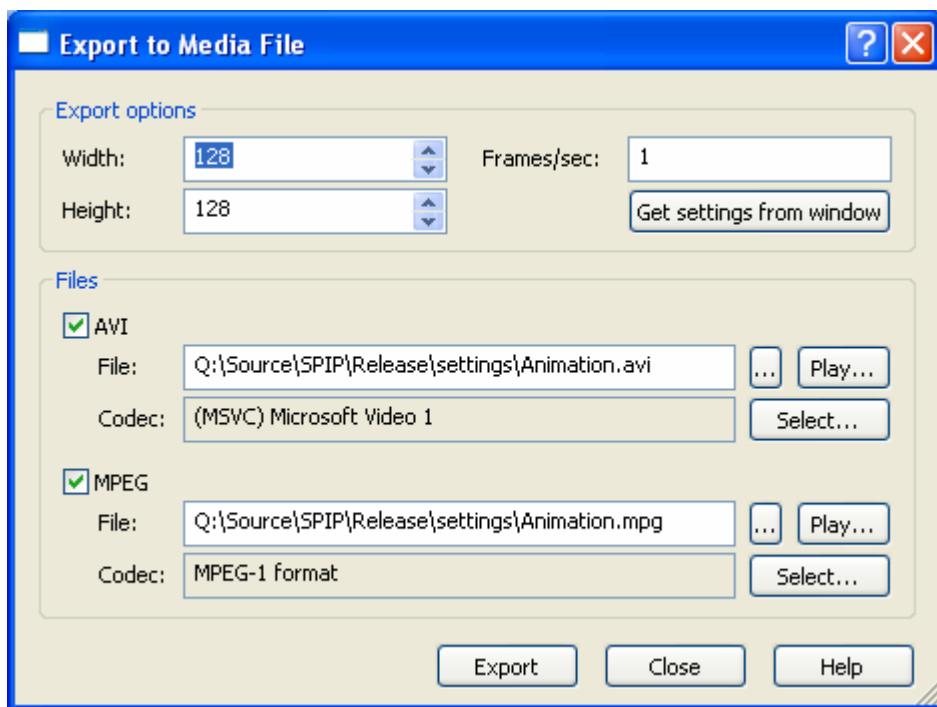
Using the slider or the frame spin buttons it is possible to preview the result of the different key frame that are automatically created in-between the different frames.

#### Saving Key frame to File

After having defined a sequence of frames you can save the anchor parameters so that they can be recalled and applied on other images; to do so click the save button  . Note, that this does only store the visualization parameters and does not create any animation file. To create the animation file see Generating Movie Files below.

### Generating Movie Files

To generate a movie file from a given sequence of frames click the export button  , which will open the menu shown below:



The animation can be exported to the following two movie file formats:

AVI              Audio Video Interleave  
MPEG              Movie Picture Experts Group

To achieve the highest quality the AVI file format should be selected but if a smaller file size is desirable the MPEG format should be considered. Typically the file size of an MPEG file will be 20 times smaller than the size of the corresponding AVI file. The disadvantage of the MPEG format is reduced quality. You can generate a pair of AVI and MPEG files simultaneously and compare their quality and file size.

The estimated size of the AVI file is shown in the output window and the MPEG file size will typically be 20 times smaller.

#### Frame Size

If you want your movie to fit a certain frame size this can be set in the top of the dialog.

#### Export

To create a movie file select the output format and output file name and press the Export button. It is possible to generate an AVI and an MPEG file simultaneously by selecting both formats.

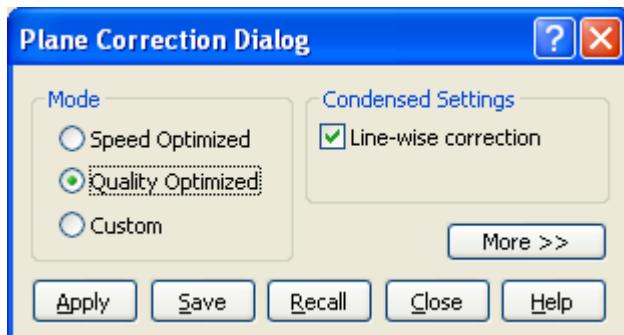
#### Play...

If you have a movie player installed on your computer you can play the generated files by pressing one of the two play buttons.

## Plane Correction Dialog

Plane correction is one of the most important aspects of SPM image correction. SPM instruments often have a non-linear coupling between the lateral plane and the Z-axis causing unwanted bow in the image. The process for plane correcting the surface image is also called "flattening". Image flattening can be a challenging process, especially when the surface structure contains steps most flattening algorithms will fail because they can not distinguish the real structure from the plane distortions. However, SPIP has dedicated tools for detecting and handling steps such that the individual steps will appear flat.

The Plane Correction Dialog offers three main modes, which are selected from the top of the dialog:



**Quality Optimized:** When selected the plane correction settings will be set such that the best possible result is achieved. This mode requires no pre-knowledge about the different plane correction techniques and can be used by the novice as well as the advanced user. This mode will combine a number of techniques that detect and handle steps such that they do not introduce flattening errors.

**Speed Optimized:** When selected the plane correction settings will be such that low processing time has a high priority.

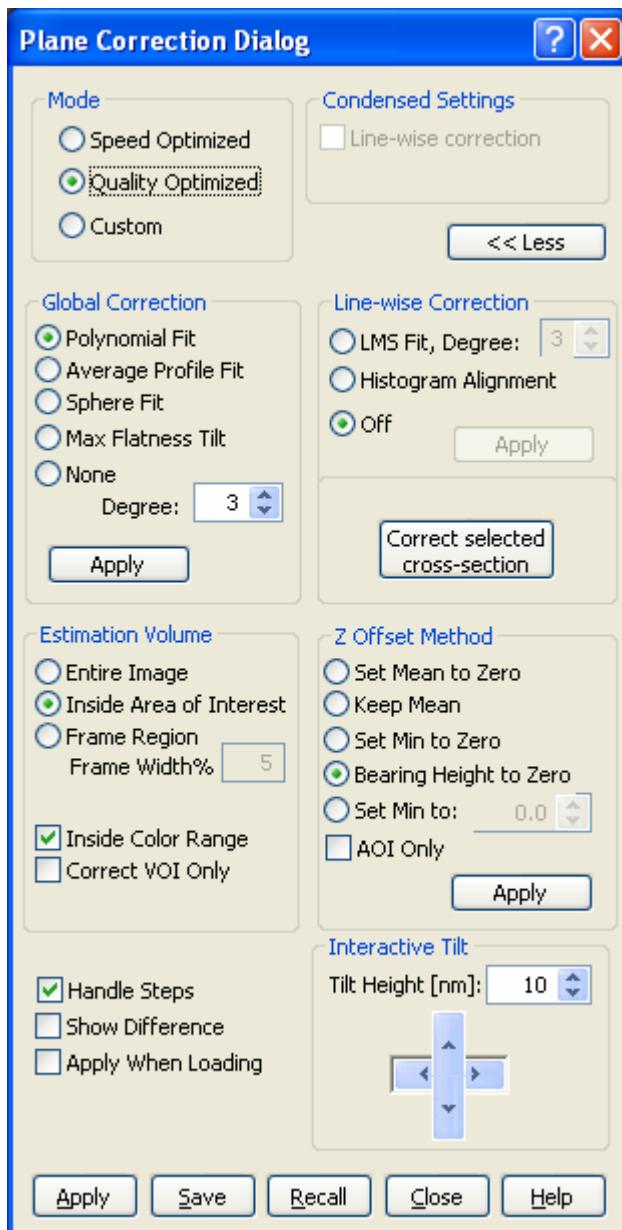
**Custom:** This mode is mainly for advanced users and offers access to all the detailed plane correction settings.

When working in the Quality and Speed optimized modes you may find it most convenient to have the dialog collapsed such that the dialog requires minimum space. Note that these modes work together with the AOI tool and the color bar markers. This means that a volume of interest can be limited and only the pixels within the volume will influence how the correction plane is calculated, see also Estimation Volume below.

**Line-wise correction** The collapsed dialog will have a single checkbox where you can define if you want to correct for line wise distortions. Line-wise distortions are typical scanning artifact occurring because the probing tip may change or pick up some contamination. When the dialog is expanded you can define in more detail how the line wise correction should be performed.

### Advanced Settings

To access all the detailed settings click the **More >>** button. The plane correction methods are grouped into three groups: Global Correction, Line-wise Correction and Z-Offset Method. In addition an Estimation Volume can be defined and interactive tilt performed.



#### Global Correction Methods:

It is possible to select between four different plane correction algorithms that subtract a fitted image to the global image:

Polynomial Fit, Average Profile Fit, Sphere Fit and Max Flatness Tilt.

**Polynomial Fit:** Slope corrects the image based on a Least Mean Square fit to the entire image or the volume defined by the Estimation Volume group box. To the image  $z(x,y)$  a plane  $zp(x,y)$  is fitted by a polynomial function of the form:

$$z_p(x,y) = z_0 + \sum_{i=1}^I a_i x^i + \sum_{i=1}^I b_i y^i + \sum_{i=1}^I c_i x y^i$$

The coefficient  $a_i$  and  $b_i$  for the polynomial function is then found by minimizing the Square Sum Error:

$$E = \sum_x \sum_y (z_p(x,y) - z(x,y))^2$$

The corrected image  $z'(x,y)$  is then calculated by subtracting the fitted plane:

$$z'(x,y) = z(x,y) - z_p(x,y)$$

#### **Profile Fit:**

The computation time for estimating the plane parameters can for some applications be inconvenient especially for images containing a large number of pixels. In those cases the number of operations can be reduced by letting the plane fit be based on the average  $x$  and  $y$  profiles. An average  $x$  profile is found by adding all individual  $x$  profiles into a single curve and the average  $y$  profile is found similarly:

$$z_{ax}(x) = \sum_{y=0}^{N_y} z(x,y) \quad z_{ay}(y) = \sum_{x=0}^{N_x} z(x,y)$$

From the  $x$  and  $y$  profiles the two sets of,  $a$  and  $b$ , coefficients is determined within a very short computation time.

#### **I Degree**

Polynomial degrees for the two Least Mean Square fit methods can be set between 0 and 5. Degrees greater than 3 are seldom recommended because the fit might then start to match the real surface structure more than the undesired plane error.

**Sphere Fit.** This will subtract an estimated sphere form.

#### **Max Flatness Tilt**

Enabling *Max Flatness Tilt* will automatically tilt the image so that the height distribution histogram will maximize the frequency a dominating height level. When SPIP detects two dominating height levels, it will maximize the sum of those two frequencies. This function has its advantage when dealing with single steps where the polynomial fit functions may fail because they will fit functions to the step rather than undesired image bow.

When setting the Global Correction method to **None** no automated Global correction methods will be performed even when "Apply When Loading" is checked.

#### **Apply (Global Correction)**

Press the Apply button in the Global Correction group box to apply the global correction method

#### **Line-wise Correction**

Small surface corrugations can sometimes be dominated by the noise in the scanner system. Typically, this creates observable steps between subsequent scan lines. Likewise, temporary contamination of the probe will cause the scan lines to be leveled differently.

In such cases the image can be corrected by leveling the individual scan lines to more probable levels. SPIP offers two methods that can be combined with the polynomial plane correction.

#### **LMS Fit**

The LMS Fit method subtracts a fitted polynomial function from each individual scan line with a polynomial degree defined by the **Degree** numerical text field.

The improvement may be astonishing. However, there might be less information about corrugations perpendicular to the scan lines. Especially for roughness measurements, this may cause underestimated values.

To achieve the best results it will often be an advantage to combine this method with the Inside Color Range check box of the Estimation Volume set. When doing so it is possible to

eliminate the influence of noise, particles and real surface corrugation and concentrate on the bow artifacts created by the scanner.

### **Histogram Alignment**

This correction technique elevates the individual x-profiles so that their height distribution obtains the best match. The result will be reflected immediately in the height distribution histogram for the image, which will show the dominating height values as sharper peaks. For structures where the average value of the profiles may vary, for example, waffle patterns for height calibration references this technique is particularly valuable. The method is especially powerful in connection with Z-calibration.

### **Apply (Line-wise Settings)**

The line-wise settings can be applied independently from the other settings using the dedicated Apply button.

### **Correct Selected Cross-section**

To correct a single scan line or horizontal line piece create at horizontal cross-section and press the "Correct Selected Cross-section" button. You can also limit the part of the cross-section, which you want to correct by applying cursors in the profile window. When the cursors are shown only the line piece between the cursors will be corrected.

The correction will substitute the pixels on the cross-section line by the average value of their upper and lower neighboring pixels.

The function is ideal for interactive elimination of local scan line distortions.

The same method can be performed by right clicking in a profile window on **Cursor Function →Correct Data Between cursors by neighboring scan lines**

### **Estimation Volume**

It is possible to limit the volume by which the fit to the image plane will be based. In this way it is possible to avoid the influence from extreme values or real surface structures not related to the scanner bow, which we want to remove. A very powerful option is to base the estimation on height values within a certain z-range defined by the color boundaries of the color bar, see Inside Color Range below

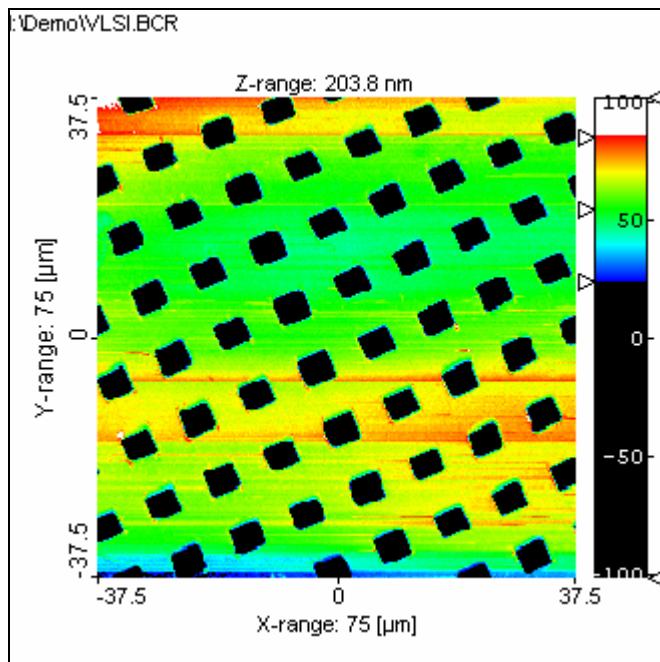
**Entire Image:** The slope correction will be based on the entire image area.

**Inside Area of Interest.** The slope correction is only based on the data within the marked Area. You can apply the Area of Interest Marking tools to define the area of interest by any shape.

**Frame Region.** The plane fit will be based only within the specified outer frame. This is particular useful when the center part of the image contains a dominating feature like, for example, an indentation that could cause a wrong estimation of the surface bearing plane.

**Frame Width,** The frame width can be set between 1 and 30% of the image width.

**Inside Color Range,** perform the estimation on the pixels having height values within the upper and lower color limits of the color bar. This enables a plane correction without influence from outliers or asymmetric distribution of e.g. pits or single steps. Below is seen how the color bar markers are used to define the Z-range, which will be used in the estimation of the plane structure; the white and black areas will be ignored.



As this option can be combined with the Estimation Area options described above it is possible to determine an estimation volume rather than just an estimation area or z-range. It is highly recommended to use this option for accurate step height measurements.

**Correct AOI Only**, only the pixels inside the Area of Interest and pixels having values within the range defined by the Color bar markers will be corrected. The surrounding will be leveled by constant values so that no or only small edges will appear.

This setting is especially useful when correcting images containing steps and where the nature of the distortion on the individual steps is different. In such case you should use the color bar markers and the AOI tools to define and correct one step at a time.

### Z Offset

The Plane Correction Dialog offers five ways of setting the Z Offset:

#### **Set Mean To Zero**

This will level the image so that the mean value of the image is set to zero.

#### **Keep Mean**

This will level the image so that the mean value of the original image is preserved after a plane correction.

#### **Set Min To Zero**

This will level the image so that the min value of the image is set to zero.

#### **Bearing Height to Zero**

This will define the bearing height as the most dominant height value (based on a height distribution histogram) and level the image so that it is set to zero. The dominant height value is identical to the value in the height distribution histogram having the highest frequency.

#### **Set Min to:**

You can also level image such that the minimum value is set at a specific value by checking the associated radio button and entering the desired min value.

#### **Apply (Z-Offset Method)**

The selected Z-Offset method can be applied independently from the other settings by clicking on the Apply button in the Z-Offset Method group box.

#### **Interactive Tilt**

The plane of the image can be tilted manually by use of the arrows and the tilt step can be controlled by the Tilt Height number entered in nm. It is possible to monitor the effect on the histogram distribution and a profile simultaneously by having these windows open.

#### **Handle Steps**

For images containing significant steps it is recommended setting the "Handle Steps" option on. In such case SPIP will combine a number of algorithms to detect and handle steps such that the flatness is optimized. This option is always applied when using the "Quality Priority" mode. A detailed description of the algorithms is a company secret and cannot be revealed. If it is important for you to document the algorithm used you should not use this option.

#### **Show Difference**

When this option is on the difference between the image before and after correction image is shown. This image is identical to the correction image and describes exactly how the image was corrected in the most recent correction.

#### **Apply When Loading**

When this check box is set the current settings will automatically be applied when opening a new image file in the following order:

Global Correction  
Line-wise Correction  
Z-Offset Correction

#### **Save / Recall**

You can save the actual settings into file such that they can be recalled again. When saving into the file called "Default.pln" you will define the default settings which will be loaded when restarting SPIP. Stored settings files can also be recalled from batch processes so that results from batch processes are independent from actual user modified settings.

#### **Apply (All)**

When clicking on the Apply button at the bottom of the dialog the selected slope correction methods will be applied on the Main Image. The result is immediately reflected in the profile curve and the histogram if open.

### **Tips and Recommendations**

#### **Monitor quality by histogram and profiles**

If you are using the Custom mode it can sometimes be necessary to process the image more times with different settings. In such case it is an advantage to monitor the histogram and a representative profile while adjusting the image plane. They are updated simultaneously with the image and you can easily see if the image is improving.

#### **Restrict estimation volume**

To avoid the influence from outliers, such as spikes, particles, pores and indentations you should apply the Inside Color Range option and the color bar markers in the image window to define a valid z-range for the estimation volume, such that the outliers will have little or no effect on the result. Likewise, you may apply the Inside Area of Interest option combined with the AOI tools to exclude outlier areas.

#### **Reducing single outliers**

If you are having specific outliers in the image which you want to reduce you can use the outlier objects filter of the filter module or the following trick:

Mark the outlier area by AOI tools such that the exterior is defined as the Area of Interest.

Select the AOI Frame, right click on it and click "Define Outside AOI's as Void Pixels"

Right click in the image on "Void Pixels→Interpolate new values"

Right click in the image on "Void Pixels→Accept"

#### **Use Undo if things fails**

While working with plane correction undesired results may occur, in which case you can take advantage of the undo function just by clicking **Ctrl+Z**. To learn more about the undo function, see the Undo section.



## Fourier Analysis and Filtering

### Fourier Dialog

The Fourier Dialog has powerful features for detailed characterization of image structures and manipulating images based on their Fourier spectrum. The Fourier tools can for example be used for:

Detection and characterization of line and lattice structures

Lateral calibration

Diagnosing time domain noise and vibration problems

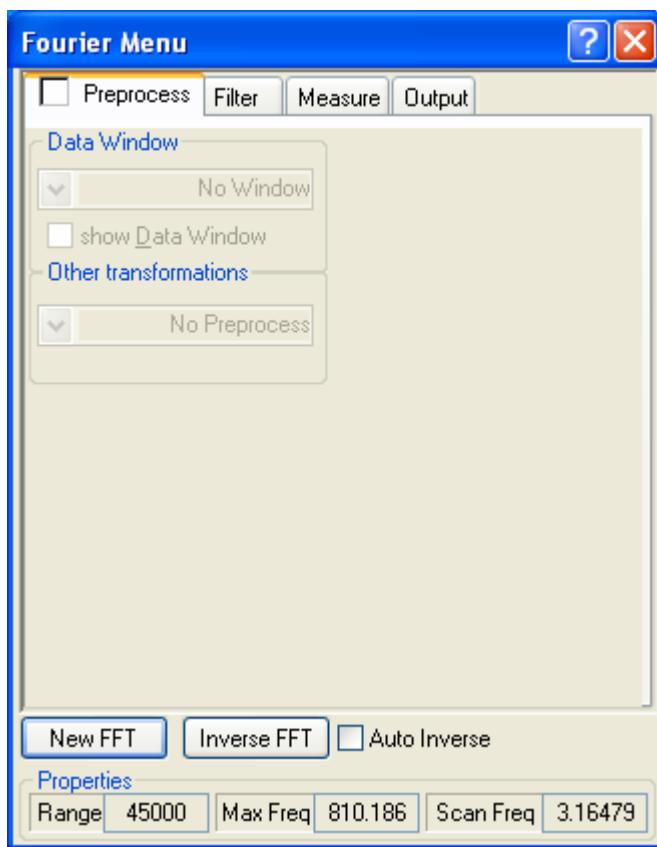
Fourier filtering by inverse transformation.

 Fourier Dialog is activated by its associated tool key or from the pull down menu

**Processing→Fourier Menu**, which will create a new Fourier Image.

The menu is closely tied to the Main Image Window, and can therefore only be accessed when the Main Image Window is open.

The menu is organized as a tab menu with four tabs:



The four tabs contain the following logical groups of functions:

**Fourier Preprocessing** defines the data window and/or other transformation of the input image to be performed before the Fourier transform is performed.

**Fourier Filtering** can predefine band filters to be performed before inverse filtering and contains strong interactive tools for removing selected Fourier components.

**Fourier Measurement** is used for detailed detection and measurement of periodicity and lattice structures. It is also possible to determine the associated time domain frequencies in Hz for diagnosis of noise and vibration problems.

**Fourier Output** defines which output windows to show and how they are scaled.

The lower part of the menu contains controls that can be accessed from all tabs:

The **New FFT** button is used for recalculation of the Fourier image. You may want to perform a new transformation when another image has been loaded into Main Image Window or the Main Image has been modified by some other procedure; or when you have changed some of the Fourier preprocessing or output options. You can also create a Fourier transform just by clicking the FFT tool key in the main menu without having the Fourier Menu open.

The used algorithms do not require any specific pixel dimension, except that there shall be an even number of pixels on the x- and y-axes. For uneven number of pixels, SPIP will automatically extend the image by an additional column or row.

SPIP applies fast Fourier algorithms for all image sizes but the best performance is achieved when the number of pixels on the axes is a power of two (radix two). Non-radix two images can be resampled to the nearest larger radix two size by right clicking in the image on "**Radix 2 Pixels**".

The **Inverse FFT** button is used for transforming the Fourier image into a spatial image, which is typically performed modification of the spectrum by the filtering tools. The produced image will be shown in its own image window and more images may appear depending on the settings in the Output tab. The inverse Fourier transform can also be performed by right clicking in the Fourier Image on "Inverse FFT". This can be convenient in connection with "Auto Erase Markings" and the "Fourier Menu" is not active.

The **Inverse** checkbox can be set to perform an inverse Fourier transform whenever the Fourier image is modified. This can create a fast (almost real-time) visual feed back of the effects of the filter settings and interactive modification of the spectrum. However, the speed depends on the actual image size and your computers general performance and for larger image it might be more convenient to have this option set off.

This option can also be set by right clicking in the Fourier Image window on "Auto Inverse FFT" when the Fourier Dialog is not active.

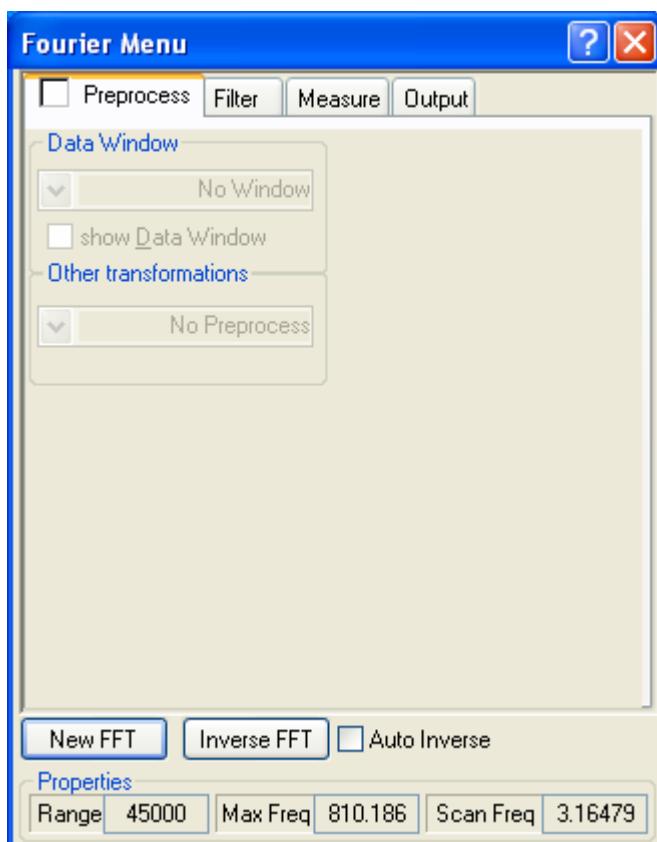
## Fourier Filtering

### Fourier Preprocessing

The Fourier Menu offers two preprocessing techniques, which can be applied to an image before the Fourier Transform is performed, these are:

Data Window: mostly used for lowering border effects and improving measurement capabilities

Other Functions: used for contrast enhancement



### Data Window

The optional Data Windows are used for minimizing an effect called spectral leakage and improving the measurement capabilities.

Discrete Fourier algorithms are created on the assumption that the input data set (image) contains an integer number of periods of an infinite number of periods. This is seldom the case and might therefore lead to undesired effects in the Fourier output. For example a curve or image dominated by a slope will in its infinite version be seen as a saw-tooth structure. As the Fourier Transformed data consist of a series of cosine functions each defined by a magnitude and phase it requires the use of higher harmonic cosine functions to describe a saw tooth structure. The resulting Fourier image will therefore contain components that are associated with the discontinuity created when repeating the images. This effect is called spectral leakage and is typically observed as stripes along the x and y axes with a magnitude that decreases as a  $\sin(x)/x$  function.

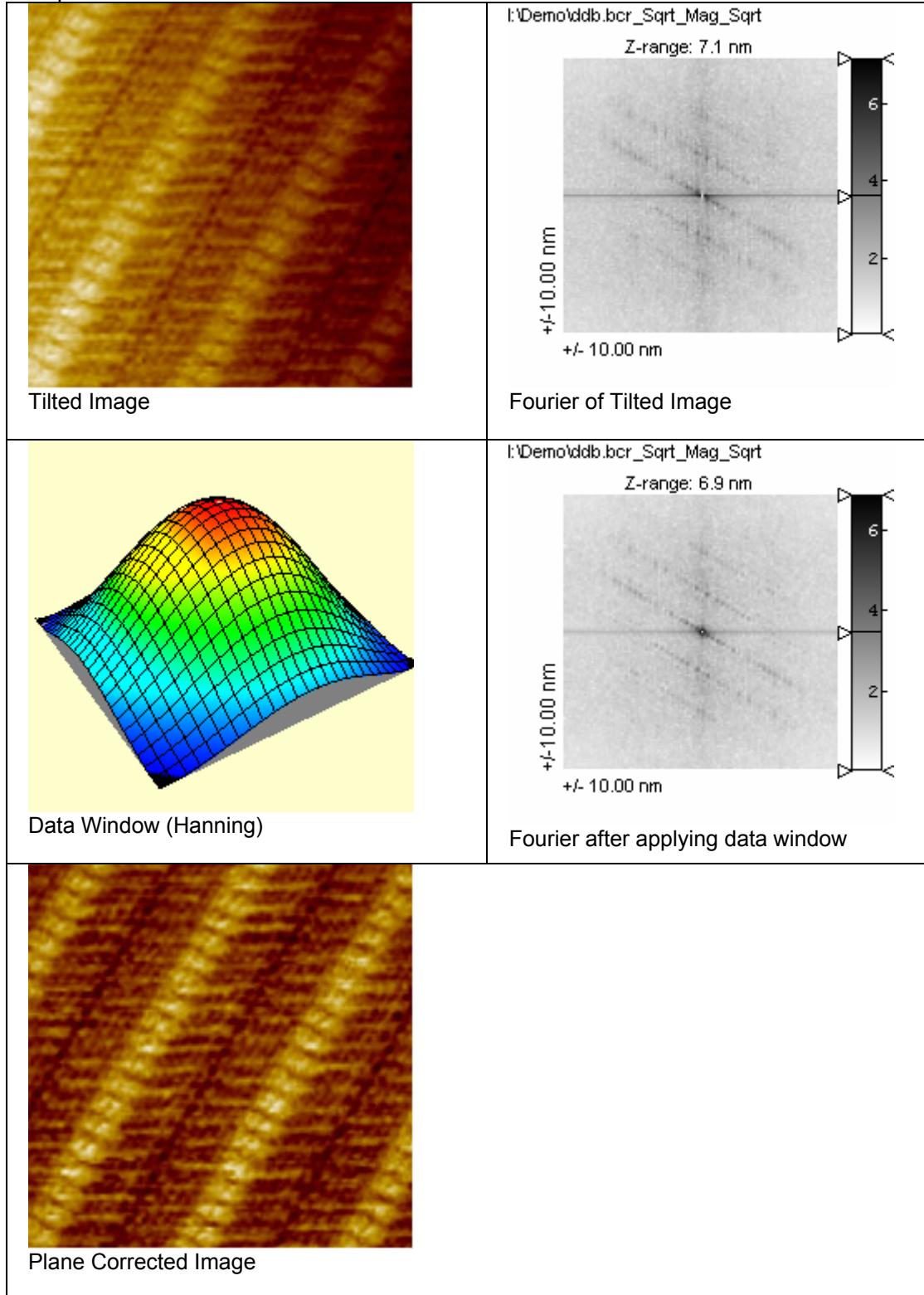
The spectral leakage can have a negative effect on measurements performed in the Fourier Image and can make it more difficult to evaluate the more interesting Fourier structure.

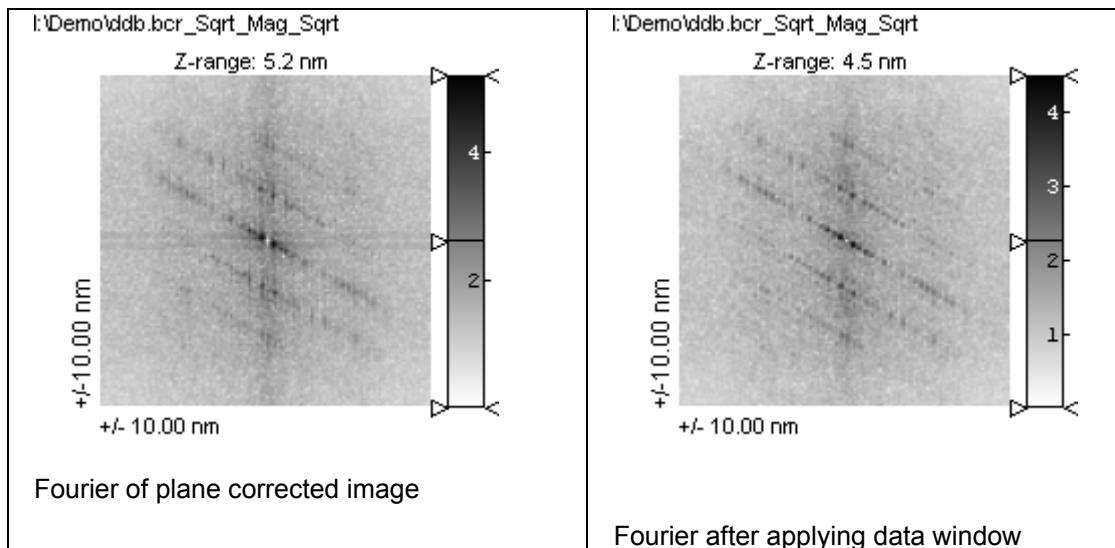
To lower this spectral leakage effect Data Windows that lower the magnitude of the border data can be applied. The side effect of the Data Windows is that the Fourier Components very next to the true Fourier peaks (Main lobe) will appear higher while the spectral leakage components further away (the side lobes) will appear smaller.

It is also worth noting that a proper plane correction of the images can reduce the spectral leakage phenomenon dramatically.

Below is shown how proper plane correction and windowing can improve the quality of a Fourier image.

The Fourier Image is scaled by a double square root to enhance the contrast of the weaker components.





SPIP offers the following Data Windows, which can be displayed by setting Show Data window on in the Output:

Hamming window  
Hanning window  
Barlett window  
Welch window

The data windows are multiplied to the image data before the Fourier Transform is performed and if an Inverse transform has to be carried in combination with Fourier Filtering it is therefore necessary to divide the Inverse Fourier result with the applied window. This requires that all window data contain non-zero values and we have therefore slightly modified the Data Windows so that no values are smaller than 0.001.

However, in combination with inverse filtering the best results are achieved when not applying data windows.

### **Other Transformations**

SPIP currently contains one other preprocessing transformation, which is at logarithmic function. This function can in combination with low pass filtering perform a so-called "Homomorphic Filtering" which can compress the brightness/height range and enhance the contrast at the same time. To perform Homomorphic Filtering follow these three steps:  
 Preprocess the data with the logarithmic function.  
 Perform a Butterworth Low-pass filtering.  
 Compute the Inverse Fourier.

## Fourier Filtering

The Fourier Filter is used for enhancing or reducing certain structures by modifying the associated Fourier components. There are often situations where it can be an advantage to apply a Fourier filter:

Reduction of noise or other undesired elements

Visual enhancement of certain structures

In combination with Roughness analysis where the user may want to measure the roughness within a certain band

To limit the unit cell detection range

The Fourier Filter tab menu contains two sub menus:

Band Filtering (Concentric Fourier Filtering), which by a few parameter settings can be used to perform:

Low-pass filtering,

High-pass filtering,

Band-pass filtering

Band-reject filtering,

Band-width filtering

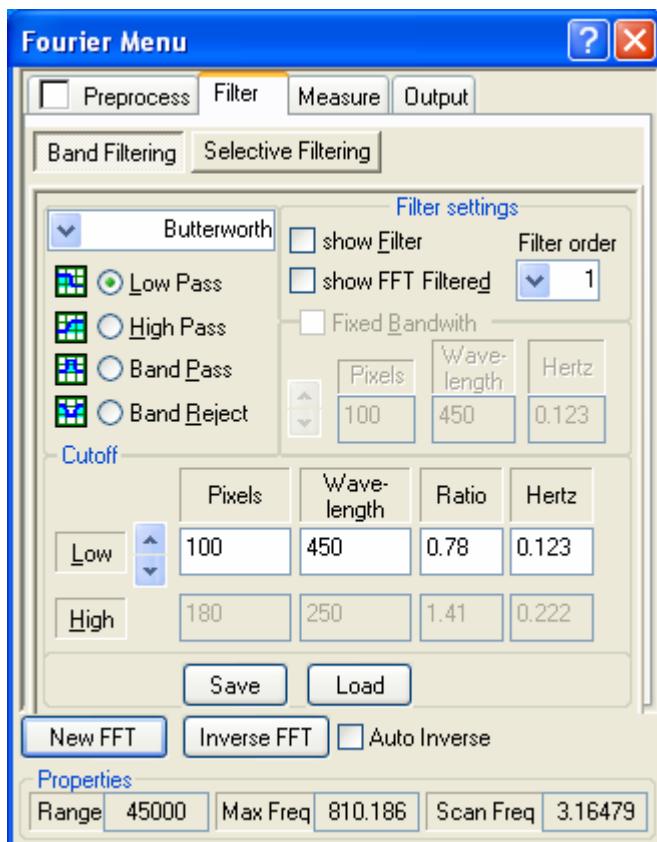
Selective Filtering, where the user interactively can remove selected Fourier components which can be selected by:

The circle, rectangle and oblique marker tools

The color bar markers or the associated Threshold Fourier Filtering scroll bars in the Fourier menu is applied for selection of Fourier components exceeding certain upper or lower values.

## Band Filtering

The Band Filtering is used to enhance or reduce frequencies within certain frequency/wavelength bands. A band filter is defined by a band type (Low-Pass, High-Pass, Band-Pass and Band-Reject), which has corresponding cut-off frequencies and by its Filter form (Ideal or Butterworth) and optionally the filter order.



The Filter Band type can be selected by their radio buttons and the cutoff frequencies by the edit fields or arrow buttons. Alternatively the cutoff frequencies can be set interactively by controlling the associated circles in the Fourier image window.

### Low Pass:

The Low pass filter will reduce the Fourier components having frequencies lower than the selected filter cut-off frequency. This will result in a smoothing or blurring of the spatial image.

### High Pass

The High pass filter will reduce the Fourier components and will typically enhance the contrast of the spatial image.

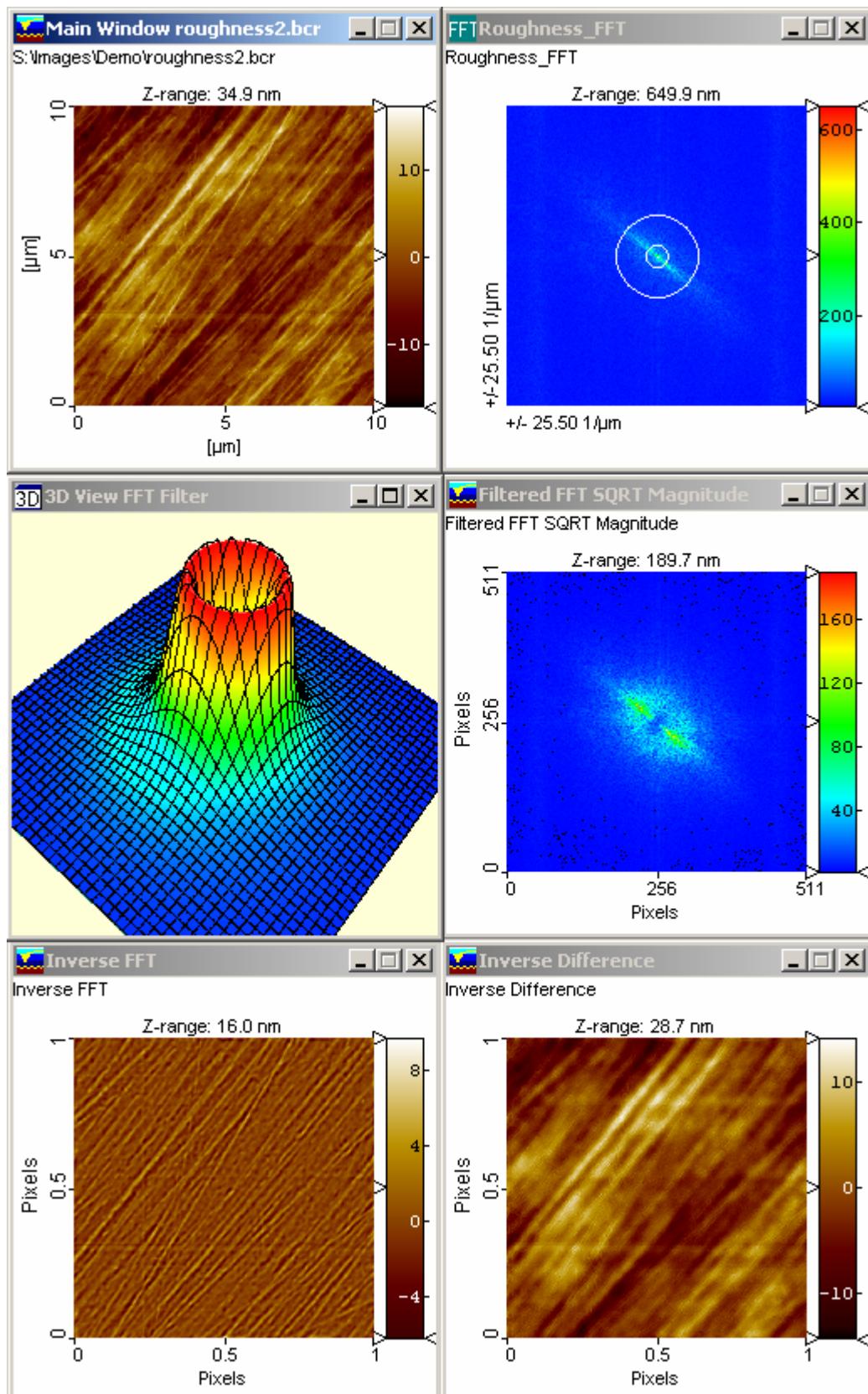
### Band Pass

A Band pass filter is a combination of a Low-pass and High-pass filter where the low-pass cutoff frequency is set higher than the High-pass cutoff frequency.

This filter type can be used for comparison of e.g. the roughness of data acquired with different instruments with different frequency characteristics. Here the filter can limit the analysis to a comparable frequency band covered by both instruments.

The Band-pass filter can also be defined by a low cut off frequency and a certain bandwidth when the Bandwidth checkbox is selected.

Below is seen a screen dump from a Band Pass filtering process:



**Upper left:** The input image. **Upper right:** the Fourier image with the upper and lower cut-off frequencies shown by circles. **Middle left:** a 3D view of the defined Butterworth band pass filter. **Middle right:** the Fourier image after multiplication with the Butterworth filter. **Bottom left:** the filtered result produced by inverse transformation of the modified Fourier image. **Bottom right:** the difference between the original and the filter result.

### **Band Reject:**

This type of filter can be used to remove a certain band of frequencies.

### **Fixed Bandwidth**

When the Fixed Bandwidth checkbox is set the band-pass or band-reject filters are defined in terms of the lower cut off frequency and the Fixed Bandwidth parameter, which will determine the upper cutoff frequency.

### **Filter Forms**

Currently two forms are implemented:

**Ideal filtering:** whereas all frequencies outside the cutoff frequency are completely attenuated.

- **Butterworth filtering:** The Butterworth filter is a more smooth function that will reduce the power (amplitude squared) of the Fourier components by 50% ( 6 dB) at the cutoff frequencies. Compared to the Ideal filter it will produce less ringing effects in the Inverse Fourier transform.

### **Controlling the Cut-off Frequencies:**

The upper and lower cut off frequencies can be controlled by the associated arrow keys.

While doing so circles in the Fourier Image will indicate the cutoff frequencies graphically and it is also possible to monitor the filter form as an image when the **Show Filter** checkbox is set.

The Cutoff circles can also be resized with the mouse in the Fourier Image Window.

It is also possible to enter the numbers directly in terms of ratio, wavelength (spatial units), pixels (Fourier Pixels) and time domain frequency (Hertz). Note, that the Hertz parameter only is valid for raster-scanned images containing proper timing information.

### **Filter settings**

#### **Filter Order**

The filter order determines the steepness of the Butterworth filter; an order of 1 will decrease the amplitude by 6 dB per octave and an order of 2 will decrease the amplitude by 12 dB per octave and so forth.

#### **Show Filter**

Checking the "**Show Filter**" checkbox will display the Fourier Filter function and changes to the filter will be reflected immediately. It might be informative to view the profile as well by putting a cross-section line across the Filter window.

#### **Show FFT Filtered**

Checking the "**Show FFT Filtered**" checkbox allows a visual check of the filtered FFT. This can be practically to see the components removed by either markers or the band filtering or even the amplitude threshold filtering.

#### **Save / Load**

If you want to apply the present filter on other images you may store it so that it can be easily reloaded or used in a Batch Process. When saving the Fourier Filter SPIP will suggest a name reflecting the Filter type and the cut off frequencies measured in pixels. Note that the filter cut off values is saved by their pixel values, meaning that the wavelength parameters will be different for image of different size.

When including a Fourier filter in a Batch Process you should use the "Fourier Filter Specific" function found in the available functions of the Batch Process Dialog.

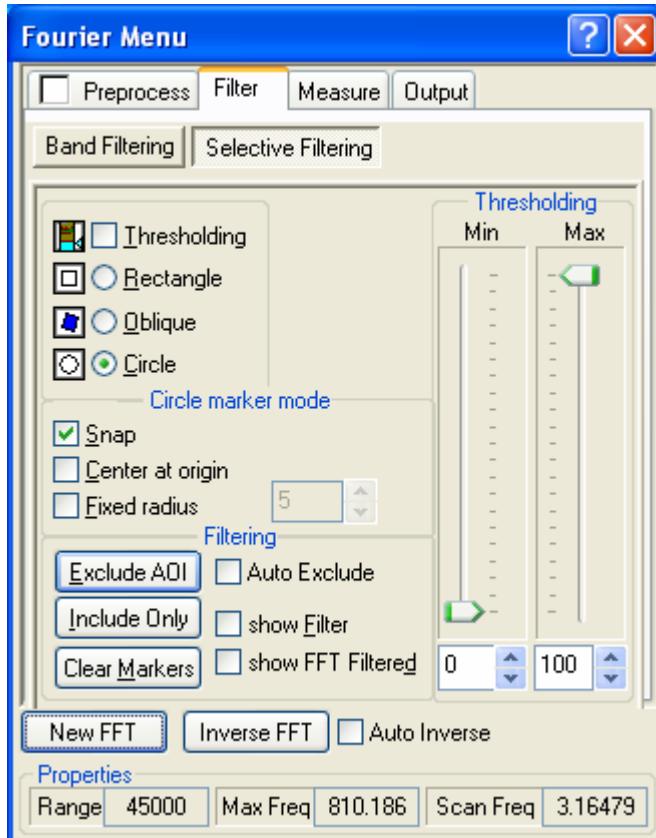
## Fourier measurement

### Selective Fourier Filtering

By use of the Selective filtering menu the user can interactively remove selected Fourier components, which can be selected by:

The circle, rectangle and oblique marker tools

The right color bar markers or the associated Threshold scroll bars in the Fourier menu, which will select the Fourier components outside the min-max range / color range..



### Rectangle marker tool

The rectangular marker tool can be selected for the Fourier menu or from the tool bar menu. Its functionality is different from its zoom functions in the spatial images. To draw a rectangle click the mouse to define the first corner then move the mouse while keeping it pressed to define the opposite corner. When the mouse is released the rectangle is defined. After having defined one or more rectangles the associated Fourier components can be set to zero by pressing "Exclude AOI". Alternatively the outside area can be set to zero by pressing "Include only". The marked areas can also be excluded automatically whenever a new shape is drawn by setting the "Auto Exclude" checkbox on.

#### **Marker tool**

When the oblique marker is active in the Fourier image it is used for marking areas of interest (AOI). This marker tool is convenient for marking an array of Fourier peaks, not parallel to the horizontal or vertical axes. The corners of the parallelogram are defined by mouse clicks: The first mouse click defines the first corner, the following mouse release determines the second corner and on the second mouse click/release the third and fourth corner are defined.

#### **marker tool**

The circle marker tool marks the area of interests by circles and can be operated in three modes defined by following checkboxes:

**Snap:** When Snap is set on the circle center is roughly defined by the first mouse click while its radius is defined by the mouse position when releasing the mouse button. The circle will then automatically be re-positioned so that its center is positioned at the highest Fourier component inside the manual drawn circle.

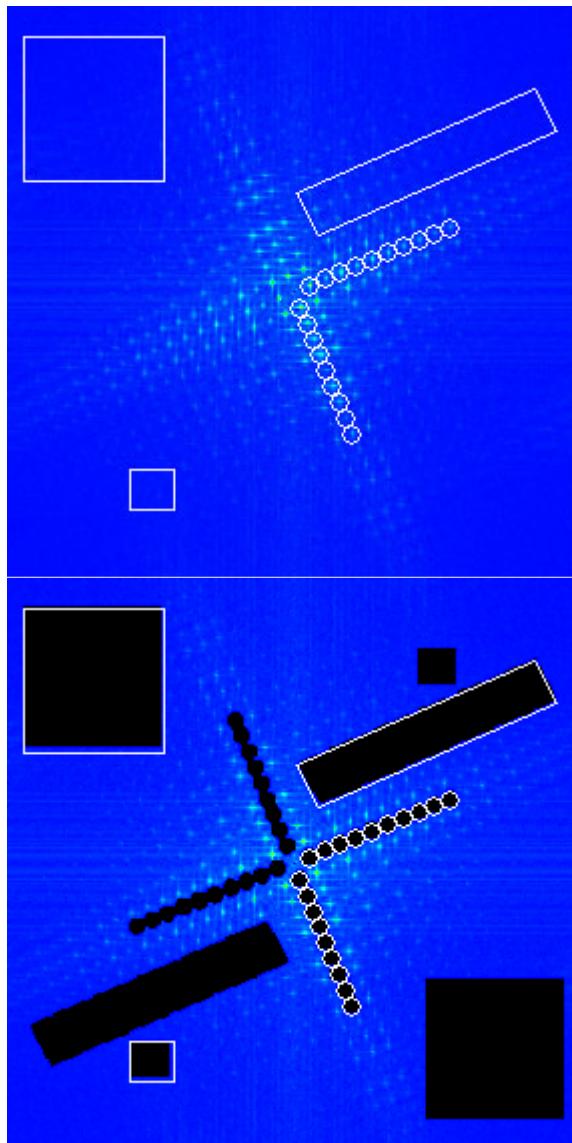
**Fixed Radius:** When this option is set on the circle will have a fixed radius given by the numeric field and the Center at Origin option will be set off. The position of the circle is defined by the mouse pointer and the Snap option.

**Center at Origin:** When this checkbox is set the drawn circle will always have the center at the origin (DC) and the Fixed Radius will be set off. You may use this function to perform low-pass, high-pass or band-pass filtering. To perform a low-pass filter mark the cutoff frequency by the circle marker and press Include Only

#### **by "Including" or "Excluding" Marked Areas**

After having defined area of interest (AOI) by the marker tools described above it is possible to set the associated Fourier components to zero by the **Exclude AOI** button or set the exterior area to zero by the **Include Only** button. The areas can also be excluded automatically whenever a new area is marked by setting the "**Auto Exclude**" checkbox on. In combination with "**Auto Inverse**" checkbox it is possible to monitor the effect on filtered spatial image immediately.

Below is seen an example with some regions marked on the left Fourier image and the right image shows the effect of excluding those regions. Note, that it is important to keep the symmetric property of the Fourier image, which is why SPIP also excludes the mirrored regions.

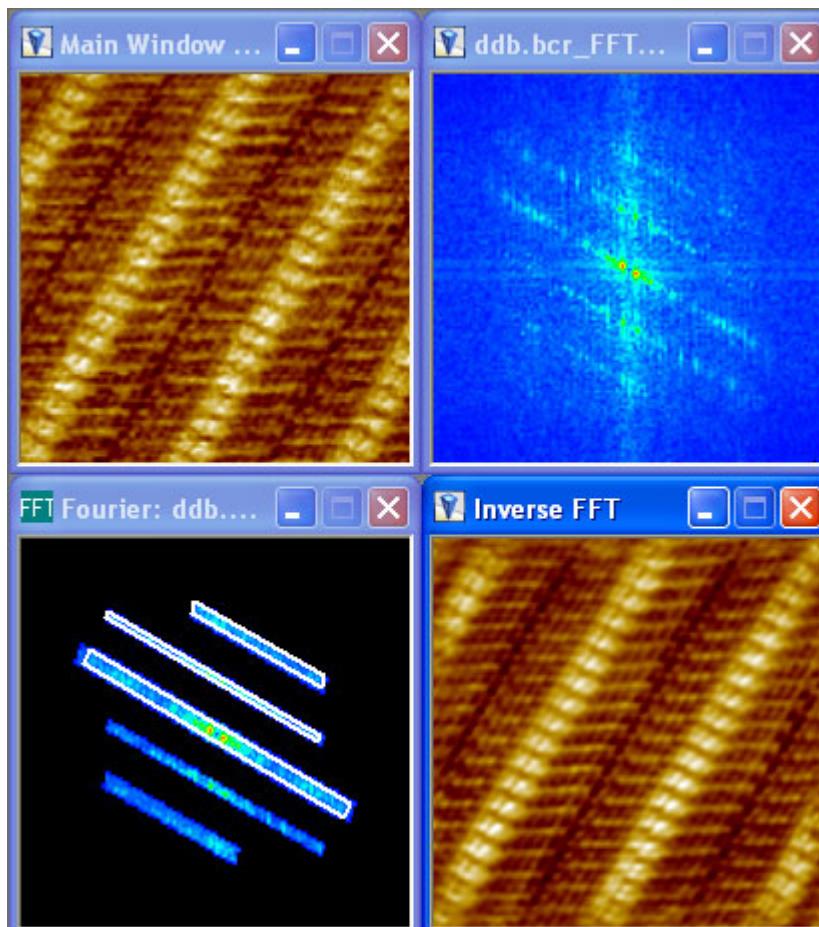


Note, that the **Auto Exclude**, and **Auto Inverse** settings also can be set by right mouse clicks in the Fourier image window without having the Fourier menu active.

When excluding areas it will work as a mask that is multiplied with the defined Band Filter and the resulting filter image can be monitored by setting "**Show Filter**" on. Likewise the resulting Fourier image after applying the filter can be view by setting "**Show FFT Filtered**" on.

Pressing the "**Clear markers**" button will clear the markers and reestablish the excluded areas.

The following shows an example of including only some Fourier components.



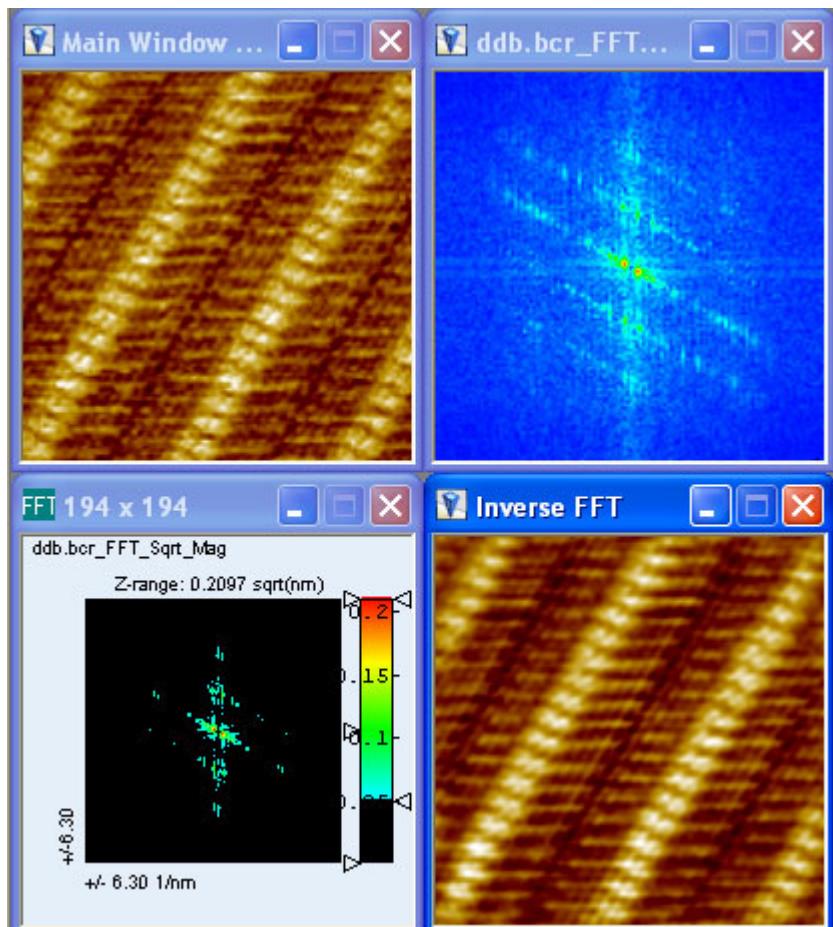
The main window holds a repetitive structure and has also a specific orientation. The effect of this can be seen in the full Fourier transform where the highest peaks form lines, oriented perpendicular to the spatial line structures. It is possible remove all Fourier components not associated with the lattice structure using the "**Oblique marker tool**" to mark the relevant lattice peaks and pressing the "**Include only**" button. The filtered result created by the Inverse Fourier function should then give a better impression of the repetitive features of the image and the distances of the side-extensions of the single elements are more distinct.

#### Fourier Amplitude Threshold Filtering

By the right Color Bar markers in the Fourier image or the corresponding Min and Max threshold scroll bars of the Fourier menu it is possible to define Fourier components to be removed based on their magnitude. Components having values lower than the min value or higher than the max value will be set to zero.

When clicking on the **Inverse FFT** button the filtered image will be shown. Checking the "**Auto Inverse**" will cause a computation of the filtered result while changing the threshold values.

When Min threshold value is set low it will mainly affect the white noise and you may regard the technique as a white noise filter. The scaling defined in the Output tab will change the sensitivity of this function. If the Min threshold is set high then only the most prominent Fourier components will appear in the filter result image. This is demonstrated in the following example.



## Fourier Output

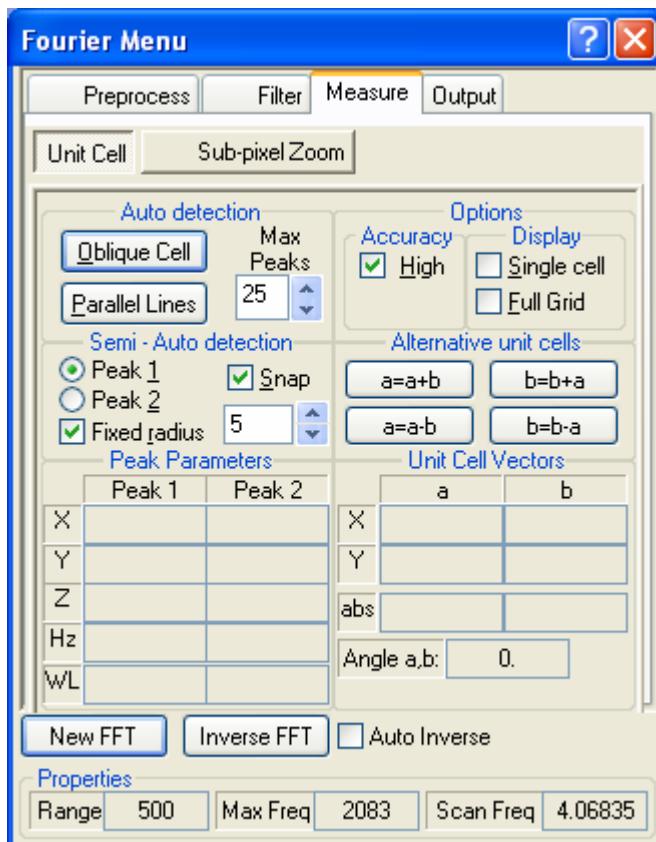
### Fourier Measurement

The Measure tab of the Fourier menu is used for measuring systematic periodicities in the image by analysis of the associated Fourier peaks at sub-pixel level. Periodicities are most often part of the true surface in which case we may want to use SPIP to detect and measure the lattice structure and maybe perform a calibration when the reference values are known. However, periodicities may also originate from coherent noise or vibration problems during the scanning process, in which case you can use SPIP to diagnose the problem and determine the time domain frequency in Hz.

#### Fourier Unit Cell detection

The spatial unit cell will be identical to the lateral unit of the spatial image and is a powerful technique for accurate characterization of lattice structures.

#### Fourier Unit Cell Detection



#### Auto Detection of unit cells

SPIP can automatically detect oblique unit cells and parallel line structures based on the Fourier image.

Press the "**Oblique Cell**" or the "**Parallel Lines**" method to start the automatic detection. If the detection is successful the numeric fields describing the unit cell are updated and the unit cell is drawn in the spatial image.

For line structures the **a** vector parameters describes the repeat distance and orientation while the **b** vector is a perpendicular vector set to a size identical to the width of the image. This makes it possible to apply the oblique marker on line structures as well.

#### Max Peaks

It is possible to change the number of max peaks for the algorithm as such to make it more or less sensitive to the weaker peaks as only the most prominent peaks are analyzed.

For noisy images where SPIP may fail to detect the lattice structure the detection algorithm may be assisted by removal of certain Fourier components, using the Fourier Filtering

section, or by changing the scaling of the amplitude values (does not require an inverse Fourier transformation).

After a successful unit cell detection the "Unit Cell and Calibration Results" dialog will appear. Here, you can enter reference values and calculate the corresponding correction factors, see <Lateral Calibration and Unit Cell Detection> for further details.

For a noisy images where SPIP might fail to detect the unit cell correctly, the detection algorithm can be assisted by exclusion of Fourier components associated with noise, see Selective Fourier Filtering.

**High Accuracy:** When this checkbox is set on, the Fourier Peaks are found by a very accurate Sub-pixel Fourier algorithm other wise the peaks are found by a faster but less accurate parabolic fit method. This setting is also used for semi-automated detections.

For further information about unit cells and unit cell detection consult the Reference Guide

### Semi-Auto Detection

By selecting two Fourier peaks associated with two corners of the reciprocal unit cell by the circle marker it is possible to determine the unit cell semi-automatically.

The associated spatial unit cell is calculated when the Peak 1 and Peak 2 pairs has been defined and the results are written in the Unit Cell Vectors box.

**1:** Having this checkbox set on, the highest Fourier component inside the circle marker will be found when ever a new circle has been defined. The co-ordinates, the corresponding wavelength and the associated time frequency in Hz will be calculated. Furthermore, the unit cell will be calculated when Peak 2 has been defined as well.

**2:** This checkbox works similarly to the Define Peak 1 checkbox.

When Snap is set on the circle will be automatically positioned with the Fourier peak at the center after releasing the mouse button.

**Radius:** When this option is set on, the circle will have a fixed radius given by the numeric field.

The position of the circle marker is defined by the mouse pointer and the snap option setting.

### Detection Settings

#### Peak Parameters

When a peak has been defined by the circle marker it's X, Y co-ordinates will be written as the Fourier pixel co-ordinates and the Z values are written as Fourier Image values using the same units as the main image. Note that the Z values will be influenced by, for example, the square root and the square functions.

Peak Parameters		
	Peak 1	Peak 2
X	2.3786	2.1221
Y	1.4175	-17.445
Z	0.03596	0.01298
Hz	4.7573	4.2441
WL	3.6114	0.56904

When the information on the scanning velocity is known the time frequency associated with the Fourier peak is calculated and shown in the Hz field. Use this feature as a diagnostic tool for characterizing noise and vibration problems. This frequency can often be found be close to the 50 or 60 Hz net frequency, a resonance frequency of the instrument or a sound frequency in the environment.

The spatial wavelength associated with the Fourier peak will be written in the WL fields. You may use this function to determine repeat distances of, for example, line structures.

#### Unit Cell Vectors

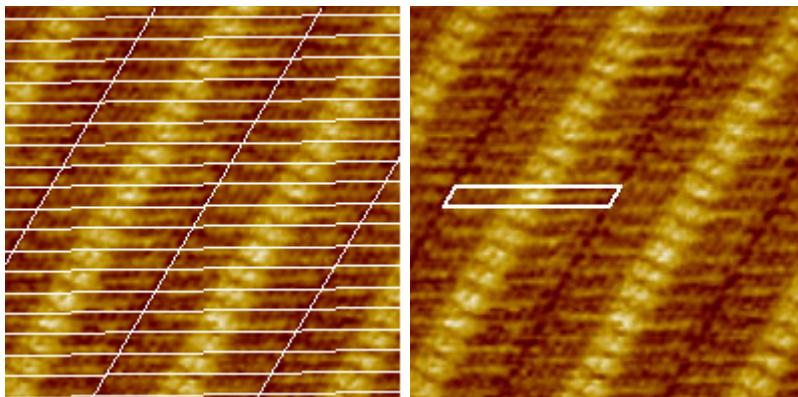
The spatial unit cell is characterized by two unit cell vectors **a** and **b** for which the co-ordinates are written in the corresponding fields. The unit of the parameters will be identical to the lateral unit of the spatial image. Also, the absolute length of the unit cell vectors and their angle are written.

Unit Cell Vectors		
	a	b
X	-3.9199	0.31852
Y	-0.47684	-0.53449
abs	3.9488	0.62220
Angle a,b:	113.86	

The result of the unit cell detection will also activate and update the Calibration and Unit Cell Results dialogue window where the correction factors are shown. Furthermore the unit cell results are written to \*.cal files, which may be used by third party programs for statistical analysis. Note that the calibration results only have meaning when the reference data exists and are set correctly. Otherwise, the unit cell detection function is a powerful technique for accurate characterization of lattice structures.

#### Showing the Unit cell

The spatial unit cell can be displayed as a "**Single Cell**" or as a "**Full Grid**". When the unit cell is displayed as a grid the grid represents the lattice structure associated with the unit cell. The spatial unit cell and the grid can be moved around with the mouse to visually inspect how well it fits to different parts of the image and as such to detect deviations from the lattice structure found. Deviations typically relates to non-linearity of the scanner.



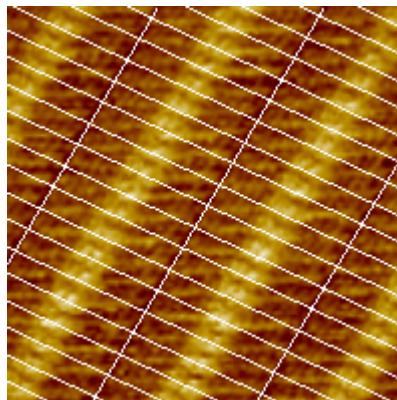
#### Alternative Unit Cells

A lattice can be described by alternative unit cells, the one SPIP displays is one having the angle between the **a** and **b** vectors most close to 90 degrees. Sometimes it might be convenient to display the detected unit cell differently to highlight the correspondence with, for example, single molecules.

For this purpose SPIP provides four buttons **a=a+b**, **a=a-b**, **b=b+a** and **b=b-a** for interactive calculation of alternative unit cells by vector addition and subtraction.

Alternative unit cells			
a=a+b	b=b+a		
a=a-b	b=b-a		

The result is displayed by the oblique marker in the Main Image and in the **a** and **b** vector fields of the Fourier Menu simultaneously.

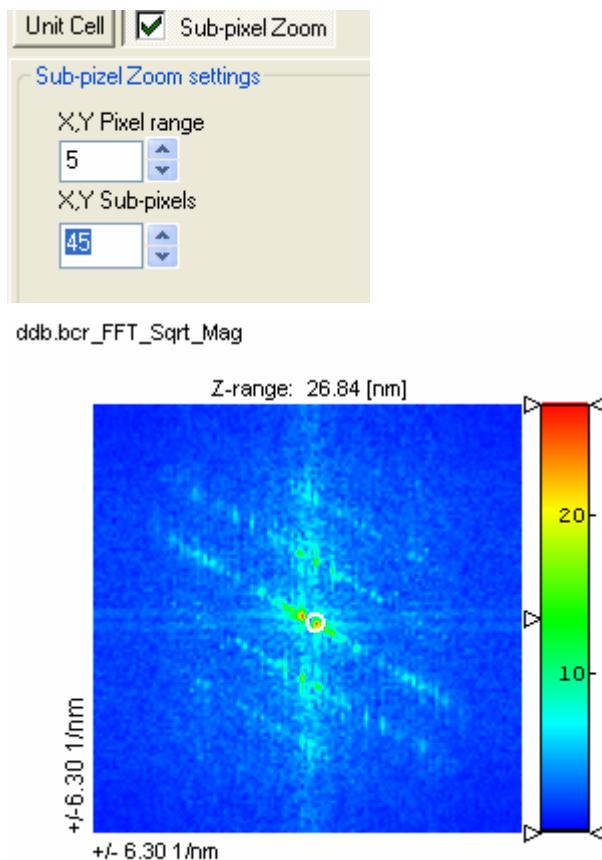


### Subpixel Zoom

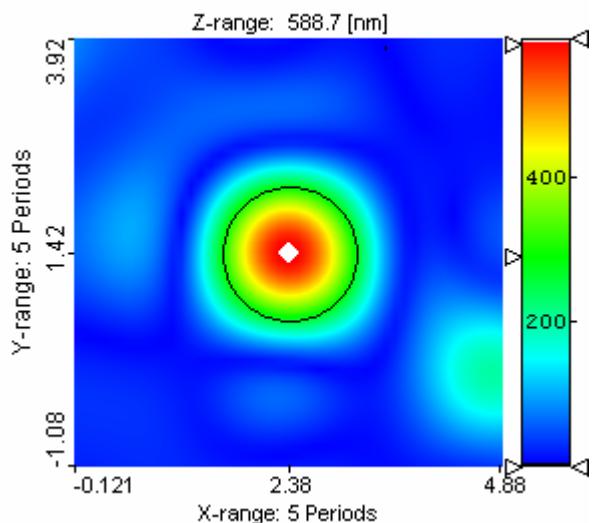
When checked a zoomed sub-pixel image of the peak will be calculated whenever a circle is drawn in the Fourier Image. This option can be applied for evaluating the sharpness of the peaks and the accuracy of the peak automated detection. It is useful to have the Snap function set on, because it will assure that the peak is put in the center.

**X,Y Pixel Range:** Defined in terms of normal Fourier pixels the size of the area, which will be zoomed.

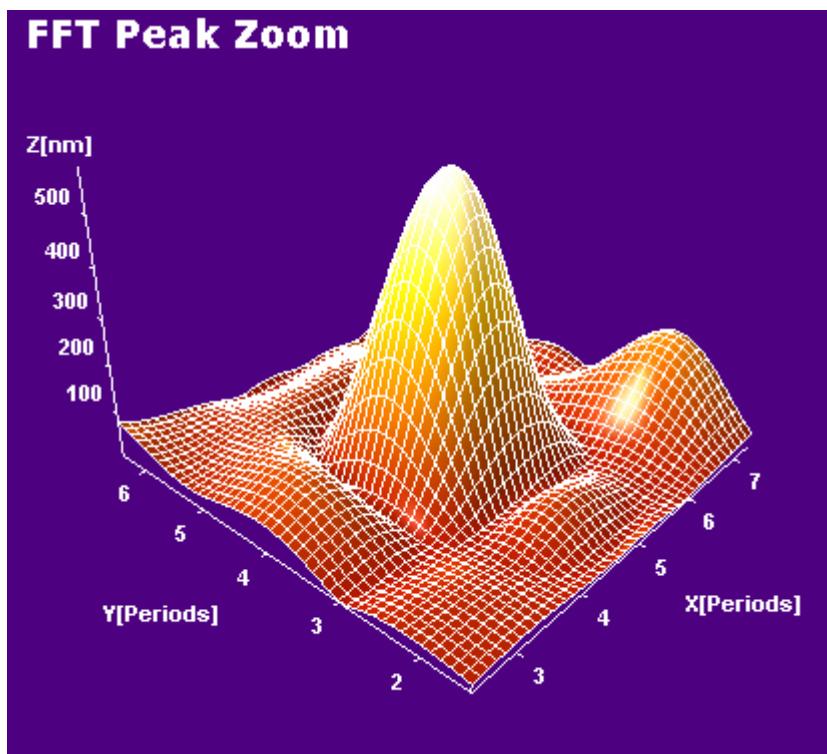
**X,Y Sub-Pixels:** Defines how many sub-pixels in each direction will be calculated. In the following a 5x5 Fourier pixel range was zoomed into an image of 45x45 pixels. The 2D-Zoom image shows automatically a circle indicating where the amplitude has decreased by a factor of two.



No Name



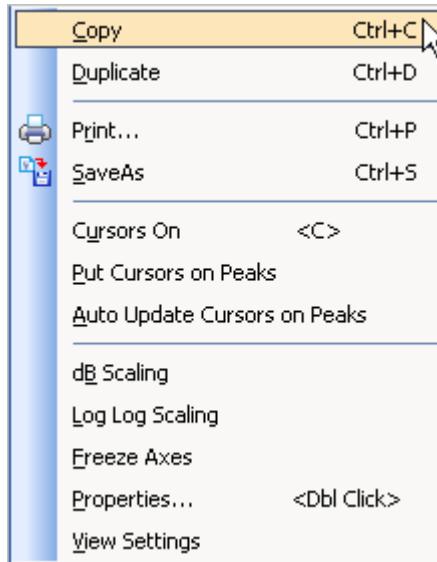
### FFT Peak Zoom



## 1D Fourier Analysis

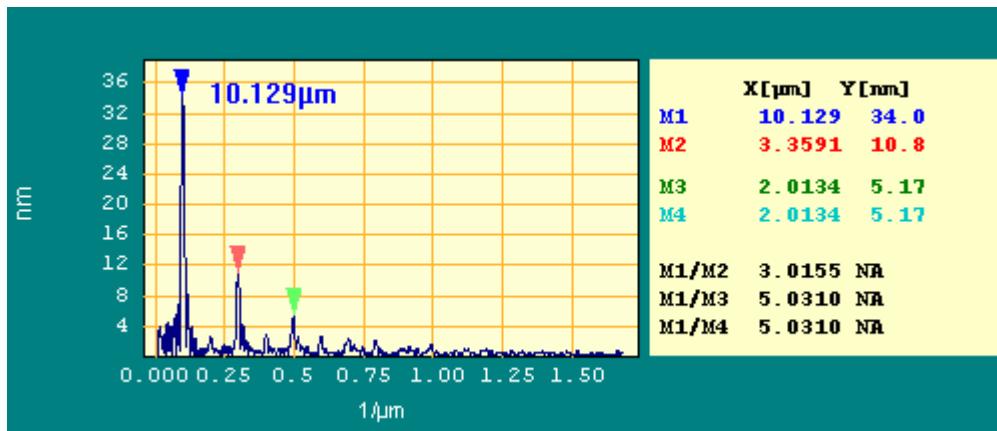
The Fourier transform of a profile is calculated when right clicking on one of the Fourier functions in a profile window. The 1D Fourier window has strong tools for analyzing periodic structures and diagnosing noise or vibration problems. To achieve the highest accuracy it will be an advantage to apply the **Fourier X 16** (Requires the Calibration Module) function of the Profile context menu.

The 1D Fourier window has its own context menu activated by the right mouse click:



**Cursor On:** When right clicking on Cursor On or pressing 'C' on the keyboard the number of cursor pairs will change between zero, 1 and 2 pairs.

The cursors can be used to measure a periodic distance (pitch) by moving a cursor to the first harmonic peak. Then the corresponding wavelength is calculated and written in the text field of the window and next the first cursor, see example below.



The **MX/M1** fields are used for testing the harmonic numbers; SPIP automatically divides the wavelength of the different cursors with the wavelength of cursor M1. In this example, M1 points to the first harmonic, i.e., the pitch, M2, M3 and M4 are pointing to the 2<sup>nd</sup>, 3<sup>rd</sup> and 4<sup>th</sup> harmonics respectively, which is confirmed by the **M2/M1**, **M3/M1**, and **M4/M1** fields. The higher harmonics can be used for getting a statically estimate of the pitch by multiplying the wavelength values by their harmonic numbers.

**Put Cursors on Peaks** (Requires the Calibration Module)

Click this function and the four highest peaks will be detected and indicated by the cursors. When using this automated technique the peak positions will be calculated at sub-sample level by parabolic fits, so that the wavelength calculations shown in the graph will have a much higher accuracy.

**Auto Update Cursors on Peaks** (Requires the Calibration Module)

This option will cause the Peaks to be detected (at sub-sample level and indicated each time the Fourier transform changes.

**dB Scaling;** The dB scaling can be used to enhance the weaker details of the Fourier transform. The maximum Fourier value will be set to 0 dB.

**Log Log Scaling**

When the profile window contains an amplitude spectrum the fractal dimension can be evaluated by the Log Log function. The fractal dimension is defined as 2.0 minus the estimated slope of the Log Log plot. The fractal dimension can also be calculated for all directions of an image as part of a roughness analysis.

**Freeze Axes;** when performing comparisons it can be useful to keep the axis frozen. Likewise it can be an advantage to duplicate a window before entering new data.

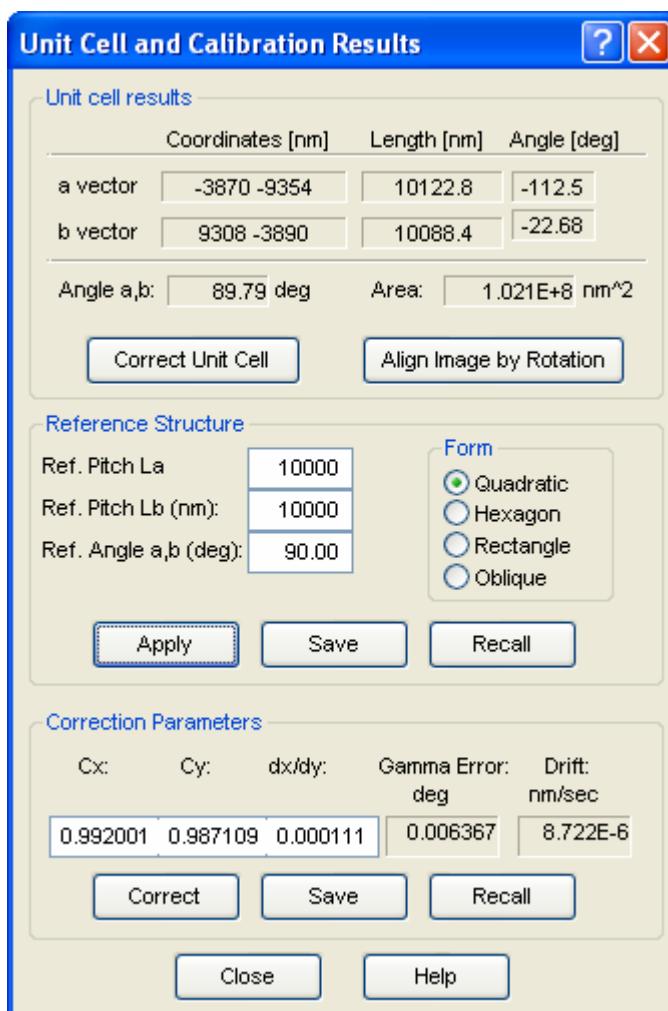
# Calibration

## Lateral Calibration and Unit Cell Detection

The lateral calibration depends on images containing structures with known pitch dimensions. The procedure can be performed in one or more steps depending on the accuracy required.

The process is started by clicking on the key for XY-calibration, .

This will automatically give you the necessary information about the unit cell, and correction factors shown in the Unit Cell and Calibration Results Menu. And if you believe that your system is linear the procedure is finished. Otherwise you should continue with the fine linearity analysis.



In the top of the menu are written the data for the detected unit cell vectors.

By clicking on **Correct Unit Cell**, the unit cell parameters will be corrected by the correction parameters shown at the bottom of the dialog. Therefore if the correction parameters are already known it is possible to correct the detected unit cell without correcting the entire image. It is often useful to rotate an image so that the unit cell or line structure is parallel to the axes, - this can be done automatically by clicking on the **Align Image by Rotation**, see more details about image rotation in the Rotation section.

### Reference Data:

Below the unit cell data, you can enter the proper reference values for the reference unit cell, the length of the two unit cell vectors and their angle.

The correction parameters can be calculated based on three unit cell forms: Quadratic, Hexagonal, Rectangular or the generic Oblique form.

#### **Save & Recall Reference Data**

The reference data can be saved into individual files and recalled again. Note that the reference files \*.crp may also contain step height information, which is preserved when saving the lateral reference data.

#### **Correction Parameters:**

Click on the **Apply** button to get the corresponding correction factors calculated.

The three correction parameters  $x_c$ ,  $y_c$ ,  $dx/dy$  are the necessary parameters for reconstructing an image with correct scaling and angles. They are described in detail in the Reference Guide Lateral Calibration by Quadratic Unit Cells.

#### **Save & Recall Correction Data**

The calculated correction parameters can be saved and recalled so that they can be applied to other images. The menu can be opened directly from the menu bar:

**Processing→XY-Calibration or Unit Cell Detection→Correction Menu**

To perform a correction by the calculated correction parameters or some entered parameters by you, click on **Correct**.

If the correction parameters were the one calculated from the current image, you can check the correction:

 A new calculation of the correction parameters should result in values close to neutral, i.e.,  $x_c = 1$ ,  $y_c = 1$ , and  $dx/dy = 0$ .

The quality of the results from this Fourier-based unit cell detection depends on the linearity of the scanner. If the image has distortion from hysteresis or some other phenomenon that causes non-uniform sampling of the surface it is advisable to continue with the Lateral Linearity Calibration.

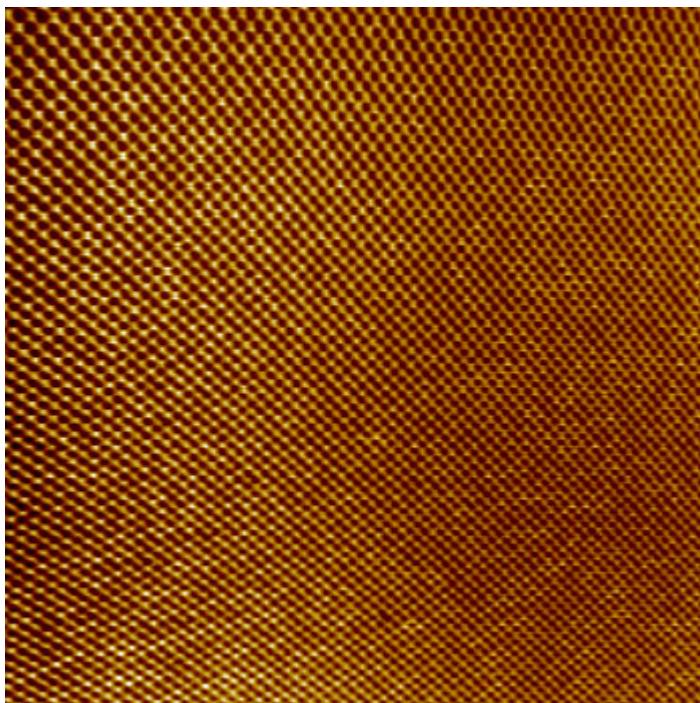
## Lateral Linearity Calibration

SPIP has two methods for linearity analysis implemented the Coarse Hysteresis Correction method and the Fine Linearity Correction method.

### The Coarse Hysteresis Correction method

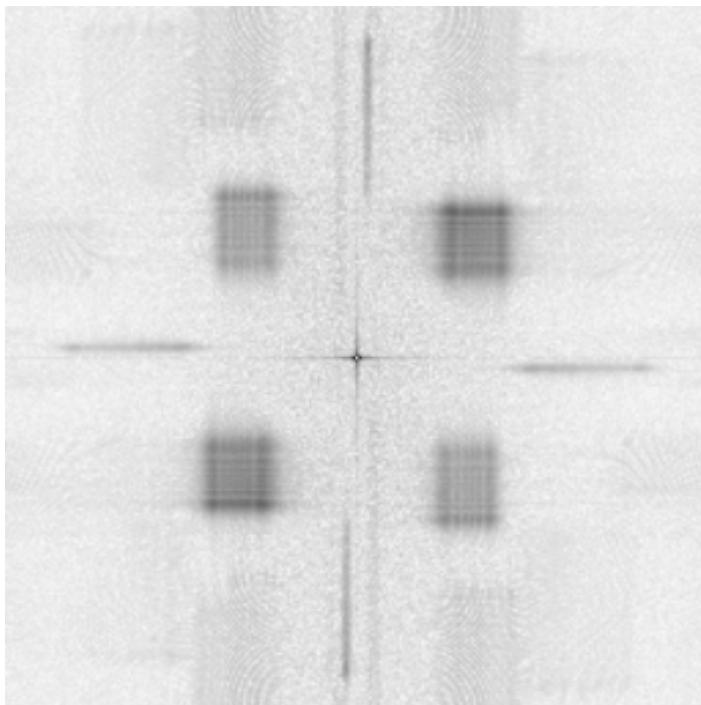
 The first applies to images where the distortions are caused by hysteresis. A 2<sup>nd</sup> order polynomial model is used for describing the hysteresis and the model is tuned so that the Fourier peaks are maximized. You can try the method on the *hyst.bcr* file which came with SPIP (to get adequate result on this specific file a license for analyzing images larger than 128 x 128 pixels is required).

 Open *hyst.bcr*.

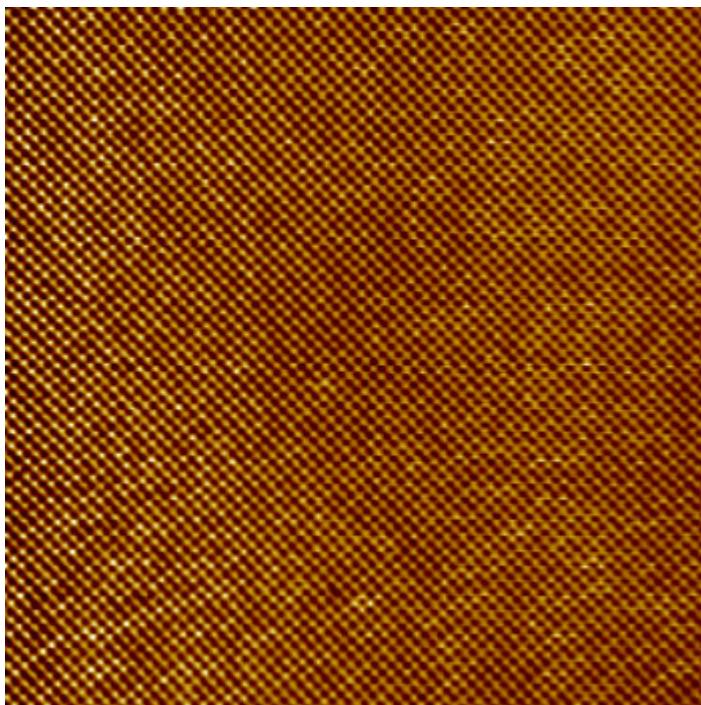


You will find that the repeat distance for the features is highest on the upper left part and smallest on the lower right part. This is an effect of non-uniform scanning caused by hysteresis. The scanner has sampled at equal time intervals but the scanning speed was lower on the upper left part where the scan started than the lower right part.

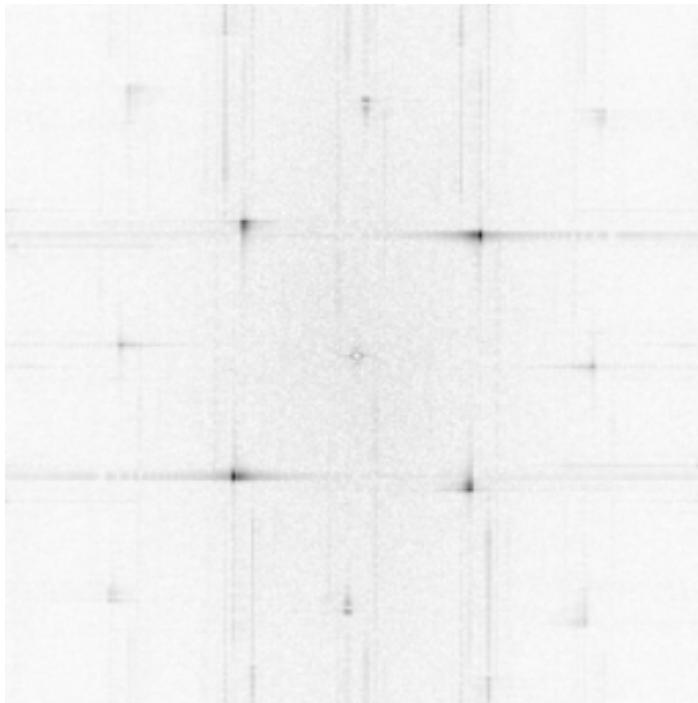
 Take a look on the Fourier image and you will see that the narrow peaks typical of calibration objects have broadened to rectangular forms:



Click on the **Coarse linearity** button and a new corrected image will be calculated:



Make a new Fourier image and you will see that the Fourier peaks associated with the real structure have been restored

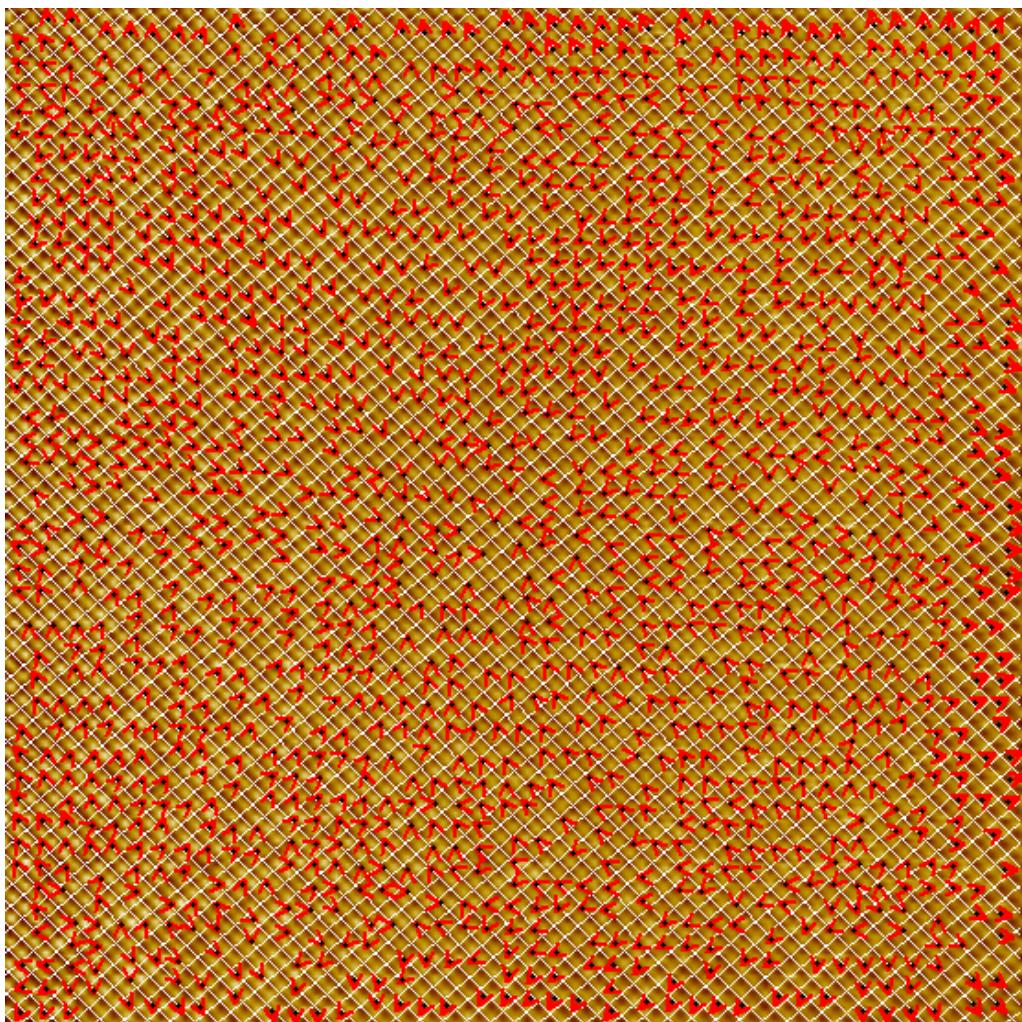


### Fine Linearity Calibration.

 The Fine Linearity Correction method is a very powerful tool for finding non-linearity even smaller than the size of a pixel. It is therefore the best method for checking the quality of high-end metrology systems.

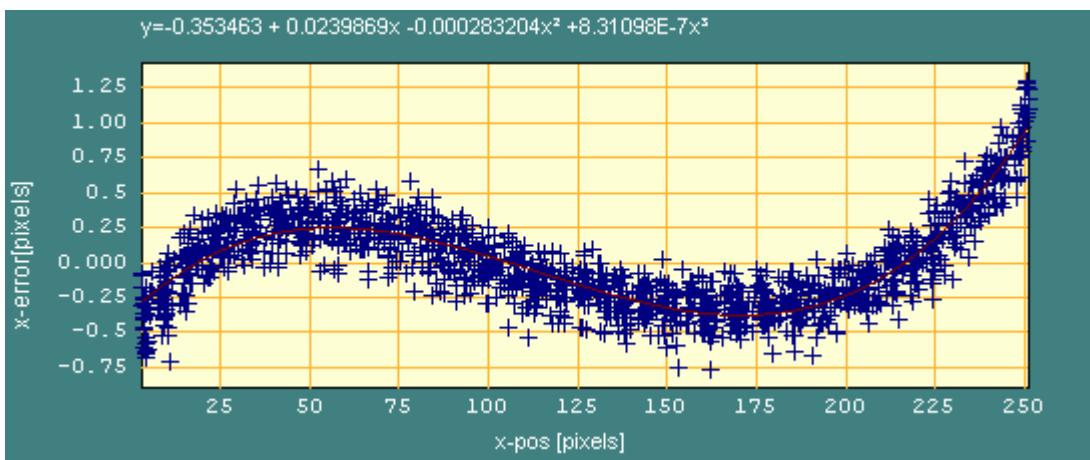
#### Example:

If you continue the with the hysteresis corrected image calculated as shown above by a fine linearity analysis  you will get a new image with the unit cell indicated together with error vectors.

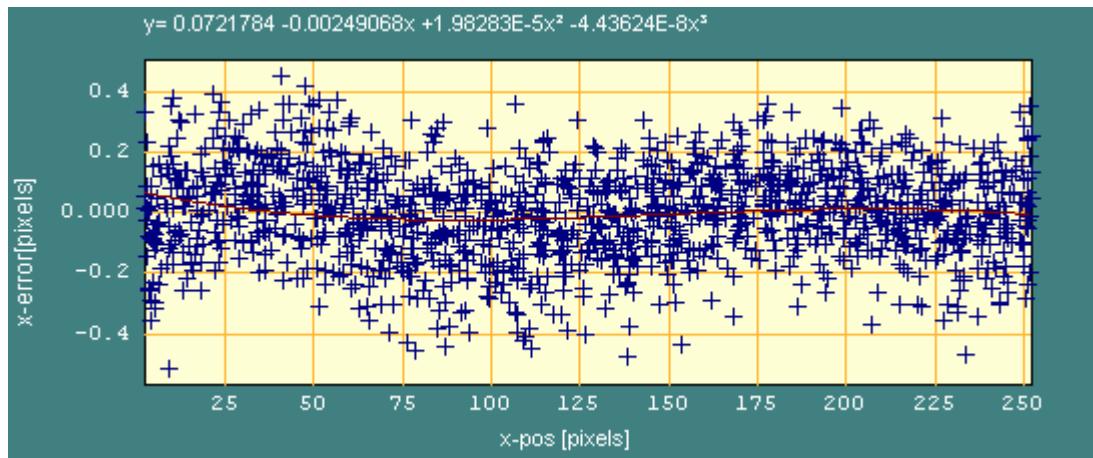


The red error vectors are of relative size and mainly used for visualizing the error direction and relative magnitude; the black points are the (0,0) anker points of the vectors. You can turn the unit cell and error vector indication off by the oblique marker tool .

The absolute magnitude of the linearity errors are best found in the scatter diagrams or the Linearity Correction Dialog where you still find some residual error within +/- 1.5 pixels:

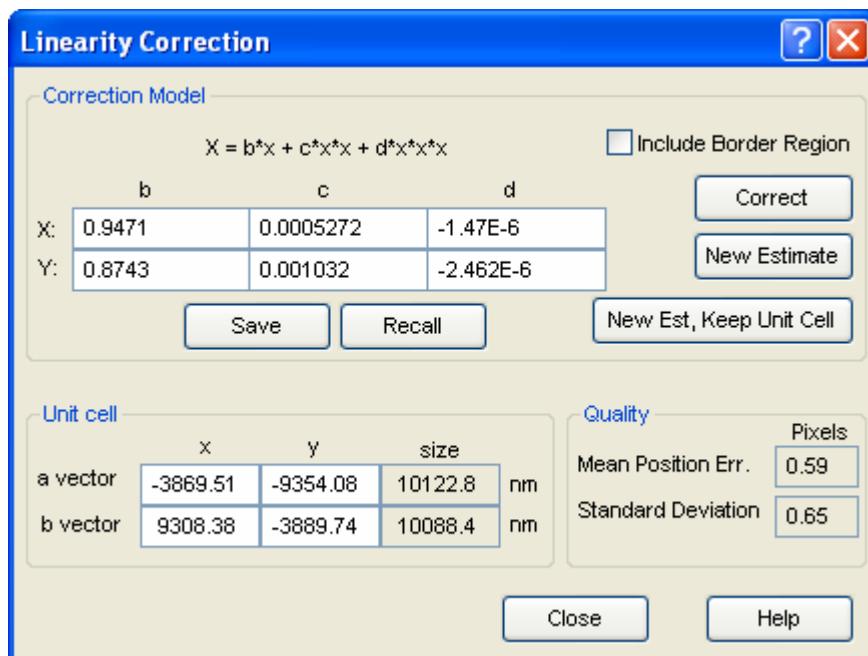


Continue by pressing **Correct** followed by **New Estimate** and you will find that all errors are in the sub-pixel regime:



The linearity analysis relies on the definition of a template, which is a representative repetitive structure. The user can define the template with the rectangle marker tool. When no selection is made SPIP will just create one which can cover a unit cell. Selecting a large template will provide the most robust result but requires more computation time. Smaller templates can provide more information about the linearity close to the image borders.

When a template is selected, the associated toolbar button starts the fine linearity analysis. If the unit cell has not been found earlier it will automatically be calculated by the Fourier method first. Then SPIP finds from the cross correlation the sub-pixel positions of all structures similar to the template shown in the zoom window. It will compare the positions with those predicted from the unit cell data. The differences are described as linearity errors, which are further, minimized by minimizing the sum of square errors (now in the spatial domain). The results are shown in the Linearity Correction Menu:



Consequently, we have quantified the non-linearity as well as the best-fit unit cell. Experiments have shown that this gives a better reproducibility than the faster Fourier method. However, the Fourier method is needed for getting a good initial estimate of the unit cell.

The overall linearity error **Mean Position Error** is also shown in the Linearity Correction Menu and more detailed information is written into the \*.linc file.

#### Correction Model

The correction parameters are based on a third-order polynomial model of the scanning system. They describe how to resample the image. A more detailed description of the parameters is found in the reference guide. It is possible to enter your own values.

#### Correct

You can apply the correction parameters on the main image by clicking on the **Correct** button.

#### New Estimate

Recheck the linearity by clicking on **New Estimate** and you should observe that the correction parameters become more neutral, that the errors in the scatter diagram reduces to the sub-pixel level and that the Mean Position Error decreases.

#### New Est, Keep Unit Cell

When clicking on this button you will get a new estimation as above but without changing the current unit cell parameters. This gives you the possibility to see how sensitive the linearity analysis is to correct estimation of the unit cell.

#### Unit Cell

The unit cell co-ordinates are found from a least error fit, except when the **New Est, Keep Unit Cell** button is used. In this case you may enter your own co-ordinates and observe how sensitive the analysis is to the unit cell co-ordinates.

#### Mean Position Error

The mean position error measure the combined X and Y dislocations. Regard also this as a quality measure for the combined  
Linearity of the instrument  
Uniformity of the surface structure  
Accuracy of the image processing.

#### Save & Recall

The calculated correction parameters can be stored and retrieved. To apply the correction parameters to a different image you can active this menu directly from the menu bar: select **Processing→Linearity→Correction Menu**.

## Z-Calibration and Critical Dimensions

### Z-Calibration and Step-height Measurement

SPIP contains more automatic and semi-automatic tools for measuring height differences in images as well as profiles. Here we described two automated methods for determining the height difference between two planes, the first is based on a height distribution histogram analysis and the second on an ISO 5436 based analysis of individual profiles. Both methods can provide a Z-correction factor when a proper reference value is provided.

The advantage of the histogram based method is that the surface form is of no importance as long as two significant plateaus can be detected while the ISO 5436 methods requires the existence of profiles from which individual grooves or lines can be defined.

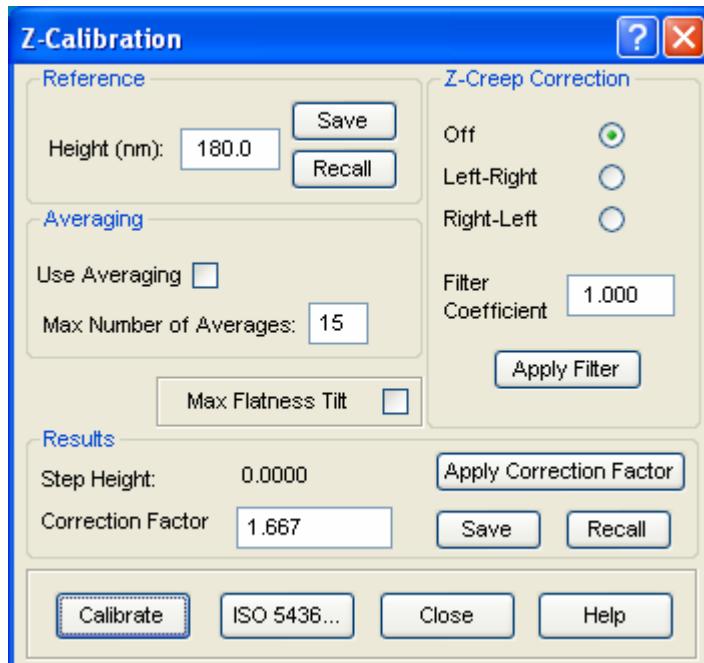
The advantage of the ISO 5436 method is that it can measure very locally at many positions and thereby produce standard deviation calculations necessary for evaluating the uncertainty.

#### Z-Measurements by Height Distribution Histogram Analysis.

The Z-calibration method based on histogram analysis assumes that your image contains two dominating height levels, for example, a waffle pattern or a bearing surface with features rising from the bearing plane. The best measurement quality is achieved with well-defined upper and lower planes, which will exhibit two main peaks in the height distribution histogram. These are the peaks SPIP will detect and use for the step-height measurement.

- The Z-calibration is activated by its associated button on the toolbar or by selecting the **Processing→Z-Calibration menu item.**
- Clicking on the **Z-Calibration** tool key will also perform a step height measurement based on histogram analysis but the dialog with advanced option will not be invoked.

Also, the Z-calibration can be performed from any height distribution histogram window by a right mouse click on "**Z-Calibrate**", Note that this includes also histograms calculated from single profiles.



Step-height reference

To get the correct correction factor calculated it is necessary to enter the reference step-height for the imaged sample. The correction factor is defined as the reference height divided by the measured height.

#### Averaging

You can choose to pre-process the image by applying the correlation averaging technique, in which case the average image is entered into the main image window.

The accuracy of the step-height measurement can often be improved by the correlation averaging technique, which will provide an average image with improved signal-to-noise-ratio. You can limit the number of sub-images to be averaged by defining the Max Number of Averages. Sub-images having the highest similarity with the defined template will be included in the average calculation first. If it is found that the possible number of matches is smaller than the defined maximum the applied sub-images will be limited accordingly and a notification is given.

By defining the maximum number of averages, it is possible to avoid distorted sub-areas, which could affect the result.

#### Creep Correction

Step-height images will often exhibit overshoot phenomena at the edges, and these overshoots can be explained by combined creep and hysteresis effects of the Z-piezo element of the scanner. They will affect the height distribution histogram and the quality of the measurement. To limit this effect it is possible apply the Creep Correction function, which adaptively finds the first-order low-pass filter that results in the best histogram, i.e., the one with the highest peaks for the upper and lower planes. Note that the found filter usually only will have little effect on other parts of the image. This is because a filter that changes too much will also destroy the slopes and thereby flatten the histogram, which is exactly not desired. If averaging has been selected this correction will be applied only to the average image.

The filter has the following form and it is the  $a$  parameter that is estimated:

$$z_x = az_x + (1 - a)z_{x-1}$$

Because creep depends strongly on the scanning direction, it is necessary to enter the original scanning direction.

The filter coefficient found will be displayed and it is possible to enter other filter coefficients and apply them to any image.

#### Max Flatness Tilt

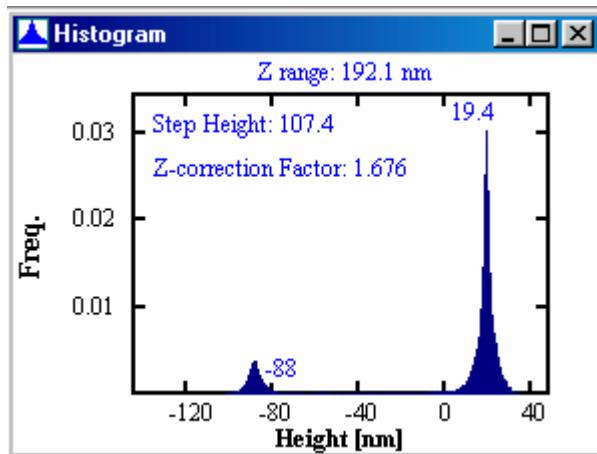
When setting Max Flatness Tilt On, the image will be tilted (first-order plane corrected) by an iterative procedure so that the histogram peaks are maximized. When the averaging option is set, the max flatness correction is applied to the average image.

#### Activation

The Calibrate button or the Enter key activates the selected calibration procedure.

#### Results

The results are indicated in the menu and in the height distribution histogram:



The Z-height values associated with the two histogram peaks are indicated at the peaks. The difference between the peaks reflects the Step-height, which is written at the upper left part of the histogram and the calculated correction factor is written below. At the very top is the total Z range for the image written. To keep track of the calibration history the result is also written to a file with extension .zcal which is a simple text file that can be imported to a spreadsheet program.

The Z-Calibration result can be checked by applying the Z-correction factor and perform a new calibration. You can also enter your own correction factor and apply it to any image.

#### ISO 5436

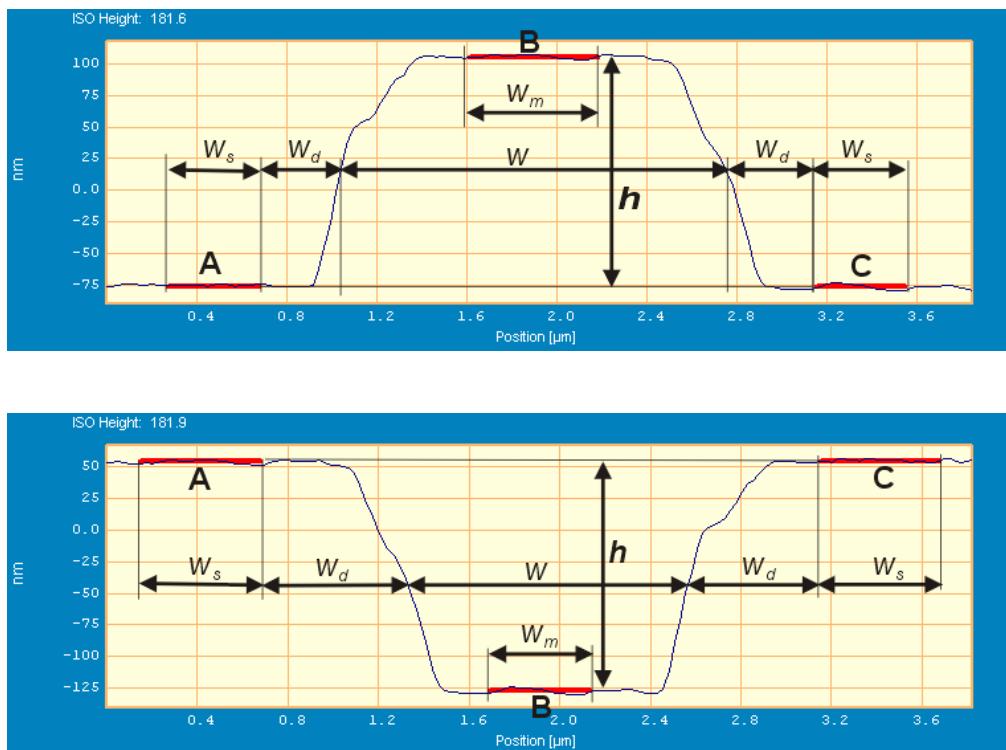
When clicking on the **ISO 5436** button the dialog for ISO 5436 based step height measurement is activated, see below.

## Z-Measurement Based on ISO 5436 Profile Analysis

Z-Measurement based on ISO 5436 profile analysis requires one or more groove or line profiles. From images these profile may be extracted automatically.

The ISO 5436 step height dialog is activated from the processing pull-down menu by clicking on Processing→Z-Calibration/Measurements→ISO 5436 or from the Z Calibration dialog described above, - or from a right click in a profile window on "ISO 5436 Step Height" / "ISO 5436 Step Height Auto Apply". When activated from a profile window the profile window will be attached to the ISO 5436 step height dialog and when activated from an image a horizontal profile will automatically be generated and attached to the ISO 5436 Dialog. The profile window provides visual feedback of the parameter settings and the results.

The philosophy behind the ISO 5436 standard is to measure the average heights at plateaus with some distance from the edges and thereby avoid the influence of the edges. For line and groove structures the active measurement areas are indicated below as A, B and C.



The length of the side areas A and C are denoted  $W_s$  while the length of the middle region B is denoted  $W_m$ . The distance of side areas A and C from the detected line edge is denoted  $W_d$ .

For groove structures the height,  $h$ , is defined as the average height of the A and C areas minus the average height of the groove area B. Similarly the height for a line structure is calculated as the average height of the line area B minus the average of the side areas A and C.

The ISO 5436 dialog offers the possibility to define several detection parameters and monitor the results:



### Object

The object radio box defines the object types to be measured, line or groove structures.

### Measurands

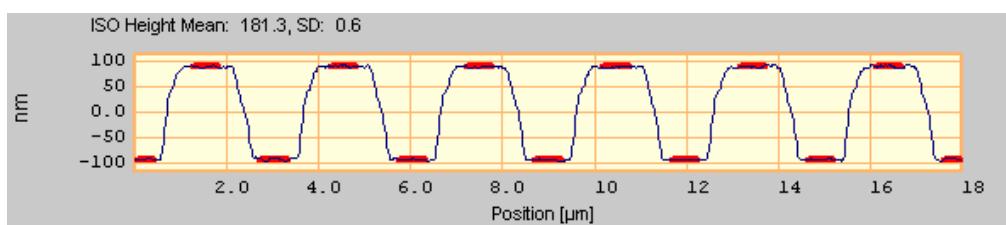
The Measurands checkboxes defines what should be measured: Height and/or Width and Slopes. This section describes Height measurements the next section explains Width and Slope measurements.

### Estimation Area

The estimation areas A, B and C are given by the length values  $W_s$ ,  $W_m$  and  $W_d$ , which are defined relatively to the detected line width  $W$ , by setting the percentage in the associated fields.

It is possible to adjust these parameters while monitoring the result graphically in the profile window in form of red line markers indicating the A, B and C measurements area and in form of the numerical results shown both in the graph and in the dialog.

When having more structures in the same profile as shown below it is possible to perform more measurements and thereby produce a mean and standard deviation result:



A good strategy for obtaining the most accurate results is to adjust the parameters so the standard deviation is minimized.

#### Reference

The height reference associated with the structure can be entered and so that the Z-Correction Factor can be calculated. When having more calibration standards available it can be convenient to have their reference parameters stored in files, which can be Saved or Recalled by the associated buttons.

#### Result

The main results of the measurement are the step height and the Z-Correction factor calculated as the reference height divided by the step height. The correction factor can be applied to an image from the histogram based Z-calibration menu described above. Also, the standard deviation which is calculated when having more than two objects in a profile / image is important as it together with the number of observation can be used for uncertainty calculations. The observation number is for single profiles referred to as "Observation on Profile" and is identical to the number of Grooves or Lines that have been measured. When measuring on an Entire Image the observation number label changes to "Observation Lines, Entire Image", which means that the observation number reflects the number of profiling lines that have been analyzed.

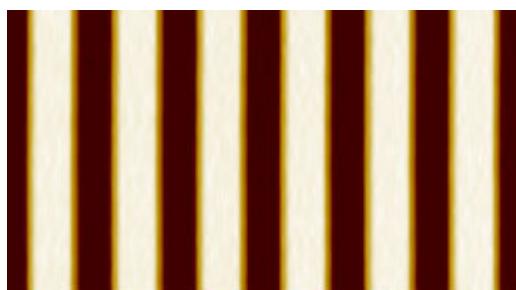
#### Profile

When clicking the Profile button the target objects (line or grooves) are detected and calculated for the current profile attached to the dialog.

#### Entire Image

When clicking the Entire Image button the target objects (line or grooves) are detected and the mean height calculated for all horizontal cross-sections of the image connected the dialog. The number of observations is reported as the number of profiles for which one or more objects was detected. The reported mean height and standard deviation is based on the mean values from each observation.

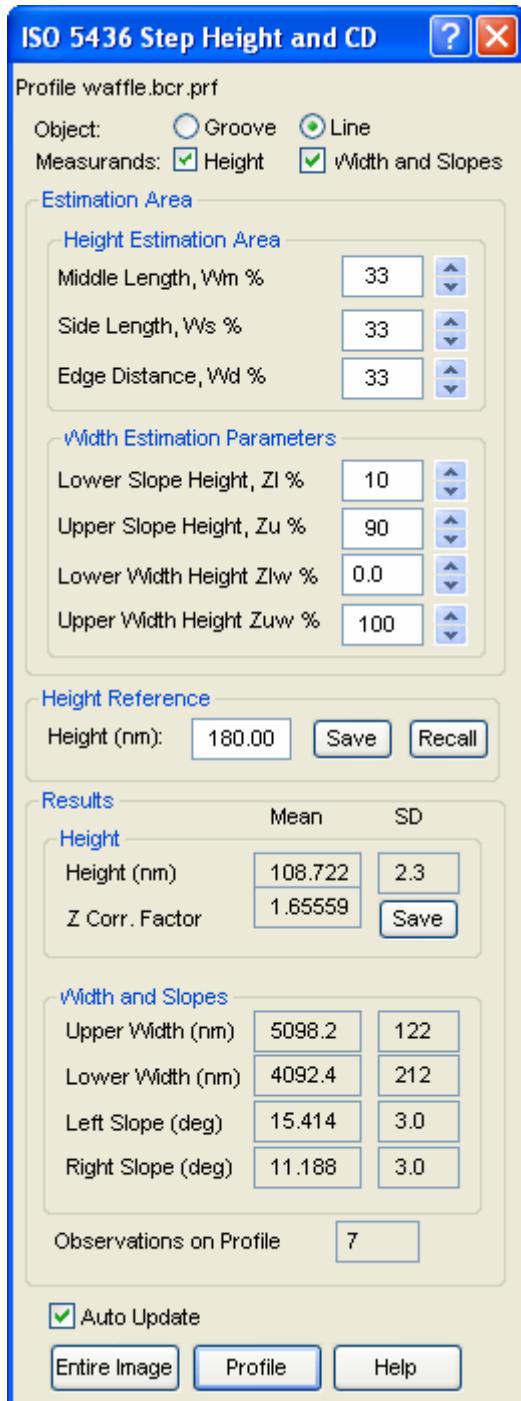
A good result requires that horizontal cross-sections exhibit one or more lines or grooves; this is best accomplished when the line structure is parallel to the y-axis as illustrated below:





## Width and Slope Measurements

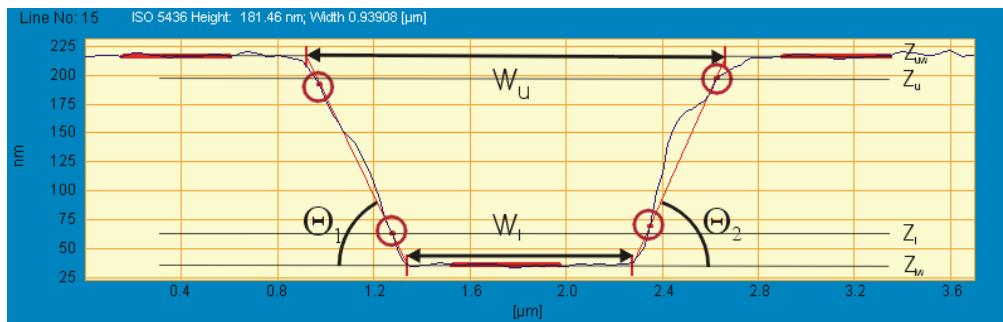
In addition to delivering a robust step height measurement the ISO 5436 method can also deliver Critical Dimensions such as width and side wall angles. The way the parameters are calculated is controlled from the dialog by defining height values relative to height values found in the step height measurement described in the previous section.



### Width Estimation Parameters

An important element in the width calculation is to determine a linear fit to the sidewalls so that width parameters can be deduced from the crossing points of horizontal lines and the

fitted side wall lines. The image shown below illustrates the meaning of the different parameters:



The Lower and Upper Slope Height parameters  $Z_l$  and  $Z_u$ , are defined relative to the upper and lower height values found in the step height calculation. The sidewall line is determined by the highest and lowest points inside the z-range given by  $Z_l$  and  $Z_u$ , - these points are marked by circles in the above image.

The Lower and Upper Width Height,  $Z_{lw}$  and  $Z_{uw}$ , defines at which height to measure the width. When drawing horizontal lines at the  $Z_{lw}$  and  $Z_{uw}$  height values the crossing points with the sidewall lines will determine the upper and lower width,  $W_u$  and  $W_l$ .

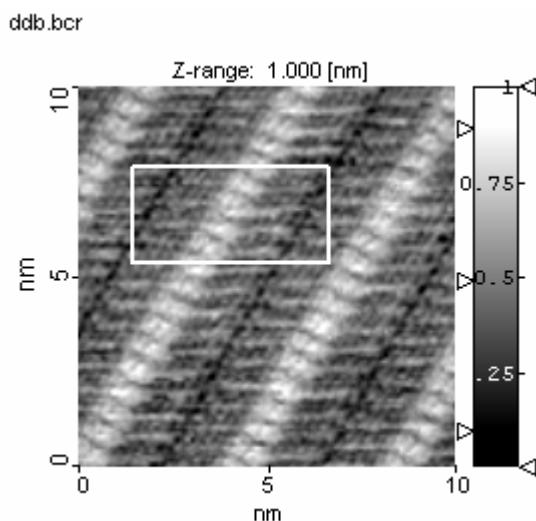
### Width and Slope Results

When the structure is successfully detected both the upper  $W_u$  and lower width  $W_l$  are calculated together with the sidewall slopes measured in degrees. The sidewall angles are indicated as  $\Theta_1$  and  $\Theta_2$ . When more structures are found on the same profile, standard deviation values are calculated such that the uncertainty can be estimated. To obtain a low uncertainty it might be desirable to increase the number of structures and if applicable to include the entire image. Please refer to the previous section for discussion on measurement in an entire image.

## Correlation Averaging

Correlation averaging is a powerful tool for analyzing images and profile data containing repeated structures like atoms, molecules or calibration patterns. The technique can find all the repeated structures and add them so that an average image of the recurrent structure is obtained. In ideal situations the signal-to-noise-ratio can be improved by the square root of the number of additions. In contrast to other filtering techniques it will not filter specific frequencies but preserve all frequencies that are represented in the repeated structure. The following example is based on an STM image of Didodecyl-benzene molecules self-assembled on a graphite substrate.

Pressing the associated key  starts the correlation averaging. If the zoom image is active SPIP will use this image as the structure that has to be recognized and averaged, otherwise SPIP automatically determines a suitable template based on unit cell detection. Let us assume you define the template by the rectangle marker tool :



The template will also be seen in the zoom window:



Start the correlation averaging by the  toolkey or from the menu: Processing→Average→Marked Area, Correlation Averaging.

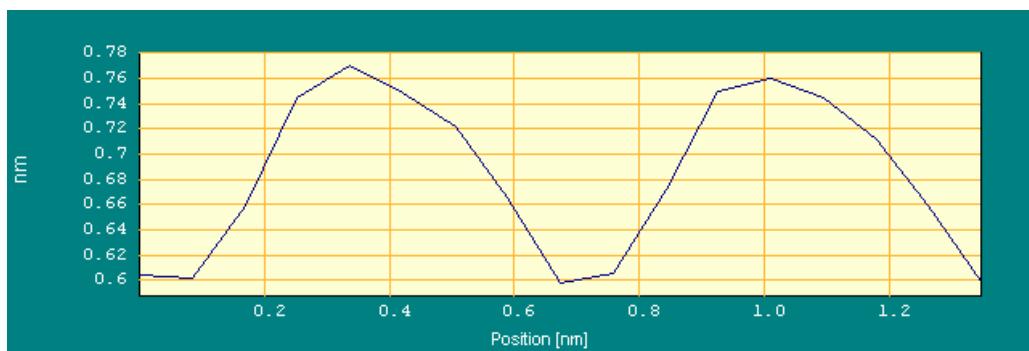
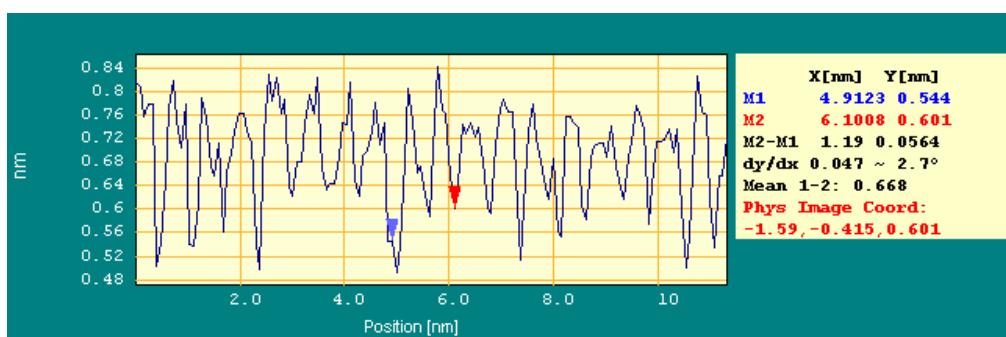
The process will create a cross correlation image displaying peaks associated with the individual areas matching the template. From the cross correlation peaks and the raw image the Average image together with the Standard deviation image are calculated. The latter will contain detailed information about the uniformity of the structures and noise in the instrument. Also, the standard deviation image may provide important information about

structural uniformity, and for example reveal details on how self-assembled molecules are attached to a substrate. The SD Image shown below displays low SD values at the right part of the benzene rings indicating that this part of the molecule is the part most fixed to the substrate.



### Correlation Averaging and Curves

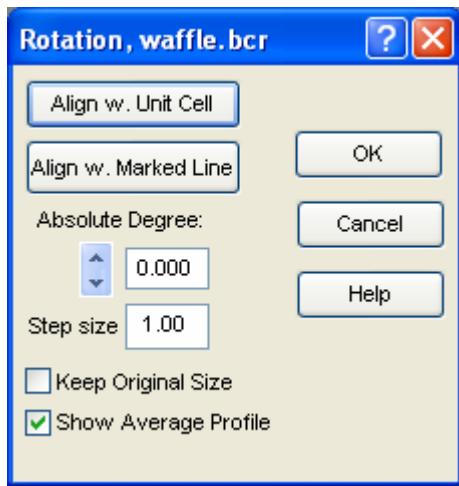
The same procedure can also be used for profiles as shown below. The first picture shows the original curve with the cursors set for marking the template defining the structure to search for. The distance between the cursors will define the final size of the average curve. You may also apply the curve zoom function for defining the template. The second curve below shows the average result.



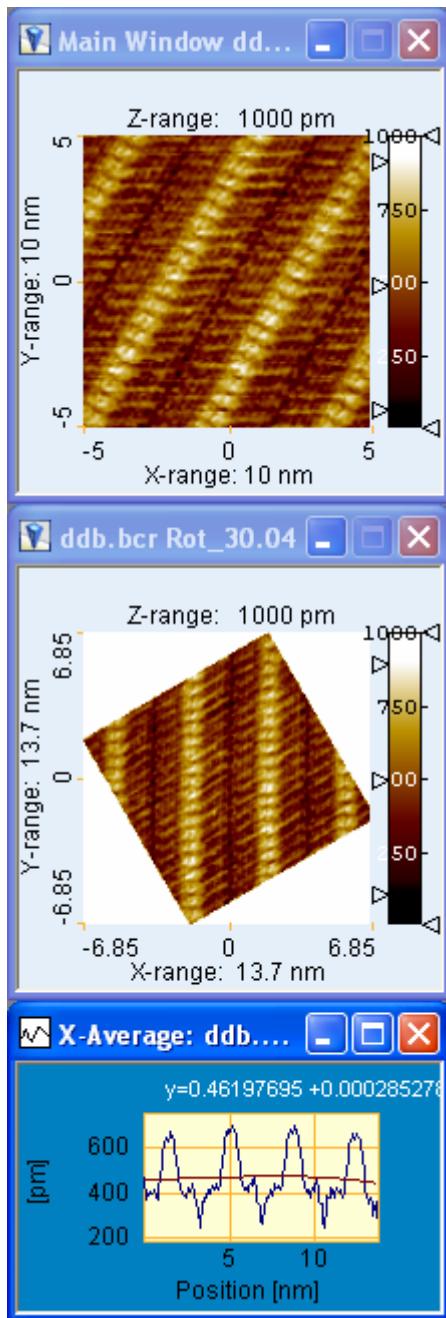
## Rotation

It is often useful to have structures of an image oriented so that they are parallel to the axes. SPIP provides three ways to rotate and image: 1) by a user defined angle value 2) by an angle defined by the line marker 3) automatically based on a calculation of the unit cell or line structure.

 The rotation dialog is activated by clicking on the associated tool button, a right click in an image window or from the Processing pull-down menu and the procedure can also be part of a batch process.



The Align w. Unit Cell function requires that a unit cell or line structure has been calculated first. If so, it can automatically perform a rotation as shown below and the optional average profile calculated as well:



The rotation angle can also be defined by a marked line or by an absolute value.

The absolute rotation angle can be changed interactively by the up-down keys while observing the result simultaneously.

#### Show Average Profile

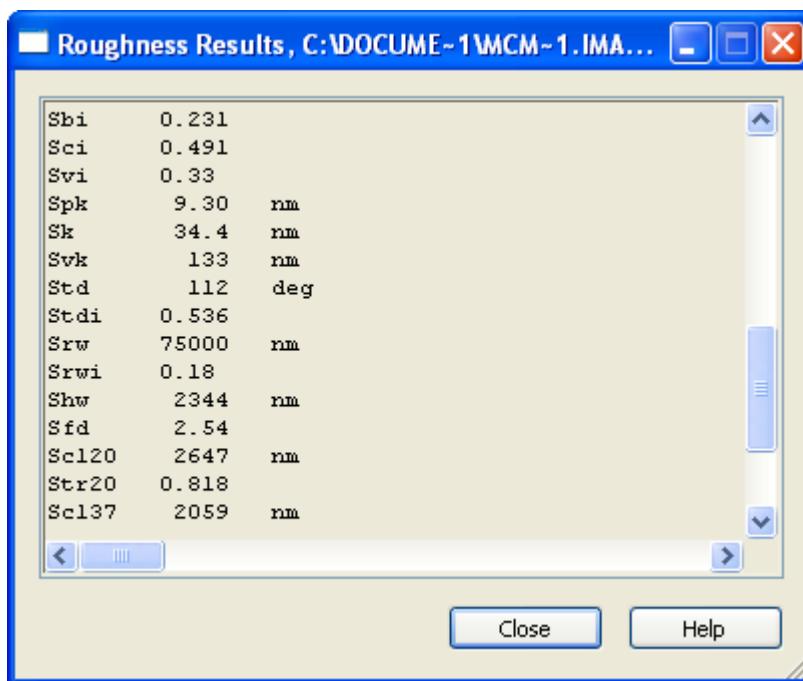
The average profile of the resulting rotation image can be shown automatically by setting the Show Average Profile check box. The averaging is done so that the void areas are excluded from the calculation and provides the best possible estimate of the average profile. See also the above example.

#### Keep Original Size

To keep the same amount of pixels in the rotated image check the Keep Original Size check box. In this case the corners of the rotated image will be excluded. When uncheck the rotated image will extended with additional pixels such that all pixels will be included.

## Roughness Analysis

Start the roughness calculation by the key symbolizing the bearing curve. The roughness analysis will then be based on the Main Image. It is also possible to calculate roughness parameters from profiles by Right Clicking in the Curve Window. For Images a large set of roughness parameters can be calculated and depending on the options defined in the Options Dialog the results may be written to files with the added extension .rgh or to the database of the ImageMet Explorer. For profiles a subset of the image parameters are calculated. For a detailed description of all roughness parameters, please consult the Reference Guide at the end of this document. Roughness parameters based on Image will have the prefix 'S' and when based on a profile the prefix 'R' is used. For example will the *Roughness Average Parameter* be denoted *S<sub>a</sub>* and *R<sub>a</sub>* for images and profiles respectively. The result file will automatically be shown in a dedicated window:



For convenience, the data is written in both a row and a column form. Depending on how you want to organize the data in a spreadsheet you can ignore one of the two forms. To put the data into a spreadsheet program just mark the data of interest and Copy Paste it to the spreadsheet program.

The files can be used for statistical analysis by third party programs. A definition of the different roughness parameters is found in the Reference Guide, *Roughness\_Parameters*.

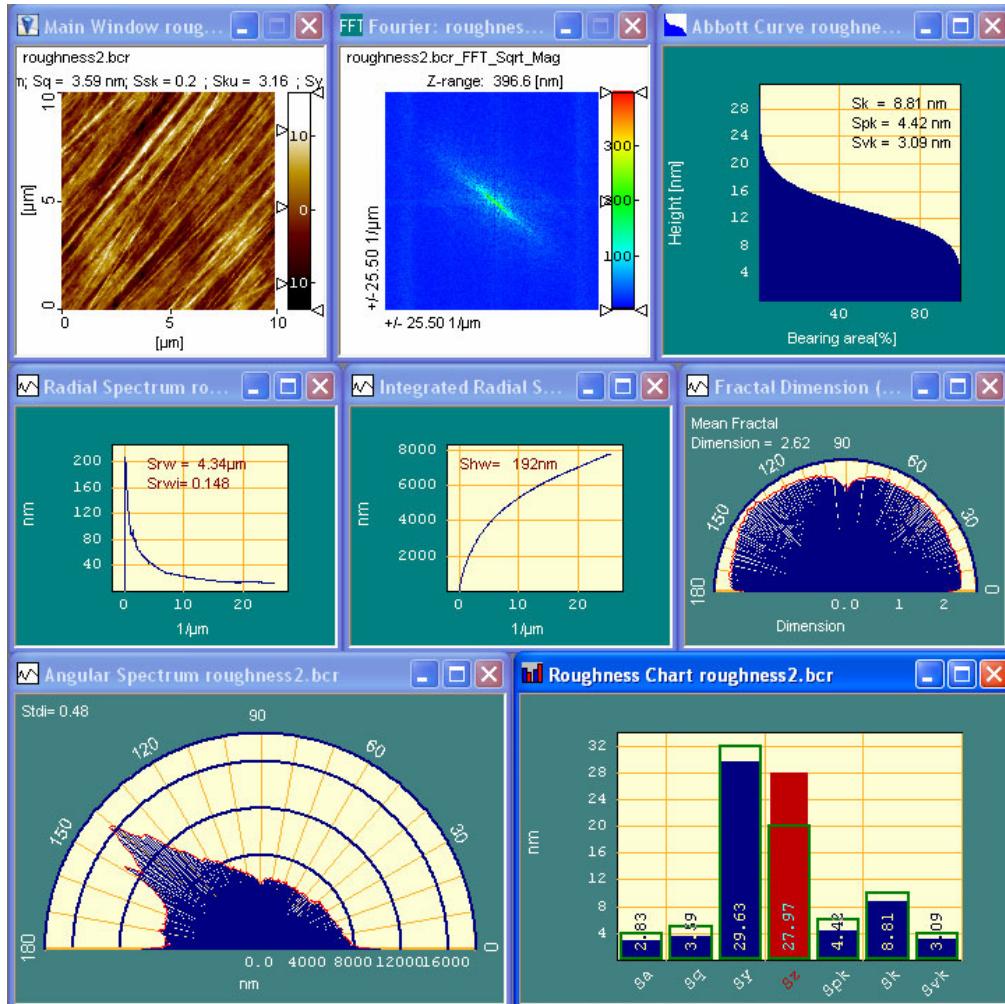
The roughness analysis will also generate the bearing curve (Abbott). In the case that the Fourier Image has been calculated the Angular Spectrum, the Radial Spectrum, the Integrated Radial Spectrum and the *Fractal Dimension* windows are shown too.

The angular spectrum and the fractal dimension are shown in Polar Plots (also called *Rose Plots*) with a value for all discrete angles between 0 and 180 degree.

The parameters depending on the Fourier image are only calculated when these parameters have been set on in the Options Dialog.

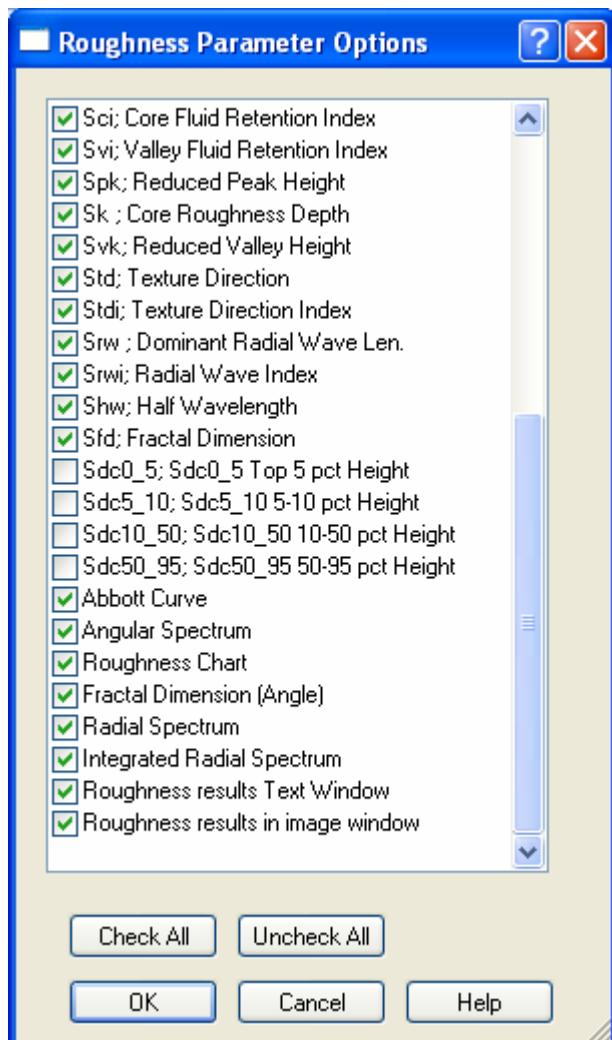
The fractal dimension is calculated for the different angles by analyzing the Fourier amplitude spectrum; for different angles the Fourier profile is extracted and the logarithm of the frequency and amplitude coordinates calculated. The fractal dimension for each direction is then calculated as 2.0 minus the slope of the log - log curves. The fractal dimension can also

be evaluated from 2D Fourier spectra by application of the Log Log function. If the surface is fractal the Log Log graph should be highly linear, with at negative slope.



### Roughness Options

To define which roughness parameters and graphs to show you can activate the roughness selection window by clicking on **Options→Preferences...→Roughness...**

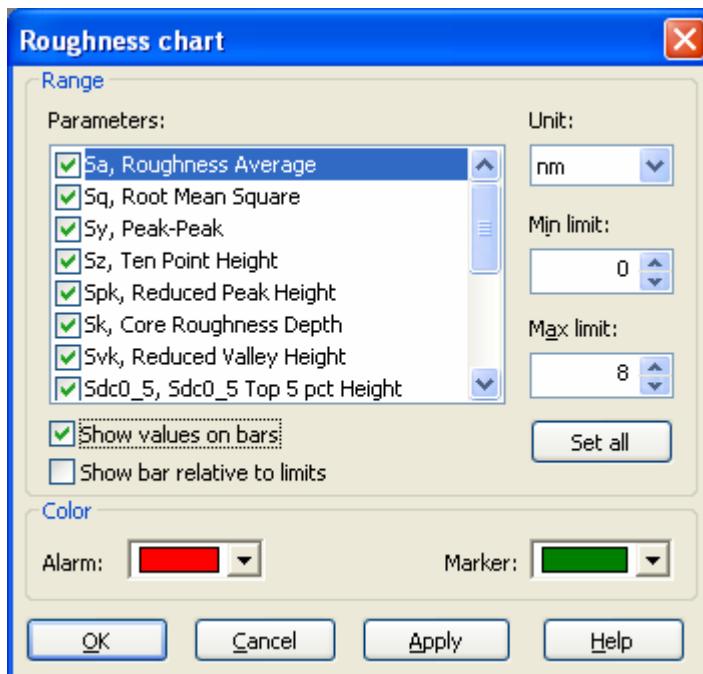


The preferred unit used for the roughness parameters can also be set in the **Options→Preferences** dialog.

## Roughness Chart

You can achieve a convenient visual inspection of the various roughness parameters by use of the Roughness Chart. To get at quick impression of how the parameters compares to tolerance values you can enter Min and Max acceptance limits for the individual parameters. Parameters exceeding the acceptance range will be marked with an optional alarm color. You may also regard the limit values as reference values for graphical comparison of roughness parameters for various images.

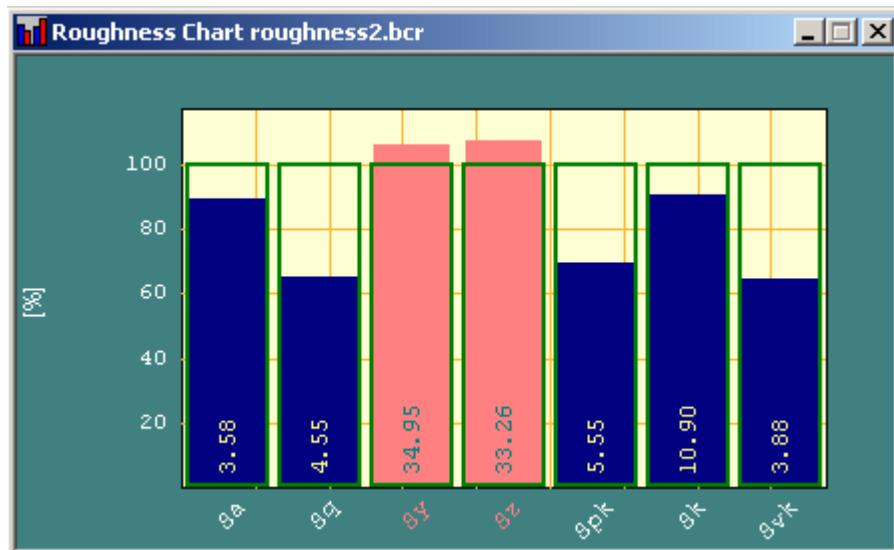
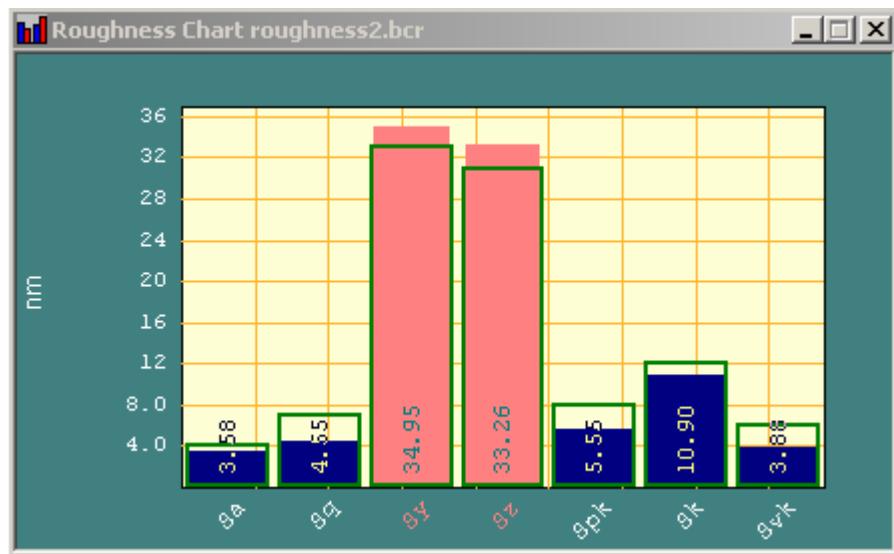
The Roughness Chart dialog which determines the appearance of the chart is activated clicking on **Processing→Roughness→ Chart set-up** or after calculation of the chart by right clicking in the Chart Window and selecting **Roughness chart setup...**



In the left pane of the Roughness chart you can select the parameters to be included. The available roughness parameters are restricted to those, which are related to the z-height and have a length unit (e.g. nm).

Max limits can be entered. Bars representing values exceeding the Min-Max range will be colored by the Alarm color. To disable the alarm and limit marker colors in the chart you must set the Min and Max limits to zero. If you do not want to see the chart you can uncheck all the parameters or turn it off by clicking on **Options→Preferences→Roughness...** and uncheck the Roughness Chart.

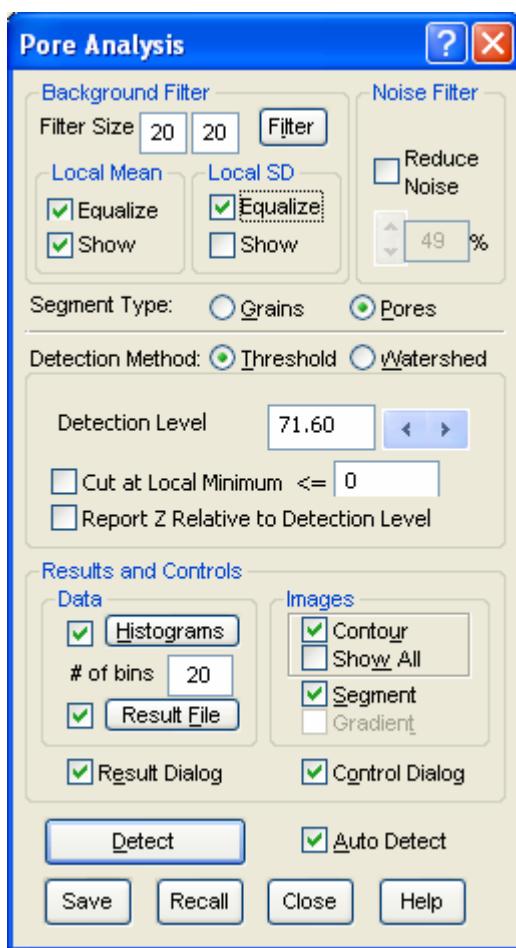
You can choose to have the roughness values shown numerically on the bars in the chart and have the bars scaled by their absolute value or relative to the defined limits. Below are seen examples of charts with absolute and relative bars together with their numerical numbers.



# Grain Analysis

## Introduction to Grain Analysis

The Grain Analysis Menu is used for detection and quantification of grains/pores or other regions for which boundaries can be defined based on height or slope conditions. We will in this text use "segments" as the general term for the regions that this module can detect. The menu is activated by the corresponding toolbar button, or by selecting the menu item Grain Analysis under Processing in the Main Menu. The menu is closely tied to the Main Image Window, and can therefore only be accessed when the Main Image Window is open.



The Grain Analysis module offers two different approaches to the task of detecting segments:

- 1) Threshold Segmentation**
- 2) Watershed Segmentation**

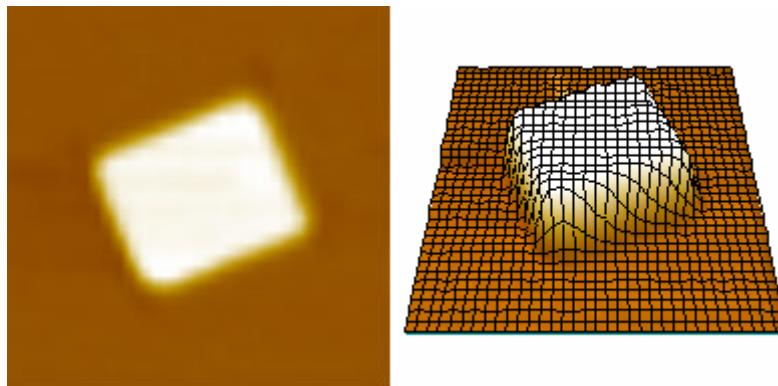
The Grain module is able to detect segments and calculate a large number of properties for the individual segments in an image. Statistics for the whole set of segment properties are calculated and results can be directed to the screen and files.

The Grain analysis module also supports batch processing and performs automated detection and reporting to text files, the ImageMet Explore Database and create HTML reports containing combined numerical and graphical results.

The following will give a brief introduction of the two segmentation methods to provide a basic understanding of the two concepts before describing the dialog controls.

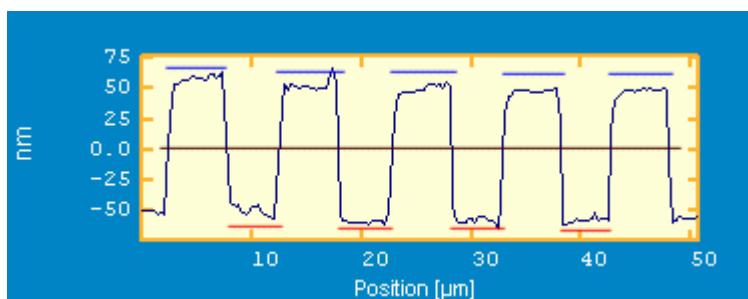
## Threshold Segmentation

For the purpose of explaining the two detection methods it is useful to regard an image as a topographic landscape. Both detection methods can then be described by considering the behavior of water in this landscape. To get a clear idea of the term topographic landscapes see the example below. At the left is an image in normal 2D view. At the right you see a projection of the topographic representation.



This metaphor applies whether the image is a true topographic image, for example SPM image, actually measuring physical heights on a surface, or the image is a conventional optical image or any other type of image.

For the Threshold Segmentation method we define grains based on a threshold level: Grains are the "islands" left when the image landscape is flooded to the threshold level. Consider the 1-Dimensional signal showed by the curve. When a threshold is chosen indicated by the black horizontal line, a binary condition is imposed. Only the part of the signal above the threshold is considered a segment/grain while the rest is disregarded. The segments are indicated by blue lines (horizontal lines at the top). Alternatively, the parts under the threshold level can be regarded as the segments to be detected, in which case we will regard the segments as pores. These are shown in red (horizontal lines at the bottom).



### Advantages

The threshold segmentation method is easy to grasp and performs very fast, so if this method performs in a satisfying way, there is no need to consider the alternative Watershed Segmentation method.

### Drawbacks

The threshold method depends on the possibility to define a threshold that works well everywhere in the image, which is not always possible. Another possible drawback is that it requires the user to select either Grain or Pores as the target segment and disregard regions not being part of the target segments, which is not always desirable.

### Alternative

If the drawbacks are not acceptable the more computation intensive Watershed Segmentation is provided as an alternative. When deciding on the detection method, be

aware of that properties for any actual segment depends on the chosen detection method. This fact is obvious when detection results are very different, because the segments found by one method are not the same as the segments found by another. But even in the case where the detected segments appear very similar results the numerical results may differ significantly. This is especially true for segment property parameters depending on height values, see the section on Reference Z-value under the topic Segment Properties

## Watershed Segmentation

This method can also be explained by a metaphor based on the behavior of water in a landscape. When it rains, drops of water falling in different regions will follow the landscape downhill. The water will end up at the bottom of valleys. In this case we do not consider the depth of the resulting lakes in the valleys. Instead we define a segment:

**For each valley there will be a region from which all water drains into it. In other words: each valley is associated with a catchments basin, and each point in the landscape belongs to exactly one unique basin.**

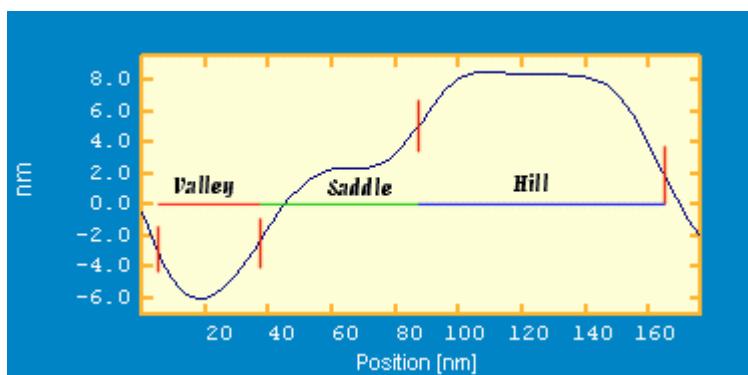
In the literature the term segment is used for these catchments basins, and in this text we will use the term segment, for both the islands found using the threshold method, and for the catchments basins found by the watershed method.

### Segmentation by the Gradient Norm

Most often a desirable result is not produced by applying the definition on the image landscape as is. Experience shows that very often the watershed technique must be applied to the gradient norm image to produce useful segmentation. In this case the method is referred to as: the watershed gradient norm algorithm.

An intuitive argument for this fact is, that the purpose of segmentation is to split the image into self-similar regions. Since a small gradient norm means small local variation, it makes sense to produce areas around points of minimal gradient. The gradient norm at a point is defined as the slope in the direction in which it is maximal. The gradient norm image is then an image produced by assigning the local value of the gradient norm to each pixel.

To explain how segmentation based on the gradient norm behaves we will consider a 1-dimensional example. In 1-D segments reduce to intervals, and the borders or curves separating different segments reduce to points. In this 1D case the consequences of implying the watershed gradient norm can be restated in another way:



Points separating segments are points of extremal slope. These are shown with short red (vertical) lines crossing the curve. The resulting segments are shown with red (the leftmost interval), green (the middle interval) and blue (the rightmost interval). The example visualizes, that segments falls naturally in three categories.

Hills : Segments containing a local maximum in the original signal.

Valleys : Segments containing a local minimum in the original signal.

Saddles : Segments containing a point of minimal slope that is not extremal.

This fact is reflected in the choice of checkboxes in the Segment Types & Limits dialog.

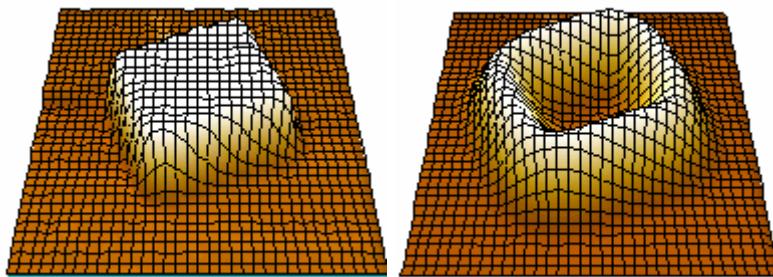
In a 2D-image the situation is a bit more complex, but the three categories persist. Both a local maximum and minimum still produce a point of locally minimal slope (in fact the slope will be zero) and hence a segment. A third category: points of minimal slope, that are neither maximal nor minimal also persists. The term saddles are fetched from a 2D setting, although it is actually misleading.

True Saddle points (points of zero slope but non-extremal) do belong to the third category, but they are a special case. All non-extremal points of minimal slope will produce a unique segment. This type of segments constitutes a third category, and due to the absence of another good short term the checkbox is labeled Saddles.

As treated in detail in the section Segment types & limits it is also possible to choose between segments based only on a type definition involving only two types: hills and valleys.

### The Gradient Norm in 2D

To reveal the "magic" concerning the use of the gradient norm image lets have a look at a 2D example. At the left is the 2D projection of the 3D topographic image landscape from above. At the right is a 3D projection of the corresponding gradient norm image.



It is seen that the catchments basin in the Gradient image corresponds to the object constituted by the single high-altitude plateau in the input image.

In some situations it turns out to be useful to apply the watershed algorithm on the input image itself instead of the gradient image. An example of this can be found in a later section dealing with the control options in the segment dialog.

### **Multi Scale Segmentation**

The Watershed Segmentation method implemented in SPIP actually works on a set of images created from the input image. Convolving the input image with a Gaussian kernel of increasing standard deviation produces the Images in this set. These images will be referred to as levels at different scales.

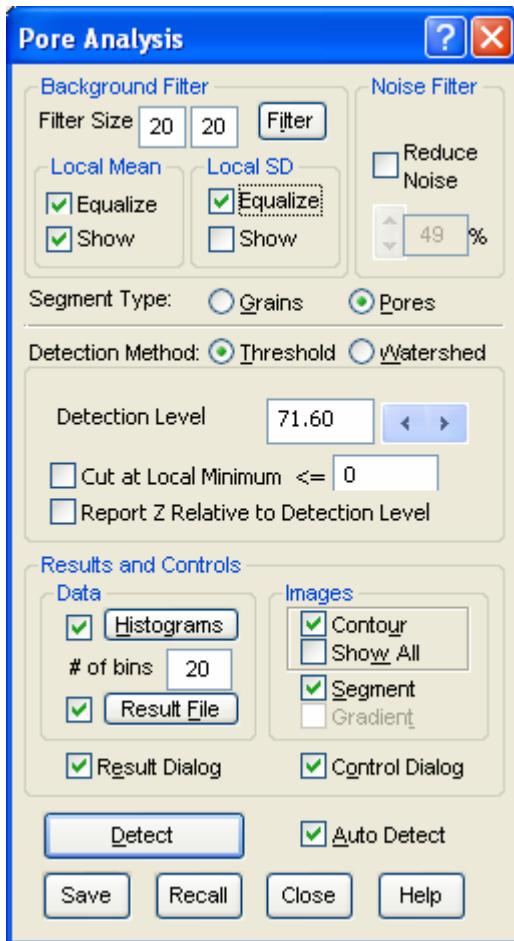
Each scale level is segmented and the segments in each level are connected over scale. Since the number of segments at a level will decrease with the Gaussian scale of the level, the connection between levels has the effect that initially small segments will be combined to produce larger segments as we climb up through the levels. The end result of this procedure is the construction of a hierarchical structure. In the terms of Graph-theory this structure is simply a tree. This hierarchy or tree over segments will be referred to as the segment-tree or just the tree.

Lookups in the segment tree are then performed governed by parameters set by the user via slider controls.

A user only has two worry about the existence of this tree regarding one particular issue. There is a trade off between performance quality and execution time. The suggested default values may have to be changed to optimize this trade off.

## The Grain Dialog

The dialog consists of five main sections grouping the different functions of the dialog.



Starting from the top of the dialog the sections are:

### 1. Preprocessing

#### 2. Detection method and mode.

This part consists of two pairs of radio buttons. The lower pair set the Detection Method, and the upper pair sets the Grain/Pore Mode:

The Grain/Pore mode defines whether grains or pores are detected. The actual mode is also reflected in the caption of the dialog. In Grains mode only pixels having z-values above the detection level are considered. In Pore mode the situation is reversed. See the Watershed Segment Definition above for details. When using the Watershed Gradient Norm for detection, the Grain/Pore option is disabled because the gradient norm is invariant with respect to inversion of z-values.

#### 3. Basic options.

This part has two different appearances depending, on the chosen method:

Basic Options in threshold Mode

Options in watershed Mode

#### 4. Output Options

#### 5. A set of buttons

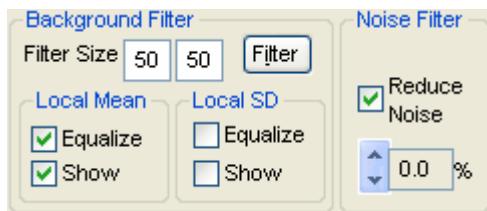
The buttons at the bottom of the dialog are self-explanatory, but note the checkbox: Auto Detect. If this is checked, all changes in the detection settings or reloading or processing of the input image it is immediately followed by an automatic detection. For large images it may be more convenient to uncheck it.

The following sections will address the sections 1, 3 and 4 in more details.

## Preprocessing

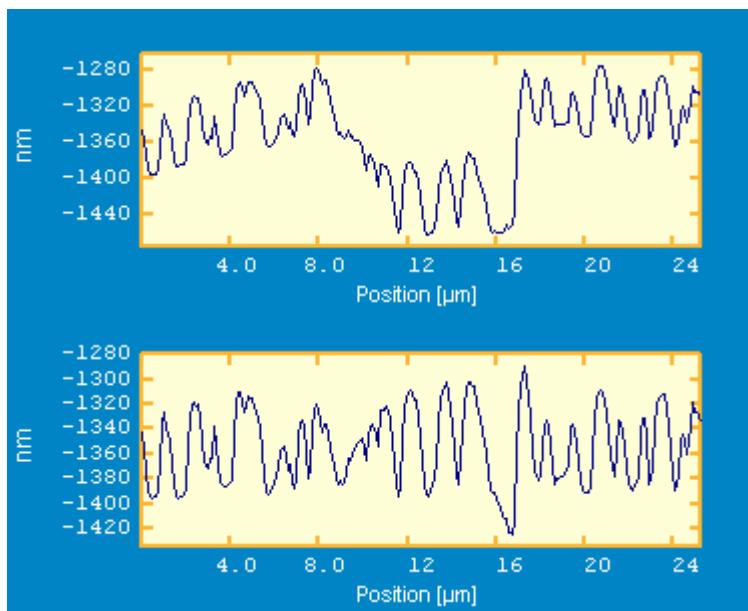
The watershed method is by nature quite robust with respect to variations in z-level at large scales. This is not true concerning the threshold method. A very simple example could be, that the image-landscape is tilted. In this case a global threshold cannot work well, and detection performance will most likely be improved by equalization of z-values.

The Grain Analysis Menu offers two types of equalization, **Local Mean equalization** and **Local Standard Deviation (SD) equalization**. The first method simply subtracts the mean value of the pixels in the local neighborhood. The **SD equalization** scales the height values by a factor given by the standard deviation of the global image, divided by the local mean of the standard deviation. Both the mean value of the local neighborhood and the local mean standard deviation is calculated using a box filter.

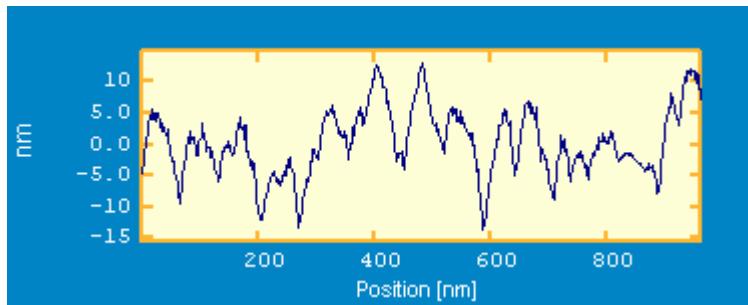


To see the calculated local mean or local SD images used for equalization set the **Show** options on. The size of the box filter used is specified in the edit boxes X, Y **Filter Size** parameters.

The example below shows a scan line sampled from an image before and after mean equalization. The original seems to have two distinct background levels. The widths of the small hills are considerably smaller than the width of the lower plateau, and this is the reason why equalization performs well.



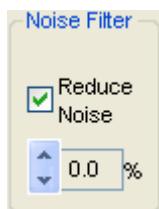
In some situations, there is no apparent background level, equalization is not very helpful and the watershed method may be a better choice. The example below displays a single scan line of this type. The scan line is samples from the full image shown in a later example demonstrating the Watershed Method.



### Noise Filter

The preprocessing part also offers a special noise reduction filter to eliminate small ridges that could otherwise trigger detection of segment borders in the Watershed method. The Filter will simply exchange small "ridge pixels" with interpolated values if the slope on the ridge is smaller than the given percentage of the maximum slope. We define a ridge pixel as a pixel having a value that is either larger or smaller than its two horizontal neighbor pixels or its two vertical neighbor pixels. In contrast to a Median filter this filter will only affect the smaller corrugations, -- to eliminate larger noise peaks a Median filter could be applied.

An increase of the Minimal Scale value in the watershed method will to some extent have a similar effect.



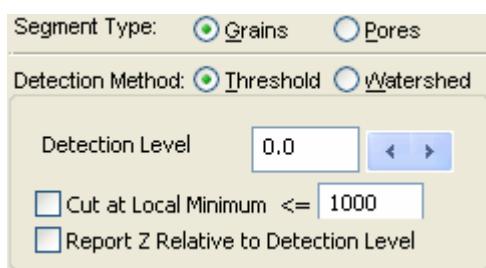
### Grain Detection Modes

#### Grain Detection Modes

The grain menu has two different appearances depending on the choice of detection method.

#### Threshold Mode

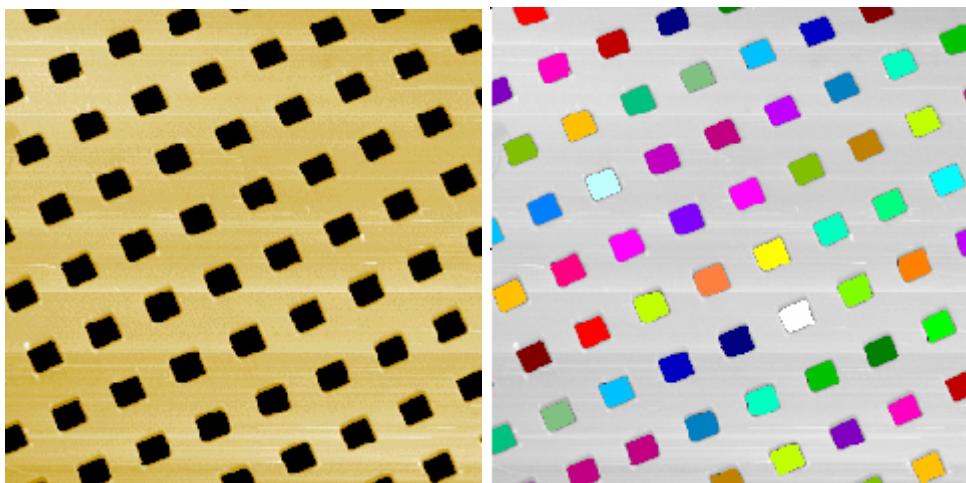
In the threshold mode the middle part of the dialog has the following appearance:



#### Detection Level

The detection level defines the minimum z-value needed for a pixel to be regarded as part of a segment. In Pore Mode only Pixels under the Detection level are regarded. The Detection level works in correspondence with the Color Scale Editor, where the Lower Color Limit of the color bar reflects the detection level. This way you will get a direct visual feedback from the colors in the Main Image. Only Pixels having a Color differing from the minimum color (usually black) will be detected. By moving the lower color limit in the color bar the Detection Level of the Grain Analysis Bar will change simultaneously.

In the example below you see an original image at the left, and the threshold detection result at the right.



#### Cut at Local Minimum

Segments that are close together can sometimes be hard to separate when the background amplitude is above the threshold level. In such situations it will help to set the **Cut at Local Minimum** option on. This has the effect that the local minima pixels will be discarded along with pixels below the threshold level.

#### Report Z Relative to Detection Level

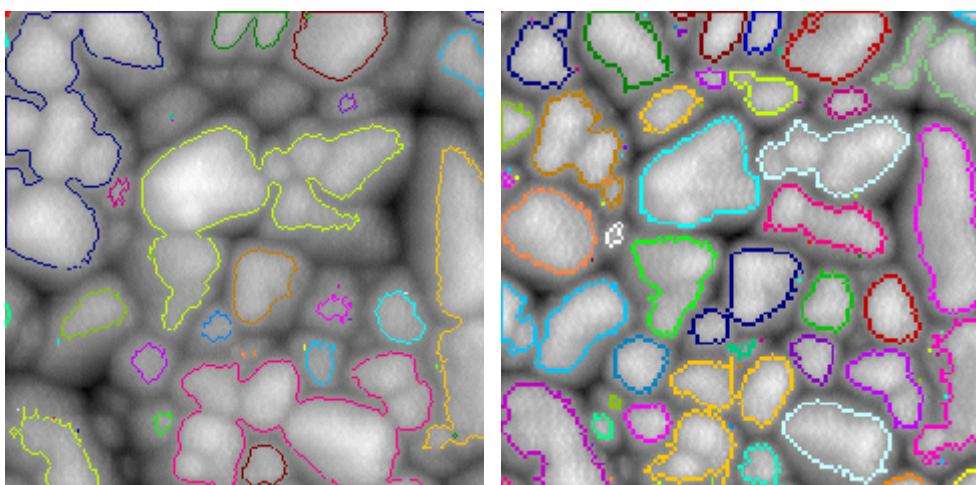
When this option is set the z values are reported relative to the detection level, otherwise the absolute values are used. When reporting absolute values it will often be an advantage to define the zero level at the bearing height. The zero level of an image can be defined by the plane correction menu, its histogram window or its profile window.

#### Cut at local Minimum Threshold

By entering a Cut at local Minimum Threshold value only Minima pixels below this value are discarded. The altitude of this additional level is always specified relative to the main threshold level. The value shown in the additional threshold edit box is the distance from the **Detection level** up to the extra threshold.

If the pores options are on, the additional threshold is situated under the main threshold level instead. As a consequence the value in the edit box is always positive and specifies how much more restrictive the extra threshold is.

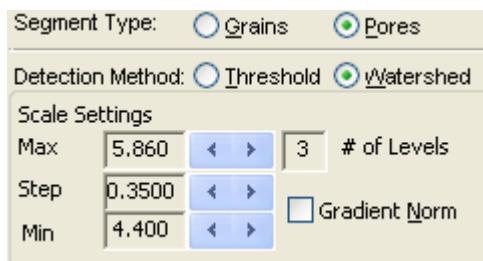
The images below demonstrate the effect of using this option:



**Tip:** Try first setting the additional threshold to a very large value. Perhaps the best result will be achieved when you split at all local minima, and then you do not have to worry about setting an extra parameter.

### Watershed Mode

In the threshold mode the middle part of the dialog has the following appearance:



### Controlling the size of the segment hierarchy

This part of the dialog handles the size of the hierarchical structure of segments mentioned in the introduction. The input variables are the set of scales at which hierarchy is build. The **min** scale is the standard deviation of the Gaussian kernel used at the smallest scale. The scale **step** is the relative scale increase performed at each level. **Max** scale is the standard deviation of the Gaussian kernel at the maximal scale. **# Levels** is the number of different scales applied.

Both the min scale and the max scale Values are always specified in Pixel units.  
The scale s at scale number i, is calculated as:

$$S = \text{min} + (1 + \text{step})^i - 1$$

This formula is chosen to achieve an exponentially growth over intermediate scales.

### The Max Scale

The most important value is the scale at the final level. As scale grows segments grow in size. Hence the maximal scale governs the maximal size of segments that can be found by lookups. This scale must be large enough to produce the segments that you need, but preferably not larger since this will increase computation time for no reason. The optimal value of this maximal scale depends among other things on the smoothness of the actual image, but as a thumb rule it has to be approximately the same size as the segments that are to be detected.

An alternative thumb rule is that a number of **levels** between 4 and 8 will work fine. This together with the **min** scale and the scale **step** will determine the max scale

### The Scale Step

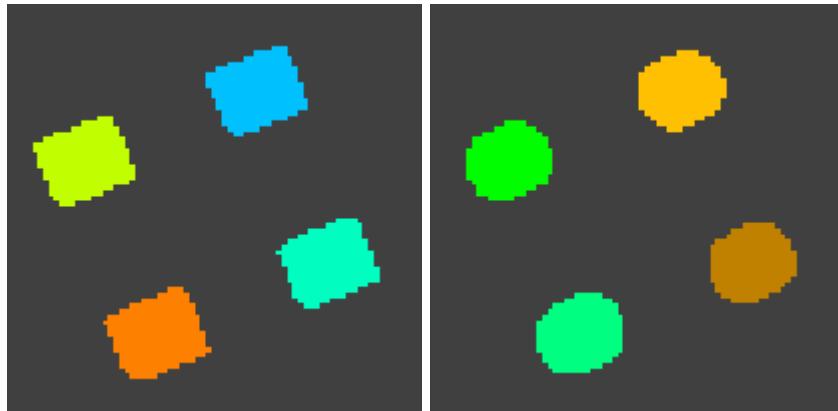
The Step value decides how well the linking over scale performs. Small steps facilitate correct linking, but increase processing time and memory demand. Settings in the range 0.1 to 0.5 will be reasonable in most cases. The default is 0.25.

### The Minimal Scale

As the max scale has strong influence on the maximal segments it is possible to detect, the min scale influences how small segments it is possible to detect. The minimal scale should usually be set to default (0.5) or lower. The Gaussian blurring at the initial scale introduces noise reduction. If this is an advantage it may be a good idea to increase the minimal scale, but notice that increasing the minimal scale may cause blurring of the detected segments

When the image at the lowest level is convolved with a Gaussian of considerable standard deviation the borders of segments will be distorted, and most segment properties like length for instance will change. If the task is merely counting of objects, this distortion may play no role and the init value may be raised substantially. This may reduce computation time considerably.

The example below demonstrates this. The left image is produced using 4 levels and a min scale of 0.5. The right image is produced using only 1 level but a min scale of 4.0. Note that the same objects are detected, but edges are severely distorted in the single level sample.



Using only a single level means that no segment tree at all is constructed. This example in fact also demonstrates that the whole purpose of building a segment tree is to produce large segments without distorting segment boundaries.

#### **Summary on choice of scale settings**

In short you will usually be on the safe side by: increasing number of levels and decreasing init value and step size. This will increase performance quality, but may result in large processing times.

#### **Initialization of the hierarchy**

Construction of the hierarchy is by far the most expensive operation performed by the grain module. Be aware that when **Auto detect** is set to on, the hierarchy will be automatically rebuilt when you change any of the watershed settings. If you check **Auto Detect**, **Watershed method** and uncheck the **Gradient Norm** checkbox, toggling the **Grain/Pore** mode will also result in auto construction of a new segment tree.

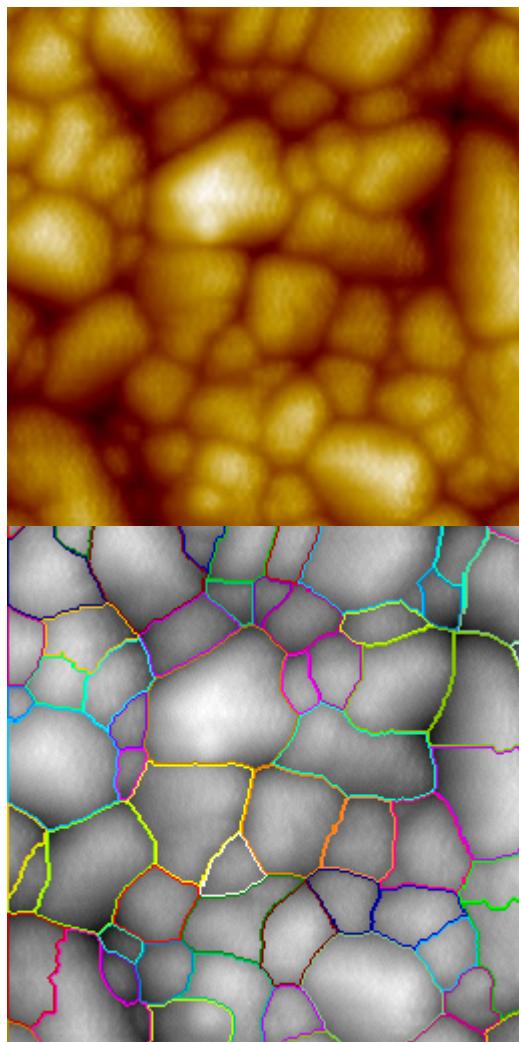
Switching from Threshold Method to Watershed Method under Auto detection will only infer construction of a new segment tree the first time unless the main image has changed. The tree is stored in background memory.

#### **The Gradient Norm checkbox**

As mentioned in the introduction the watershed algorithm usually is applied on the gradient norm image. This option is default on, but if the checkbox is unchecked the watershed algorithm runs on the original image itself. If the **Grain/Pore** radio buttons is set on pores, the watershed will be applied on the inverted image. Using the water metaphor, gravity is reversed and water runs uphill. Right clicking the image window and choosing **Invert** will achieve the same. In the later case the image display will also be inverted. Both options applied simultaneously cancel out.

See the introduction for a 2D example for an example of a topographic image together with its Gradient Norm Image.

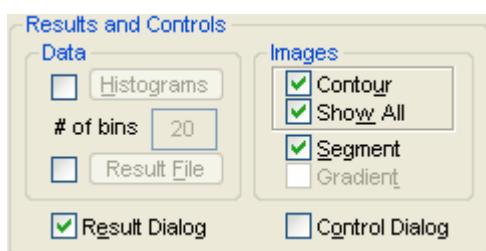
Below is demonstrated an example where it is an advantage to have the **gradient norm** unchecked.



The reason that the watershed method in this example performs well directly on the input image is due to its somewhat special structure. Our one visual system will notice the canyon like structures separating the images in individual hills. This means that the watershed method will detect these hills directly if the direction of gravity is inverted forcing water to run upwards. Hence the catchment's basins will be localized around the hilltops. When the requested segment type is set to Grains the inversion is automatically performed and you do not need to think about it.

### Grain Output Options

In this part of the dialog the graphical output options and numerical reporting to files is controlled.



### Image Outputs

In addition to the main window the grain module works with three optional extra image windows.

### Segment Image

The segment window shows the result of the detection. All non-excluded segments are marked by a random color, and by left-clicking a grain in it the properties of the actual segments will be displayed in the Result Dialog.

### Contour Image

The Contour window only differs from the grain window in three ways.

The Segment boundary (contour) is showed instead of the full segment. The contours are shown as an overlay on the original image; this may be more convenient for the purpose evaluating the detection performance.

When the option: **Show All** is checked, all contours inclusive the ones excluded manually or by the Segment Types & limits dialog are shown. This feature only applies to the contour window

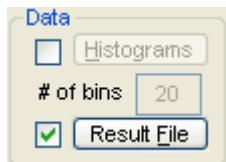
Segments cannot be left clicked to access their properties in the Result Dialog.

### Gradient Image

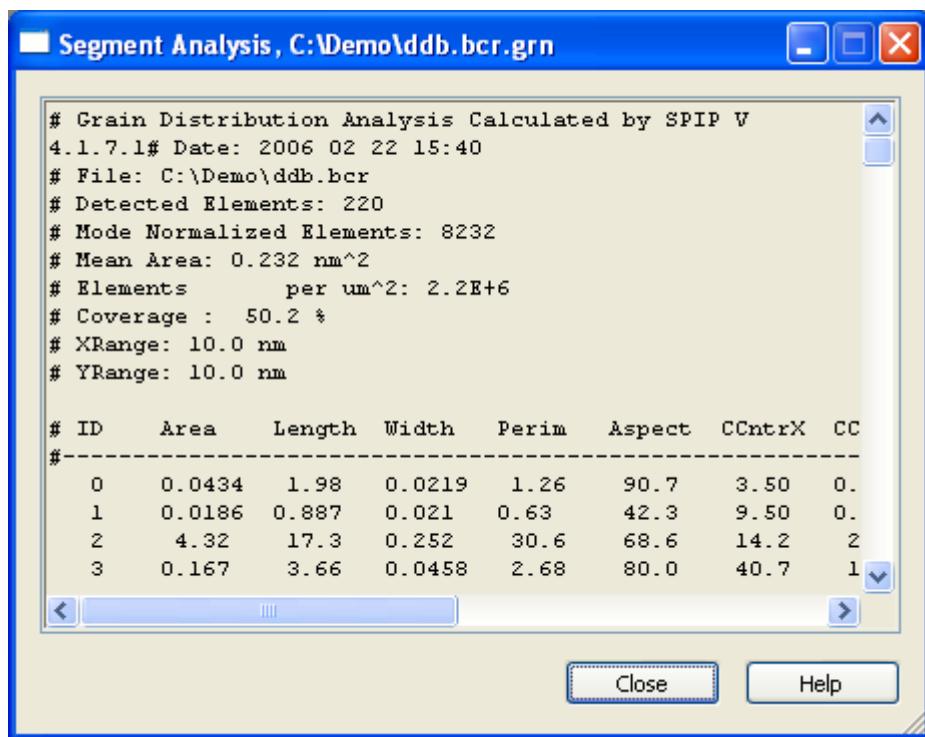
The Gradient window shows the gradient image at the maximal scale specified in the Watershed options sub dialog. It may be a help to get an intuitive feeling of the detection method, and help to choose the proper value of the maximal scale. Checking **gradient window** on, will only result in a gradient window in watershed mode, when gradient norm is checked.

All three optional windows can be toggled of and on.

### Data Output

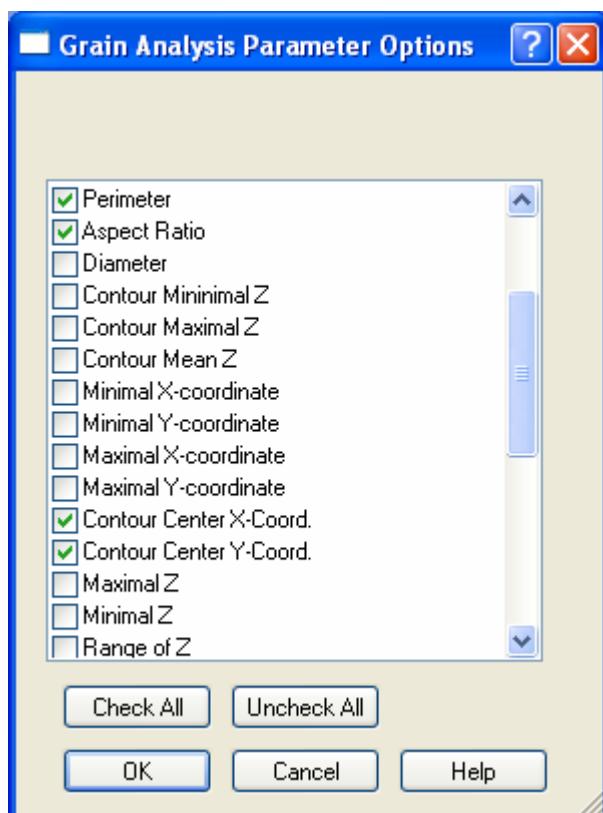


Output to text file or database can be set on or off in the **options dialog** found in the **main menu** bar. In the Segment dialog there is a checkbox: **Result file** If this is checked segment properties will always be written to file, and the file will be automatically opened in a dedicated window. You may Copy & Paste the data from this window to a spreadsheet program.



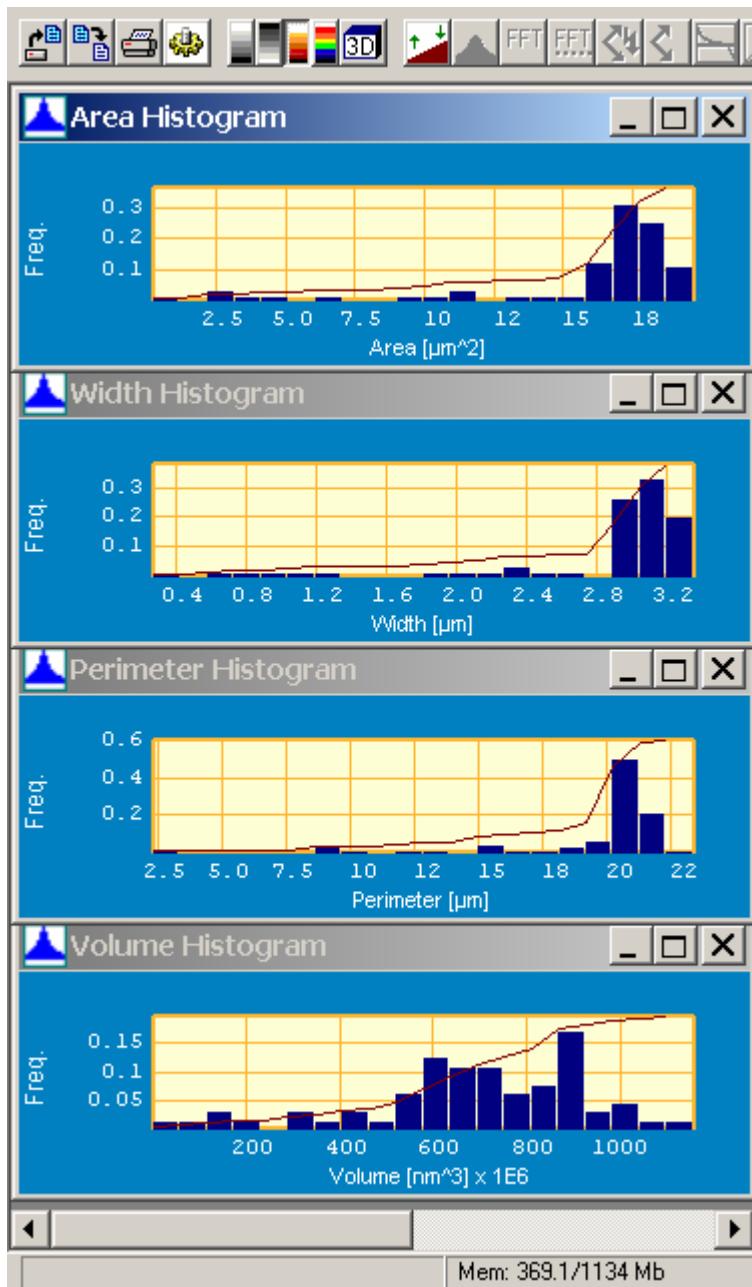
To view the results in a condensed summary you may click the "Result Dialog" on.

By clicking the Result file button beside the checkbox, you get access to the **Segment Analysis Parameter Options**. In this dialog you can specify which of the segment properties calculated by SPIP, you want to be written in the result file or in case of Batch Processing into the HTML report.

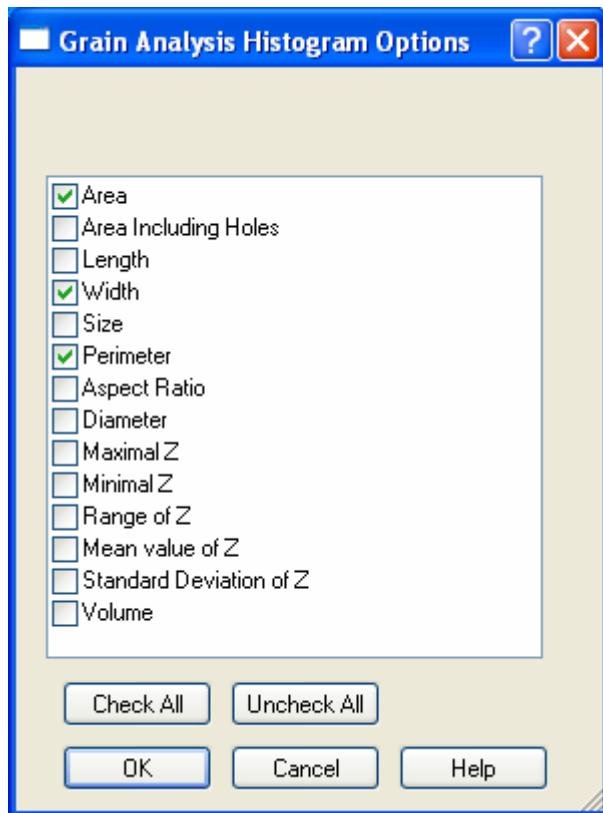


## Histograms

The **histogram** checkbox and button works exactly the same way as the result file checkbox and button. The only difference is that histograms are output to screen in individual windows, instead of data to file. Below is seen an example of possible Histograms:



The **histogram button** will open a dialog where you can specify for which segment properties you want to have distribution histograms shown.

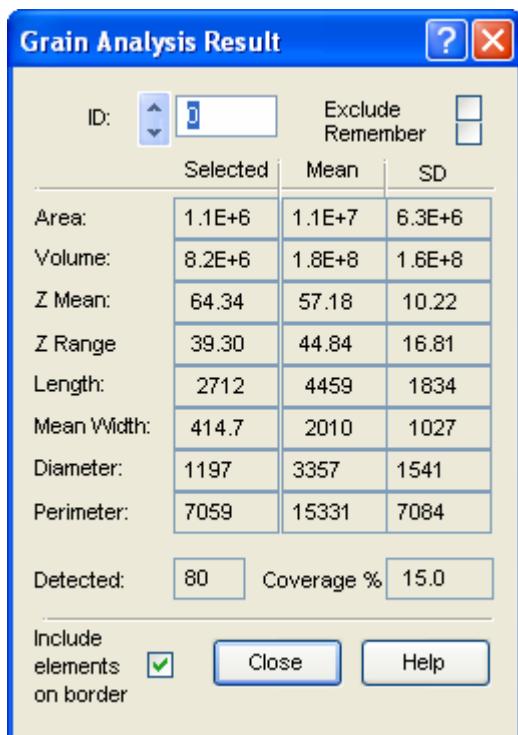


#### Save and Recall

The settings shown in the dialog can be saved and recalled by the "Save" and "Recall" button so that settings for specific application can be retrieved easily. Likewise, the specific grain analysis settings files can be applied from the Batch Processor. The extension for the grain settings files is ".grs".

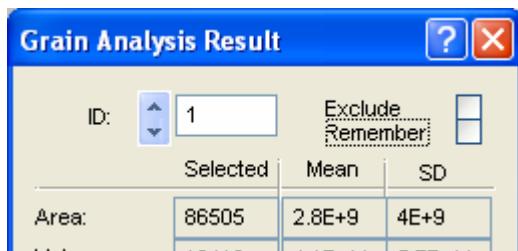
## The Grain Result Dialog

The detection result is visualized in the Segment Image. If the Write to File option is checked in the main Grain Analysis Dialog results are written to text files with the added extension .grn and/or to the database of the ImageMet Explorer. The text file contains tab-separated text and can easily be imported to a spreadsheet program. Concerning image and histogram outputs to screen see the section: Grain Output Options



In the Grain Analysis Result dialog the properties of individual objects can be manually inspected. The Grain/Pore ID's can be entered or defined by clicking in one of the found objects in the Grain Image Window. It is possible to exclude individual grains manually by checking Exclude.

Below the exclude checkbox is an additional checkbox: Remember. When this is checked the exclude status of the particular grain is fixed and will independent on limit changes in the: Segment types & limits dialog. On a new detection all remember flags will be set off.



The Result dialog also offers to exclude all grains at image borders. This way partial border segments will not affect the statistics but it will lower the coverage percentage.

When an object is excluded no matter what reason its colors will turn into gray in the grain window. Excluded Segments are also excluded from Segment statistics and output to file.

Note that the Result Dialog also supports the correspondence between the segments shown in the Segment Image Window and the data in the result file. The ID number off a particular Segment is shown in the Segment dialog, when it is clicked in the Segment Image or the Contour Image.

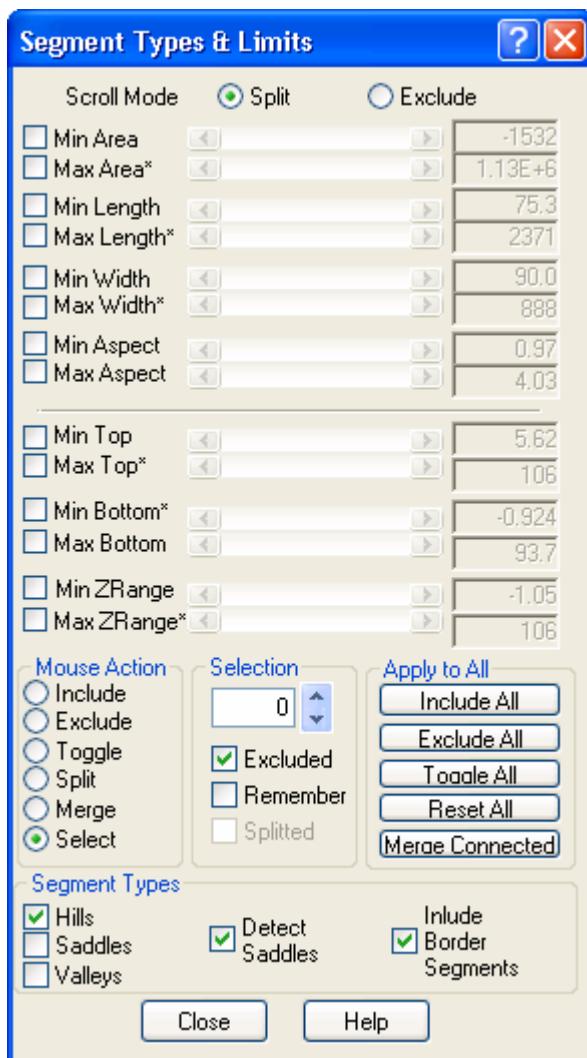
Here the Segment ID is 0, which is the default after detection.

The reverse is also possible: if you write an ID in the edit box, you can find the corresponding segment in the image. By toggling the exclude box, the color of the corresponding segment in the segment window will toggle between gray and some non-gray color.

Information on the actual calculations performed to find the segment properties is found in the section: Segment Properties.

## Segment Types & Limits Dialog

The "Segment Types & Limits Dialog" is activated from the main Grain Dialog by clicking the **Control Dialog** checkbox.



The dialog offers the possibility to specify ranges for a fixed set of parameters and in. The dialog has slightly different functionalities in the Threshold and the Watershed modes as will be described in the following.

### In Threshold Mode

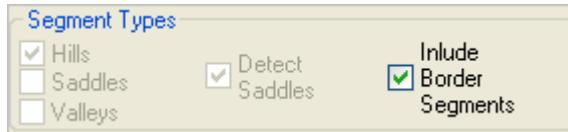
In Threshold mode it's straightforward. Each of the seven parameter controls works the same way. As an example let's consider the top one the area controls.



The idea is simply to offer the possibility of discarding segments having areas outside the range between the chosen min area and max area. The effect is precisely the same as when manually excluding individual segments in the result dialog. In this case however the effect is global: All segments outside the specified ranges are discarded. These segments will not be considered in any of the various grain statistics or outputs that SPIP offers.

At the left of each pair of sliders there is a checkbox. Sliders and their settings are only active if the checkbox is checked. Any number of parameters can be checked simultaneously, but it is advised to examining the effect of each slider isolated first.

At the bottom part of the dialog is situated an additional set of checkboxes. In threshold mode only one of them is accessible namely the **border** checkbox. If unchecked all grains touching the image border are excluded. This checkbox is identical to the same one in the Result Dialog. It is merely duplicated here for convenience.



### Defaults

After detection all parameter limits are defaulted to the smallest possible and largest possible setting for the segments in the actual image. This means that as default no segments are discarded at all. Each time detection is performed the sliders are reset to their defaults. The actual values of the defaults are automatically updated during detection.

### Changing the Limits

The sliders are automatically scaled, which means that the user does not have to worry about the actual physical values of the parameter values. The user can simply position the sliders guided by the image feedback in the Segment Image and/or the Contour Image. Feedback on the fly requires **Auto Detection** set to on. The text boxes right to the sliders will displays the absolute values corresponding to the slider positions.

**Tip:** It may be convenient to be able to see all segments including the excluded ones while pulling the parameter limit sliders. If the **Show All** checkbox in the output images part of the main dialog is checked all contours will be visible in the contour Window.

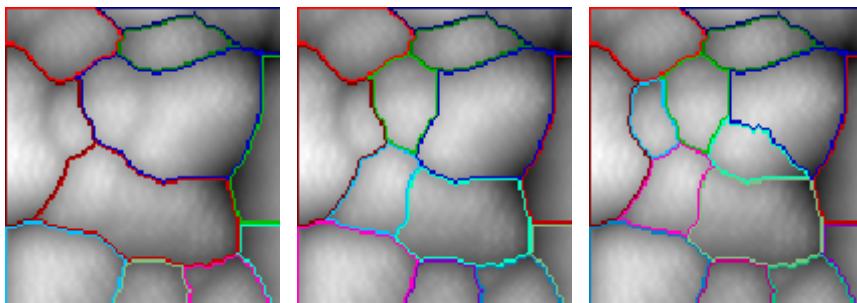


### In Watershed Mode

#In Watershed Mode the functionality of the dialog is a bit more advanced:

As explained in the introduction part SPIP builds a tree over the set of segments. Some of the sliders settings control the lookups in the tree and these sliders are marked with an asterisk (\*). At the root of the tree very large segments are build by merging many smaller segments. The marked sliders control how far up in the tree segments should be chosen. If for instance the maximal value of the area is decreased, and the **Scroll Mode** is set to **Split** you will notice that segments superseding this value will be split into smaller segments. When Scroll Mode is set to **Exclude** the segments superseding the limits will be excluded.

The example below shows how segments have been split by decreasing the Maximum Area limit:



The other half of the slider limit pair (In the Area case the minimal value) works as in threshold mode. If Segments are under the limit they are excluded. If the maximum area is set to a very small value, it may happen that the hierarchy does not hold any sub segments corresponding to a given segment. In this case the segment cannot be split and will remain too large. Since it in this case does not meet the requirement it will be excluded like in threshold mode.

### True Scale Space Parameters

When segments are merged some parameter values will be growing monotonically. For instance it is obvious that the area can only grow never decrease. Because of this the maximal area is a True Scale Space Parameter, and a good choice for controlling lookups in the hierarchy. These True Scale Space Parameters are marked with asterix '\*'.

<input checked="" type="checkbox"/> Min Area	<input type="button" value="&lt;"/>	<input type="button" value="&gt;"/>	1.91E+5
<input checked="" type="checkbox"/> Max Area*	<input type="button" value="&lt;"/>	<input type="button" value="&gt;"/>	9.84E+5

Note that the maximal z-value will always increase when segments are merged, but the minimal z-value will always decrease. That is the reason that the: Min Bottom is the only minimal value marked considered a True Scale Space Parameter.

Neither the minimal nor the maximal value of the Aspect ratio is a true scale space parameter, so it does not control lookups, but works entirely as in threshold mode.

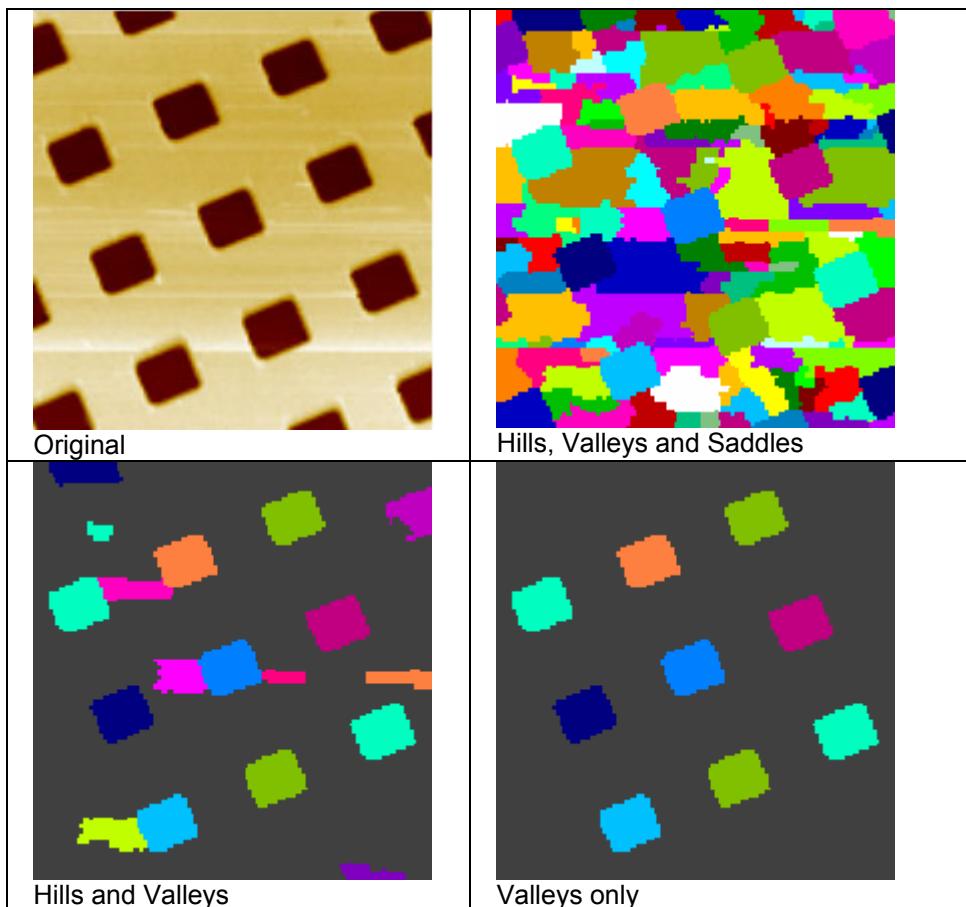
<input type="checkbox"/> Min Aspect	<input type="button" value="&lt;"/>	<input type="button" value="&gt;"/>	0.97
<input checked="" type="checkbox"/> Max Aspect	<input type="button" value="&lt;"/>	<input type="button" value="&gt;"/>	2.44

### Segment Types

In addition to the parameter limit ranges, SPIP offers a few extra options for choosing segments. These are accessed via checkboxes in the lower part of the dialog.

Segment Types			
<input checked="" type="checkbox"/> Hills	<input checked="" type="checkbox"/> Detect	<input checked="" type="checkbox"/> Include	
<input type="checkbox"/> Saddles	<input checked="" type="checkbox"/> Saddles	<input checked="" type="checkbox"/> Border	
<input type="checkbox"/> Valleys		<input checked="" type="checkbox"/> Segments	

As discussed in a bit more detail in the introduction, it makes sense to consider three mutually exclusive classes of segments: **Hills**, **Valleys** and **Saddles**. The checkboxes allows you to specify which of the categories you want to include and control the result as illustrated below. The first upper left image is the original; the upper right is the Segment Image showing all segments. In the lower left the Segment Images contains only the valleys and hills while the Segment image lower right only contains the valleys.



The actual definition of the three categories is as follows:

If the maximal z-value is inside the segment, that is, not on the segment contour/border the segment is a **Hill**.

If the minimal z-value is inside the segment, that is, not on the segment contour/border the segment is a **Valley**.

If neither is the case, i.e., both the minimal and maximal values are found on the contour the segment is a **Saddle**.

#### **Note.**

Actually these definitions allow a segment to be both a Hill and a Valley simultaneously, but the Gradient Watershed Norm Algorithm makes this very unlikely. Should it happen excluding saddles, hills or both will exclude the segment.

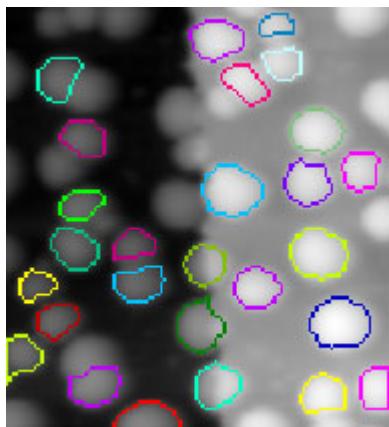
#### **Detect Saddles Option**

By experiment it is found that in some situations, it is better to operate with only two categories: Hills and Valleys. In threshold mode these correspond to the grain versus pore option. The extra checkbox: **Detect Saddles** at the right of the saddle checkbox determines whether to classify segments in two or three classes.

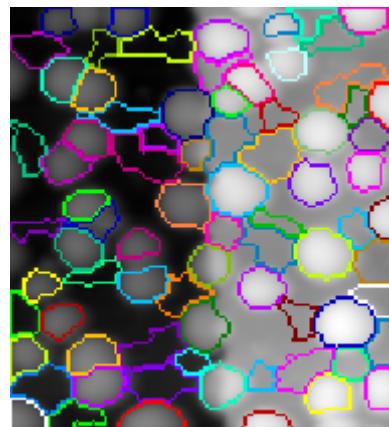
With **Detect Saddles** checked the saddle class is defined, which means that you can choose between 3 classes, as in the example given above. If **Detect saddles** is unchecked the saddles class does not exist and hence it makes no difference whether you exclude saddles or not. Instead the set of segments that would otherwise be classified as saddles, are split into two half's. One half is included in the hill class, the other in the valley class. In this case another definition of the two classes is used:

- If the mean z-value of the segment is larger than the mean z-value on the segment contour the segment is a **Hill**
- If the mean z-value of the segment is smaller than the mean z-value on the segment contour the segment is a **Valley**

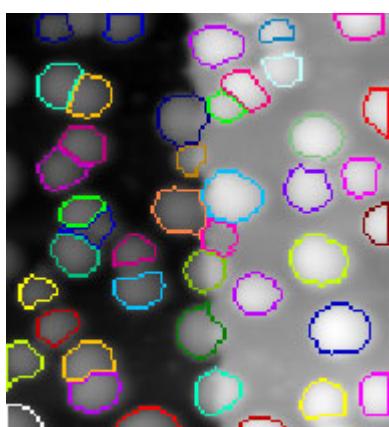
To demonstrate this feature an example is given below. The first image shows detected Hills when **Detect Saddles** is checked, and the second shows both Hills and Saddles. The third image shows Hills with **Detect Saddles** unchecked.



Hills only, Saddles checked



Hills and Saddles



Hills only, Saddles un-checked

Note that the first image contains too few segments, the second too many, but the third image seems to contain the desired segments. Also, note that the segments are found in spite the fact that the Z-value has two very different levels in the two image-halves. No Pre-processing was performed in this example and as such it demonstrates a situation where the Watershed method is more feasible than the Threshold method.

#### Individual Segment Control

The middle part of the dialog offers functions for individual modification and monitoring of selected segments:

<b>Mouse Action</b>	<b>Selection</b>	<b>Apply to All</b>
<input type="radio"/> Include <input type="radio"/> Exclude <input type="radio"/> Toggle <input type="radio"/> Split <input type="radio"/> Merge <input checked="" type="radio"/> Select	<input type="text" value="0"/>	<input type="button" value="Include All"/> <input type="button" value="Exclude All"/> <input type="button" value="Toggle All"/> <input type="button" value="Reset All"/> <input type="button" value="Split"/> <input type="button" value="Merge Connected"/>
<input type="checkbox"/> Excluded <input type="checkbox"/> Remember <input type="checkbox"/> Split		

The radio buttons in the left frame defines which action that will be performed when you click on a segment in the Segment Image or the Contour Image.



The following Mouse Actions can be selected:

Include	The segment selected with the mouse will be included as part of the result.
Excluded	The segment will be excluded.
Toggle	The segment status will toggle between included and excluded
Split	If in watershed mode the segment will if possible be split
Merge	This mode requires the user to click on two different segments, which then will be merged into one segment.
Select	No action will be performed on the selected segment but its current Exclude state will be shown in the Selection box to the right.

#### Selection State

The Selection state frame box shows the modification state of the selected segment and it is possible to **Exclude** the segment.



When the **Remember** checkbox is checked the Exclude state will be preserved when modifying the Min Max limits with the scrollbars and the Scroll Mode is set to **Exclude**. Use the **Split** checkbox to split a segment found at a smaller scale level in the Multi Scale Segmentation. This function is only active when Scroll Mode is set to Split.

#### Apply to All Functions



The following Apply to All Functions Actions can be performed:

Include All	Include all detected segments
Exclude All	Exclude all segments
Toggle All	Toggle the Include/Exclude state of all segments
Reset All	Reset all Include/Exclude, Split and Merged states to the original detected.
Merge Connected	Merge all segments that are connected to each other.

**Include Border Segments**

When checked all segments on the border will be included. As the area of these segments typically will be observed as being smaller it will typically cause the mean size parameters to be smaller.

## Segment Property Issues

This section contains a short description of some relevant issues concerning the definitions and calculations of various segment properties.

### Units

For topographic images all properties are calculated and written in nm units regarding both X, Y and Z values. If you load a windows bitmap or some other format that does not include information on physical units the units will be defaulted by SPIP. You can change these defaults by right-clicking the image, which will open the Image Properties Menu that offers you the possibility to specify new units.

### Coordinate system

For the Grain Analysis Origin is set at the center of the 1st pixels in the first row. In image windows on screen this is the uppermost leftmost pixel. The x-coordinate is measures along rows (horizontal) and the y-coordinate along rows (vertical).

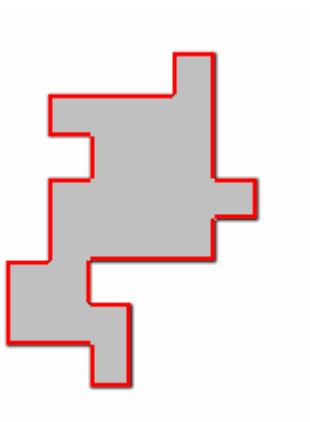
The first pixel have center coordinates (0,0). In an image consisting of M columns and N rows the center of the last pixel (lowermost rightmost) have coordinates (M-1, N-1).

### Definition of Contours

All contour parameters are calculated by considering the outer contour of the segment.

#### Outer Contour

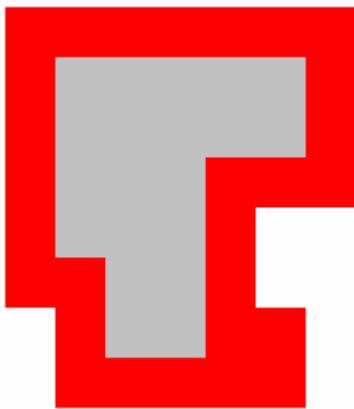
What is meant by the outer contour is illustrated by the sample contour below.



The contour is located between the pixel center points implying that for a single pixel segment the maximal distance between two contour points will evaluate to the value  $\sqrt{2} \sim 1.414$ .

#### Inner Contour

When properties involving z-values on the contour are calculated, the inner contour is used. The inner contour pixels is identical to the border pixels of the segment see below.



### Contour coordinates

Contour coordinates are also between pixels, so for an image having its units set as the x and y coordinates the contour coordinates will be half-integer valued. As a consequence the difference between the maximal and minimal x coordinate for the whole image is M, when the image has M Rows. The area of the total image (sum of all segment areas) equals to  $N \cdot M$ .

### Reference Z-Value

Some of the segment properties/parameters like for instance the Volume require that a reference value for the z-values be chosen. When detection is performed by the Threshold method the threshold is the reference value. This means that the volume of a segment is calculated as the volume of the part that is above the threshold value. (In Pore mode the situation is reversed.) As a consequence some of the segment properties may change dramatically with respect to the threshold value, even when the visual feedback has not changed much.

When detection is performed by the watershed segmentation method the reference is the mean z-value of the inner contour. There is only a single exception from this rule: The contour mean z-value it self. Instead of holding the trivial value zero it is assigned the absolute z-value of the contour mean. If the user should prefer all properties based on z-values expressed in absolute values instead of relative values, these are found by adding this absolute offset.

Note that since the z-reference depends on the chosen method, the segment properties may differ dependant on the detection method, even if the detection results are (almost) identical with respect to the x/y -coordinates of the contours.

### Definition of the Segment Properties

The following segment parameters can be reported to files and their histogram distribution can be shown.

**Area:** Area not including possible holes inside the segment.  
(Holes are only detected in threshold mode;

**Length:** The maximal distance between two points on the outer contour.

**Width:** Area inclusive Holes divided by Length.

**Perimeter:** Length of outer contour.

**Aspect ratio:** Length divided by width.

**Diameter:**  $2 * \sqrt{\text{Area inclusive Hole divided by PI}}$ .  
Evaluates to the true diameter for a circle

**Contour Center X/Y-coord:** x/y-coordinate to center of mass if the segment was flat.

**X/Y-coord of mass center:** x/y-coordinate to center of mass.

**XMin, YMin, XMax and YMax :**

The coordinates of pixels on the outer contour. This means that they have an offset of one half compared to the positions of the pixel centers

**Size:**  $\text{Max( XMax-XMin, YMax-YMin )}$

**Global Grain and Pore parameters.**

In addition to the calculation individual segment properties SPIP will also calculate the following grain/pre results:

**Detected Elements**

**Mode Normalized Elements**, where the number of elements has been normalized by use of the Area mode parameter. This means that the total number of elements is calculated as the coverage area divided by the typical area value. This is especially useful when segments area overlapping so that they cannot be separated.

**Elements Per square um**

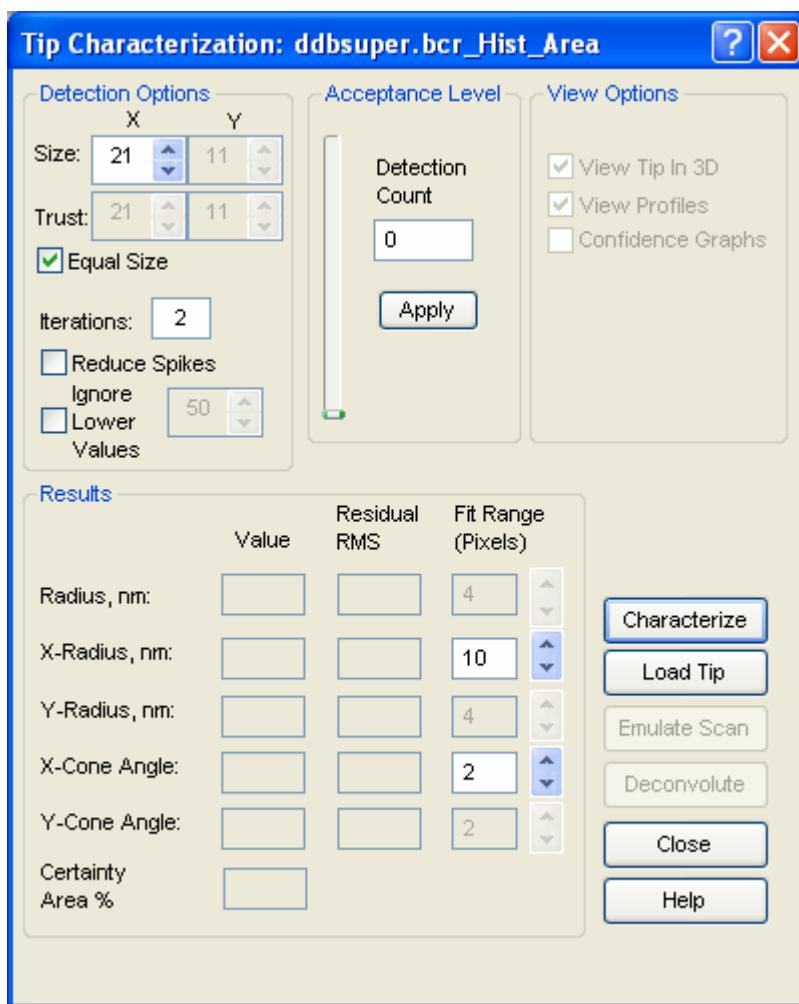
**Coverage Pct.** The percentage of the surface covered by the detected grains/pores

## Tip Characterization

The SPIP tip characterization module allows you to characterize the tip or stylus used for scanning the actual image. The basic methods used are very similar to the blind reconstruction method described by J. S. Villarrubia and P. M. Williams et. al.

 The tip characterization can run on topographic images and profiles and activated by its tool key or the Tip Characterize menu item found in the right mouse menu or the Processing sub-menu. If you have the Batch Processing option included in the software you can also run the tip characterization and *Deconvolution* in a batch process and combine it with other functions and thereby improve your productivity. There are four tip processing functions available for batch processing: Tip Deconvolute, Tip Characterize, Tip Load and Report Tip Characterization to HTML.

Likewise, it is possible to combine the Correlation Averaging on repeatable structures and thereby minimize the influence from noise.



In the Tip Characterization menu different detection parameters influencing the result can be set. It is important to notice that if we can assume that there are no image distortions, apart from tip artifacts; SPIP will be able to calculate the *worst case tip*. The worst-case found tip is able to scan all parts of the surface with its apex but might be sharper in reality.

### Detection Options

### Size

The Size parameters defines the number of pixels for the tip to be estimated, uneven numbers in the range 3 to 255 are possible values for the X-dimension while the Y-Dimension can be set between 1 and 255; Having uneven pixels means that the tip apex always will be centered.

The X, Y tip length can not exceed half of the respective surface image length. By setting the Y-length to 1 pixel it is possible to calculate the x-profile of the tip rather than a tip image. This is useful for 1 dimensional surface structures where tip information only can be obtained from one direction.

### Iterations

The Iteration number determines how many times the recursive algorithm will run through the image. First time the tip is evaluated only from the true maximums. Based on this tip we can create the *Certainty Map* by emulating a tip scan. This image tells us which part of the image that is scanned by the apex and can be trusted. In the second iteration all local maximums in the trusted image areas are used for further tip estimation and a new *Certainty Map* is created. Third and higher numbers of iterations are similar to the 2<sup>nd</sup> but now all trusted pixels are included. The computing time depends linearly with the number of iterations and it will seldom be necessary to use more than 3 iterations.

### Trust

*Trust pixel area* defines how many pixels are trusted in 2<sup>nd</sup> and following iterations.

When estimating a large area of a tip the uncertainty of the border points will be much lower than the center pixels and can reduce the *Certainty* surface area because it will be difficult for the tip to enter the lower surface levels. This means that there will be fewer places where tip shape information can be deduced resulting in a too blond tip. If this is a problem it can be an advantage to define the *Trust pixel area* to be smaller than the tip area meaning that we are ignoring the tip outer parts when calculating the certainty area.

In most cases you should keep the Trust area equal to the tip size but especially when performing the characterization on pores rather than particles this option can be useful.

### Reduce Spikes

Depending on the image quality the tip characterization result may be influenced by noise and this is especially true when there are noise peaks creating maximums that are going to be used by the first iterations of the characterization algorithm. In these cases it is therefore important to have an *intelligent* way to reduce noise peaks. When the Reduce Spikes option is set, the tip is pre-calculated using only the first iteration described above. From the x and y profile of the tip the slopes at the very apex are evaluated. If the slopes at the very apex is higher than the slopes just below this is regarded as a noise artifact and the height at the tip apex is then lowered so that the slopes at the apex does not exceed the slopes just below. Using the knowledge of the noise reduced tip we are now able to detect all parts of the image where we have peaks sharper than the tip and then reduce these values so that they in the following iterations doesn't causes the sharpness of the tip to be overestimated. Note that the input image will be changed by this procedure, but you can regard the technique as an intelligent way of detecting and removing noisy peaks.

### Ignore Lower Values

By checking this checkbox it is possible to ignore peaks in the lower parts of an image. This will lower the processing time and limit the unwanted influence from small noise peaks. This is especially useful when applying dedicated tip-characterizing samples where the vital information is found in the upper part of the structure.

The level can be defined by the color bar or the associated arrow keys.

### Acceptance Level

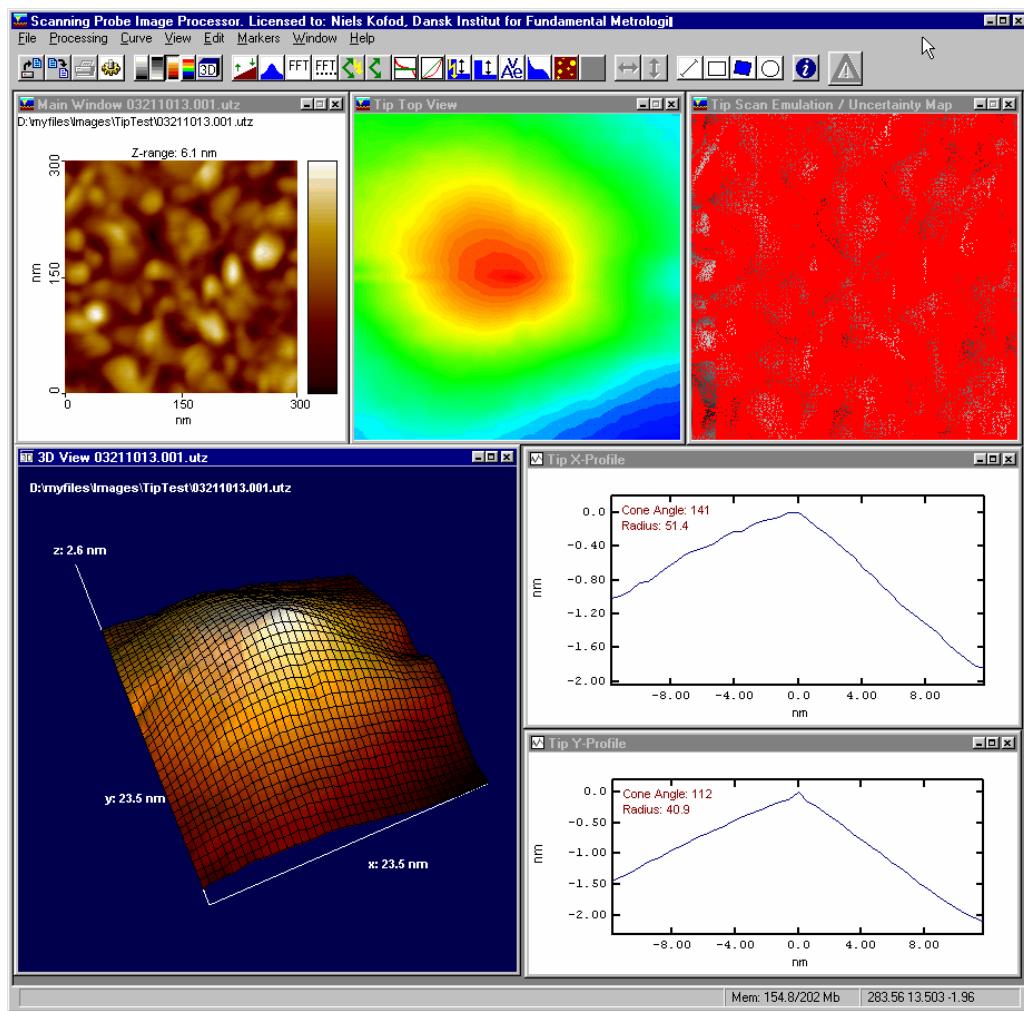
If there is noise in the image, especially spikes, the sharpness of the tip can easily be overestimated. In such cases it is a good idea to increase the tip detection count, which is the number of occurrences in the image that a certain part of the tip would be *inside* the surface. This can of course not be true but is a way of ignoring the spikiest parts of the image. After the tip has been characterized you can set the detection count interactively by the scroll bar

and in real-time observe how it changes the estimated tip. Note that the Acceptance level will influence the *Certainty Map* and thereby alter the tip estimation after 1<sup>st</sup> iteration in the tip estimation algorithm.

### Characterize

When pressing the **Characterize** button the tip characterization will be started and it will be based on the image window for which the tip characterization was invoked the first time. Below is seen a screen dump after a tip characterization with the estimated tip seen in top view and 3D perspective. The gray image is the *Certainty Map* and is the result of a tip scan emulation by the estimated tip and the surface image. The red marks indicate the positions where the tip is probing the surface with other parts than its apex. Also the tip x- and y-profiles can be shown with their estimated tip radius (based on a circle fit) and the cone angles.

The following image is an AFM image of an evaporated gold film; kindly provided by the Danish Institute of Fundamental Metrology and demonstrates a blind reconstruction of the AFM tip.



### Load Tip

After having estimated a tip you can save it in the BCR format, load it again and use it for *Deconvolution* of other images. Note that only tips saved in BCR format can be loaded. If you have a tip in another format you may be able to use SPIP to convert the tip image to BCR format.

If the resolution (physical distance between pixels) of the loaded tip is different from the image to be *de-convoluted* the tip will be resampled to obtain the same resolution and a message will be given.

### **Emulate Scan**

By the Emulate Scan push button it is possible to scan the Main Image with the current tip shown in the Tip Top View window, this process is also called *dilation*. The resulting image is called the Certainty Map because areas un-touched by the tip apex are detected and marked with the red color.

It is possible to use this function on artificial tips and surfaces and learn how different tips can affect the observed images and the quantitative results.

### **Deconvolute**

*Deconvolution* is important for correct line width measurements and can also assure more accurate results in particle size analysis and roughness measurements.

Pressing the **Deconvolute** button will calculate a new image based on the Main Image and the actual tip shown in the Tip Top View window, this technique is also known as *erosion*. The process has only meaning when the surface structure has sharper edges than the tip. In such cases it is partly possible to correct for the width of the tip, which otherwise causes line width and the lateral size of particles to be overestimated.

## **Results**

A number of quantitative results can be extracted from at tip characterization process, which can be reported into Word files or HTML files when using batch processing and/or the Active Reporter

Tip Radius: is determined by a sphere fit to the estimated tip. Small radii characterize quality tips. The Radius is calculated from a sphere fit to the NxN center pixels where N is specified by the Fit Range input field. You can turn off the calculation by setting the Fit Range to zero.

Tip X- and Y-Radius: is determined by a sphere fit to the estimated tip. Small radii characterize quality tips. The Radius is calculated from the N center points where N is specified by the X, Y Fit Range input fields. The fitted semicircle is shown in the profile window by default, but can be turned off by turning "Show Fitted Curve" off, which is done by right clicking in the curve window on Curve Fit. Alternatively you can avoid the calculation and display of the semicircle by setting the Fit Range to zero.

Tip X- and Y-Cone Angles: is determined by a linear fits to the two sides of the estimated tip. Small cone angles characterize quality tips. The two lines are estimated from the N/2 point s on each side of the tip, where N is specified by the X, Y Fit Range input fields. The fitted cone angle is shown in the profile window by default, but can be turned off by turning "Show Fitted Curve" off, which is done by right clicking in the curve window on Curve Fit. Alternatively you can avoid the calculation and display of the cone angle by setting the Fit Range to zero.

Certainty Area: is the percentage of the surface that could be probed by the tip apex. If this number is low you could consider exchanging the tip with at sharper one.

Profiles: it is optional to view the tip x and y-profiles; if they are on they will also display the profile radii based on circle fits to the N center points, where N is defined by the associated Fit Range input fields. The fitted circles can be visualized by setting Show Fitted Curve On. Likewise, they will show the Tip Cone Angles, which are calculated based on linear fits to the each side of the estimated tip where the estimation region is given by the associated Fit Range input fields.

### **Residual RMS**

For the fitted spheres and cones the residual RMS value is calculated. For good fits the RMS value will be low. Depending on the tip and its general form the RMS value may also indicate the roughness of the tip.

### Saving the numerical results

Depending on the options defined in the Options Dialog the numerical results may written to files with the added extension *.tip* or to the database of the **ImageMet Explorer**

### View Options

#### View Tip in 3D

If you have the 3D Visualization Studio included in the software you can automatically visualize the tip in 3D.

### View Profiles

The tip x- and y-profiles can be shown with their estimated tip radius (based on a circle fit) and the cone angle.

### Confidence Graphs

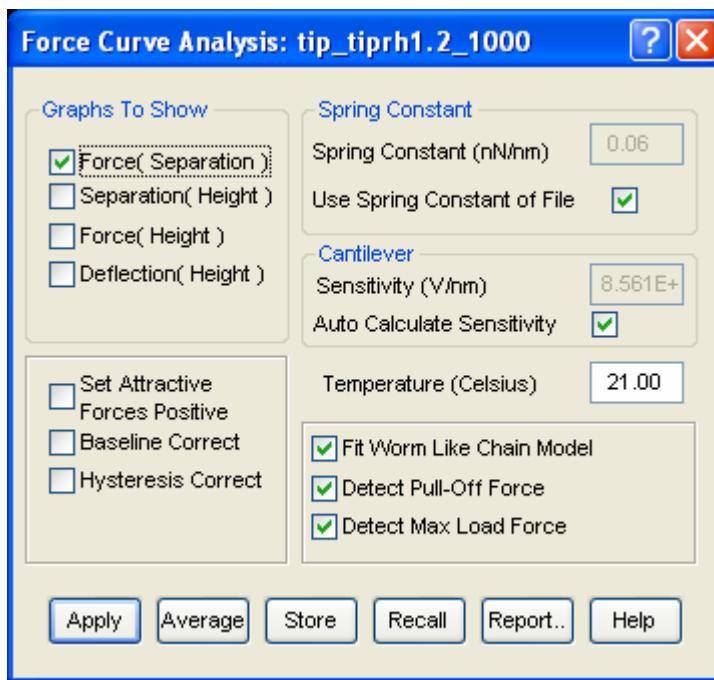
It is possible to display how the different quantitative results depends on the Detection Count Setting: Tip Radius, Tip Height (Height range of estimated tip), and X,Y Cone Angles. This may help you to optimize the Detection Count selection and estimate a tip based on a compromise between small noise influence and high utilization of the image information.

### Hint

The outer pixels of the estimated tip will often have a high uncertainty simply because there is not enough information in the surface image. In such cases it can be practical to show these pixels as invisible, which is done by manually defining them as Void Pixels. This is performed the Tip Top View window and will also have effect when it is put into the 3D window.

## Force Curve Analysis

The force curve analysis menu is activated either automatically when opening a file with force curve data or selecting the menu item Force Curve Analysis in the right mouse key menu of a curve window or the curve menu of the menu bar.



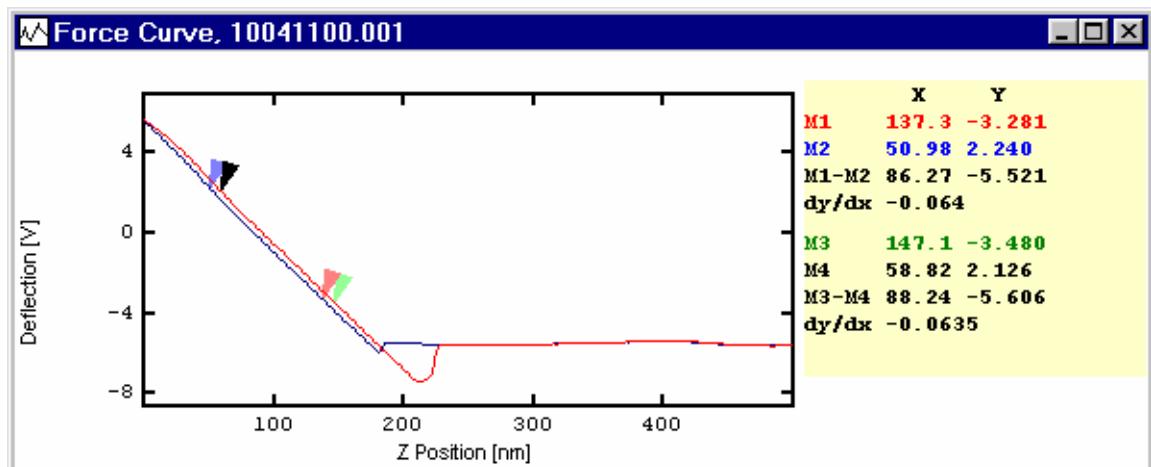
The menu enables the creation of new graphs where force and separation are calculated based on the spring constant and the deflection signal as function of the height.

The cantilever sensitivity (V/nm) can be calculated automatically from the slope of the **extending (blue curve)** or **retracting curve (red curve)** where the repulsive forces are dominating. The deflection measured in nm is calculated by dividing the deflection voltage with the cantilever sensitivity and the separation between sample and cantilever can be calculated from the sum of deflection and the height signal (where low height values means that the sample is close to the sample). SPIP will set the found minimum separation to zero. The Force values are calculated from the product of the cantilever spring constant (nN/nm) and the calculated deflection [nm].

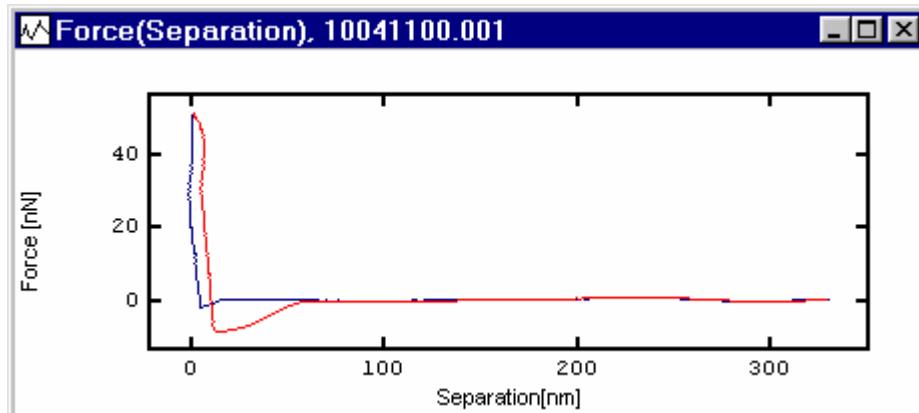
Sometimes it might be most convenient to show the attractive forces as positive and the repulsive forces as negative forces, e.g., when analyzing curves from unfolding protein experiments. This can be set by the Set Attractive Forces Positive check box.

It is possible to enter a spring constant or let SPIP read it from the file if it is included.

The cantilever sensitivity can be calculated automatically or entered manually. In the latter case the sensitivity can be evaluated from by use of the cursors. Setting two cursors on one of the curves in the engage region will cause the slope  $dy/dx$  corresponding to the cantilever sensitivity to be calculated. There is a cursor pair available for each curve (extending and retracting), see below.



In this case the calculated Force (Separation) graph looks as below, although the x-coordinates are non-equidistant spaced it is possible to activate the cursors and perform measurements as on normal curves.



When Fit Worm Like Chain Model (WLC Model) is checked a WLC model will automatically be calculated from each detected unfolding event. The model is based on the following formula:

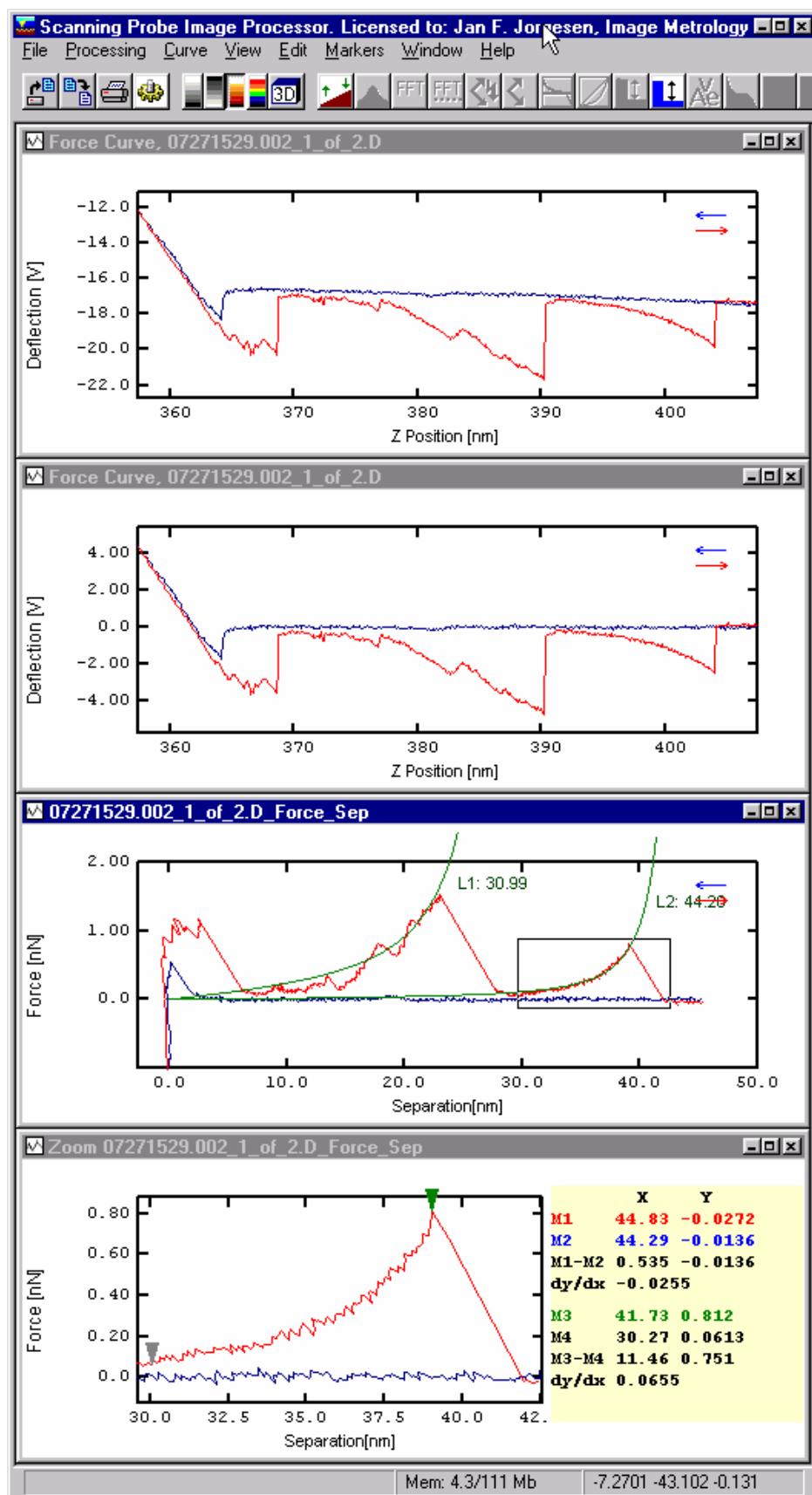
$$F(x) = \frac{K_B T}{l_p} \left[ \frac{1}{4(1-x/L_c)^2} + \frac{x}{L_c} - \frac{1}{4} \right]$$

Where  $F(x)$  describes the Force as function of separation  $x$ ,  $K_B$  is the Boltzmann's constant,  $T$  the temperature in Kelvin,  $l_p$  the persistence length and  $L_c$  the Contour Length, which is presented as the result in the graph.

It is also possible to force a WLC fit to a certain part of the curve defined by the zoom box for this purpose right click in the Force Separation Graph on Force WLC Fit Inside Zoom.

When more than two unfolding events are detected the individual Contour Length results will be displayed as function of the event index. The slope of this graph is automatically calculated and reflects the domain contour length in the protein.

Below is seen an example of a Worm Like Chain Model analysis, the upper graph is the raw curve, below is a Base Line Corrected version and then the Force(Separation) graph with two fitted WLC models is shown with a zoom at the bottom. Data Courtesy of Michael Wrang Mortensen, Danish Institute of Fundamental Metrology.



Detect Pull-Off Force Enables the calculation of the pull-off force on the retraction curve, which will be shown in the Force(Separation) graph.

**Detect Max Load Force** Enables the calculation of the Max Load force, which will be shown in the Force(Separation) graph.

#### **Temperature**

In order to get the Persistence Length values of the Worm Like Chain model calculated it is necessary to enter the temperature during the pulling experiment.

When Base Line Correct is set on SPIP will automatically fit a 3<sup>rd</sup> order baseline to the approach curve (Ignoring the contact regime). This base line is then subtracted from the approaching curve as well as the retraction curve. The base line estimation region can also be defined manually by the zoom box, it will then be processed by a right click in the **Deflection(Z)** curve window on **Base Line Correct Within Zoom**.

**Hysteresis Correct:** This option will cause SPIP to shift the retracting curve so that it will overlap with the extending curve in the contact region.

When the **Apply** button is pressed the requested curves are calculated and shown but in contrast to when the **OK** button is pressed the Force Curve Menu stays active.

The entered settings can be saved to Force Curve Settings (\*.fcs) files and defined as default by saving the settings to the file called *Default.fcs*.

#### **Average:**

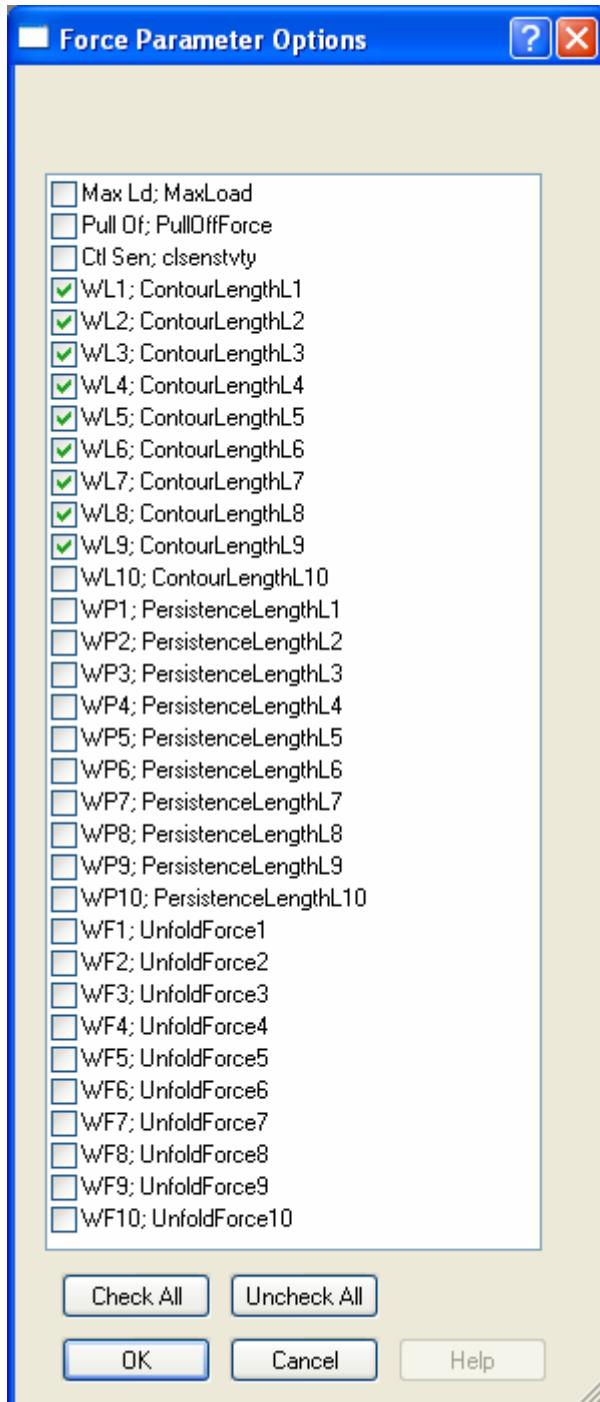
To perform force curve averaging of multiple force curves all the curves of interest should be loaded into the SPIP program first. Then, when pressing Average SPIP will find all force curves of same type as the active force curve connected to the dialog and perform the average calculation.

Curves of size or type different from the active force curve will automatically be ignored. The quality of the result depends strongly on the alignment of the curves and the program will prompt you for selecting one of two alignment methods. The first is based on an alignment of the minimum curve values, which typically is related to the pull-off point. The second method performs the alignment by minimizing the mean square sum difference.

After averaging you can turn the average curve into the active force curve by right clicking in it is window on **Force Curve Analysis**.

### Report Options and Batch Processing

By clicking the Report Options button it is possible to define which parameters that will be reported during batch processing. A batch process including Force curve analysis will automatically generate an ASCII file with a table of the numerical results for the individual force curves and add a summary table showing the statistical values. Likewise optional reports in HTML and MS Word can be generated. For high throughput it might be desirable not to include the HTML and MS Word reports, to save processing time.



## Continuous Imaging Tunneling Spectroscopy (CITS)

The Continuous Imaging Tunneling Spectroscopy (CITS) module allows you to visualize and handle I/V spectroscopy data. The availability of this function depends on the file format used by the STM vendor. If your file format is not supported please contact us for an upgrade.

When opening a file SPIP checks if there is CITS data included in which case it will display three windows containing the following images:

Topographic image.

CITS Volume image

Spectroscopy image

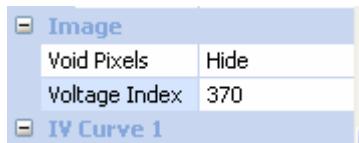
In the CITS Volume Image window the current is shown for a selected voltage. This window can be overlaid with a grid indicating the positions of the individual I/V acquisitions and the individual I/V curves can be selected and shown in an IV Curve window.

To show the individual IV curves click on the IV Spectroscopy Curve tool key.

When clicking in the volume image the I/V curve acquired nearest to the associated mouse position will be displayed in an IV curve window and the position will be marked by a cross. It is possible to select more IV curves and have them shown in the same IV Curve window.

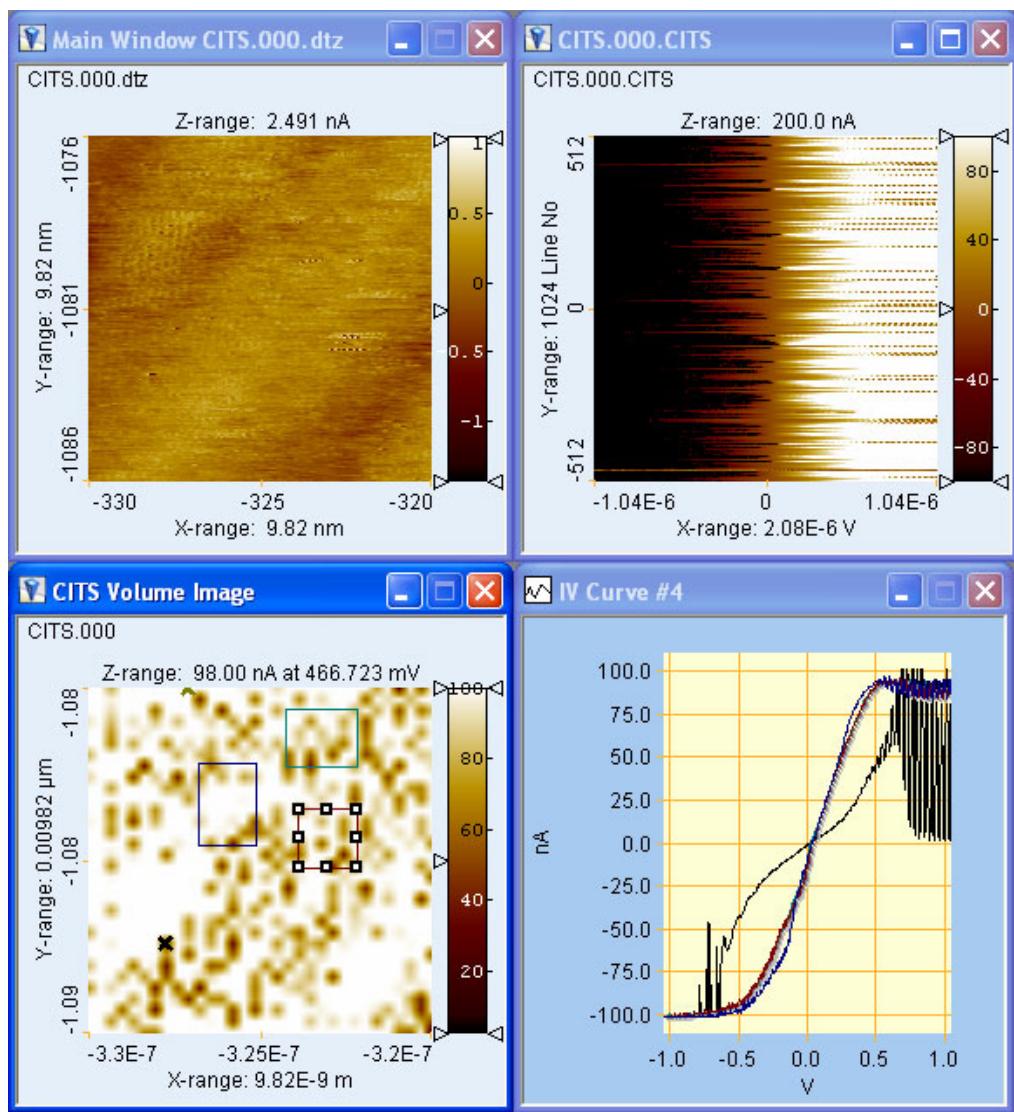
Once selected, IV curves at other positions can be shown by dragging the IV cross mark. By drawing rectangles the IV curves acquired inside the boundary of the rectangle will be averaged and shown in the IV curve window. Different colors are used to distinguish between the selected IV curves.

For the CITS Volume image the voltage can be selected from the View Settings Pane by the Voltage Index parameter found in the Image group:

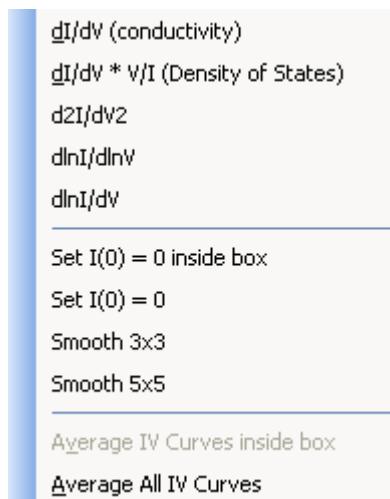


In the spectroscopy image each horizontal line represents an I/V Curve. The lines are ordered by the acquisition time with the first curve shown in the upper line.

The CITS data shown below is kindly provided by Abdou Hasssanien, Electrotechnical Laboratory, Tsukuba, Ibaraki, <http://www.etl.go.jp/>. It demonstrates the selection of three regions for which average I/V curves have been calculated and shown in the IV Curve window. Likewise a single I/V curve has been selected, which is shown by the cross marker.



By right clicking in a CITS image its context menu with dedicate spectroscopy functions will appear:



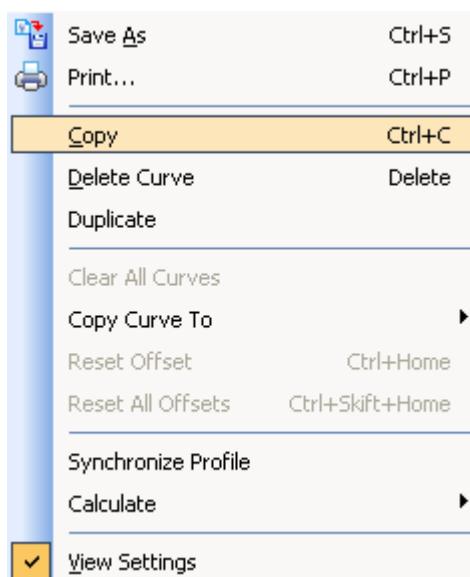
The CITS Volume and the Spectroscopy images can be transformed to show other properties e.g., conductivity ( $dI/dV$ ) data or the Density of States ( $dI/dV * V/I$ ) using the context menu.

To correct the current values by an offset value such that the current will be zero for zero voltage press the Set  $I(0) = 0$  or Set  $I(0) = 0$  inside box.

To smooth the IV curves press Smooth 3x3 or Smooth 5x5, which will cause a calculation of average IV profiles for each x,y based on the 3x3 or 5x5 neighborhood.

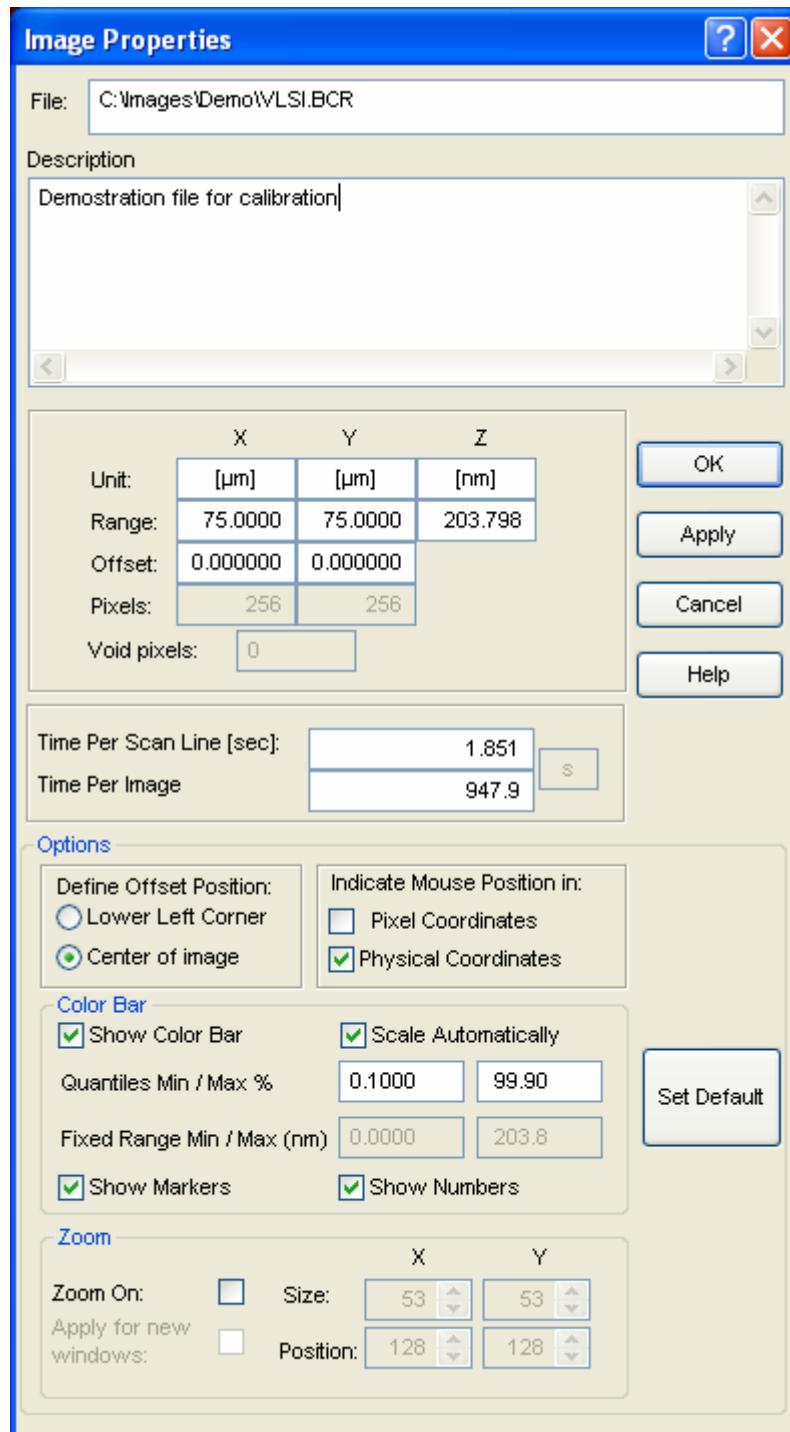
Average IV curves can be calculated by clicking on Average All IV Curves or Average IV Curves inside box. In the latter case the zoom box must be present.

The context menu of the IV curve window allows you to clear the individual curves or to copy individual curves to the Single Profiling window, which provides more measurement tools.



## Image Properties

To view and edit the image properties click on the right mouse key and select properties:



**File:** You can enter a new name for the image, which will be used as file name when saving the image. This will also change the caption of the image window and can be practical for demonstration purposes.

### Description:

You can edit the description, which can be saved into STM-BCR (\*.bcr) files.

### Units:

The units for the three axes can be defined, but the numerical values will stay unchanged. Depending on the range of the different dimension SPIP might show length using the most appropriate units. Currently SPIP recognizes the following length unit abbreviations:

- Å, A: Ångstrøm
- nm, nanometer
- µm, um, micrometer
- mm, millimeter
- cm, centimeter
- in, inch
- m, meter
- km, kilometer

The units are also recognized when included in brackets, e.g., [um]

### Range:

The range can be changed for all three dimensions. This is particularly useful for graphical formats like tiff, bitmap and jpeg where the physical size of the image area is not included in the file.

When changing the Z-range the Z-values will be scaled so that the difference between the maximum and minimum values equals the entered Z-range.

### Offset:

The offset parameters describe the physical position of the image area relative to the scanner / acquisition instrument.

### Timing Information

The timing information defines how fast the image area was scanned (and has only meaning for scanned images). These parameters are important for correct calculation of time domain frequencies when diagnosing noise and vibration problems using the Fourier Menu.

### Options

There are several options, which will determine how the current image will appear and can be set at defaults.

#### Define Offset Position

The offset position can be associated with the center of the image or the lower left corner.

#### Mouse Position Information

When the mouse cursor is located in an image window its position relative to the image coordinates are written in the lower right corner of the program window. These coordinates can be expressed in pixels or in physical dimensions.

#### Color Scale

The color scale can set to cover the full z-range or a fraction of the image automatically or to cover a fixed range. The latter can be useful for comparing images.

When "Scale Automatically" is set on, it is possible to define a quantile range such that the left color markers of the color bar are set to the min and max quantiles (the color markers will determine the contrast of the image, see the "Colors" section). This is a strong technique for achieving a good contrast even in images containing extreme values and the color markers will also provide a good indication of the outlier height values.

When setting the min and max quantiles to 0% and 100% respectively the color markers are set to the associated minimum and maximum values of the image.

Here, you can also define if you want to have the color bar shown by default. When saving this option as default it will only apply to images of same class, i.e., Main Image, Fourier Image and others.

**Zoom Options**

When zooming using the rectangular marker tool it can often be convenient to have a zoom box of a certain size or position. The numbers entered will be in terms of pixels of the raw image and work independently of the actual window size. When checking the "Apply for new windows" checkbox new image window will have set their zoom box size and position as shown.

**Set Default**

When pressing Set Default all parameters defined in the Options frame will be saved along with the associated image class: Topographic image or Fourier Image. For the Show Color Bar Initially SPIP will also distinguish between the Main Image Window and other topographic image window, thereby you can have the Main Image to appear differently from the other topographic images.

## Filter Dialog

### Introduction to Filters

The SPIP Filter Module provides a comprehensive set of predefined spatial filters and tools for designing dedicated filters. You can use the various filters for getting nice presentations and robust measurements by noise reduction or to emphasize certain textures.

The filtering techniques implemented in the SPIP program are divided into the four groups:  
Linear Filters (smooth, sharpen, edges,...)

Specific ISO Standard Linear Filters

Non-Linear Filters (median, outlier objects, statistical differencing)

- Fourier filtering

The filters described here are all spatial filters while Fourier filtering (Frequency domain filtering) is part of the Fourier module and is described in the Fourier section.

For information on how to use the filter module the following sections are included:

Introduction to the filter module

Using the template dialog

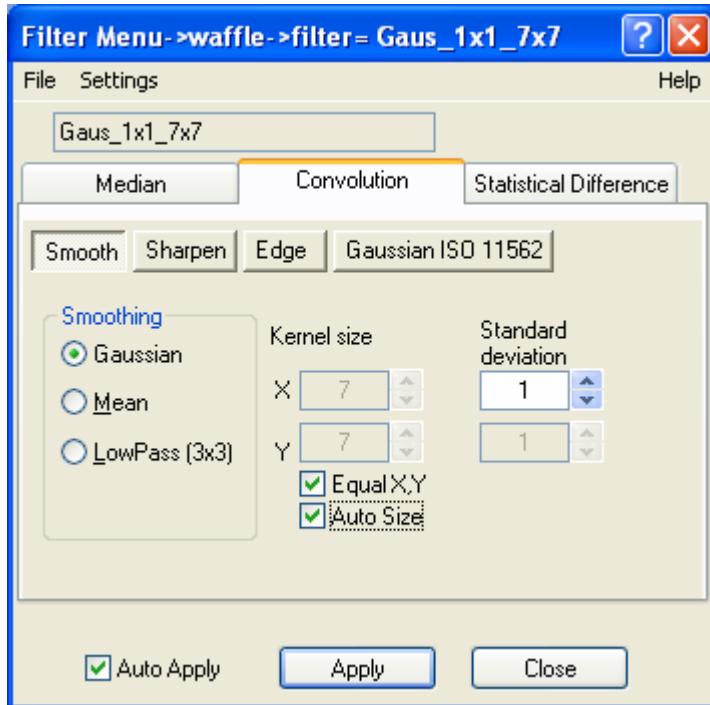
Overview of the different filters

Filter Border Mode

Output Options

## The Filter Dialog

To perform a filtering process Right click on either a 2d Image window or a curve window. In the pull-down menu, press "filters" and the filter menu appears with a possible list of filters available as shown below. Note, the availability of the filter module depends on your license.

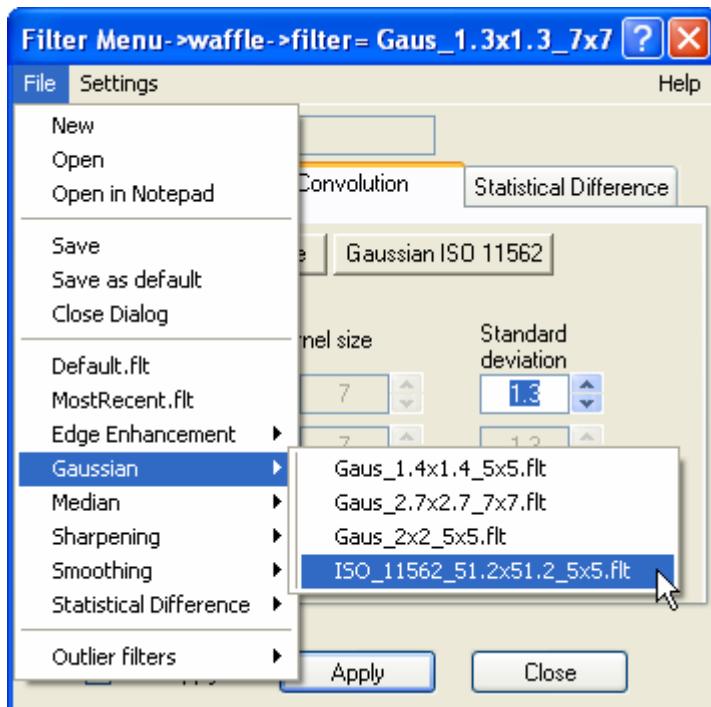


By use of this filter dialog different filters can be created, loaded, shown and altered. The filter dialog has three tab dialogs where Convolution, Median or Statistical Difference filters can be chosen. When the convolution filters tab is selected four groups of convolution filters can be selected: Smooth, Sharpen, Edge and Gaussian ISO 11562. At all times the title bar contains the name of the filter source.

### Apply

To apply a selected filter, just press Apply. Alternatively set the "Auto Apply" checkbox on and every change of filter parameters will be applied immediately to the source image. The auto apply button is most practical for checking the effect of smaller kernels where the filter effect can be monitored in almost real-time while modifying the filter parameters. Larger kernels require more computation time and it may therefore be more convenient to disable the Auto Apply option.

### File (Loading Filters)



The different predefined filters can be loaded from the "Filter Dialog" as shown above. The "File" button is used to load pre-defined filters from the hard disk.

The filter module is delivered with a number of predefined filters and the user has tools for designing and storing user-defined filters. By directly choosing any of the available filters the filtering takes place and the result will be shown as indicated in the output options.

These predefined kernels can also be loaded from the "Filter Dialog" using the "Load" command. The filters can be found in a map called "kernels" in your SPIP program directory.

#### **Open**

Allows opening a kernel file from a diskette, CD or hard disk. Normal file extension for the added filters are: ".flt". Other files can be searched for by changing the type of files to (\*.\*) all files. The software is capable of reading filter kernels from ASCII files, where the parameters are organized on one line per row of data.

#### **Saving Filters**

When saving a filter kernel file in a sub directory of the kernel directory, the file will appear in the Filter Dialog automatically next time the "File" button is pressed. It is also possible to create a limited number of maps. The default extension for the filters files is .flt. The kernel filters are in ASCII format and can be viewed and edited in notepad.

When the filter is saved as a default filter this filter will be used when running batch processing.

## Overview of the Different Filter Types

SPIP™ has the following spatial filters implemented in the Filter module

### **Linear Convolution (kernel) Filters**

#### **Smoothing**

Parametric LowPass

Mean filter

Gaussian Standard deviation Smoothing

#### **Sharpening**

HighPass (Unicrisp - Laplacian)

Laplacian of the Gaussian /Mexican Hat

#### **Edge Enhancement**

Gradient (Roberts, Prewitt, Sobel, Pixel Difference )

Laplacian

### **ISO Standard Filters for surface analysis**

ISO 11562 Gaussian profile filter for surface analysis

ISO 13565 Deep Valley - Gaussian profile filter for surface analysis

### **Non-linear Filters**

Median filtering, for noise removal

Outlier Objects Filter for recovery of areas covered by contamination and spike elimination

Statistical Differencing

Local Mean equalization

Local Standard Deviation equalization

## Linear Convolution Filters

### Introduction to Linear Convolution Filters

Linear convolution filters are based on a filter kernel that is convoluted with an image or in the 1 dimensional case a curve. The filter kernel it self can be considered as an image (or in 1D as a curve) and also viewed as such. The SPIP program makes it easy to modify the filter kernel and display the kernel in 2D, 3D or for one-dimensional filter kernels as curves.

The Linear filter kernels provided are divided into the following categories:

- Smoothing (Low Pass, Mean, Gaussian)
- Sharpening (High Pass)
- Edge enhancement & Laplace
- ISO standard filters

The mathematical description of a convolution with a filter kernel K of size N x M and an Image I is described below.

$$C(x, y) = \frac{1}{k} \sum_{i=-N/2}^{N/2} \sum_{j=-M/2}^{M/2} K(i, j) I(x - i, y - j)$$

To avoid a general amplification of the data the sum of products are normally scaled by a factor  $1/k$ , where k is the sum of the kernel coefficients.

$$k = \sum_{i=-N/2}^{N/2} \sum_{j=-M/2}^{M/2} K(i, j)$$

The simplest form of a convolution kernel is 1x1. Then the output data depends only on the value of the input data at the position (x,y) and the convolution becomes a gray-level transformation, which is also called mapping.

### Smoothing Filters

Smoothing filters are also called low-pass filters because they let low frequency components pass and reduce the high frequency components.

The impulse response of a normal low-pass filter implies that all the coefficients of the mask should be positive. Low-pass filtering in effect blurs the image and removes speckles of high frequent noise. Larger masks will result in more blurring effect. To avoid a general amplification or damping of the data the sum of the filter coefficients should be 1.0.

Different types of smoothing are available:

- Parametric LowPass
- Mean filter
- Gaussian Smoothing

In practice the low-pass filter can be used for creating high pass filters by subtracting the filtered result from the original image or by some other combination of the input image and the filtered result as described in the "Unsharp Masking" section.

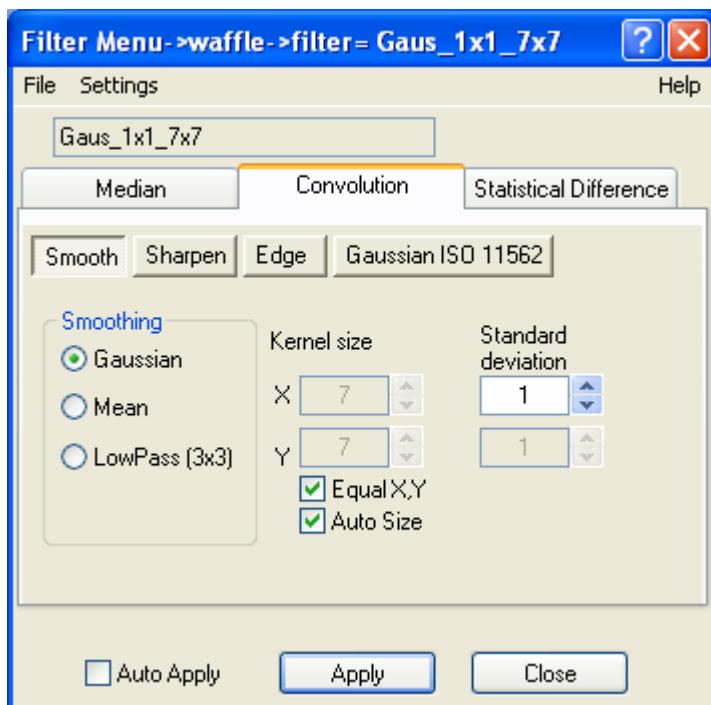
### Gaussian smoothing

Gaussian smoothing is often applied because the noise or the nature of the object observed might be of a Gaussian probable form. A two-dimensional Gaussian Kernel defined by its kernel size and standard deviation(s). Below are the formulas for 1D and 2D Gaussian filter shown  $SD_x$  and  $SD_y$  are the standard deviation for the x and y directions respectively.

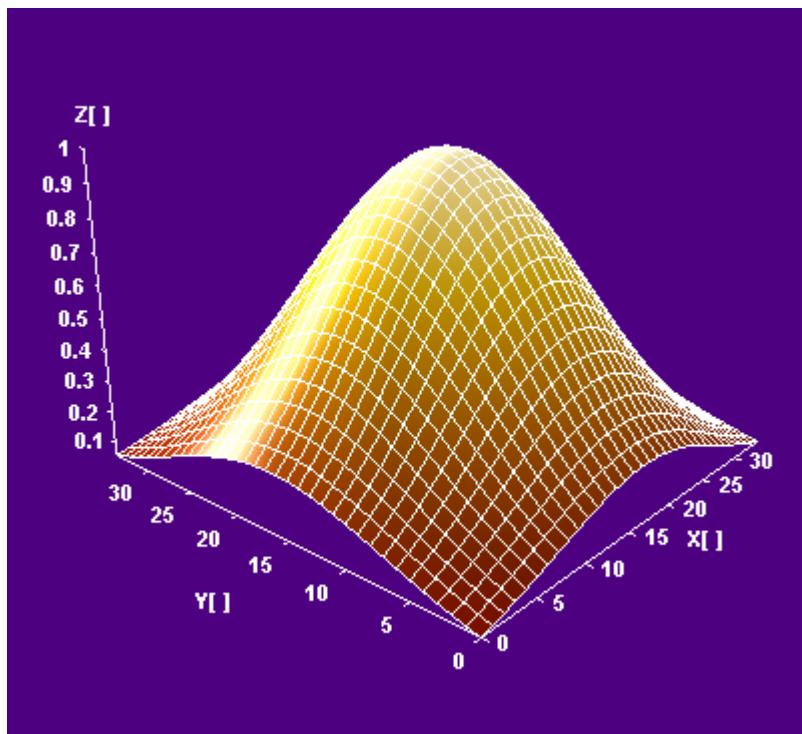
$$K_{1D}(i) = e^{\frac{-i}{2 \cdot SD}},$$

$$K_{2D}(i, j) = e^{\frac{-i}{2 \cdot SD_x}} e^{\frac{-j}{2 \cdot SD_y}}$$

The Gaussian filter works like the parametric LP filter but with the difference that larger kernels can be chosen.



Below a Gaussian filter is shown in 2D top view with horizontal and vertical cross sections and also in 3D view. The Gaussian function shown has a standard deviation of 10x10 and a kernel size of 35x35 pixels. Notice that a large part of the kernel for the y direction contains values very close to zero due to the low standard deviation in this direction. During the filtering process the filter kernel will be normalized so that it will not introduce a general amplification of the height values.



### Kernel Size

The size of the kernel should normally be selected large enough so that the kernel coefficients of the border rows and columns contribute very little to the sum of coefficients. By selecting a kernel size parameters six times the standard deviation the border parameters will be 1% or lower than the center parameter.

It is recommended to use the Auto Apply setting and having the Difference image included in the Output options such that the filter effect can be monitored in detail.

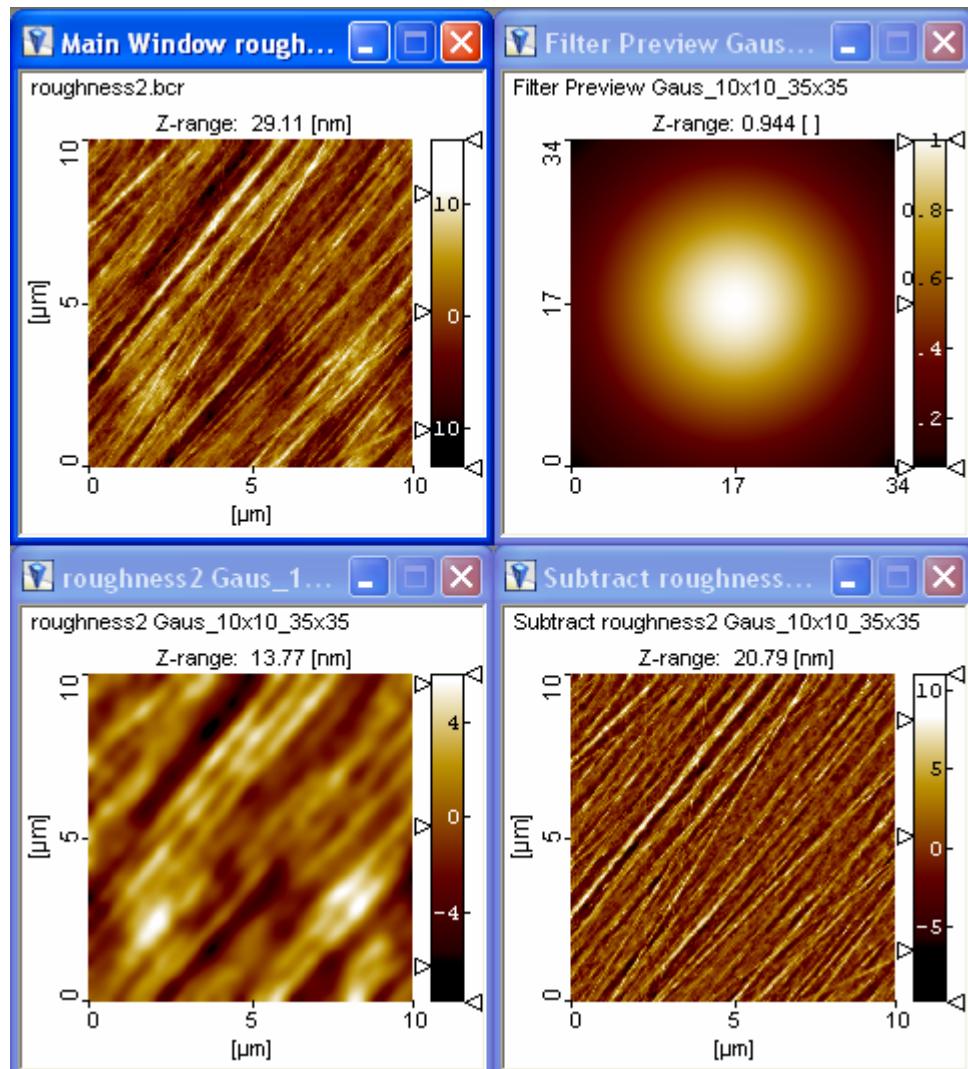
### Standard Deviation

The standard deviation for a two-dimensional kernel is the radius in pixels containing 68% of the integrated magnitude of the coefficients. Increasing the standard deviation will increase the effective kernel size.

The Gaussian kernel can be used to perform an unsharp masking filter by subtracting the result from the original and can in this way serve as an ideal high pass filter. This is discussed in the "*High Pass Filter*" section.

A special implementation of the Gaussian filter is the ISO 11562 Gaussian profile filter, this filter is discussed in the ISO standard section. The shape of the filter is equal to the Gaussian filter described here, but the Gaussian ISO filter is defined by a cutoff wavelength measured in physical length units (e.g. nm or  $\mu\text{m}$ ) determining which shorter waves should be reduced.

Below is seen a filtering example where the input image is shown upper left and the filter kernel upper right while the smoothening result is monitored lower left. The lower right image is difference image between input image and the filter result. While the smooth filter result reflects the long waves (waviness) the difference image reflects the short waves of the image.

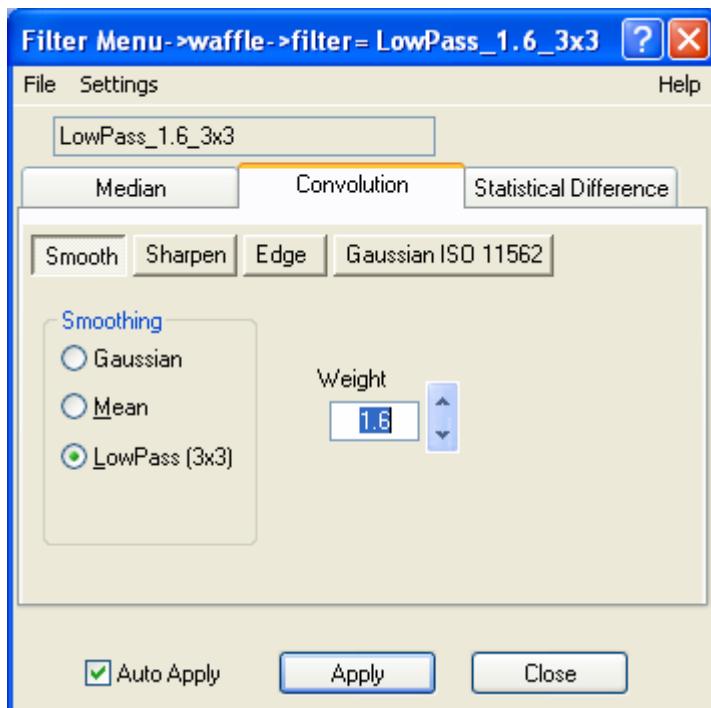


### Parametric Lowpass

A parametric lowpass filter is given by a 3x3 kernel where the coefficients are determined by a factor b, when b is equal to 1 the parametric LP is equal to a mean filter.

$$C(b) = \left(\frac{1}{b+1}\right)^2 \begin{bmatrix} 1 & b & 1 \\ b & b^2 & b \\ 1 & b & 1 \end{bmatrix}$$

The b parameter can conveniently be applied by the up-down keys of the Template dialog:



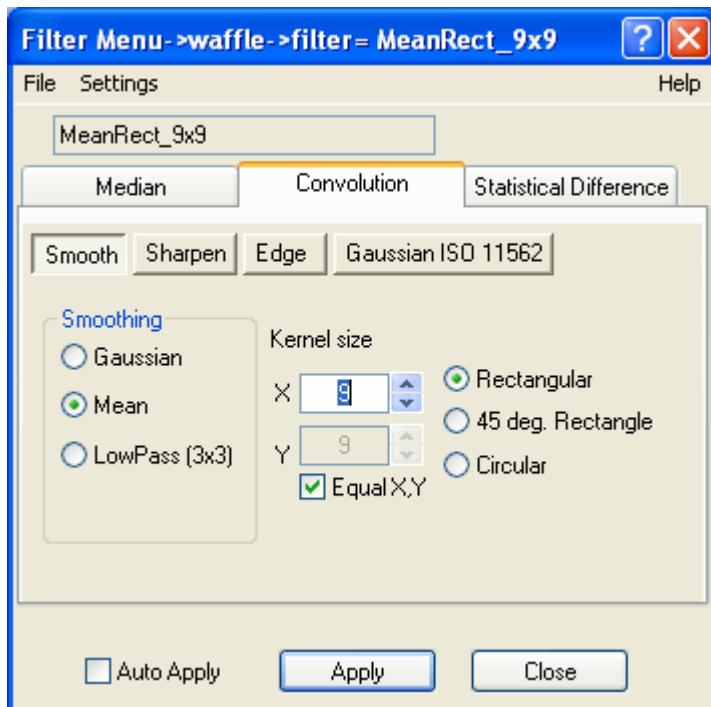
When the "auto apply" checkbox is checked the effect can be observed in almost real-time.

### Mean Filter

The mean filter is the simplest type of low-pass filter; here all the coefficients have identical values. Its characteristics are defined by a kernel width, height and shape. If obvious image deviations occur mostly in only one direction the smoothing can be adjusted by changing the shape of the filter to lie accordingly. When the size of the kernel increases the smoothing effect increases.

When the neighborhood considered is too large blurring and other unwanted effects can appear in the data set.

The selection of Kernel Size and form is a compromise between reduction of noise and a low blurring effect.



Different shapes for the Mean filter can be selected:

- Rectangular shape (normal)
- 45 degrees turned rectangle shape
- Circular shape (= octagonal for smaller kernels).

A Simple 3x3 mean rectangular filter is defined by:

$$C = \frac{1}{K} \begin{bmatrix} 1 & 1 & 1 \\ 1 & 1 & 1 \\ 1 & 1 & 1 \end{bmatrix}; K = 9$$

$1/K$  is the scaling factor, which can be applied to avoid general data amplification or damping.

### Kernel Size

The smoothing effect depends on strongly on the filter kernel size the larger the kernel the larger is the smoothing effect. With large kernel sizes the smoothed value becomes more dependent on values lying further away from the current position. The choice of kernel size is a compromise between a desired noise reduction and keeping the image sharpness.

### Sharpening Filters

Sharpening filters are used to enhance the edges of objects and adjust the contrast and the shade characteristics. In combination with threshold they can be used as edge detectors. Sharpening or high-pass filters let high frequencies pass and reduce the lower frequencies and are extremely sensitive to shot noise.

To construct a high-pass filter the kernel coefficients should be set positive near the center of the kernel and in the outer periphery negative.

The sharpening filters are divided into the following groups:

- High Pass Filters (Uni Crisp)
- Laplacian of Gaussian / Mexican Hat filters.
- Unsharp Masking
- High Boost filtering
- Difference of Gaussians

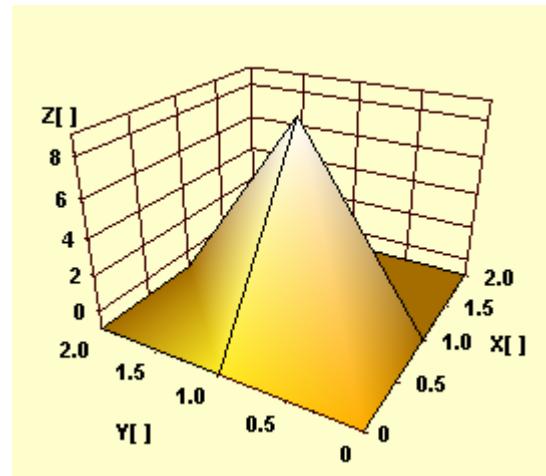
**Kernel Size**

Typical kernel sizes are 3x3 to 7x7 but larger kernels can also be applied.  
When checking "Equal" check box the X and Y kernel size are kept equal.

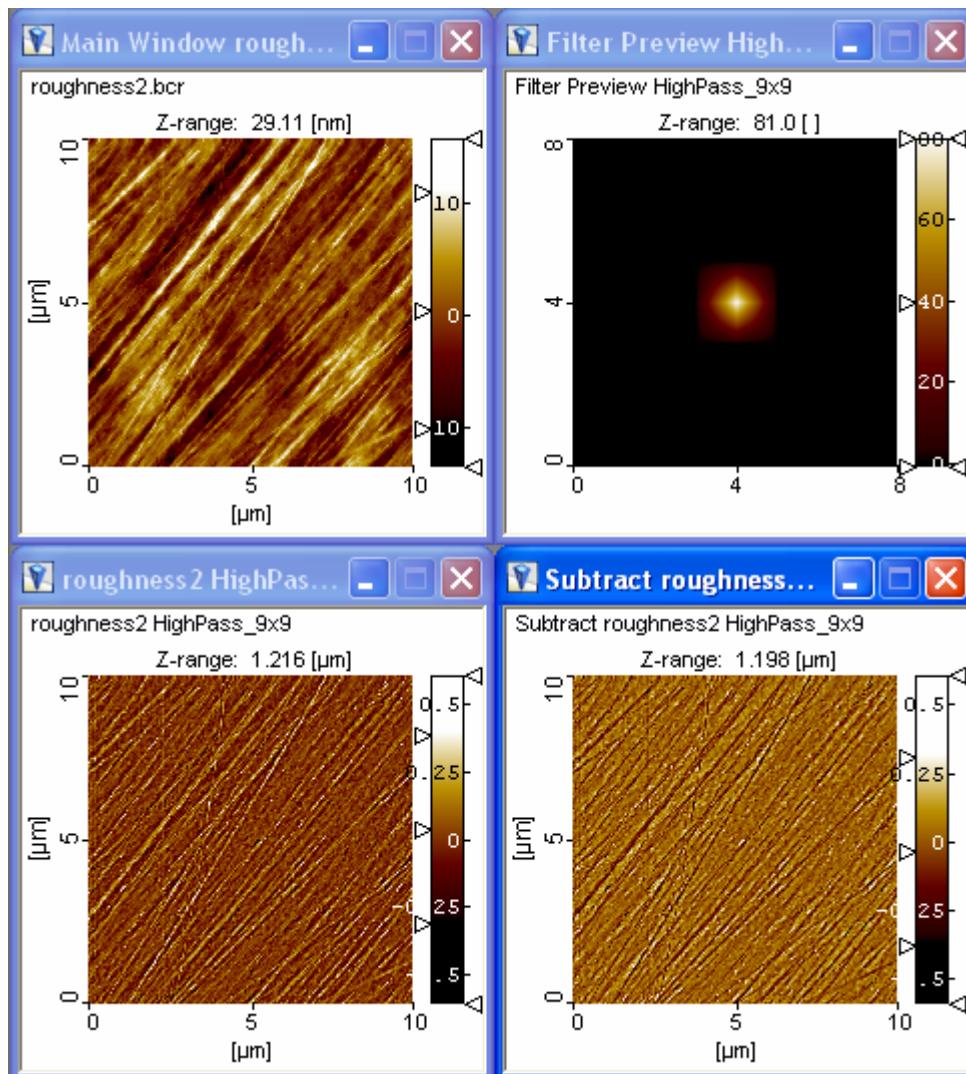
## High Pass Filters

The UniCrisp is seen as the most standard combination of a Sharpening or High Pass filter. By varying the Kernel size of the Kernel different sizes of the UniCrisp kernel can be chosen.

$$\text{uni\_crisp} := \begin{bmatrix} -1 & -1 & -1 \\ -1 & 9 & -1 \\ -1 & -1 & -1 \end{bmatrix}$$



The following is an example of the output from a 9x9 HighPass Filter.

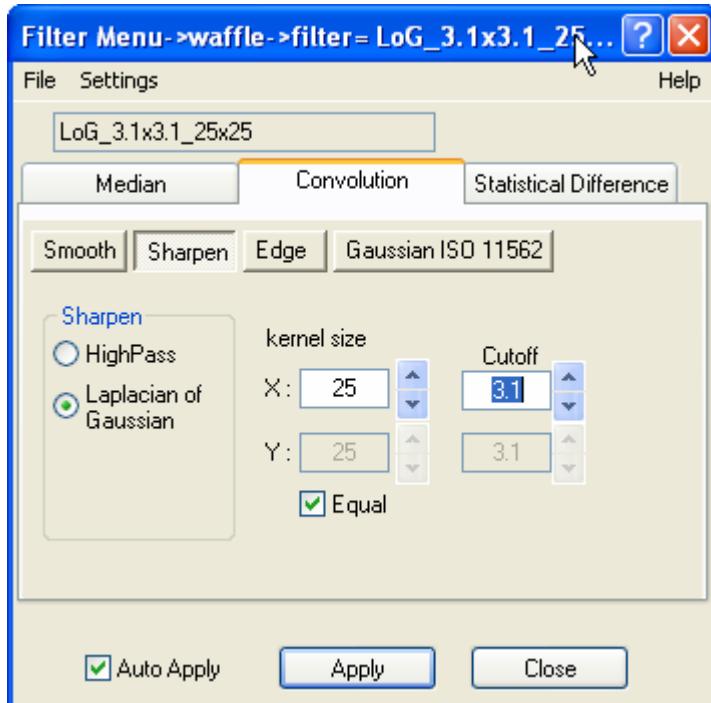


### Laplacian of Gaussian Filters

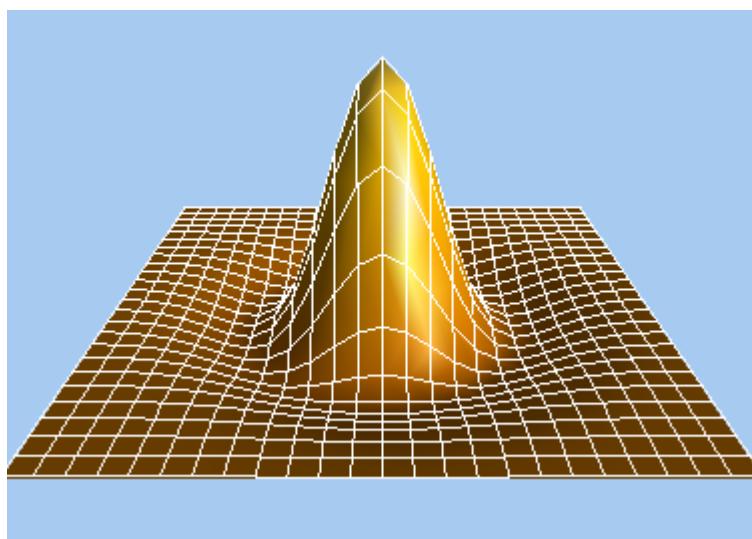
The Laplacian of Gaussian filter (LoG) is a combination of a Laplacian and Gaussian filter where its characteristic is determined by the  $\sigma$  parameter and the kernel size as shown in the mathematical expression of the kernel:

$$LoG(i, j) = \frac{1}{\pi\sigma^4} \left(1 - \frac{i^2 + j^2}{2\sigma^2}\right) e^{-(i^2 + j^2)/2\sigma^2}$$

The shape of the filter is defined by from template menu:



Here it is a good idea to set "3D Filter Preview" on in the Output Options so that the shape of the kernel can be monitored in 3D while modifying the kernel parameters:



Because of the shape Laplacian of Gaussian filters are often called Mexican hat filters. The kernel size should be selected large enough to contain the negative values otherwise its effect reduces to a Gaussian smoothing filter.

## Edge Enhancement Filters

Edge enhancement filters, enhances the local discontinuities at the boundaries of different objects (edges) in the image. An edge in a signal is normally defined as the transition in the intensity or amplitude of that signal.

Most of the edge enhancement filters are thus based on first and second order derivatives and different gradient filters are also common to use.

The edge enhancement filters are divided in the following groups:

- Gradient (Roberts, Prewitt, Sobel , Pixel Difference)
- Laplacian

### Gradient edge enhancement

The gradient of an image  $I(x,y)$  is defined along two orthogonal directions:

$$G_x(x,y) = \partial I(x,y) / \partial x \quad \text{and} \quad G_y(x,y) = \partial I(x,y) / \partial y$$

This operator is approximated in the discrete case as introduced by Roberts.

The output of such filters consists of positive and negative intensities and emphasizes the high frequency details of the image. When the sensitivity for noise is too high larger kernels should be considered to approximate the derivative operators.

The **Roberts** and **Prewitt** kernels are implemented by convolution with the different kernels to respectively enhance the edges at 0, 45, 90 and 135,... degrees.

Other typical kernels are the **Sobel** kernels.

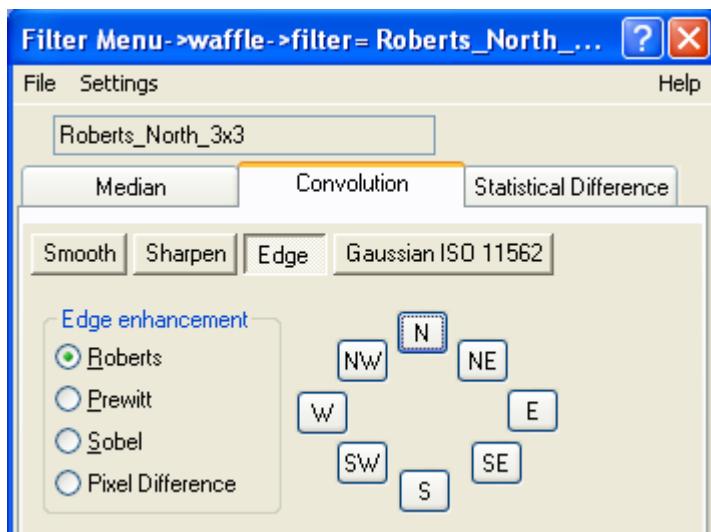
### Roberts edge enhancement kernel

This kernel focuses on the diagonal pixel differentials, which emphasizes corners more clearly but can blur together small horizontal or vertical features.

This can also be seen in the shape of the kernel.

Example:

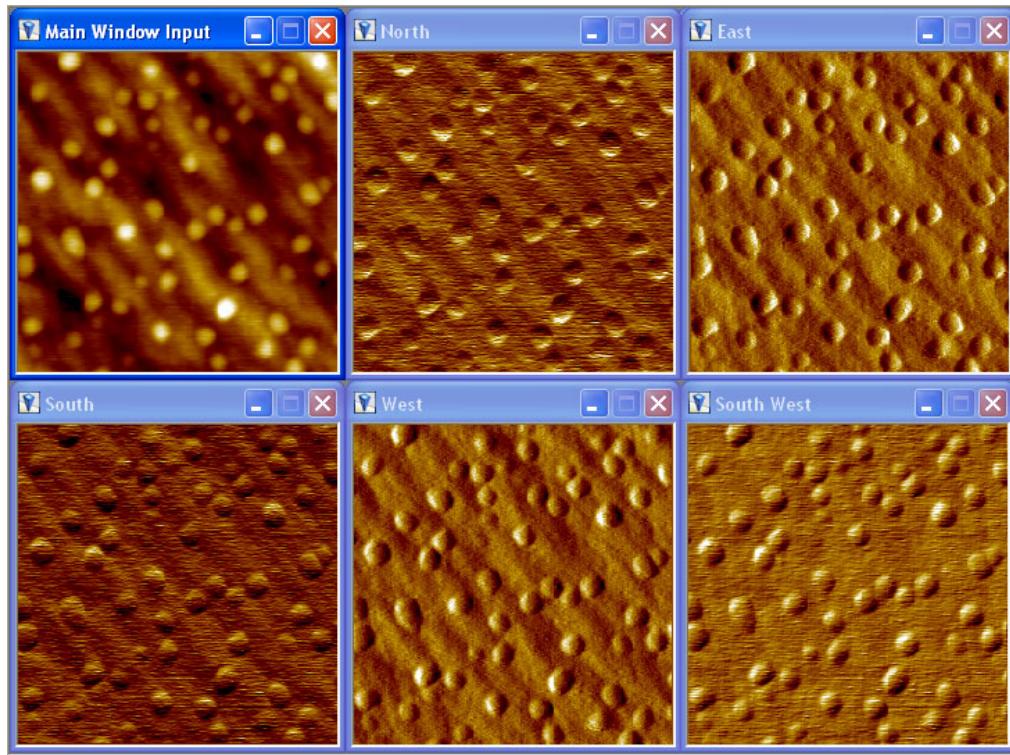
0	0	0
0	-1	0
0	1	0



Example: Roberts edge enhancement in different directions

The following example shows a zoomed part of an image containing some grain particles. When selecting any of the buttons above the different gradients can be retrieved from the data. Here an output is shown with the corresponding result.

Below is seen the results for the Roberts filer applied in 5 orientations (N,E,S,SW and W).



Notice that in the different filtered outputs some grains are better visible than in others.

#### **Prewitt edge enhancement kernel**

considers the orthogonal and diagonal pixel differentials equally.

Example:

1	1	1
0	0	0
-1	-1	-1

#### **Sobel edge enhancement kernel**

provides a more uniform edge enhancement although it still gives increased weight to the orthogonal pixels over the diagonal pixels.

Example:

1	2	1
0	0	0
-1	-2	-1

#### **Pixel Difference**

The Pixel difference edge enhancement filter is very similar to the Roberts edge enhancement filter and the output will be alike but for opposite directions.

0	0	0
0	1	0
0	-1	0

### Laplacian Edge enhancement

The Laplacian filter separates itself from the other edge enhancement filters because it uses second derivative information about the intensity changes in an image through a difference equation.

What is happening is that the difference of the center pixel is taken with every surrounding pixel, and then averaged. At edges this differential will be large and elsewhere it will be small, leaving highlights only in the areas where sharp differentials, or edges, occur. In the discrete domain the simplest approximation to the continuous Laplacian is to compute the difference of slopes along each axis.

$$\nabla^2 B := \frac{d^2}{dx^2} B + \frac{d^2}{dy^2} B$$

The Laplacian operator can be defined in a two-dimensional plane as:

$$2D(x,y) = \partial^2 I(x,y) / \partial^2 x + \partial^2 I(x,y) / \partial^2 y$$

In the discrete case it is approximated by the 4 connected grid as:

$$L(x,y) = -I(x-1,y) -I(x+1,y) -I(x,y-1) -I(x,y+1) +4I(x,y)$$

This four-neighborhood Laplacian can be generated the following kernel:

$$K = \frac{1}{k} \begin{bmatrix} 0 & 0 & 0 \\ -1 & 2 & -1 \\ 0 & 0 & 0 \end{bmatrix} + \begin{bmatrix} 0 & -1 & 0 \\ 0 & 2 & 0 \\ 0 & -1 & 0 \end{bmatrix} = \frac{1}{4} \begin{bmatrix} 0 & -1 & 0 \\ -1 & 4 & -1 \\ 0 & -1 & 0 \end{bmatrix}$$

## ISO standard Filters

The Specific filters are implemented according to general standard specifications.

ISO 11562 Gaussian Profile Filter for surface analysis

ISO 13565 Deep Valley - Gaussian Profile Filter for surface analysis

### ISO 11562 Gaussian Profile Filter

The ISO standard ISO 11562 describes how to separate the long and short wave content of a surface profile (roughness and waviness). Here the specifications are extended to cover images as well.

The filter kernel for a Gaussian filter is expressed as:

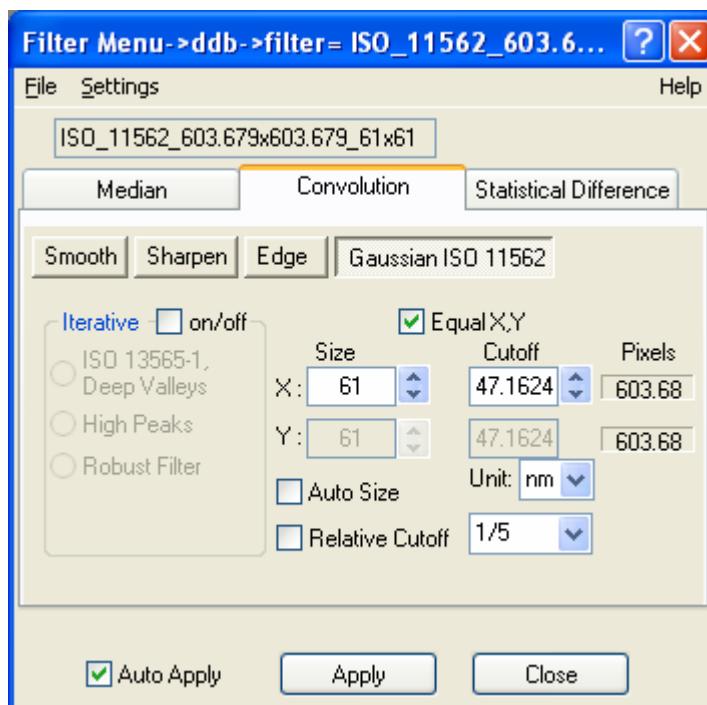
$$S_{1D}(i) = \frac{1}{\alpha\lambda} e^{-\pi\left(\frac{i}{\alpha\lambda}\right)^2}, \quad \alpha = \sqrt{\frac{\ln(2)}{\pi}} = 0.4697,$$

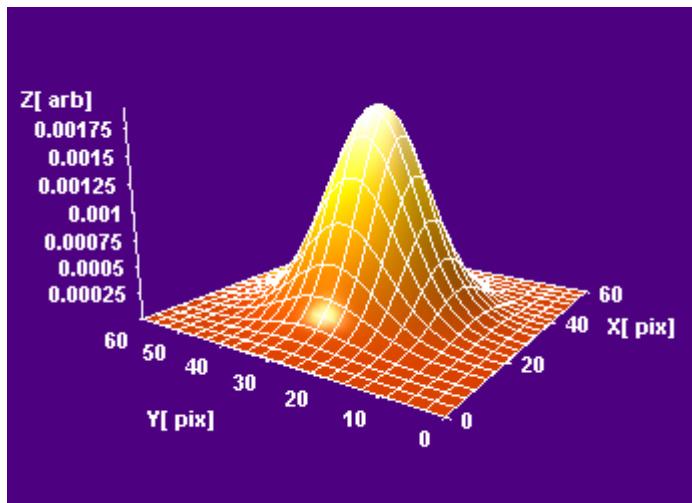
where  $\lambda$  is the cutoff wavelength.

The two dimensional Gaussian kernel is constructed by multiplication of horizontal and vertical 1D Gaussian kernels:

$$S_{2D}(i, j) = S_{1D}(i) \cdot S_{1D}(j)$$

In the image below a Gaussian kernel is shown in a one-dimensional form by a cross section of the 2D filter kernel. Notice that the height of the kernel is normalized to 1 and the values at the beginning and end of the 1D-kernel approaches zero.

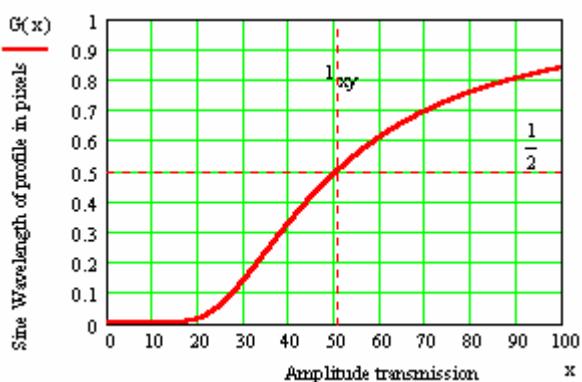




The transmission characteristic for a Gaussian filter can be obtained by Fourier transformation of the filter kernel and the damping factor as function of wavelength  $\lambda$  can be expressed as:

$$G(\lambda) = e^{-\pi \left( \frac{a\lambda}{l} \right)^2}$$

This is shown graphically for a filter with a cutoff wavelength  $\lambda$  corresponding to 51 pixels. It is seen that the damping factor is 0.5 at the cutoff wavelength.



### Kernel Size

The kernel size can be defined individually for the x and y directions. It should be selected so that a significant part of the Gaussian function is included in the kernel. This is obtained if the kernel size is 5 times or larger than the cutoff wavelength measured in pixels. It is possible to have the kernel size adjusted automatically by checking the Auto Size **checkbox**.

### Cutoff wavelength

The Cutoff wavelength can be defined by physical units, e.g., nanometers and the corresponding pixel length will automatically be displayed.

The cutoff wavelength can also be chosen from the drop down menu with sizes varying from 1/1 to 1/10 of the image size. The standard prescribes a cutoff wavelength of 1/5 of the profile evaluation length.

When the "Relative Cutoff" checkbox is checked the corresponding cutoff wavelength is calculated from the chosen value in the drop down menu.

### Size

When this option is checked the filter kernel size is automatically calculated so that a significant part of the Gaussian function is included in the kernel. This means that the kernel width and length will be 1 or two pixels larger than the cutoff wavelength.

## ISO 13565 "Deep Valley" and related filters for extracting waviness and roughness data

The ISO 13565 standard specifies an iterative method to separate waviness and roughness from profiles, by use of the Gaussian profile filter ISO 11562 and elimination of influence of deep valleys. The direct output from a Gaussian filter is a smooth version of the image mainly representing the *waviness* of the data while the difference between the raw data and the *waviness* data mainly is representing the surface roughness.

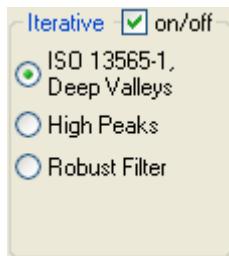
Here the ISO 1D standard is generalized to cover 2D surfaces, as there are no defined 2D standards yet.

The standard specifies a cutoff wavelength that is 1/5 of the evaluation length and specifically mentions the following examples:

Standard Relationship between the cut-off wavelength and the evaluation length

	Evaluation length
0,8	4 mm
2,5	12,5 mm

The ISO 13565 Deep Valley filter is selected by setting the iterative checkmark.



The Filtering process to determine the roughness profile is carried out in several stages. When the "Full Output" option is checked the different stages will be drawn in different windows.

- 1) A first estimation of a reference profile is determined by applying the ISO 11562 filter Gaussian filter using a cutoff wavelength that is by default 1/5 of the evaluation length.
- 2) All valley portions of the source profile below the reference profile set equal to the corresponding value of the reference profile.
- 3) The same filter is applied on the corrected profile and the result is the reference profile relative to which the assessment of the profile is performed.
- 4) The roughness profile is obtained from the difference between the source profile and the reference profile. This is the curve on which roughness parameters should be calculated. This procedure is generalized so that it also works on 2D images even though there are currently no standards for filtering images.

### High Peaks

A similar procedure can be performed by checking the "High Peaks" instead of ISO 13565-1 filter deep valleys. This filter removes the peaks instead of the valleys. This is not part of the ISO standard but very useful for filtering instrumentation artifacts often seen in scanning probe instruments.

### Robust Filter

The Robust Filter is an advanced combination of the Deep Valley and High Peaks filters, as it will minimize the influence from all extreme values in an iterative process:

First the image (or profile) is filtered by the plain Gaussian filter

The difference between the original and the filter output is generated and the median value of the absolute differences calculated.

Extreme points are defined as positions where the absolute error differs more than two times the median value of the absolute difference. These points are then substituted by the Gaussian filter output.

The procedure steps 1-3 are repeated three times.

The resulting *waviness image* is subtracted from the original surface image, which generates the "roughness image" from which robust evaluation of the roughness can be performed.

## Non-Linear Filters

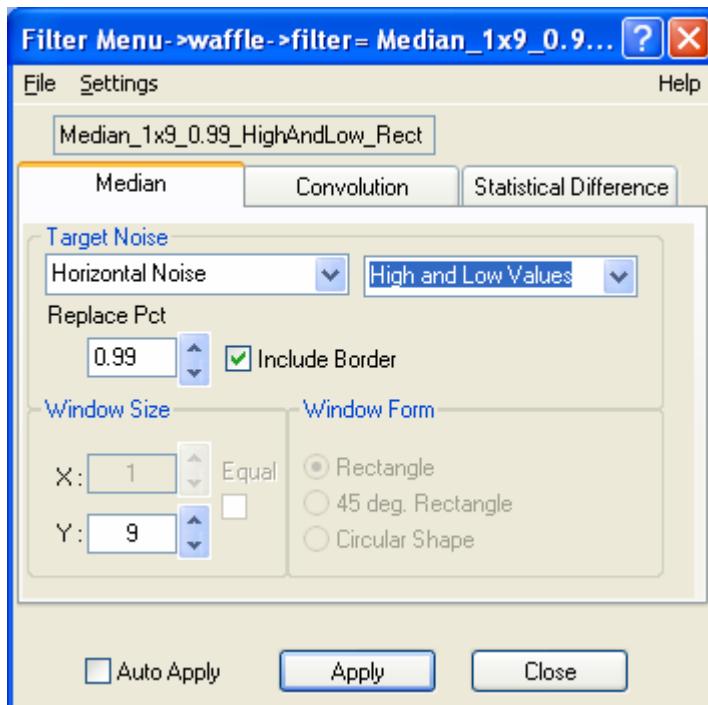
There are three types of non-linear spatial filters implemented:

- Median filtering, for noise removal
- Outlier Objects Filter, for recovery of areas covered by contamination and spike removal
- Statistical Differencing, for contrast enhancement

## Median Filtering

The advantage of a median filter is that it is very robust and has the capability to filter only outliers and is thus an excellent choice for the removal of especially shot noise and horizontal scanning artifacts.

A median filter is performed stepwise by moving a data window of specified size over the image. If the center value in the data window differs more than a certain value from the median value it will be exchanged by the median value. The threshold value determining whether or not to modify a pixel value depends on the local standard deviation within the data window. The higher the standard deviation is the higher the threshold value will be set.



### Target Noise

The target noise specifies the type of noise the filter should reduce. There are four options:

**Horizontal Noise:** This is mostly used for removing bad scanning lines or stripes that often occurs for images, such as SPM images, acquired in raster scans with the horizontal direction as the fast scanning direction. In this mode the x-size of the data window will be fixed to 1.

**Vertical Noise:** This works as above but for noise in the vertical direction. In this mode the y-size of the data window will be fixed to 1.

**Non Directional Noise:** This mode is used for reducing noise with our specific directionality. The x and y size of the data will be set equal.

**Customize:** This mode allows setting the data window of any size and shape

### Noise Level.

The noise level for the target noise can be set to:

**High Values:** In this mode only outliers having values higher than the median value can be modified. Therefore, this mode is good for reducing artifacts which are above the normal image plane.

**Low Values:** In this mode only outliers having values lower than the median value can be modified. Therefore, this mode is good for reducing artifacts which are negative.

**High & Low Values:** This mode will modify both high and low values based on their distance from the median values.

#### Replace Pct

The Replace Pct. value determines the percentage of pixels that will be modified. When set 1.0 only the 1.0 percent worst outliers will be modified. In this way possible to perform very gentle filtering leaving the most pixels intact but still get a significant noise reduction. In many cases removing between 1-5% of the values would be an effective median filtering, removing outliers without blurring the image.

#### Window Size

The data window size can be adjusted in both x and y directions. By having for example a  $1 \times 5$  kernel the filter will only be sensitive to corrugations in the y-direction. Kernels for median filters are typically small, lower than or equal 9 pixels in length.

**Include Border** If this option is checked the also the pixels at the border can be filtered by applying the border-mode as specified in the border-mode settings dialog.

#### Window Form

It is possible to define the data window shape different from the default rectangular form and make it more or less sensitive to particular directions:

- **Rectangular** (default) shape



- **45 degrees** turned rectangle shape

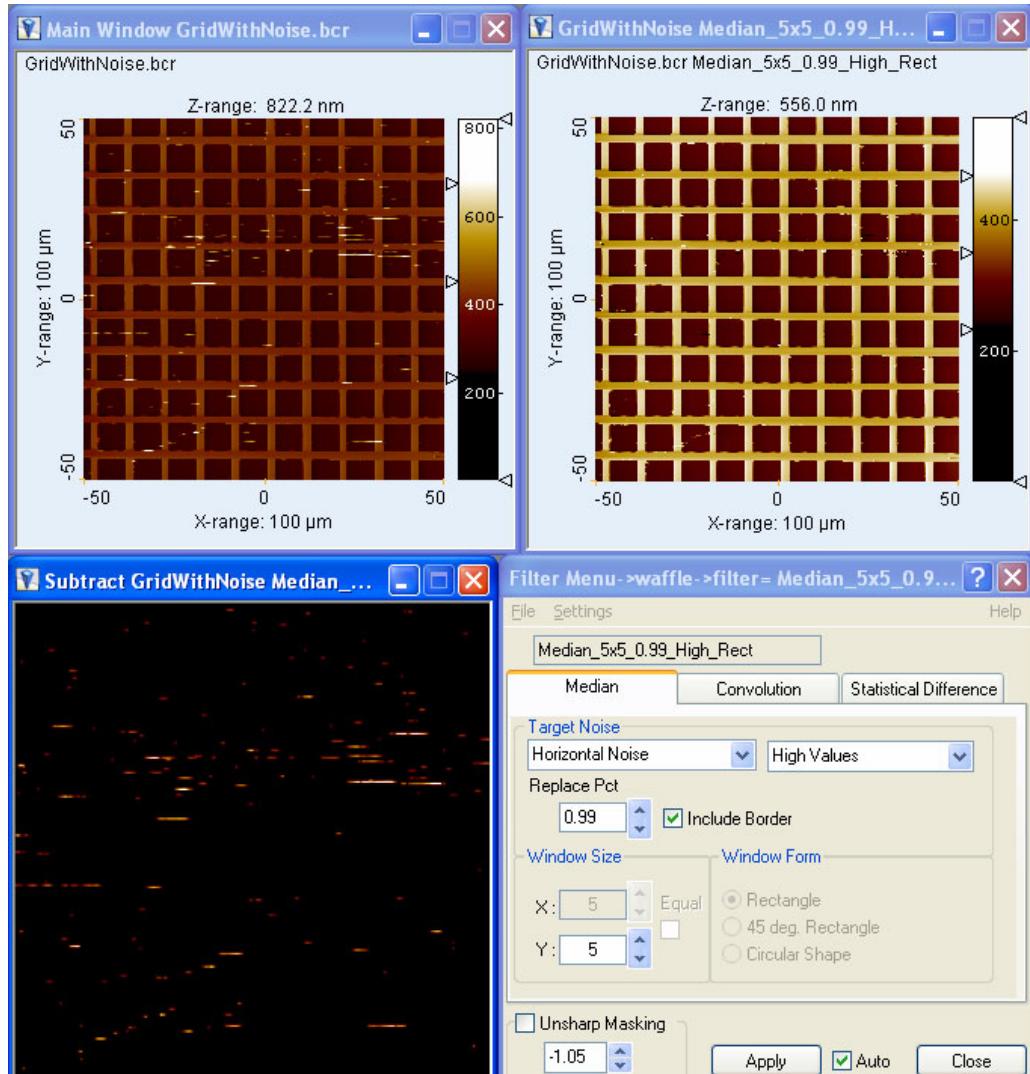


- **Circular shape** (= octagonal for smaller kernels).



### Example

Below is seen an example of an image distorted mostly by short horizontal lines. By defining a  $3 \times 7$  Median mask we achieve a filter that is extremely selective for this type of artifact. The bottom image shows the difference between the original image and the filtered result. It clearly displays the removed line artifacts and in addition also the "under shoot" artifacts typically occurring when scanning across steep slopes.



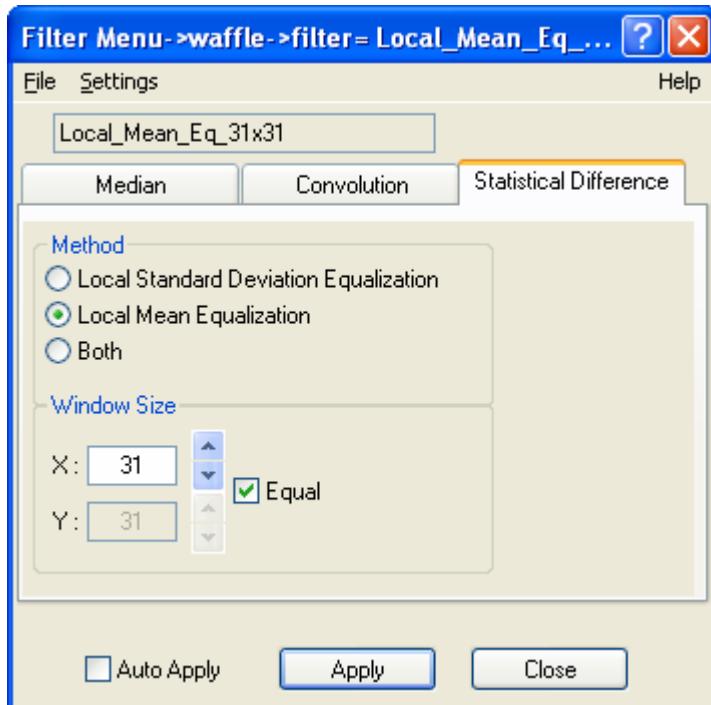
## Statistical Differencing

### Method

The statistical differencing dialog offers two ways to enhance the contrast:

- Local Mean equalization.
- Local Standard Deviation equalization.

Either one or both methods can be performed on the data set.



### Local Mean equalization.

This method simply subtracts the mean value of the nearest neighbor pixels within the filter window:

$$O(x, y) = I(x, y) - \frac{1}{M \cdot N} \sum_{i=-N/2}^{N/2} \sum_{j=-M/2}^{M/2} I(x + i, y + j)$$

This is a powerful way to reduce long-range waves and image bow.

### Local Standard Deviation equalization

The Standard Deviation (SD) equalization scales the height values by a factor given by the SD of the global image,  $\sigma_g$  divided by the local standard deviation  $\sigma_l$  found in the filter window.

$$O(x, y) = I(x, y) \frac{\sigma_g}{\sigma_l}$$

This way the local SD and contrast will appear the same all over the image.

When "Both" is checked both Local Mean and Local Standard Deviation equalization will be performed.

### Kernel size

The filter window, i.e., the number of pixels used for calculation of the local mean and SD values is defined by the X, Y filter kernel Size parameters. To have the desired effect the kernel size should be chosen so that it is larger than the size of the features being studied but smaller than the long range structure, which should be suppressed.

When the equal check box is set the X and Y kernel size parameters will be set equal when using the up down buttons.

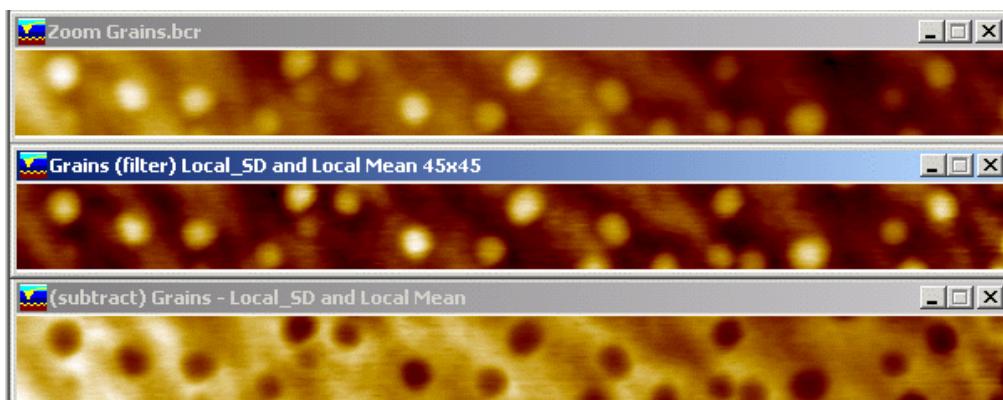
#### **Auto Apply and Apply**

The auto apply button can be checked so that every modification of the filter settings will cause the filter to process immediately so that the effect can be monitored simultaneously. Otherwise clicking on the Apply button will apply the currently defined filter.

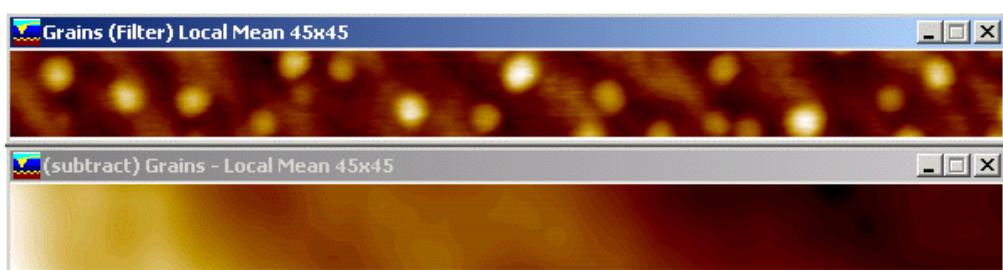
The auto apply function is a good way to interactively define the filter that gives the best result. However, for larger kernels the response time may be so long that it is more practical to turn off this feature.

Below is seen an example of an image filtered by the Statistical Differencing filters:

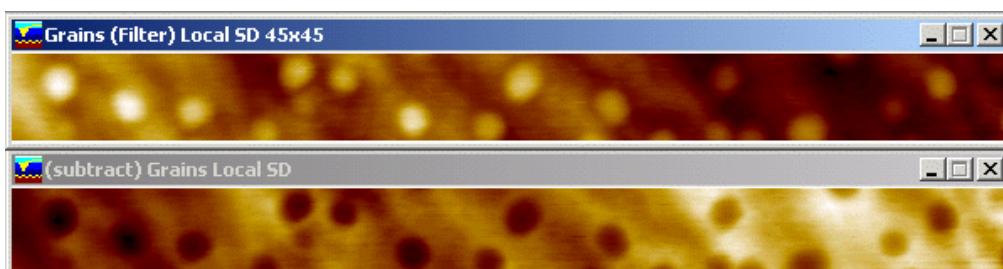
- 1 Zoomed portion of a Raw Image with some grains (512×512)
- 2 Filtered result from a combined Local Mean Equalization and Local SD Equalization filter (Kernels size 45×45). The individual grains are here more visible
- 3 Difference between the raw image and the filtered image



- 1 Filtered result from a Local Mean Equalization filter (Kernels size 45×45)
- 2 Difference between the raw image and the filtered image



- 1 Filtered result from a Local SD Equalization filter (Kernels size 45×45)
- 2 Difference between the raw image and the filtered image



## The Outlier Objects Filter

The Outlier Objects Filter is a strong tool for detecting outliers and filling in the most probable values by interpolation of neighboring pixels, where the aim is to get the truest representation of the image. SPIP will detect a particle when some part of it exceeds a certain level and will then determine its boundaries at the positions where the slope of the particle flattens or changes sign. A user-selected Exchange Method will then fill the pixels inside the particle boundary. Instead of particles it is also possible to detect and remove spikes exceeding a certain slope threshold.

### The Outlier Objects Filter Dialog

The Outlier Objects Filter is activated by from the right mouse menu item "Filter Outlier Objects" or from the Processing pull down menu of the SPIP menu bar.



#### Objects to be removed

The upper part of the dialog defines which object should be removed, **Particles**, **Pores**, **Spikes** or **Negative Spikes**. And the detection area can be narrowed down to include the **Zoom Box Only**.

#### Particles and pores filtering options

The **Detection Level** is set as a percentage of the z-range of the image. Because the Z-range of the image will lower for each filter process it will be possible to filter the image gradually by setting a high detection level and pushing the Apply button more times. The detection level will be reflected on the color bar so that you see which part of the images will be handled as objects to be filtered. Likewise you can also define the color bar of the image or the color scale editor. For particles the upper color scale limit will define the threshold value and for pores the lower color scale limit is associated with the threshold value.

### **Spike filtering options**

When the "Spike Exceeding Slope" is checked the slope level for detecting a spike can be set. A spike is here defined as a local maximum, or minimum for negative spikes, where the slope  $dz/dx$  or  $dz/dy$  exceeds the set slope level. Here, we regard maximum values as pixels which two neighboring values in x or the two neighboring values in y are smaller and vice versa for minimum values. Thereby it is possible to remove structures, which look like ridges, see example below.

Notice that for scanning probe images the maximum measurable slope is limited by the shape of the tip. If spikes have slopes larger than at the tip apex we have a good indication of a noise artifact, which should be filtered. This spike filter is therefore also very good for preprocessing images before tip characterization, which success depends on how well local maximums can be trusted.

The slope of the tip depends may be different seen from different directions and it might also have been mounted so that for example the tip is able of scanning side walls in one direction. In such situations high slopes in one direction may be acceptable but not in the others and therefore necessary to handle the directions individually. To do this you can with the direction check boxes (Up, Down, Left and Right) define which slopes the spike detection algorithm will check against the given slope threshold value.

### **Exchange Method**

There are six methods for filling new values into the "bad" pixels:

**Horizontal Interpolation**, where new values are inserted by interpolation of the neighboring values in the x-direction. This method is recommended for structures mainly oriented in the x-direction.

**Vertical Interpolation**, where new values are inserted by interpolation of the neighboring values in the y-direction. This method is recommended for structures mainly oriented in the y-direction.

**Min Value**, where a fixed value equal to the minimum value of the image is entered.

**Mean Value**, where a fixed value equal to the mean value of the image is entered

**Median Value**, where a fixed value equal to the median value of the image is entered

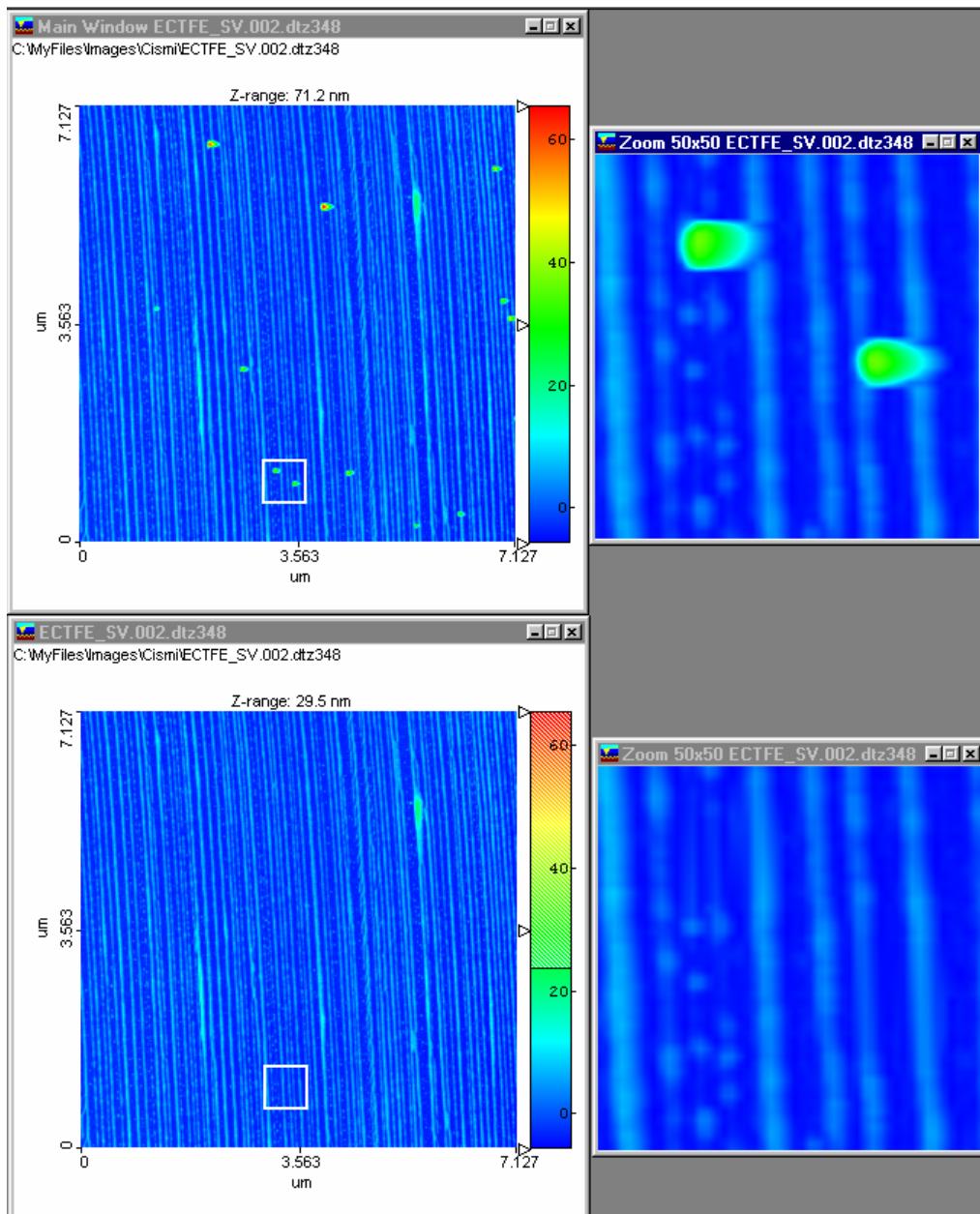
**Fixed Value**, where a value defined by the user is entered

**Mark as Void**, The outlier pixels will be marked as void pixels.

### **Particle removal example**

Below is seen an example of an AFM image with a fiber structure suffering from some contamination particles before and after filtration. At the top is the raw image together with a zoom image focusing on two contamination particles and below is seen the same areas after filtration. The **Synchronized Multi Zoom** function has been used to set the zoom boxes at the exact same locations in the two images.

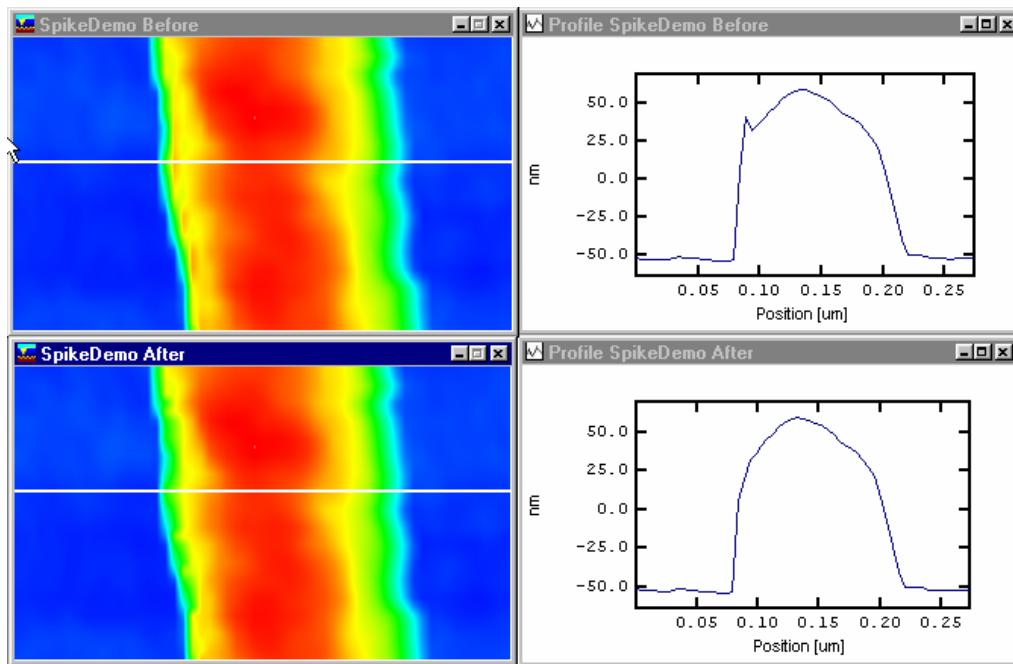
In this case the vertical interpolation method has been applied because the fiber direction is roughly parallel to the y-axis and it is seen that particles have been removed with very little or no damage to the fibers and we will be able to quantify the fibers much better by the Grain Analysis function.



### Spike Removal Example

The next image demonstrates the effect of the Spike filter. The raw image at the top suffers from overshoots on the left wall, which is probably due to a change of probe angle when the probe moves from low high friction to low friction. Such a spike may cause a tip characterization to overestimate the sharpness of the tip and it should therefore be eliminated before the tip characterization takes place.

In this case the spikes have been exchanged by horizontal interpolated values and the result shows successful spike elimination with no damage to the remaining image



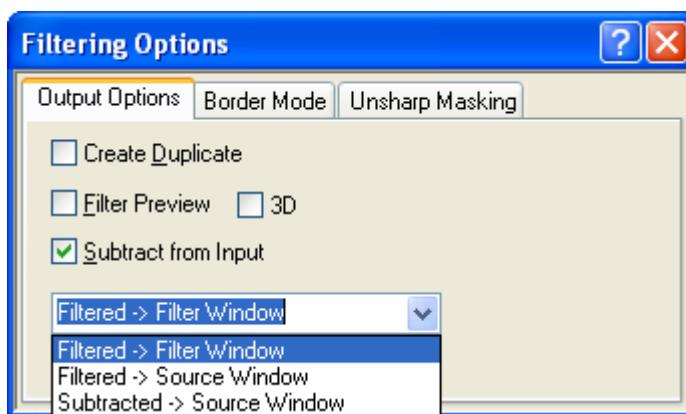
## Filter Options

In the settings dialog it is possible to set up several general settings like:

- output options
- specifying the border mode (explained in the advanced section)
- defining the optional "Unsharp Masking" mode

## Filter Output Options

By specifying the output options the filtered version will be either placed in a new window or put in the place of the original data.



Three additional windows might be created depending on the current marked checkboxes:

### Duplicate

When the Create Duplicate option is checked, the filter results will always be shown in a new SPIP-Window, otherwise the same window is used for the filter results. This option is useful for checking the difference between the effects of different filters.

### Preview

When this option is checked the corresponding spatial filter kernels impulse response is shown in either a flat 2D image or in a 3-dimensional view. Previewing the filter gives a better understanding of the characteristics in the filter and allows the user to visually inspect for mistyped values kernel values.

### Subtract from input

When this option is on the difference between the original data and the filtered result is shown. If the filter is of a low pass (smoothing) type the subtraction will have a high pass characteristic and thus highlight the shorter waves. For more information about this technique refer to the unsharp masking method found in the advanced filtering section. When the "subtract from input" option is set and a median filter is used, the altered data points can easily be spotted.

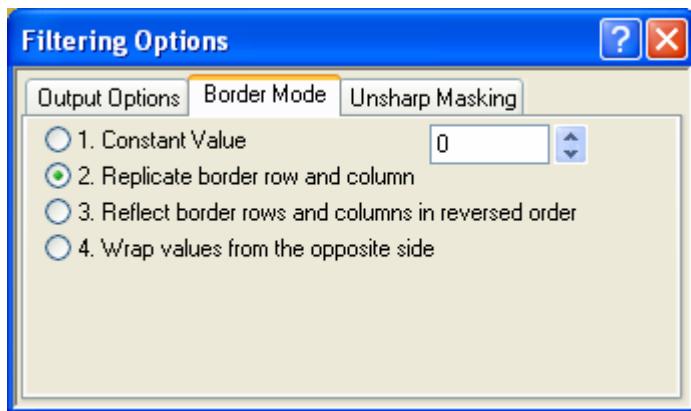
### Result in Source Window

This option places the result back in the original source window after performing the calculations. This is useful when the filter is used for preprocessing in an analytical sequence; otherwise it is more convenient to have the source window fixed and dedicate another window for the filtered result.

### Result in Main Window

Places the result back in the Main SPIP window after performing the calculations.

A kernel filter does not directly apply to the borders of the images; when the center of the kernel is placed on a border pixel some part of the coefficients of the kernel will be located outside of the data set. For performing a filter convolution at the borders and avoiding unwanted border effects different strategies can be applied. The difference between the strategies becomes most apparent for larger filter kernels. The simplest strategy is to ignore the border regions and just filter those pixels located so the filter kernel doesn't overlap the image borders. All other strategies are in principle based on an enlargement of the image. The different modes can be defined in the Settings menu seen below:



The following border mode currently exists:

#### **1. Constant value**

The values outside the border are replaced by a user defined constant value. An appropriate value will often be the mean value of the image. Plane corrected images are leveled so that the mean value equals zero.

#### **2. Replicate border row and columns**

Here the data found in the (first or last) row or column is duplicated to the enlarged temporary data.

#### **3. Replicate border row and columns in reversed order**

- The pixels are "mirrored" at the borders.

#### **4. Wrap values from the opposite side**

- The data found at the opposite border of the image is used to fill the enlarged data and make it continuous.

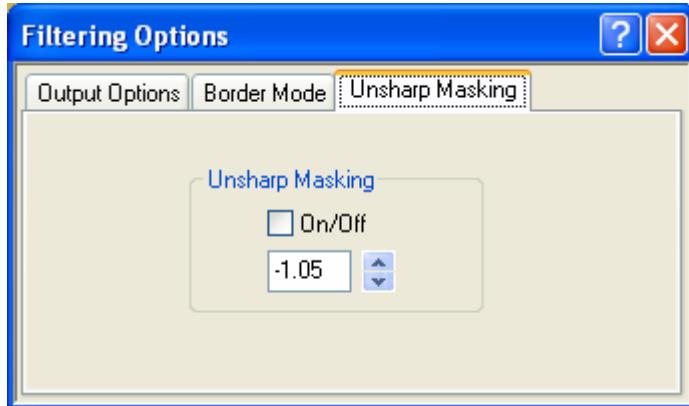
Applying the border mode to a specific border:

The border mode can be set for one or more of the 4 borders (Left, Top, Bottom and Right) by the check marks at the bottom of the dialog.

When no border handling is selected the border pixels will remain unchanged.

## Unsharp Masking

An optional "Unsharp Masking" mode can be set in the filter options dialog:



Unsharp masking is a filter technique where the output from a filter is combined with the input image:

Depending on the sign of the Unsharp Masking parameter ( $\alpha$ ) the filter combination will be as follows

$$UM(x, y) = |\alpha| I(x, y) + \text{Filtered}(x, y), \text{ for positive values of } \alpha$$

$$UM(x, y) = |\alpha| I(x, y) - \text{Filtered}(x, y), \text{ for negative values of } \alpha$$

In the special case where  $\alpha$  equals -1.0 and the applied filter is a low pass filter the UM filter becomes a high pass filter:

High Pass = Original - Low Pass.

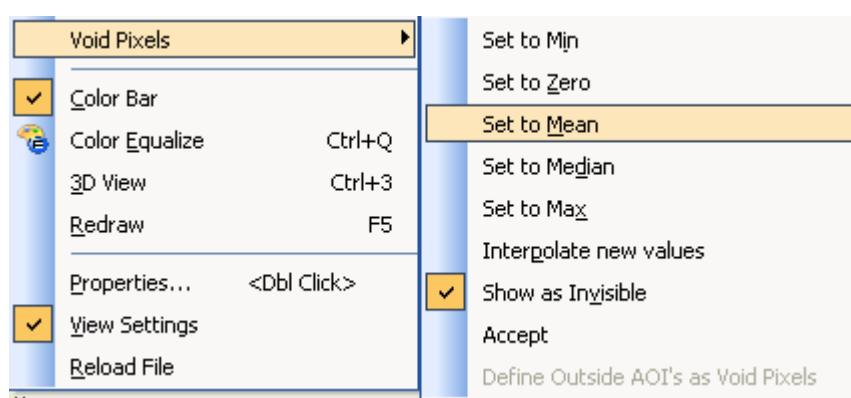
This effect can also be obtained automatically by setting the *Subtract from Input* check box in the Output Option in the Filter Settings.

When  $\alpha > 0$ , more of the original image is added to the filtered result. When the filter type is of high pass type this restores partially the low-frequency components lost during the high-pass filtering operations.

## Void Pixels

Some Images may contain "void pixels", which are pixels that could not be measured by the instrument. This is often true for interference microscope images, which need a proper reflectance in order to measure the height values. This may also be true for objects with holes for examples rings. Void pixels can be handled as invisible when drawing in 2D or 3D or they can be shown by other inserted values.

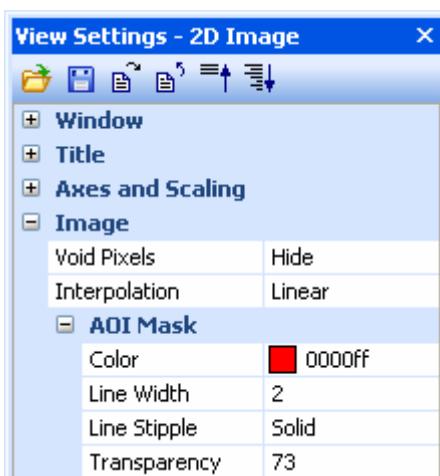
For randomly located void pixels it might be desirable to show their interpolated values while structures with real holes is better shown with the void pixels invisible or for example with the minimum value of the valid pixels. You can define how to handle void pixels by right clicking **Void Pixels:**



The selected option will also have effect on the calculation of histograms and the simplest 1st order statistical roughness parameters. If "Show as Invisible" is set they will not be included in these calculations and they will simply be ignored when calculating plane correction parameters. More complex roughness parameters depending on Fourier analysis will make use of the inserted values. New values can be inserted by selecting one of the choices for the menu. The new values may be accepted by the "Accept" button, meaning that there will be no more void pixels contained in the image.

The number of void pixels contained in the image is shown in the upper part of the Image Property Menu.

You may also find it convenient to use the View Settings for setting the visibility of the Void Pixels:



#### **Defining new void pixels**

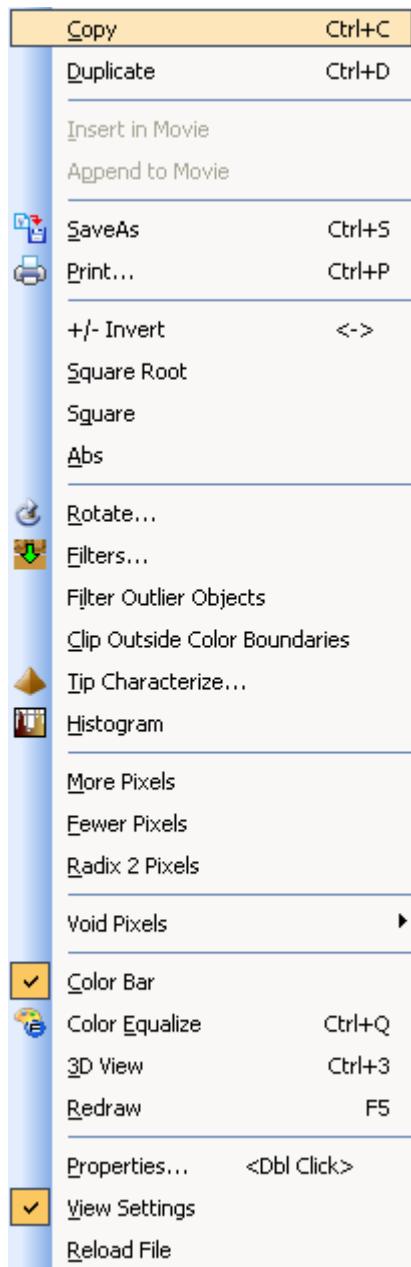
New void pixels can be defined manually by pointing to a pixel, which should be defined as a void and then clicking on the **Delete** key and the mouse key simultaneously. Likewise, a void pixel can be defined as valid by combining the **Insert** key and the mouse key.

Defining a larger region of pixels as void pixels is done by combining the Zoom box with the **Delete** button; likewise regions can be redefined as valid pixels by combining the **Insert** key with movement of the Zoom box.

Defining void pixels can be appropriate in combination with for example tip characterization where the most outer pixels can have a high uncertainty and therefore better shown as invisible.

## Multiple Image analysis

It is possible to have several images open at the same time and you can use the Right Mouse Key Menu to Duplicate, Exchange with the Main Image or Send to the Main Image for a more detailed analysis:



### Image Comparison by Cross Correlation, Image Alignment and Image Subtraction

It is possible to analyze differences of very similar images by subtracting an image from the Main Image. Before subtraction it can be an advantage to align the images by right clicking on **Align To Main** or **Processing→Operate With Main→Align All Images To Main** (requires the Calibration or Movie Module), which will shift the current image in the x-y plane to give the best match defined by the cross correlation function.

When having more images of same size open it is possible to create profile at the exact same positions using the Synchronized Multi Profiling tool.

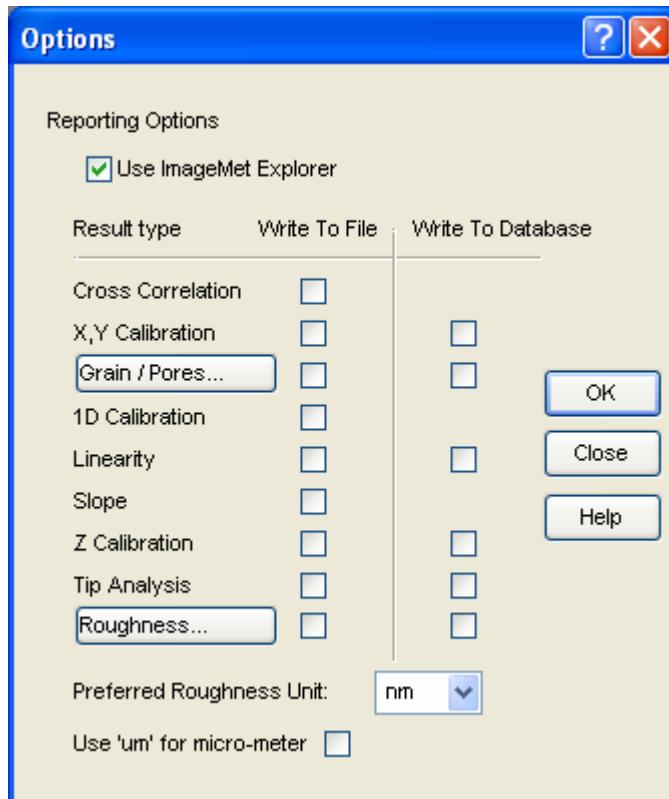
To open a group of files you can Drag Drop group of files or even entire folder branches from ImageMet Explorer or the MS Windows Explorer.

It is also possible to create a movie or a slide show of your images. First open the Movie Dialog and then add the images (frames) to the movie by right clicking on **Add to Movie** in the image window.

# Options

## Options Dialog

The Options Dialog is used for defining where to save analytical results; to individual text files and/or to the ImageMet Explorer database. Most other options can be defined and set as defaults along with the dialogs for the different functions.



**Use ImageMet Explorer:** When this option is off no results will be entered to the database and browsing with ImageMet Explorer will be deactivated.

### Text Files

Storing results to text files can have the advantage of containing more detailed information, which can be imported to, e.g., spreadsheets.

You may import the files into a spreadsheet program and create your own presentations of the results. Typically the fields are tab separated and '.' is used as the decimal character (Most European countries use ',' as decimal character). Therefore, depending on your nationality settings you might need to replace '.' in numbers with commas.

### Database

Saving results to the database has the big advantage that they can be viewed automatically when browsing through the files using the ImageMet Browser, - can be part of a search criteria of the ImageMet Finder, - or contained in reports of the ImageMet Reporter.

Note when the write options are active previous results will be overwritten with no prior warnings.

**Cross Correlation:** When performing cross correlation alone or in combination with linearity analysis the cross correlation peaks, sorted by amplitude can be written to text files where the name is given by the name of the source file a the extension .cross

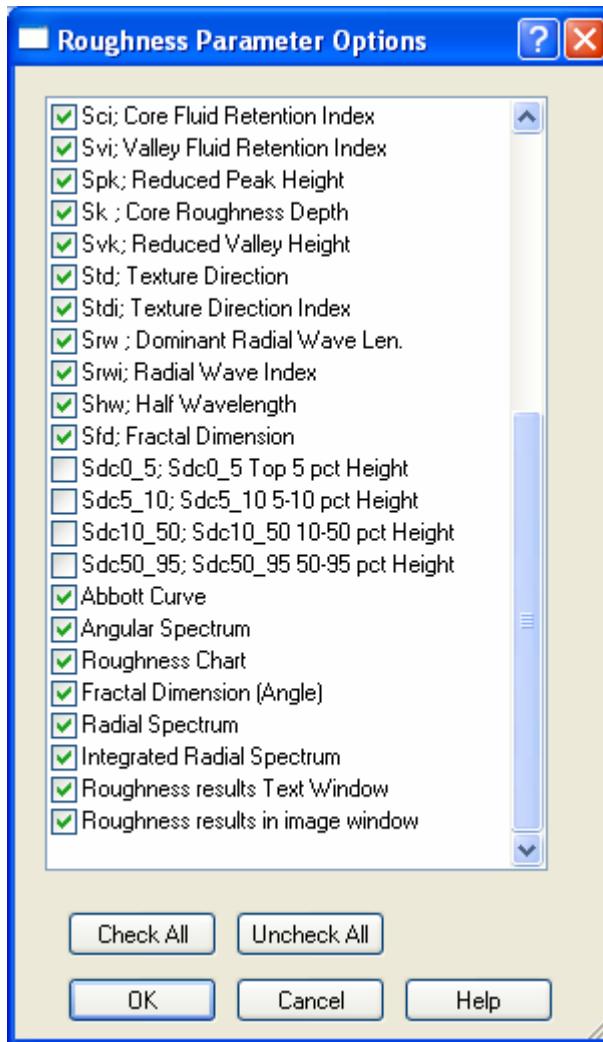
**X,Y Calibration:** Results from lateral calibration can be written to text files and the database file. The text files will have the extension *.cal*.

**Grain / Pores:** Statistical Results from Grain and Pore analysis can be written to text files and database. The files will have the extension *.grn* and will contain detail information about each particle/pore.

**1D Calibration:** Results from a 1D Calibration (parallel lines) analysis can be stored to text files with the extension *.lin*

**Linearity:** Linearity analysis results consisting of error description as well as correction parameters can be written to text files and database. The text files will have extension *.lin*

**Roughness:** Roughness parameters can be written to text files and database. The text files will have extension *.rgh*. When clicking on the "**Roughness**" button the calculation of individual roughness parameters can be set On/Off:



Note that when deselecting parameters depending on the Fourier transform, those parameters will not be shown on the screen either.

**Slope:** Slope correction parameters used for correcting the image plane can be stored in text files with extension *.slope*

**Z Calibration:** Z-calibration results can be saved in text files and the database. The text files will have the extension *.zcal*

**Tip Analysis:** Tip analysis results can be saved in text files and the database. The text files will have the extension *.tip*

**Preferred Roughness Unit:** Although SPIP is handling all height values in nanometers you can define another unit for reports of roughness results.

## Active Modules

The "Active Modules" dialog shows which modules are active and the maximum number of pixels that applies to your license. The dialog is especially useful in an evaluation process where you want to decide which modules to include in your license.

A module can be in three modes: Enabled, Disabled or in Demo

If SPIP is in demonstration mode you can disable those modules

By un-checking the individual modules SPIP will remove and disable the associated buttons and menu items so that you see which features you get when choosing a specific combinations of modules.

The dialog will automatically appear when running in evaluation mode, which happens when no valid license is found. In such case SPIP will be running in reduced resolution, typically 128x128 pixels. The dialog can also be activated from the main menu by selecting **Options → Active Modules**.



## Interfacing to SPIP

### Opening files by the user Interface

SPIP offers a number of ways by which you can open a data file from the user interface:

- **File→Open:** standard way of opening files with out the ImageMet Explorer.
- **File→Open by ImageMet Explorer:** Activated ImageMet Explorer from where you can enter files into SPIP by double clicking, by use of the dedicated tool key or by Drag-Dropping selected files. See ImageMet Explorer for more information.
- **File→Import by Heuristic File Importer:** This will activate the Heuristic File Importer dialog from where you can open data files of formats unknown by SPIP. See the Heuristic File Importer for more information.
- **Drag Drop:** You can Drag Drop one or more files from other program supporting the Drag Drop technique for example the Microsoft File Explorer.
- **Send To:** By putting a short cut to SPIP into your Send To folder you can send files to SPIP from the Microsoft File Explorer by right clicking on SPIP in the Send To menu.

The Send To folder is typically found in:

C:\Documents and Settings\YourUserID\SendTo

- **Command Line:** SPIP can be started from the command line with optional data file names as parameters. The parameters should be space separated and written in quotes when the names include space characters, see example:

C:/Programming Files/Image Metrology/SPIP/Spip.exe "file 1.img" "file 2.img"

The complete command line syntax definition is shown below:

```
SPIP [/?] {/p [group :] plugin} {/b batchfile} {filename [: subimage] }
  [/d [: logfile] [: name {, name}]]
  /?                               Displays this help text
  /p                               Activates the specified plugin function
    group                         Plugin group filter (case sensitive)
    plugin                         Plugin to run (case sensitive)
  filename                        The name of a data file to open
  /b                               Activates batch processing, supersedes autorun mode
    batchfile                      Name of the batch file to process the data file
    subimage                        The image in the file to open (number or "last")
  /d                               Runs SPIP in diagnostic mode
    logfile                        The name of the file to which log text is saved
    name                            The name of program group(s) to log
```

The above techniques enable selection of multiple files and to have a the AutoRun.batch Batch Process run automatically when active.

### Interfacing to other Programs

SPIP offers a number of ways by which other software programs can interface with SPIP:

- **The Sniffer:** Used for automated processing of new files stored to a defined Sniffer Folder. See The Sniffer section for more information.
- **Shell Command:** If you are programming other programs and want to process data in SPIP you can store the data into a file and have a Shell command calling SPIP with the file names as arguments, see command line example above.

**Plug-in Interface:** This programming tool enables you to retrieve data from SPIP and have SPIP to view and process data given by the Plug-in. See the "SPIP Plug-in Interface for Programmers" for more information.

# ImageMet Explorer

## The ImageMet Explorer™, Introduction

The ImageMet Explorer™ is a productivity tool adding a new dimension to image and data handling. It has an integrated database that allows you to browse quickly through your data files and view them as thumbnails. For all recognizable image and curve files thumbnails and other characteristics are automatically entered to the database from where they can be retrieved on the fly while browsing your files. Furthermore, important analytical results from the Scanning Probe Images Processor, SPIP, can automatically be stored in the database so that you never lose important results. You have the flexibility to enter descriptions, assign categories or create hyperlinks to individual files. Although very powerful the usage is so easy that no prior knowledge about data base programming is required.

Image Explorer™ is a combination of three subprograms: ImageMet Browser, ImageMet Finder and ImageMet Reporter which all take advantage of the underlying database:

### **ImageMet Browser: Organizing and managing files and folders**

The browser allows you to browse through your files with an interface and functionality that covers most of what is found in the Microsoft Explorer that is part of your operating system. In addition Image Explorer™ offers thumbnail view for the most common microscope formats and an extra **Info Pane** where characteristics and results for individual files can be viewed. Furthermore, it is possible to enter descriptions, assign categories and links to related files, web sites, or for example contacts in your contact database file.

### **ImageMet Finder: Searching for images, files and folders**

The ImageMet Finder also covers most of what is found in the search utility of the Microsoft Explorer and additionally it allows you take advantage of the integrated database. It enables searching for images with certain attributes, for example measurement conditions, results within certain ranges, categories, and / or links.

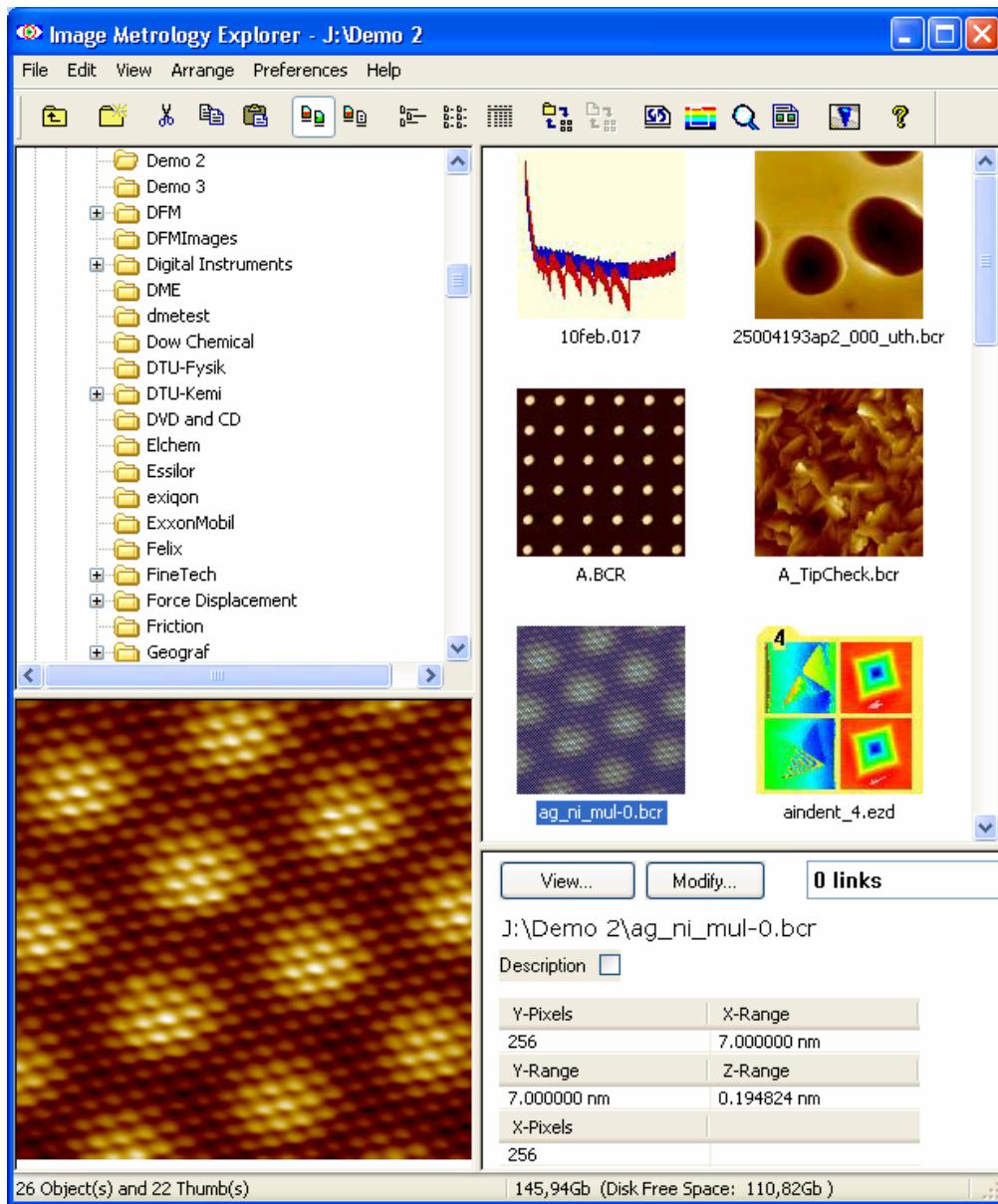
### **ImageMet Reporter: Reporting data files to HTML**

With the ImageMet Reporter you can create HTML reports containing groups of image or profile files. The report can contain graphical presentation of the images or profiles themselves and selected characteristics and results retrieved from the database.

The Image Explorer™ is an optional module of the Scanning Probe Image Processor and its availability depends on your current license.

## The ImageMet Browser

The ImageMet Browser is activated from the SPIP program by File→Open or the corresponding tool key  and you will see a Browser window similar to the one below:



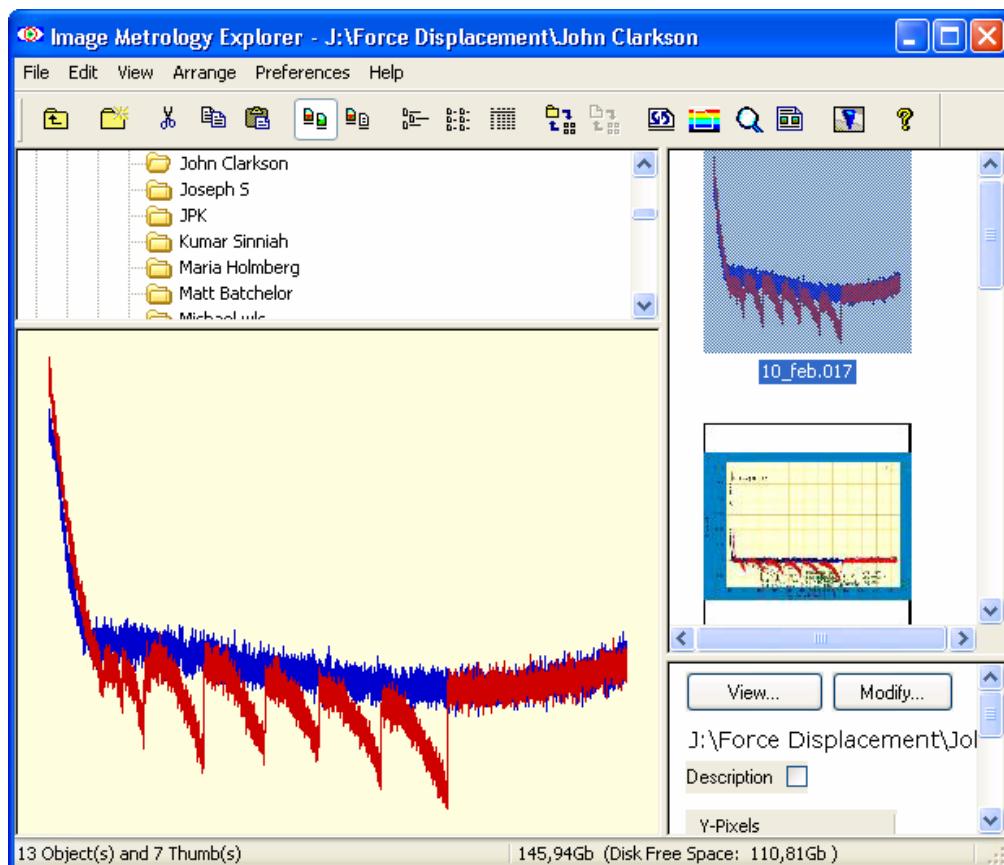
The ImageMet Browser contains four Panes:

The **Folder Pane**, upper left, where you can select the directories you want to browse. This window works very similar to the Microsoft Explorer and the same Right-Click functions are provided.

The **File List Pane**, upper right, where the individual files can be viewed as thumbnails, icons or text lists. Compared to Microsoft Explorer this window has the advantage of being able to visualize all the SPIP recognizable microscope file formats including force curves and profiles. From this window it is possible to select one or more files and open them in the main program. It is even possible to explore and open individual data object from files containing more images or curves.

The **Info Pane**, lower right, where the characteristics of the selected files can be viewed and edited. Here you can also assign categories and links to related files or e.g. contacts.

The **Preview Pane**, lower left, where an enlarged view of the selected data files is viewed. The size of the image is determined by the size of the pane and the actual size can be defined by moving the borders between the panes. Images will keep their x,y aspect ratio while curves will be scale to use the full preview area, see the force curve example below:



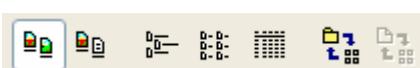
When you start browsing a directory the first time Image Explorer™ will automatically check if the files are of recognizable formats, in which case the basic information are retrieved and entered into the database together with a thumbnail. Browsing a directory a second time will appear much faster because Image Explorer™ will take advantage of the information stored in the database.

#### **Opening a file:**

To open a file, just double click on the file in the File List Pane. If it is a SPIP recognizable file it will be opened in the SPIP program while other files are send to their associated programs. You can force any file to be opened in SPIP by **Drag Dropping** or clicking on the **Send To SPIP** tool key. If the file is of non-recognizable format the Read a Special File Format dialog will be invoked and you can instruct SPIP on how to read the file. It is possible to select more files and open them simultaneously.

#### **Changing the file view mode:**

ImageMet Explorer provides more view modes that can be selected by their associated tool keys:



#### **Thumbnail View:**

This will limit the view to SPIP recognizable image or curve files for which thumbnails can be created. The size of the thumbnails can be defined in the in the Default View Settings.

#### **Combined Thumbnail and Icon View:**

All recognizable files are shown as thumbnails and other files are shown with at default icon.

 **Small Icons:**

All files are shown with their associated icons row wise in the most compact form.

 **List:**

All files are shown with their associated icons column wise.

 **Details:**

All files are shown row wise with columns for Name, Size, Type, Modified time, Description and Categories

 **Expand Multi Data Files**

Files containing more images or curves can be show in an expanded view with one item per data object (image or curve) or as a single item. When shown as a single item in thumbnail view mode a folder thumbnail overlaid smaller thumbnails of the first four data objects are shown. The folder thumbnail will provide the number of data objects stored in the multi data file. If you have more multi data files containing larger data set you may find it most convenient to show multi data files as single items.

 **Expand Selected Multi Data File**

When the files are shown with one item per file, individual selected data files can be viewed in expanded view by clicking this tool key or double clicking on the file. This may be the most convenient way to explore folders with multi data files containing many data objects.

## Default View Settings

To change the thumbnail size click **Preferences→Thumbnail Size**.



Selecting the thumbnail size is a compromise between the wish to view nice detailed thumbnails and the required disk space of the data base file and processing speed. Because the thumbnails are in compressed format it is hard to set up strict formulas to the space required space per thumbnail; typically a 128\*128 thumbnail will occupy 1 kbyte.

Note, that when changing the thumbnail size all the thumbnails currently stored in the database having a different size now will adopt the new size. This is done on the fly while browsing but can slow down browsing until all thumbnails are updated. You can also update the thumbnails of the current directory by pressing **F5**.

For image containing height information the thumbnail colors will reflect the currently selected color scale of the SPIP program. For graphical color images, e.g., jpeg, tiff or bmp image the thumbnails will adopt the colors directly. To change the color scaling for one or more selected files to the active color scale of SPIP, press **F5** to refresh the thumbnails.

**Viewing and entering database information in the Info Pane:**

In the Info Pane optional parameters for the selected files are displayed and additional information in form of description, hyper links, and categories can be entered to the database.

[View...](#)    [Modify...](#)    <http://www.imagemet.com/>

D:\myfiles\Images\Demo 2\Waffle.bcr

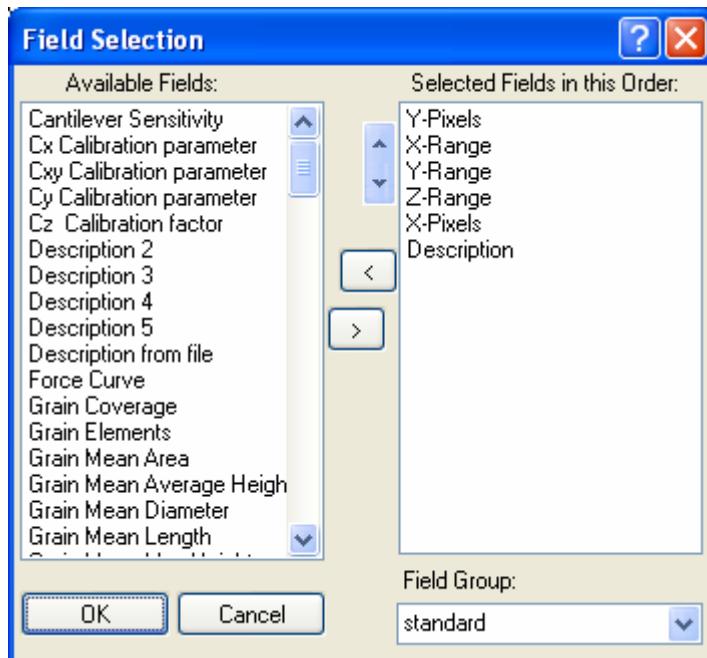
Description

**Waffle Calibration structure**

Y-Pixels	X-Pixels	Z-Range
256	256	191.343 nm
Y-Range	X-Range	
75 nm	75 nm	

**View Parameter Selection:**

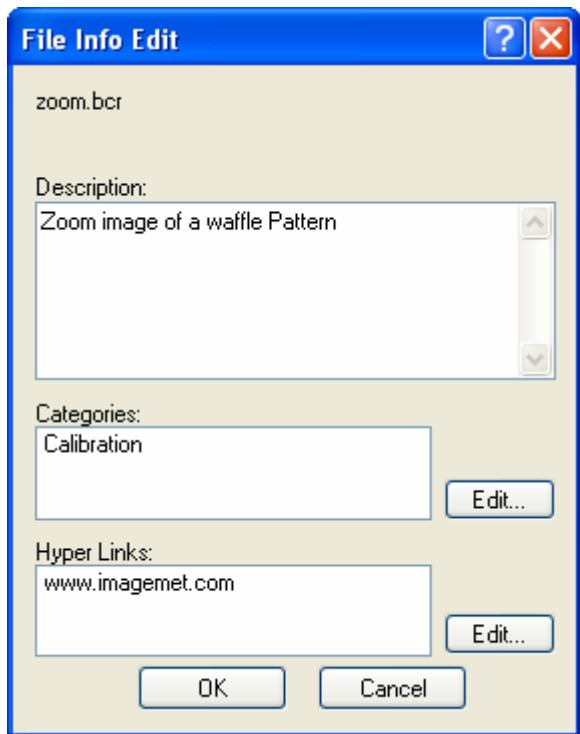
To define which parameters you want to display, press **View..** and move the desired Available image info parameters to the Selected image info list by double clicks or the '**>**' keys. and you can use the arrow keys to define the order.



It is possible to create more lists under different names and it can be practical to use names that associates with the parameter types, e.g. Calibration, Roughness

**Modifying description, links and categories**

To modify or add information in stored in the database press **Modify**.

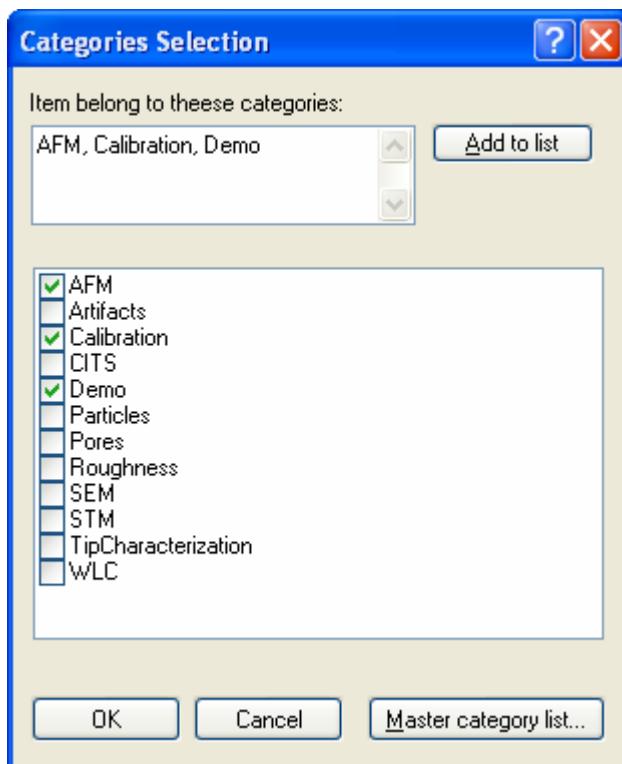


### Description

Depending on the actual file a description may already have been set at load time. You can edit the description field in free text style.

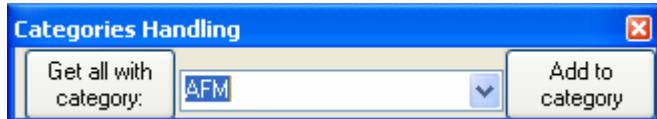
### Categories

For easy and fast search of images for families of images it is convenient to assign logical categories. Press Edit next to the Categories list to define and set new categories:



The categories can be written comma separated in the upper edit field or selected from already defined categories shown below. When entering a non-existing category it will be automatically be added to the Master Category List and made available for other files.

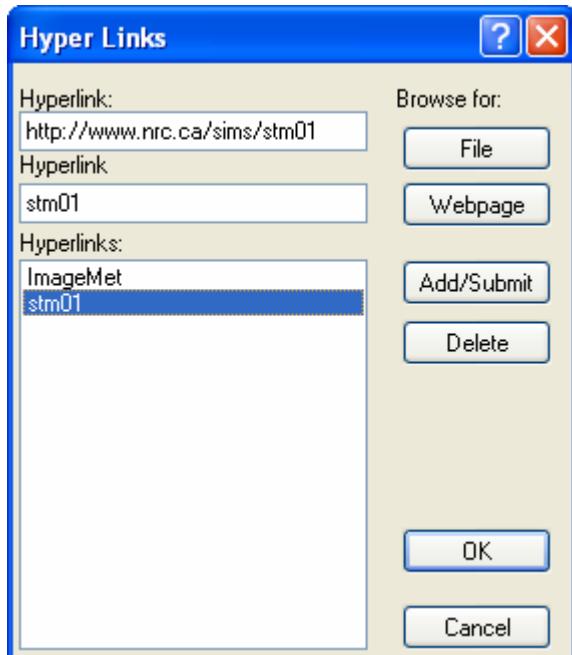
A quick way to find all files belonging to a certain category is by the Category Handler, which is activated from the menu File→Category Handling.



Select the Category you are looking for and press Get all with category  
You may also use this menu as a convenient way to assign the same category to all selected files.

#### **Hyper Links:**

It can be very convenient to create links to files, data entries or objects associated with a file. Having defined a link you can jump directly to the link with at single mouse click.  
To define a new link click on Edit, next to the link list.



You can enter the links directly or browse for a file or Webpage.

Examples of links are:

c:\myfiles\images\demo\demo-report.doc

<http://www.imagemet.com/>

[outlook:Contacts/~Person](#)

Where the latter requires the Microsoft Outlook mail program and is a convenient way to create links to people associated with the file. Similar links may also be created for data fields in other third party file types.

## Common Tasks

### Copy and Move a file(s) or folder(s)

Click the drive or folder you want to work with.  
Click the file or folder you want to copy or move.



#### Cut:

This button corresponds to Edit→Cut and cuts a selected object to the clipboard.



#### Copy:

This button corresponds to Edit→Copy and copies a selected object to the clipboard.



#### Paste:

This button corresponds to Edit→Paste and places the content of the clipboard to the selected folder

To select consecutive files or folders to copy or move, click the first item, press and hold down SHIFT, and then click the last item.

To select files or folders that are not consecutive, press and hold down CTRL, and then click each item.

To select all files press CTRL+A.

It is advised to copy the different files and folders by use of ImageMet Explorer if you do want the same changes performed on the database; otherwise some of the information might not get linked correctly.

### Browsing shared folders on another computer over the network

Browsing files over the network is like browsing your locale computer, but depending on how the network is configured it will appear slower.

To locate files on another computer, click on **My Network Places** or **Network Neighborhood**.

Locate the computer in which the shared folder is located.  
Choose the shared folder you want to browse.

You can assign a drive letter for shared folders that you connect to often.

To map a drive letter to a network computer or folder follow the following description:

Open Windows Explorer.

On the Tools menu, click Map Network Drive.

In Drive, select the drive letter to map to the shared resource.

In Folder, type the server and share name of the resource, in the form of \\servername\\sharename. Or click Browse to locate the resource.

### Change file or folder properties

Right-click the file whose properties you want to change.

On the File menu, click Properties.

To change properties for archiving, indexing, compression, or encryption on NTFS drives right-click the file, click Properties, click Advanced, and then select the options you want to change.

### Tool key supported functions

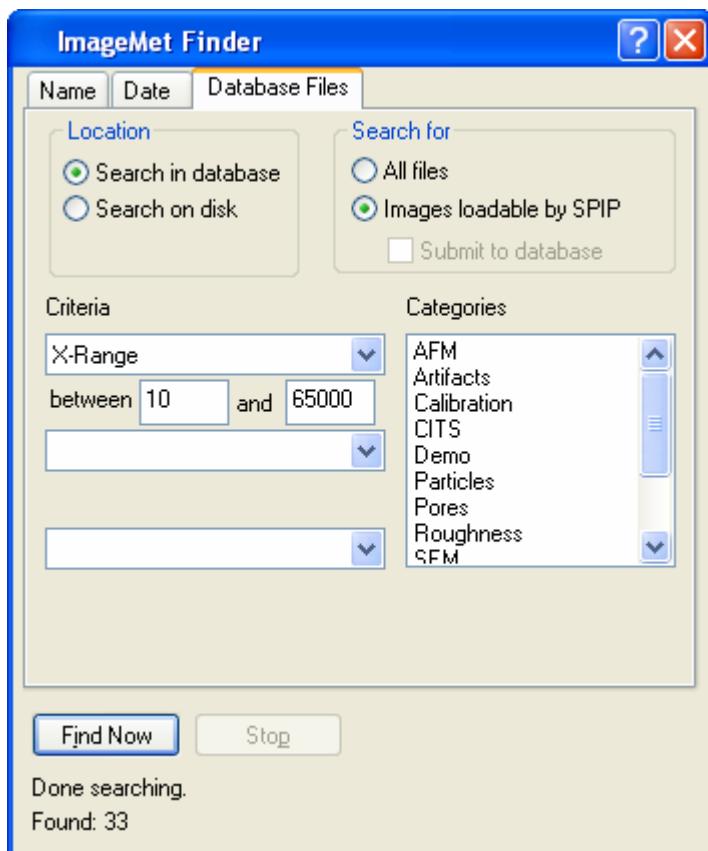
Most common functions can be accessed directly from the toolbar and/or by short cut keys:

	Selects the parent folder of the current folder in the directory tree
--	---

	Ctrl + X: Cuts one or more selected objects to the clipboard.
	Ctrl + C: Copies one or more selected objects to the clipboard
	Ctrl + V Places the content of the clipboard to the selected folder.
	F8 Changes the view mode to thumbnail mode. Only data files for which a thumbnail can be created are shown, the size of these can be set in the preferences dialog.
	F9 Shows thumbnails for recognizable files and icons for other files, the size is dependent of the settings in the preferences dialog.
	F10 Shows a file list with small icons and names.
	F11 Shows a file list with small icons and names.
	F12 Shows details, with name, size, type, modified time, description from the data base and categories.
	File→Find Activates the ImageMet Finder, from which files with certain characteristics can be found. The results will be shown in the File View Window and the Info View and Image Window will reflect selected files.
	Expand Multi Data Files into one thumbnail per image or show just one thumbnail per file.
	Expand Selected Multi Data File into more thumbnails. Same function is obtained by double clicking the file.
	File→Report Enables the ImageMet Reporter for the currently selected files. If nothing is chosen than it is assumed that the complete content of the list view or all the viewable thumbnails will be used.
	Use this button to open the selected file(s) the SPIP main program.
	Start the help program.

## The ImageMet Finder

To activate ImageMet Finder click the corresponding tool key  or select the menu item **File → Find**. You will see that the ImageMet Finder menu is very alike the find menu of Microsoft Explorer, but with additional search capabilities for parameters that can be extracted from the files a stored in the database.



Note, you can use the ImageMet Finder to build up the ImageMet database in one step; by entering the wildcard symbol '\*' and setting the Database check box **Submit found images to database** all files in the selected directory and its subdirectories will enter the database with thumbnails and other characteristics. Depending on the number of data files this may take a while but afterwards you will be able to browse all the directories much faster and searching for files will also be functioning faster.

The search result will be displayed in the File List Pane of the ImageMet Browser where you can investigate the files for further details, load them into the main program or create a report using the ImageMet Reporter.

### Name Tab

Use the fields in the Name Tab to define names and locations for the files you want to find. It is possible to use wildcards and an empty name field will be regarded as '\*' enabling us to find all files in a given directory tree.

### Date Tab

Select the Date tab to specify file modification time intervals for the search criteria.

### Database files

Select the Database tab to enter search criteria related to recognizable image or curve files. Found files not already included in the database can be submitted to the database automatically when the Submit to Database check box is set. The search criteria can also be limited by checking the checkbox Search only files submitted to database. When this selection is chosen more specific search criteria can be used.

Click **Find Now** to start finding the files satisfying the entered search criteria. During the search process you will have the option to stop the searching by pressing the **Stop** push button

## The ImageMet Reporter

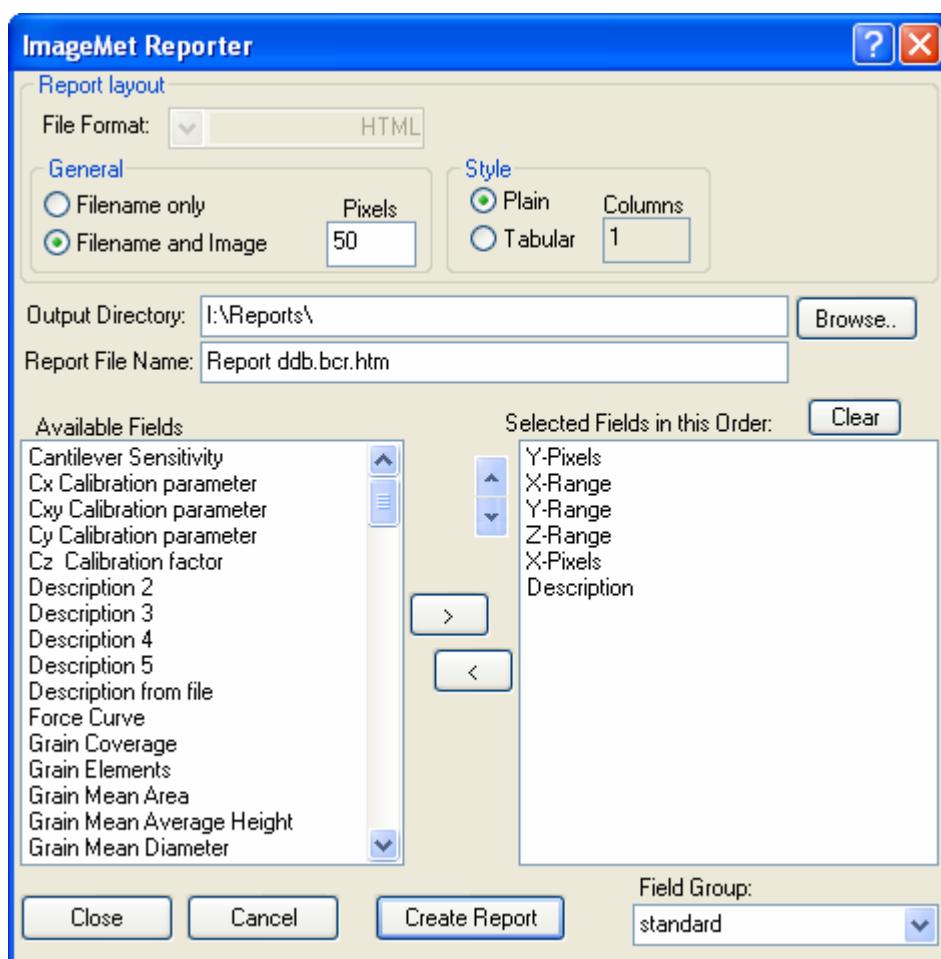
The ImageMet Reporter is designed for creation reports containing catalogs of selected data files, including the images or curves themselves together with its characteristics and calculated results.

To create a report first select the images in the File List Pane, which you want to include in the report, then activate the ImageMet Reporter by its associated tool key and define the output settings.

If no files have been selected the reporter will include all files in the current directory. Note also that it is possible to create reports including more folders by selecting files from the output of the ImageMet Finder

### Format

The currently available format is the HTML format, which makes it easy to include your data on web sites.



### General Reporting Options

It is optional to include image of optional size or just to show the filename.

### Reporting Style

The report can be written in two styles:

the Plain style where the files with the selected characteristics are shown row wise below each other.

the Tabular style will create a report with one column per file, with the image and file name shown on top and below the selected data fields.

### Data Fields

From the available data base fields you can choose which you want to have included in the database. The available fields are the same as seen in the File Info Pane and at the lower left you can conveniently select predefined groups of fields or define new groups

### Report generation and viewing

The report generation will start when clicking the OK button and when finished your default web browser will open and show the results. If you want have the report to appear differently just change the options and click OK again. Depending on your browser it might be necessary to perform a refresh to update the file content the 2<sup>nd</sup> time.

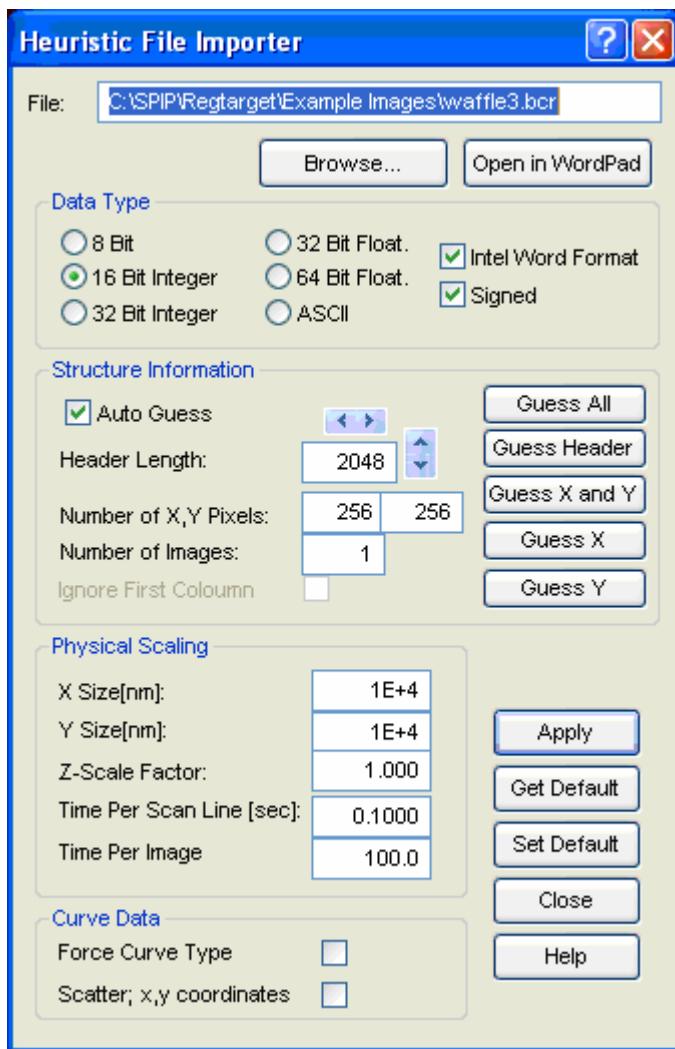
Below is shown a typical report defined with 3 columns and image of the size of 100 x 100 pixels.

**SPIP Report 2001-01-01 10-00.htm - Microsoft Internet Explorer**

C:\MYFILES\SPIP\Reports\Report S/Images_Demo 2.htm			
Image			
	<a href="S:\Images\Demo 2\Waffle.bcr">S:\Images\Demo 2\Waffle.bcr</a>	<a href="S:\Images\Demo 2\Test.dt2">S:\Images\Demo 2\Test.dt2</a>	<a href="S:\Images\Demo 2\Grains.bcr">S:\Images\Demo 2\Grains.bcr</a>
Y-Pixels	256	2	512
X-Pixels	256	500	512
Z-Range	191.327 nm	176.77 nm	10.642 nm
Y-Range	75 um	3.99942 um	500 nm
X-Range	75 um	49.9994 um	500 nm
Description	Created by SPIP 1.9222 Original file S:\Images\Demo 2\Waffle.bcr Calibration structure		Created by SPIP 1.9222 Original file S:\Images\Demo 2\Grains.bcr Particles
<hr/>			
Image			
	<a href="S:\Images\Demo 2\DDDB.BCR">S:\Images\Demo 2\DDDB.BCR</a>	<a href="S:\Images\Demo 2\CrossCorrImg.jpg">S:\Images\Demo 2\CrossCorrImg.jpg</a>	<a href="S:\Images\Demo 2\200x1.jpg">S:\Images\Demo 2\200x1.jpg</a>
Y-Pixels	128	908	1250
X-Pixels	128	952	1664
Z-Range	1.00357 nm	255 nm	255 nm
Y-Range	10 nm	907 Pixels	1249 Pixels
X-Range	10 nm	951 Pixels	1663 Pixels
Description	Created by SPIP 1.9222 Original file S:\Images\Demo 2\DDDB.BCR Didodecyl benzene self assembled molecules		

## Heuristic File Importer

When trying to open a file that is not directly supported by SPIP, the Heuristic File Importer Dialog is activated. You have the option to let SPIP guess the structure or provide SPIP with some information about the format. This way you will be able to read almost any file excluding files containing compressed data. For accurate measurements, it is necessary to enter the correct physical scaling parameters.



### File

This field initially contains the name of the file, which format was not recognized by SPIP. By putting in a name for a file that is recognized you can force SPIP to read the file in a different way. This can be a temporary solution when your microscope vendor has changed the format, for example, included multiple images in the same file. If such a situation occurs, please contact Image Metrology so that we can implement a proper solution.

### Data Type

SPIP currently supports four binary word types in addition to ASCII. It is important that you enter the correct word type and if you are in doubt consult your microscope manual or just try the different possibilities. Most SPM file formats consist of a fixed-sized header describing the image followed by  $N_x \times N_y$  16 bit signed integers. You will usually be able to distinguish a correctly read image from a wrong.

**Intel Word Format**

The binary words are usually in the Intel format. However, if your data source is a UNIX or Macintosh workstation it is more likely that you need to turn off this setting.

**Structure Information****Auto Guess**

By checking the Auto Guess check box you can conveniently have SPIP to guess the structure information whenever the Data Type is modified or a new file is defined. However, if you are repeatable opening files of a certain structure it might be desirable to keep the structure fixed by turning off the Auto Guess function.

**Header Length**

The Header Length is the number of 8-bit bytes in front of the raw data.

**Number of X,Y Pixels**

The number of X and Y Pixels in the X and Y directions determine the number of pixels in the image. SPIP assumes that the data are produced in a raster scan, *i.e.*, there are Ny scanlines each of Nx points.

**Guess All**

In many cases you can successfully let SPIP guess the size of the header and the number of X, Y points. The guess will be based on the Data Type setting and the size of the file.

**Guess Header**

If you know the number of X, Y pixels you can let SPIP guess the header size so that it fits to the settings and the size of the file.

**Guess X,Y**

If you have entered a known header size you can let SPIP guess the number of X,Y pixels that will fit to the settings and the size of the file.

**Guess X**

Let SPIP Guess the number of X pixels and keep the header and Y pixels fixed.

**Guess Y**

Let SPIP Guess the number of Y pixels and keep the header and X pixels fixed.

**Physical Scaling**

For quantitative analysis in absolute numbers, it is important that data for the physical dimensions of the image are entered.

**X, Y Size**

The X, Y size should be entered in nanometer, - a future release of SPIP will give you the option to define other units. If your image is representing other units you might enter these in the Image Properties Menu

**Z-Scale Factor**

The Z-scale factor is the factor by which the read pixels should be multiplied in order to achieve the correct height information.

**Time Per Scan Line**

The two timing parameters are important if you want to extract time related information. Sinusoidal 50 Hz noise signal added to the Z-data, for example, can be detected in the Fourier Image and quantified as a 50 Hz noise.

**Time Per Image**

The Time Per Image is usually 2 Ny times the Time Per Scan Line. However, some systems may perform some additional scanning outside the visible scan-line causing the time per image to be larger.

**Force Curve Type**

Mark this checkbox if the data present force curves

**Scatter x,y Coordinates**

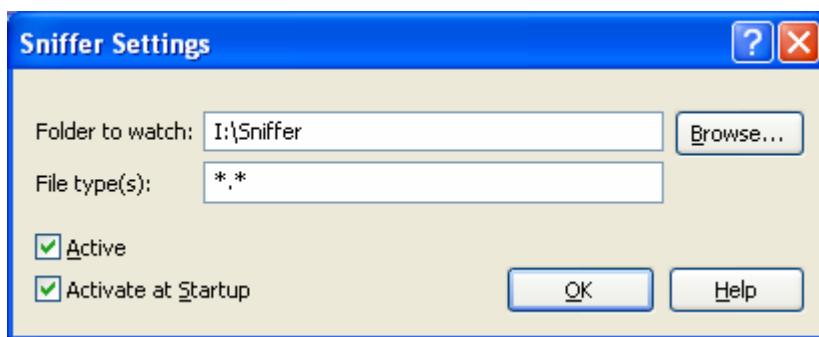
Mark this checkbox if the data presents scatter data with x,y coordinate pairs.

## The Sniffer

The Sniffer is used for automated view and processing of data whenever data files are written to a defined "Sniffer Folder". You can for example have a microscope producing image files to a network folder and SPIP to process such files whenever they are generated. In combination with the Batch Processor and the ActiveReporter you have a powerful automation tool for analyzing and reporting.

Basically the function of the Sniffer is analogous to other ways of opening files, for example by File→Open or Drag Dropping from the ImageMet Explorer (see the section Interfacing to SPIP for more alternatives). The difference is that it is run automatically whenever there are new data files to process and requires therefore no user interaction.

The Sniffer status is controlled from the Sniffer Dialog, which is opened from the File→Sniffer menu item.



### Folder to Watch

The Folder to Watch field of the Sniffer dialog defines the "Sniffer Folder", which SPIP will be watching whenever the Sniffer is set active.

### File Type(s)

In the File Type(s) field you can by use of wildcards specify which files should be handled by the Sniffer. If you want to include more than one file type just enter more specifications separated by spaces, for example: "\* .img \* .map \* .tif \* .0???".

Specific file types can also be excluded by specifying the file type with a '-' (minus sign) as prefix. For example "\* -\*.bak ~\*.\*" will include all files except those with extension .bak and those files starting with ~ (tilde character) .

### Active

The Sniffer will only be active when the Active check box is set.

### Active at Startup

If you want the Sniffer to be active when starting the program, check the "Active at Startup" checkbox. This might be convenient when you are using the same Sniffer Folder frequently.

### Sniffer Processing Issues

The Sniffer implementation is event based and will normally not use CPU resources unless new files are put into the Sniffer folder. While other systems are generating new files to the Sniffer Folder the Sniffer will use a few extra resources to check when the files are closed and ready for processing.

When the Sniffer is activated it will register the existing files in the Sniffer Folder so that only files, which did not exist at the activation time, can be processed. The list of registered files will be reset whenever the OK button is pressed.

Result files generated by SPIP will not be processed.

## ActiveReporter

### ActiveReporter Introduction

The ActiveReporter is used for creating user defined reports. You can define the content and layouts of reports by use of templates. Templates are plain documents, so it is easy to create new defined or modify existing ones to fit a particular purpose.

To define a value or a picture (for example image, curve, dialog or screen dump) from SPIP to be entered in a report, an Active X component called a SPIP Control is inserted in the template. You can work with the SPIP Control and define the values or graphical output which SPIP shall provide during reporting.

The only difference between the template and the report is that all SPIP Controls in the report are replaced by their corresponding value or image.

The templates are Active because SPIP automatically calculates requested values or graphs when processing the SPIP Controls included in a template. There are only a few parameters for, which it is necessary for user to perform a semi-automated measurement.

Currently Microsoft Word documents (.doc files) are supported as the only template and report format; please refer to Word ActiveReporter Overview for more information. However, the design opens for support of other formats in the future.

# Word ActiveReporter Overview

## Introduction to Word ActiveReport

Word ActiveReporter is the ActiveReporter implementation for Microsoft Word 2000 and 2002 (XP). This means that both the template and report format is the standard Word document (.doc).

The following sections will describe how to generate templates and reports based on the Word ActiveReport tools:

## The Word ActiveReporter Dialog

## How to create a Word ActiveReporter template

## How to create a Word ActiveReport for a single image/curve

## How to create an ActiveReport through batch processing

## SPIP Control Properties Dialog

## **Supported Microsoft Word versions**

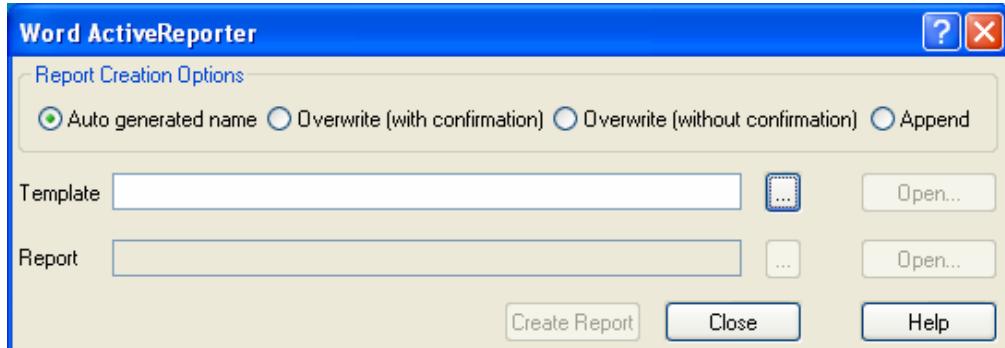
Word ActiveReporter has been tested with the following versions of Word:

- Microsoft Word 2000 Service Release 1a (SR-1a)
  - Microsoft Word 2000 Service Pack 3 (SP3)
  - Microsoft Word 2002 Service Pack 2 (SP2)
  - Microsoft Word 2003 Service Pack 2 (SP2)

Please contact Image Metrology if you experience problems with other versions of Microsoft Word 2000 or 2002.

## The Word ActiveReporter Dialog

The Word Active Reporter Dialog is selected by the "Word ActiveReporter..." item in Processing menu or by clicking the associated icon on the tool bar .



## Report Creation Options

Use the radio buttons to define how new report files are generated:

**Auto generated name:** The report will be written to a new file with a unique name

Overwrite (with confirmation): The report will be written to the specified file. If it already exists it will only be generated if you confirm SPIP to do so.

**Overwrite (without confirmation):** The report will be written to the specified file. If it already exists it will be overwritten without notification.

**Append:** The report will be appended to the specified file. If it does not exist it will be generated.

### Template Selection

The template is selected by entering its name or by selecting the file using the browser button. Use the Open button to check and modify the template. It is possible to have the template open while generating the report.

### Definition of Report File name

Unless you have chosen to use the "Auto generated name" option you will need to enter a name for the report to be generated. After generation you can use the Open button to check the result. Note, you it is necessary to close the report if you want to generate a new report with the same name.

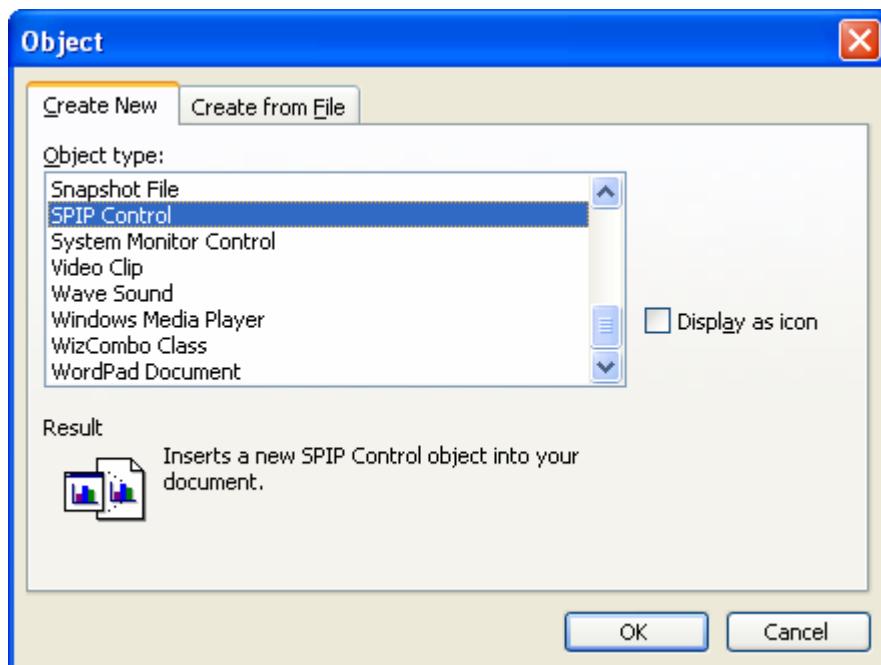
### Create Report

To generate the report just press the "Create Report" button. During the generation of the report you will see a progress bar being updated for each processed SPIP control while the SPIP program may generate requested results.

## How to create a Word ActiveReporter template

Open Microsoft Word.

- 1 Start with an empty document or load an existing template to modify. Predefined template examples can be found in the "Word Templates" folder of the SPIP program and can conveniently be opened from the Word ActiveReporter dialog.
- 2 To insert a SPIP Control in the Word Template Press <Insert, SPIP Control...>. You can then select the SPIP Control as shown below:



Below is seen an example of a SPIP control object as it might appear in the Word template

```
{ SPIP "Roughness" "Sa" "Value" }
```

- 3 The SPIP Control can be resized as desired. To define the SPIP parameter associated with the SPIP Control right click on it and select <SPIP Control Object→Properties...>.

You can find more details on how to set the different SPIP Control options in the "SPIP Control Properties Dialog " section.

- 4 Insert as many SPIP Controls as needed. This can now be done as describe above or by copy & paste of the previously created controls.
- 5 Save the template.

### **How to create a Word ActiveReport for a single image/curve**

Open the image or curve the report shall describe.

Select the "Word ActiveReporter..." item in Processing menu or click <Word Reporter icon>.

This will open a Word ActiveReporter Dialog

Set the report creation options, template filename and report filename. Please refer to Word ActiveReporter Dialog for more information.

Changes to the template can be made by clicking the template Open button, but remember to save the template before creating the report.

Click the Create Report button to create the report.

Click the report Open button to see the result. Note, remember to close the report before trying to append new report sections to the file.

For report generation of data files groups please refer to How to create an ActiveReport through batch processing . There you will also learn how to generate summary reports containing statistical values for the processed data files.

## SPIP Control Properties

A SPIP Control is an ActiveX component corresponding to a value or image in SPIP.

It is used in templates to define where to insert a SPIP value or picture. In word templates the SPIP Control Property dialog is activated by Right clicking on the SPIP control and selecting <SPIP Control Object →Properties...>.

The available fields are logical grouped and selected from the Group field, which will determine the available fields. A field may contain a numerical parameter or a Picture.

### Numerical Field Options

A numerical field can be reported in the following modes:

- Value: The value of associated with the processed data file
- Max, Mean, Min, SD, Count: Which are the statistical parameters calculated from a batch of files using the Batch Processor and are primarily used in combination with summary reports. The availability of the statistical parameters depends on the selected field.  
It is furthermore possible to report the values with or without units, or just the unit. The latter is most suitable for creation of tabular reports, where the name and units are written at the top of the table columns.

### Picture Display Options

The picture display option is used to control the sizing of the final images entered to the reports:

- Keep Aspect Ratio best fit: The image is placed inside the borders of the SPIP Control while keeping the original aspect from SPIP. This ensures that the image will never become larger (but may become smaller) than the SPIP Control.
- Keep Aspect Ratio fixed width: While keeping the image's original aspect from SPIP, the height of the picture is changed until it has the same width as the SPIP Control. The image may become higher than the SPIP Control.
- Keep Aspect Ratio fixed height: While keeping the image's original aspect from SPIP, the width of the picture is changed until it has the same height as the SPIP Control. The image may become wider than the SPIP Control.
- Stretch to fit: This will stretch the picture to fit the area of the SPIP control exactly.  
Note that this can create undesired distortion of images.

### Picture Resolution factor

To achieve a good resolution of the final printout you can set the Picture Resolution factor higher than one. When set to for example 2.0 the number of pixels contained in the image will be the double of the pixels it covers in the Word window when the zoom is set to 100%. Thus this will provide more details in printouts.

### Picture resolution scale font

This property applies to images only and is used in conjunction with Picture resolution factor. It causes SPIP to scale the font size for text on images so that it will have a readable size even if the picture resolution factor is very high or low.

### Set as Default

Stores the current property values as the default for new SPIP Controls.

### Info tab

Then info tab displays possible error messages from SPIP when the value or picture associated with the SPIP Control could not be calculated during generation report generation. In such cases the SPIP control will reappear in the report rather than the requested value.

### Wrapping style in MS Word documents.

The wrapping style of a SPIP Control can be used to control how the value or image is presented in the report:

- If the SPIP Control's wrapping style is "In line with text" and it refers to a text value, the value is simply inserted as text replacing the SPIP Control. The size of the SPIP Control is ignored.
  - If the SPIP Control's wrapping style not "In line with text" and it refers to a text value, the SPIP Control is replaced by a text box with the same size as the SPIP Control and the text value is inserted in this text box.
  - If the SPIP Control refers to an image, the image replacing the SPIP Control gets the same wrapping style as the SPIP Control.
- Please refer to Word's help system for more on setting wrapping styles for objects.

## Word ActiveReporter performance issues

The processing time for generating reports depends on a number of factors:

- The number of SPIP Controls contained in a template will influence the loading time of the template as well as the processing time.
- Tests have shown that the use of tables can slow down the report generation. This is probably because Microsoft Word's rendering algorithms (which is run for every new exchange of a SPIP Control with a value or image) is computation intensive. Therefore, if the processing time is of major concern the use of tables should be avoided. However, it might be practical to design a template by use of tables and then convert the table to tab separated text when the design is ready.
- A large amount of temporary files in the *windows\Profiles\user\Local Settings\Temp* folder can slow the report generation down because Word is scanning this folder when generating unique filenames for temporary files. Therefore, it is recommended to clean up this folder regularly.

## Word ActiveReporter Troubleshooting

**Problem:** There is no "SPIP Control" on the "Objects" dialog in Word

**Solution:** The control has not been registered correctly or Word has not yet discovered the object. Try rebooting the computer and if this does not help: Reinstall SPIP.

**Problem:** The SPIP Controls are visible in the Word document but cannot be selected, resized or have their properties changed.

**Solution:** Word is not in design mode. SPIP Controls (like other ActiveX controls) cannot be modified unless Word is in design mode. To enter the design mode you can do the following:

Click **Tools→Customize...** and check the Control Toolbox on. In the Control Toolbox you will then be able to enter the design mode by clicking the Design Mode button: .

Please refer to Word's help system for more information on how to put Word in design mode.

**Problem:** Some of the SPIP Controls in a template have not been replaced in the report.

**Solution:** There was a problem calculating the value or image to replace the SPIP Control. The error message is displayed in the control or can be read on the info tab in the SPIP Control's properties dialog. This may happen if a requested parameter is not applicable for the current data or because some other SPIP settings have prevented a parameter to be calculated.

**Problem:** The Group and Field values displayed on the SPIP Control are not the same as in the properties dialog.

**Solution:** This is behavior by design. Please refer to SPIP Control Properties for more information.

**Problem:** Word stops during creation of report with the message: "The server threw an exception".

**Solutions:** This means that an internal error in MS Word has occurred. Close all Word documents. Use the Windows Task Manager to possible invisible MS Word programs; they will appear with the "WINWORD.EXE" name. If this does not help, try to restart SPIP or the computer.

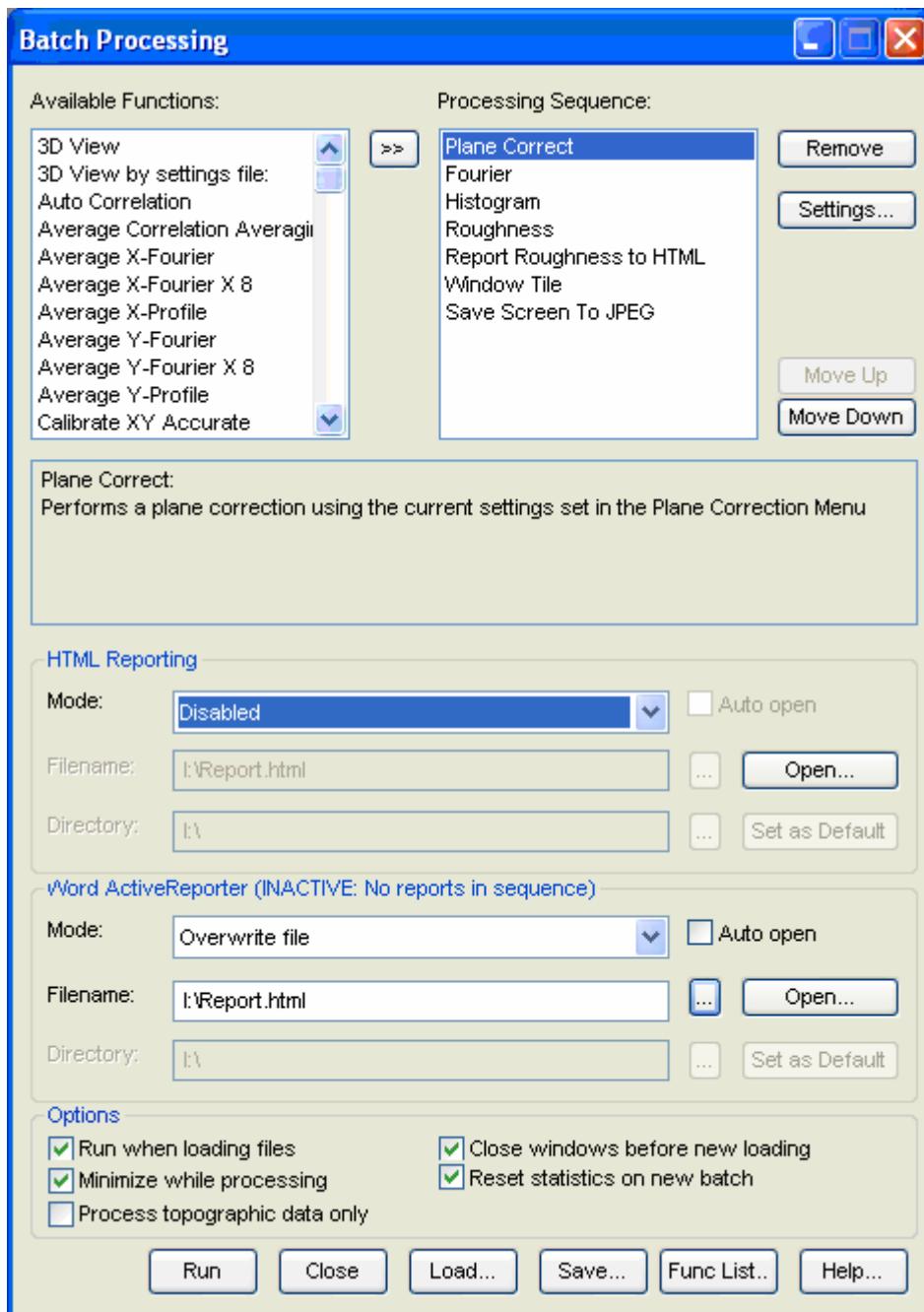
If the error consequently happens for a specific word template it might be necessary to rewrite the template from scratch.

Such errors may occur when the MS Word program is in focus and handling keyboard input. It is therefore recommended not to use the keyboard during report generation.

## Batch Processing

The Batch Processing dialog enables you to design your own processing sequence and create reports for each file opened. A group of files can for example be drag dropped from ImageMet Explorer or selected from the Open File Menu and process automatically. The Batch Processors automation features can be further enhanced when combined with the ActiveReporter, The Sniffer and the Plug-in Interface.

 The menu is activated by the corresponding tool key or from Processing→Batch Processing.



The processing sequence can be selected from the left list box by double clicking or by the add ( >> ) button. In the information box below there will be written a short description of the selected function.

The sequence order can be changed by the "**Move Up/ Move Down**" bottoms; the top most command will be processed first.

For certain processing steps there are associated settings which can be viewed and set when the "**Settings**" button is active.

The colors of the selected batch process indicate possible abnormalities:

- **Black:** means that everything is normal
- **Gray:** means that the function is not available because the **required** module is not included in the license. These functions will be ignored when running the batch process.
- **Red:** Indicates a problem with the settings of the function, typically a reference to a missing file. Such functions are ignored during a batch process.

To save memory it is a good idea to delete the current windows whenever a new file is loaded; this is set by the "**Close Windows Before New Loading**" check box.

Setting the checkbox "**Run when loading files**" will cause the sequence to be performed when ever loading a new file or a group of files, but only when the batch dialog is open.

To avoid the Batch Processing Dialog to overlap the SPIP image data windows it is a good idea to set the "**Minimize while processing**" checkbox on.

Setting the checkbox "**Reset statistics on new batch**" will cause all generated statistics from, e.g. roughness and grain analysis to be reset before processing a new batch of files. In situations where the Batch Processor is running one file at a time, it might be desirable not to reset the statistics so that the statistics of a larger group of files can be reported together.

Such a setup may be relevant when using the Sniffer to send files generated by your microscope to the Batch Processor whenever a new file is generated.

When setting "**Process topographic data only**" only images which have a length unit as z-unit and therefore considered as a topographic image will be processed. This is particular useful when processing files containing more types of images, such as phase images, which are not relevant for e.g. roughness analysis.

The **Load / Save** buttons allows you to save and retrieve the designed sequences. A default processing sequence can be defined by saving the settings into the *Default.batch* file. SPIP comes with a number of sample files, which can be loaded by the **Load...** button

Note, that during the batch process current defined reference parameters for calibration will be applied. You can in the corresponding menus store your preferences as the default settings, which will be loaded at program start.

The different analytical operations available in the Batch Processing menu applies mainly to the Main Image Window, but it is possible to put the image from the most recent generated window for example a gradient images into the Main Window and then process with all the optional batch operations.

When running the information box will inform about the status If the batch process.

## Available Batch Functions

The following lists the currently available Batch Functions. To get an up-to-date list of available functions in your version of SPIP click the "**Func. List..**" button.

Function Name	Description	Required Module
3D View	Creates a 3D view of the Main Image using the 3D default settings	3D Visualization
3D View by settings file:	Creates a 3D view of the Main Image using 3D view settings stored in a 3D	3D Visualization

	settings file	
Auto Correlation	Calculates the Auto-correlation image	Basic
Average Correlation Averaging	Correlation Average using an auto selected template	Correlation Averaging
Average X-Fourier	Calculates the average Fourier spectrum of all X-Profiles	Basic
Average X-Fourier X 8	Calculates the average Fourier spectrum of all X-Profiles with 8 times normal resolution	Basic
Average X-Profile	Calculates the average X-Profile	Basic
Average Y-Profile	Calculates the average Y-Profile	Basic
Average Y-Fourier	Calculates the average Fourier spectrum of all Y-Profiles	Basic
Average Y-Fourier X 8	Calculates the average Fourier spectrum of all X-Profiles with 8 times normal resolution	Basic
Calibrate XY Accurate	Calibrates the XY unit cell using sub-pixel Fourier transforms at the Fourier Peaks. The correction parameters are based on the current reference parameters	Calibration
Calibrate XY Fast	Calibrates the XY unit cell using polynomial fits to the Fourier Peaks. The correction parameters based on the current reference parameters found in Processing→XY Calibration→Correction Menu	Calibration
Calibrate XY Linearity	Determines the Linearity, Unit Cell, and XY Correction parameters based on combined Fourier and Cross Correlation analysis. The correction parameters are based on the current reference parameters	Calibration
Calibrate Z	Calculates the step height based on Histogram analysis. The Cz correction parameter is based on the reference parameter set in the Z-Calibration Menu	Calibration
Calibrate Z Advanced	Calculates the step height based on optional Averaging and Histogram analysis. The Cz correction parameter is based on the reference parameter set in the Z-Calibration Menu	Calibration
Coarse Hysteresis Correction	Calculates 2nd order x-,y-hysteresis functions and corrects the Main Image	Calibration
Color Brown Scale	Applies the predefined Brown Color Scale	Basic
Color Default Scale	Applies the user definable default Color Scale	Basic
Color Gray Scale	Applies the predefined Gray Color Scale	Basic
Color High Contrast	Applies the predefined High Contrast Color Scale	Basic
Color Reverse Gray	Applies the predefined Reverse Color Scale	Basic
Crosssection Profile	Show the Cross-section Profile window	Basic
Correct X,Y,Angle	Corrects for X, Y scaling and angle error. The correction parameters are based on the actual settings, which can be from the most recent calibration performed in the processing sequence	Calibration
Correct XY Linearity	Corrects the XY Linearity by the actual 3rd order linearity model, which can be from	Calibration

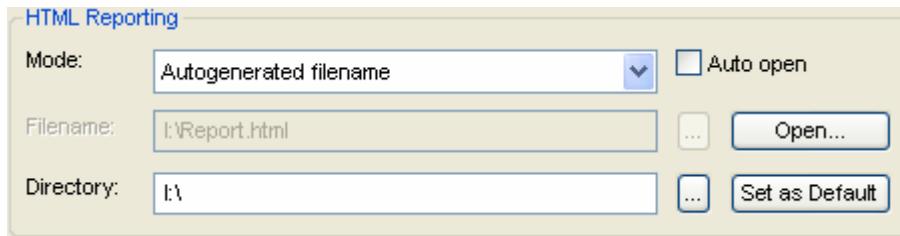
	the most recent calibration performed in the processing sequence	
Correct Z	Corrects the scaling by the actual Cz scaling factor, which can be from the most recent calibration performed in the processing sequence	Calibration
Detect Lines	Detects Parallel Line Structures / pitch, by Fourier analysis. The result is shown as a unit cell with orthogonal vectors	Extended Fourier
Filename Extend Number	Extend the filename of the Main Image with an incremental number.\ This way results from the same image, such as roughness parameters, can be saved in different result files	Basic
Fine Linearity Correction...	Performs a linearity analysis, same as "Calibrate XY Linearity"	Calibration
Filter	Filter the image using the currently defined filter (stored in Kernels\Default.fit)	Filter
Filter Specific	Filter the image using specific filter settings stored in a File	Filter
Force Curve Analysis	Perform force analysis	Force Curve Analysis
Fourier	Performs a Fourier transform of the Main Image	Basic
Fourier Curve	Performs a Fourier transform of the Most Recent created curve	Basic
Fourier Curve X 8	Performs a Fourier transform of the Most Recent created curve, With 8 times resolution	Basic
Fourier Filter Specific	Filter the image using specific Fourier filter settings stored in a File	Extended Fourier
Gradient_Norm	Calculates the Gradient Normal Image. The result is saved in a new image	Basic
Gradient_X	Calculates the X-gradient Image. The result is saved in a new image	Basic
Gradient_Y	Calculates the Y-gradient Image. The result is saved in a new image	Basic
Grain Analysis	Detects Grains and/or Pores	Grain and Pore Analysis
Grain Analysis Specific	Detects Grains and/or Pores using specific settings stored in a settings file	Grain and Pore Analysis
Histogram	Calculates the Height Distribution Histogram of the Main Image	Basic
Inverse Fourier	Performs an Inverse Fourier transform of the Fourier Image	Extended Fourier
Mirror X	Mirrors the Main Image X-wise	Basic
Mirror Y	Mirrors the Main Image Y-wise	Basic
Pixels Fewer	Decreases the number of x,y pixels by a factor of two	Basic
Pixels More	Increases the number of x,y pixels by a factor of two	Basic
Pixels Radix 2	Increases the number of x,y pixels to the nearest radix two numbers	Basic
Plane Correct	Performs a plane correction using the current settings set in the Plane Correction Menu	Basic
Print All	Prints a screen dump of the SPIP program	Basic
Print Main	Prints the Main Image to the printer	Basic

Quadrangle Curve Fit	Perform a quadratic curve fit	Calibration
Recall Default Correction	Recalls the default corrections parameters saved in Default.cp. Use this when an image need to be corrected before calibration, which will define new correction parameters	Calibration
Report Calibration to HTML	Reports the X, Y, Z calibration results for the Main Image to the HTML report, including linearity parameters	Calibration
Report Force to HTML	Reports the most recent calculated Force Curve parameters to the HTML report	Basic
Report Grain/Pores to HTML	Reports the most recent calculated grain/pores statistics to the HTML report	Grain and Pore Analysis
Report Roughness to HTML	Reports the most recent calculated roughness parameters to the HTML report	Roughness
Report Tip Characterization to HTML	Reports quantitative tip characterization results: Radius, Height, Angles, Certainty Area	Tip Characterization
Report Quadrangle Fit to HTML	Reports the most recent results from quadratic fit to profile to the HTML report	Calibration
Rotate 90 Deg	Rotate 90 degree	Basic
Rotate Align unit cell	Rotate so that the unit cell / line structure comes parallel to the axes	Basic
Roughness	Calculates the Roughness Parameters. The results can be reported to HTML	Roughness
Save Screen To JPEG	Save the SPIP Screen to JPEG using a file name based on the Main Image. The file will be included in the HTML report	Basic
Sobel	Enhances edges by a Sobel operation on the Main Image. The result is saved in a new image	Basic
Tip Characterization	Characterizes the tip used for scanning the main image	Tip Characterization
Tip "Deconvolute"	"Deconvolutes" the main image with the current tip	Tip Characterization
Tip Load	Loads a tip that can be used for "Tip Deconvolution"	Tip Characterization
Unit Cell Accurate	Same as "Calibrate XY Accurate"	Calibration
Unit Cell Fast	Same as "Calibrate XY Fast"	Calibration
Void Pixel Interpolate new Values	Interpolate new values for the void pixels	Basic
Window Duplicate	Duplicates the active window	Basic
Window Duplicate Main	Duplicates the Main Image Window	Basic
Window Close All	Closes all SPIP windows	Basic
Window Close All Dialogs	Closes all SPIP Dialogs	Basic
Window Close All Except Main	Closes all SPIP windows except Main Image Window	Basic
Window Close Main	Closes the Main Image Window	Basic
Window Inverse FFT To Main	Put the Inverse (Fourier Filtered) FFT Image to the Main Window for further operation	Extended Fourier
Window Tile	Tiles all windows, useful for screen dumps	Basic
Window Tile 1 Column	Tiles all windows, in one column, useful for screen dumps	Basic
Window Tile 2 Column	Tiles all windows, in two columns, useful	Basic

	for screen dumps	
Window Tile 3 Column	Tiles all windows, in three columns, useful for screen dumps	Basic
Window Tile 4 Column	Tiles all windows, in four columns, useful for screen dumps	Basic
Window Most Recent Image To Main	Put the image of the most recent created image window to the Main Window for further operation	Basic
Window Save All In ASCII	Saves all individual images and graphs in ASCII (*.asc) format (no loss of data)	Basic
Window Save All In BCR	Saves all individual images and graphs in BCR (*.bcr) binary format (no loss of data)	Basic
Window Save All In BMP	Saves all individual images and graphs in BMP (*.bmp) graphics format as it appears on the screen	Basic
Window Save All In BMP 1:1	Saves all individual images and graphs in BMP (*.bmp) graphics format with the same number of pixels as the raw image	Basic
Window Save All In JPEG	Saves all individual images and graphs in JPEG (*.jpg) graphics format as it appears on the screen	Basic
Window Save All In JPEG 1:1	Saves all individual images and graphs in JPEG (*.jpg) graphics format with the same number of pixels as the raw image	Basic
Window Save All In NanoScope	Saves all individual images originated from a NanoScope file version 4 or higher in NanoScope (*.nsc) binary format (no loss of data)	Basic
Window Save All In TIFF	Saves all individual images and graphs in TIFF (*.tif) graphics format as it appears on the screen	Basic
Window Save All In TIFF 1:1	Saves all individual images and graphs in TIFF (*.tif) graphics format with the same number of pixels as the raw image	Basic
Word Report by Template	Create a MS Word report based on a selected template.	Batch Processing
Word Report Preface by Template	Create a MS Word report preface based on a selected template. The preface will be inserted at the start of all reports in the batch process.	Batch Processing
Word Report Summary by Template	Create a MS Word report summary based on a selected template. Only one summary will be produced for each batch process.	Batch Processing
Zoom	Create a Zoom image using the default zoom size and position	Basic

## HTML Reporting in Batch Process

Reporting to an HTML file in a batch process can be carried out automatically when the **HTML Reporting Mode** is set differently from Disabled.



You may define the HTML file name or let SPIP automatically generate a unique name based on the current date and time of day in this case the file will be located in the SPIP/HTML directory.

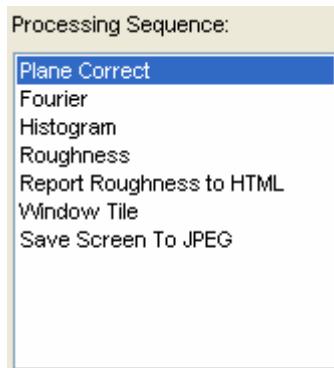
During the batch processing screen dumps can be saved in JPEG files, which will be saved in the same directory as the HTML report file or to the directory of the Main Image file in the situation where HTML reporting is disabled.

Numerical results can be saved together with the screen dumps by including Report functions in the Processing Sequence. Currently the following HTML reporting functions are available:

- Report Calibration to HTML
- Report Force to HTML
- Report Grain/Pores to HTML
- Report Quadrangle Fit to HTML
- Report Roughness to HTML
- Report Tip Characterization to HTML

These functions will also enable reporting of statistical mean and standard deviation values for the file sequence at the end of the HTML report.

The sequence example shown below will produce a HTML report with calculation of roughness parameters and a screen dump for each file in the sequence and will finally enter statistical results at the end of the HTML report.



### HTML Report Customization

Currently the layout of the HTML reports is fixed meaning that colors etc. cannot be modified. However, a logo for the report can be included in the HTML report by having the logo in a file called *Logo.gif* this file should be located in the same directory as the HTML file. Similarly operator information can be included in the header by writing this information into a plain text file called *Operator.txt*.

### Word Reporting in Batch Process

To set up a batch process containing word reports select one or more of the Word Report functions from the available functions. There are three types of Word templates to select:

**Word Report by Template:** This template will be run for each file entered to the batch process and the results appended to the selected report file.

**Word Report Preface by Template:** This template will only be run at the very beginning for each batch process and is suitable for defining the page layout and labeling names for tabular outputs.

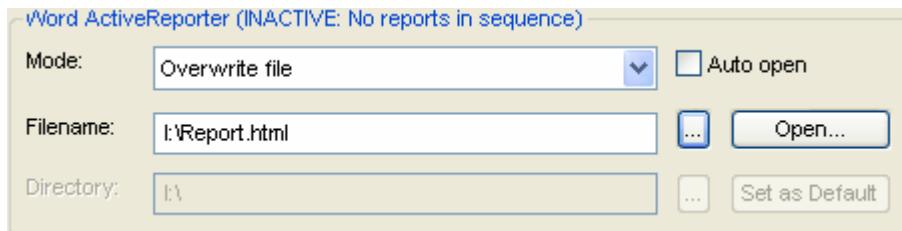
**Word Report Summary by Template:** The template will only generate output when all the files in a batch have been processed. Thus, it is suitable for reporting statistical results like mean and standard deviations

When selecting a word template function you will be asked to specify the template file. The template can hereafter be opened by use of the **Settings** button or exchanged by another template.

Note that it is possible to run a batch process containing nothing else as a word template because the template will instruct SPIP which processes to perform.

**Report modes:**

Use the **Mode** Combo box to select the name of the report to be generated:



**Autogenerated filename :** The report will be written to a new file with a unique name. The folder for the file is selected by the "Directory" field.-

**Overwrite file (prompt):** The report will be written to the specified file. If it already exists it will only be generated if you confirm SPIP to do so.

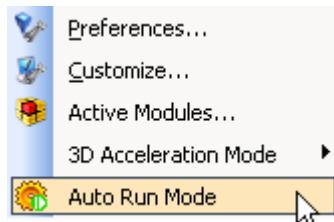
**Overwrite file:** The report will be written to the specified file. If it already exists it will be overwritten without notification.

**Append to file:** The report will be appended to the specified file. If it does not exist it will be generated.

## Auto Run Mode

The Auto Run Mode is used for processing and displaying data the same way every time a data file is opened without having to activate the Batch Processing dialog. You may for example always want to have a 2D image shown next to a 3D rendered image and with profile and histogram windows shown below.

The Auto Run Mode turned is on/off by clicking it on in the Options pull down menu:



The processing sequence for the Auto Run Mode is defined in the Batch Processing file called "AutoRun.Batch", which can be generated for the Batch Processing dialog. If this file does not exists the Batch Processing dialog will open when activating the mode.

To assure that the windows will appear with certain size and position you may do the following:

Turn Window→Tile Automatically on

Turn Window→Duplicate Main Automatically off

Open a data file and for each of the automatically generated data windows stretch and position them as desired.

**For each data window click Window→Set Window Size and check "Apply when Tiling".**

You may also use the Window Size dialog for adjusting the window size.

You may change the order of appearance by modifying the "AutoRun.batch" file in the Batch Processing dialog.

## **Batch Processing Trouble Shooting**

The big advantage of Batch Processing is the large amount of data that can be processed automatically. This also means that large amount of results can be generated. Therefore you should always make sure that you have sufficiently disk space available before activating a large batch process.

### **Resource leak in Windows XP SP2**

There is a known error in the Windows XP Service Pack 2 operating system, which may create resource leaks such that only approximately 800 data windows can be created during a session. This error is described by Microsoft article Q319740

The error is related to the Windows theme interface and can be solved by turning it off. To do this, follow these steps:

Click Start, and then click Control Panel.

Click Appearance and Themes, and then click Display.

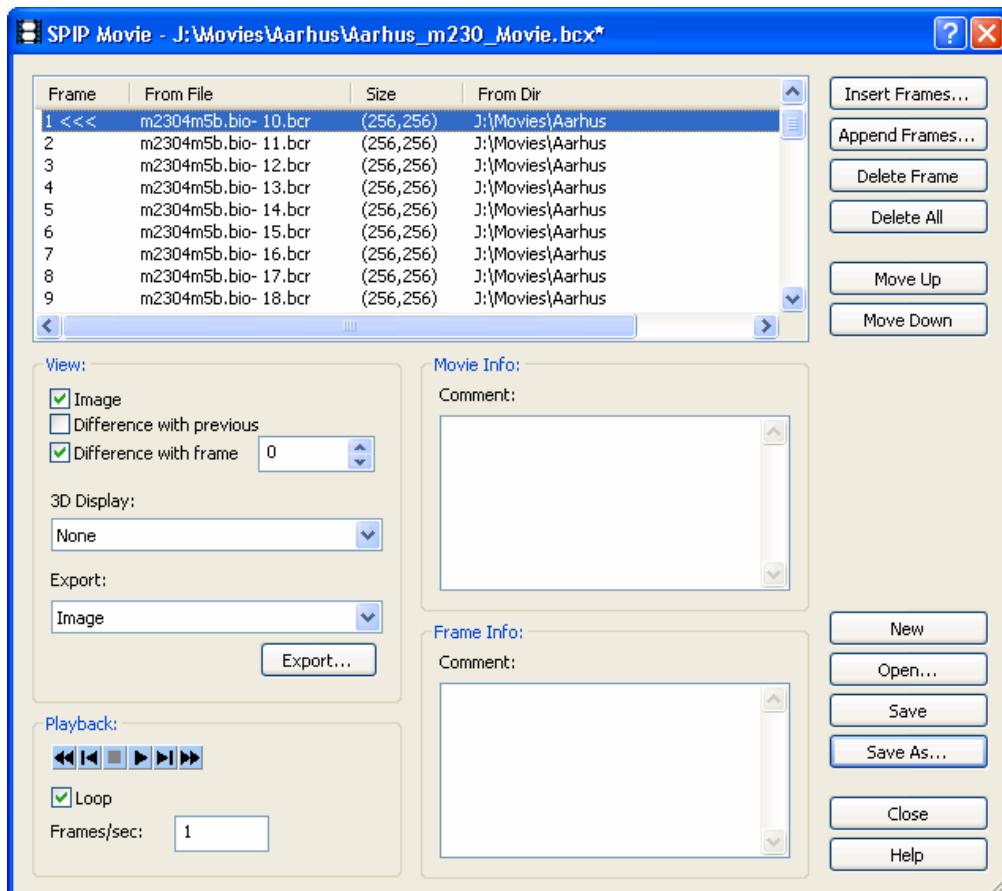
On the Themes tab of the Display Properties dialog box, click Windows Classic in the Theme list.

Click Apply, and then click OK.

## Movie and Time Series Analysis

The Movie Dialog allows you to define a sequence of frames which you can then play back inside SPIP or export to externally playable formats (AVI or MPEG). By setting up analyses (e.g. [Histogram](#) or Profile) on the playback window this feature allows Time Series Analysis to be carried out.

The dialog is activated by selecting the Processing→Movie... menu item, by using the keyboard shortcut **Shift+Ctrl+M** or clicking the toolbar button .



### Working with movies

When the movie dialog is opened the last loaded movie will be reloaded. If it is unavailable then a new, empty movie will be opened. The current movie can be saved, another movie can be loaded, or a new movie can be created using the appropriate buttons. The filename of the currently loaded movie is shown in the title bar of the dialog.

It is possible to add or edit a comment to the movie by using the Movie Info comment field. This comment is saved as part of the movie file.

### The frame sequence

The frame sequence of the currently loaded movie is shown at the top of the dialog. The currently selected frame is indicated by the symbol "<<<" shown next to the frame number. The list also shows the filename and directory of the image file that was imported to make that frame, and the point size of the frame.

If a movie contains frames of different point size (e.g. 128x128 and 256x256) then the "Difference with ..." view functions will not be available.  
It is possible to enter individual comments for each frame, by using the Frame Info comment field. These comments are saved as part of the movie file.

## Inserting frames

Use the "Insert Frames..." or "Append Frames..." button to select one or more files to be inserted in the image sequence. If adding the file(s) will result in the movie containing frames of different point size then a warning will be shown that "Difference with..." functionality will be unavailable.

Any image file readable by SPIP can be added. The file is read and a copy of the image is inserted as a frame in the movie, along with information about the image file it was generated from.

Please note that it is also possible to add files by dragging them from e.g. Windows Explorer or ImageMet Explorer onto the Movie Dialog.

Adding frames from other open SPIP image window is possible by right clicking on Insert in Movie or Append to Movie. Furthermore, all open images can be appended to the movie by clicking on **Processing→Transfer→Append All Images to Movie**.

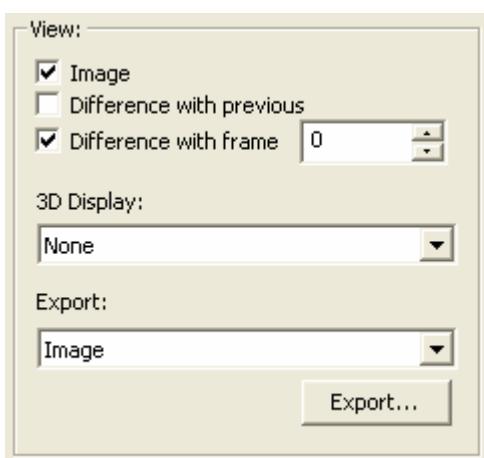
## Deleting frames

Use the "Delete Frame" button to delete the currently selected frame, and use "**Delete All**" to clear the list of frames. If the remaining frames are all of the same point size then the "Difference with..." view functions will be enabled (see Adding Files)

## Changing order of frames

The current frame can be moved to a different position in the sequence by using the "**Move Up**" and "**Move Down**" buttons.

## Viewing and playing frames



Use the three checkboxes to select what playback windows to show. Please note that the difference views are only available if all frames in the movie have the same point dimensions. The difference images are generated by subtracting the Z-values point for point, without regard for the physical X- and Y-dimensions.

The selected views of the current frame will be shown as normal image windows in the SPIP window, and it is possible to apply the normal analysis functions to the view windows. When the selection changes, the content of the view windows are changed to show the new current frame. Any analyses applied to a view window will be updated to reflect the new selection.

When one or more of the checkboxes are checked, it is possible to select one of the views for 3D display using the **3D Display** combo box. It is also possible to select one of the views, the 3D display, or a screen dump of the full SPIP window client area for export to AVI or MPEG (See Export Movie to Media File for details).

Exporting the full SPIP client area is useful for generating externally playable movies of time series analyses involving e.g. Histogram calculation, because the histogram curve window in this way will be included in the exported media file.



To play the movie inside SPIP use the playback buttons. Their functions are (left to right):

- Go to first frame in movie (frame 0)
- Go to previous frame
- Stop playback
- Start playback (starting with current frame)
- Go to next frame
- Go to last frame in movie

Check the **Loop** checkbox if you want the movie to play continuously. If left unchecked then the movie will play till the last frame is reached, whereupon playback will stop and current frame will be reset to what it was prior to playback.

The **Frames/sec** value is the desired frame rate. For large images or large view window sizes this frame rate might not be achievable. Playback will then proceed as fast as possible. Use high values (e.g. 20) to achieve animation effects, or low values (e.g. 0.1) to achieve a slide show effect.

## Getting Good Results

To get good results it might be desirable to perform some preprocessing of the images. In particular correction of plane distortion and lateral drift should be considered.

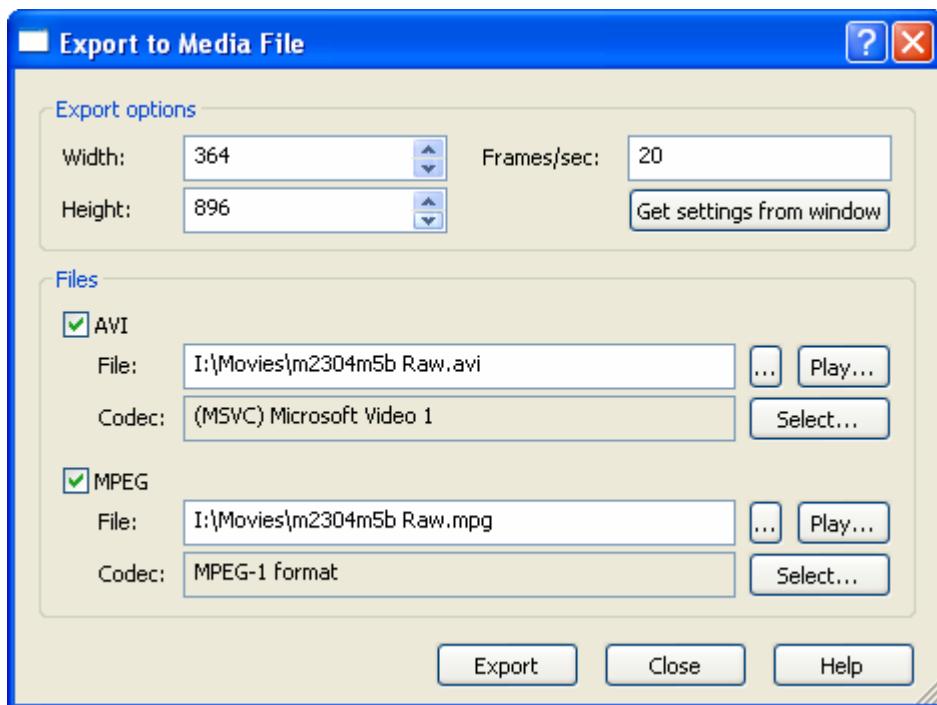
Plane correction can be performed for each image while having it in the Main Image Window or be applied as part of a Batch Process . The Batch process should include a command for saving the corrected image. After the corrected images have been written to file they can be added to the Movie as described above.

Lateral drift correction can be performed on the individual images by right clicking on "Align to Main" or on all opened images by clicking on **Processing→Operate with Main Image→Align all Images to Main**. The corrected images can then be added to the movie by right clicking on Add to Movie.

Correction of a particular frame can be perform by transferring it to the Main Image Window and perform the correction by the available tools. To transfer frames to the Main Image Window right click on **To Main Image**.

## Exporting to Media Files

The export dialog is used for setup of exports of animated sequences.



The **Export Options** group allows setting the parameters for the export. For screen dumps, setting the output frame size is not possible.

The **Files** group allows selection of which formats to export to, and selection of output file(s). The "**Play...**" buttons will launch the registered media file player (usually Windows Media Player) with the specified file.

Click the "**Export**" button to perform the export. If the specified file(s) exist you will be prompted for overwrite permission. A progress bar dialog will be displayed, which also allows you to cancel the export operation.

### Selecting the proper export format

There are differences between export formats, so it is important to select the proper format. Use these simple guidelines to make the proper choice:

If you need the best possible image quality, select AVI rather than MPEG.

If you have selected a low frame rate (<1) then exporting to MPEG may result in a very large file, depending on the number of frames in your movie. If this is a concern, choose AVI rather than MPEG.

If you have a large number of frames in your movie then exporting to AVI may result in a very large file. If this is a concern, choose MPEG rather than AVI.

## SPIP Plug-in Interface for Programmers

The intention of the SPIP Plug-in interface is to provide an easy way for users to exchange data with the SPIP program. There are mainly three types of operations you can perform with the interface.

Retrieve Images or curves from SPIP windows and apply your own specialized analysis software.

Manipulate data by your own algorithms and view the result in the SPIP windows.

Create your own data and use SPIP's analytical and visualization tools. The data can come from your own control and data acquisition software integrated with SPIP, your own file reader or artificially created data.

This way you get all the advantages of all the SPIP processing features including file handling and visualization while you can concentrate on your own specialized data processing and data creation.

You can get easy access to your functions by defining associated buttons that will appear in the SPIP Menu. Your plug-ins can include data processing functions as well as dialogs.

The following is a short *Getting Started Introduction*; the SPIP Plug-in Functions section of the reference guide contains more detailed information about the available interface functions.

### Compilers and Programming Environments

SPIP comes with a project generator that can create the following ready to build programming project types:

Microsoft Visual C++ 6.0SPIP\_Plug\_In\_Wizard\_for\_Microsoft\_Visual\_Studio\_C\_6\_0

Microsoft Visual Basic 6.0SPIP\_Plug\_In\_Wizard\_for\_Microsoft\_Visual\_Basic\_6\_0

Microsoft Visual C++ .Net

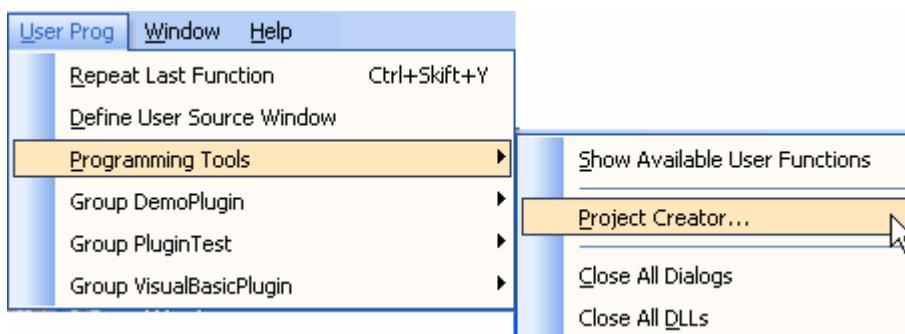
Borland C++ Builder 5 and 6

For other compilers you may use the code generated for one of the supported compilers. The interface is based on COM technology and every programming environment that can create plain DLLs, COM DLLs or ActiveX DLLs can be applied for creation of SPIP Plug-ins.

Below is described how to create and build the different types of projects.

### User Prog Menu and Programming Tools:

In addition to the user defined Plug-ins the User Prog menu contains a number of convenient functions.



Repeat Last Function will repeat the most recent Plug-in function that has been processed and its shortcut is **Ctrl+Shift+Y**.

The Define User Source Window function is useful when using user-defined dialogs. When a user dialog is created it will be connected to the active data window, - the User Source Window. Whenever the dialog retrieves data it will get it from the User Source Window.

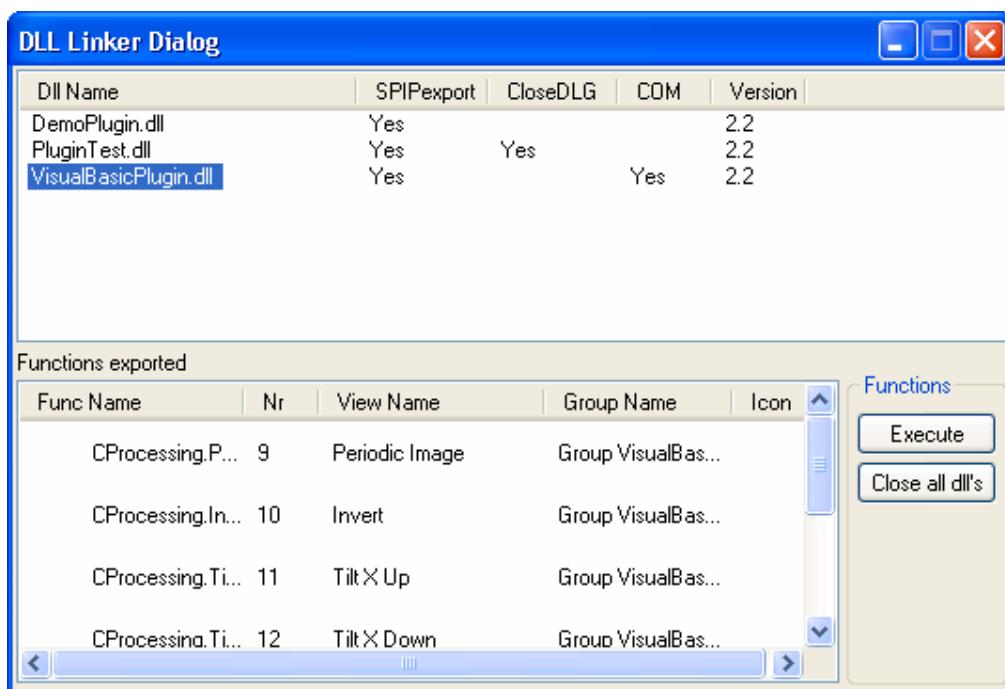
However, another data window can be defined as the User Source Window by clicking **Define User Source Window** or just **Ctrl+W**.

### Programming Tools

The User Prog menu comes with a predefined submenu called Programming Tools, where you find useful utilities that can be applied when creating and trouble shooting your own Plugins.

#### Show Available User Functions.

To get information on the available DLLs and Plug-in functions click on **Show Available User Functions**. The DLL Linker Dialog will then show a list of available DLL files. It will be indicated if the DLLs include the **SPIPExport** function necessary for creating the User Menu. Likewise, the presence of the **CloseDLG** function is indicated; For C++ projects SPIP needs to call this function when closing Plug-in dialogs. The Version number is associated the data exchange functions and used for checking the comparability with the current SPIP version. For each DLL you can get information about the available Plug-in functions, their source code name and number in the **User Prog** menu, Menu item name and the name of its menu group, and you have to possibility to process the functions from the dialog by clicking **Execute**.



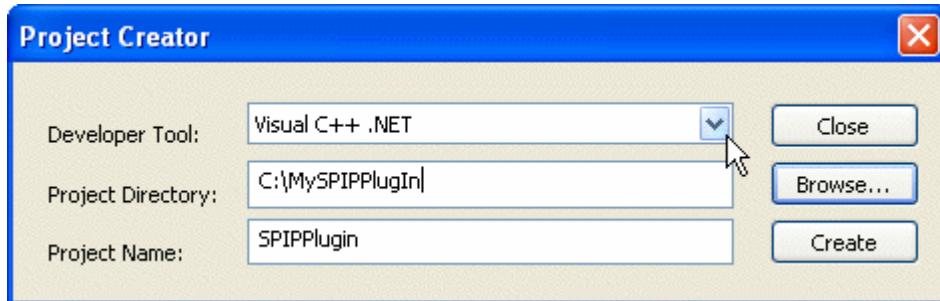
#### Close All Dialogs will close all user defined dialogs.

**Close All DLLs** will close all user defined dialogs and free the connections to the DLLs. This enables you to modify and test a Plug-in without having to restart SPIP.

The **Start MS Visual C++, MS Visual C++ .Net Creator, Start MS Visual Basic, and Start Borland C++Builder** menu items are provided for your convenience and will be active when the associated compilers are found present on the computer.

## SPIP Plug-in for Microsoft Visual Studio C++ 6

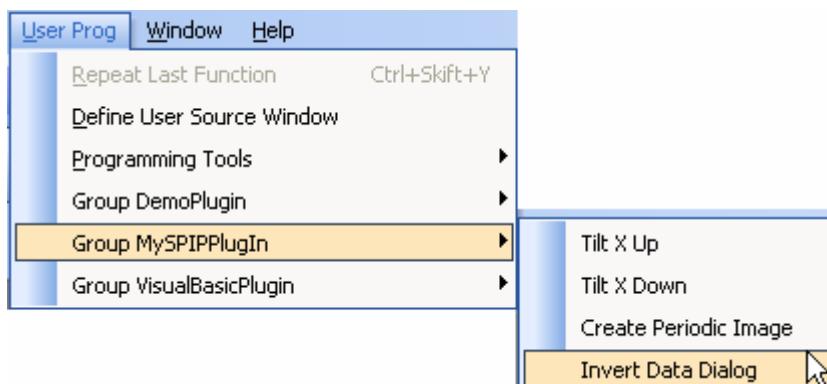
To create a Microsoft Visual Studio C++ 6 plug-in project click **User Prog→Programming Tools→Project Creator** and select **Visual C++ 6.0** as the Developer Tool:



To build the generated project open it .sln file in Visual studio The Project is now ready go be build: click **Build→Build MySPIPPlugIn.dll** (or other name given by you) and the resulting dll will put into the SPIP\UserDLL folder where it is automatically found by SPIP next time SPIP is started and the menu items defined in the project are automatically inserted in the **SPIP→User Prog** menu.

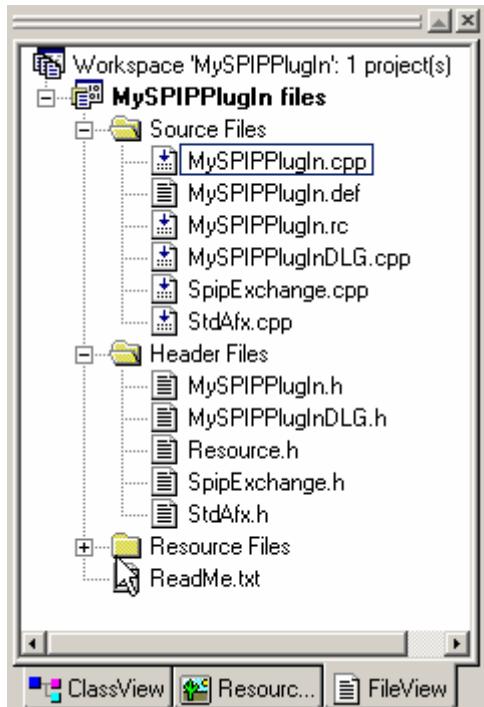
The predefined example functions are called Tilt X Up, Tilt X Down, Create Periodic Image and Invert Data Dialog. You can modify these functions and use them as inspiration for new Plug-in functions.

Restart SPIP and try to click on the Plug-in example Menu Items found in the **SPIP→User Prog** menu.



### Modifying the Code

The files generated by the wizard can be viewed in the FileView of the project. You need just to concentrate on the *MySipPlugIn.cpp* and the *MySipPlugInDlg.cpp* files; - the latter is not generated if you decided not to include a dialog in the project.



The only SPIP class you need to know is the `CSpipExchange` class, which contains methods for retrieving and sending data to and from SPIP Windows. Once a `CSpipExchange` object is defined a connection between the object and the SPIP program is created.

Below is seen the simple `TiltXUp()` example function, which retrieves the data from the active SPIP client window and add the x pixel index to the pixel values.

Finally the modified image is displayed in the SPIP source window.

```
extern "C" __declspec(dllexport) int TiltXUp()
{
    CSpipExchange b;

    if (!b.Get_ImageData())
        ::AfxMessageBox("No data in window", MB_OK, NULL);
    return 0;
}

int i = 0;
for (int y=0;y<b.SizeY;y++)
    for (int x=0;x<b.SizeX;x++, i++) {
        b.Data[i] += x;
    }
// Show the tilted image in the source window
IM_PWIN pShow=NULL;
b.Show_ImageData(&pShow, "TiltX", IMF_SOURCE);
return true;
}
```

You can modify this code to suit your needs or copy it to a new function with a different name.

To define the Plug-in functions that should appear as Menu Items in the SPIP program one call to **AddToSPIP** for each Plug-in function should be included in the **SPIPExport()** function:

```
void SpipExport()
{
    AddToSPIP("TiltXUp"      , "Tilt X Up",   "Group MySpipPlugh", 0 );
    AddToSPIP("TiltXDown"    , "Tilt X Down", "Group MySpipPlugh", 0 );
    AddToSPIP("PeriodicImage", "Create Periodic Image", "Group MySpipPlugIn", 0 );
    AddToSPIP("InvertDataDialog", "Invert Data Dialog", "Group MySpipPlugIn", 0 );
}
```

The first parameter in the **AddToSPIP** function should be identical to the name of the function (except for Borland compilers where you need to include an underscore in front of the name, e.g., `_TiltXUp`). The second parameter is the friendly name that will appear as the menu item text. The third parameter is the Group Name, which enables you to group the Plug-in functions to different submenus; when setting this parameter to NULL the menu item will appear at the outer level. The last parameter is reserved for future use of icons.

### **Modification of the dialog**

To design the dialog click the **ResourceView** tab in the Workspace and double click the first dialog. After for example a button you can go to its event handler by double clicking on it. Here you can enter the desired function of associated with the button. Refer to the MS Visual C++ documentation for more details on how to create new buttons and setting up event handlers.

### **Debugging the Code**

Debugging of the Plug-in code can be performed from the Visual C++ environment, just select **Build→Start Debug→Go** and enter the `spip.exe` program as the executable file.

To rebuild the project and restart a debug session you will need to unload your DLL by pressing User **Prog→Programming Tools→Close All DLLs** alternatively you will need to restart SPIP. After creating complete new menu items it is necessary to restart SPIP.

For further information about the available functions refer to SPIP Plug-in Functions For C++ in the reference guide.

### **Working with void pixels**

It is possible to define pixels as being Void Pixels by setting them to the maximum floating point value, `FLT_MAX`. This way you can have the pixels to show up as invisible see the following code, which will create a donut where only the donut ring itself is visible.

```
extern "C" __declspec(dllexport) int Donut()
{
    CSpipExchange b;
    if (!b.Create_ImageData(200,200))
        ::AfxMessageBox("No Image Data Created",MB_OK,NULL); return 0;
    int mx = b.SizeX/2;
    int my = b.SizeY/2;
    float Radius = mx/2.0f;
    float RadiusSqr = Radius*Radius;

    float OuterRadius = (float) mx;
    float OuterRadiusSqr = OuterRadius*OuterRadius;
    float VoidVal = FLT_MAX;

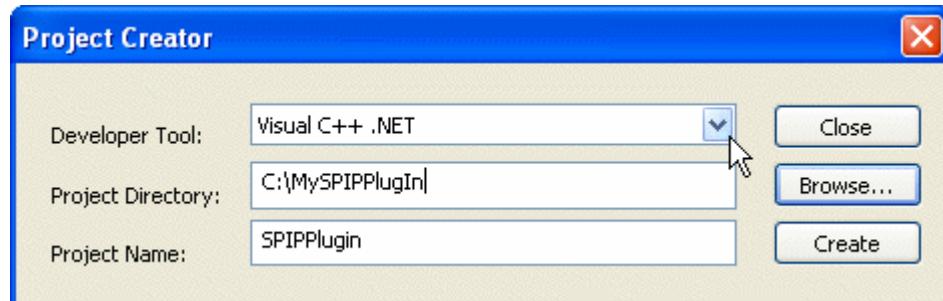
    float MeanRadius = (OuterRadius+Radius)/2;
    int i = 0;
    for ( int y=0;y<b.SizeY;y++) {
        for ( int x=0;x<b.SizeX;x++, i++) {
            float distsqr = (float) ((x-mx)*(x-mx) + (y-my)*(y-my));
            if (( distsqr > OuterRadiusSqr) || ( distsqr < RadiusSqr) )
                b.Data[i] = VoidVal; // Mark pixel as Void / Invisible
            else{
                float dist = (float) sqrt(distsqr);
                float z = dist - MeanRadius;
                b.Data[i] = (-z*z)/1000;
            }
        }
    }
    b.Put_YRange(1000.);
    b.Put_XRange(1000.);
    b.Put_Xunit("nm");
    b.Put_Yunit("nm");
    b.Put_Zunit("nm");
    b.Put_Orgfilename("Donut");
    // Show Image in new window
    IM_PWIN pShow=NULL;
    b.Show_ImageData(&pShow,"Donut", 0);
    // Show Image in 3D window
}
```

## The Scanning Probe Image Processor, SPIP™ V. 4.2

```
pShow=NULL;  
b.Show_ImageData(&pShow,"Donut", IMF_3D);  
return true;  
}
```

## SPIP Plug-in for Microsoft Visual C++ .Net

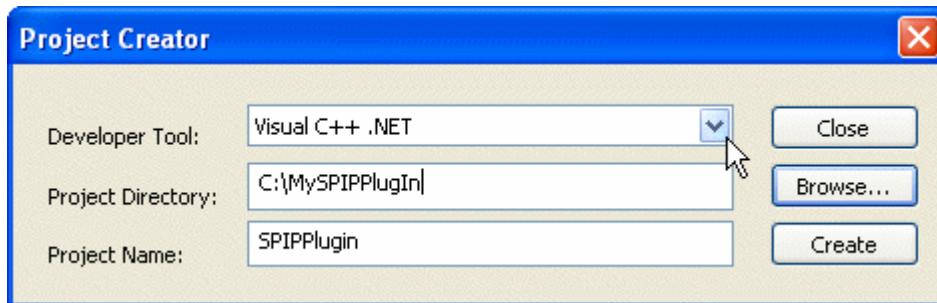
To create a Microsoft Visual C++ .Net plug-in project open click **User Prog→Programming Tools→Project Creator...** and select Visual C++ .Net as the Developer Tool:



The generated project contains code similar to the VC++ 6.0 code shown above and you can refer to that section on how to modify the code.

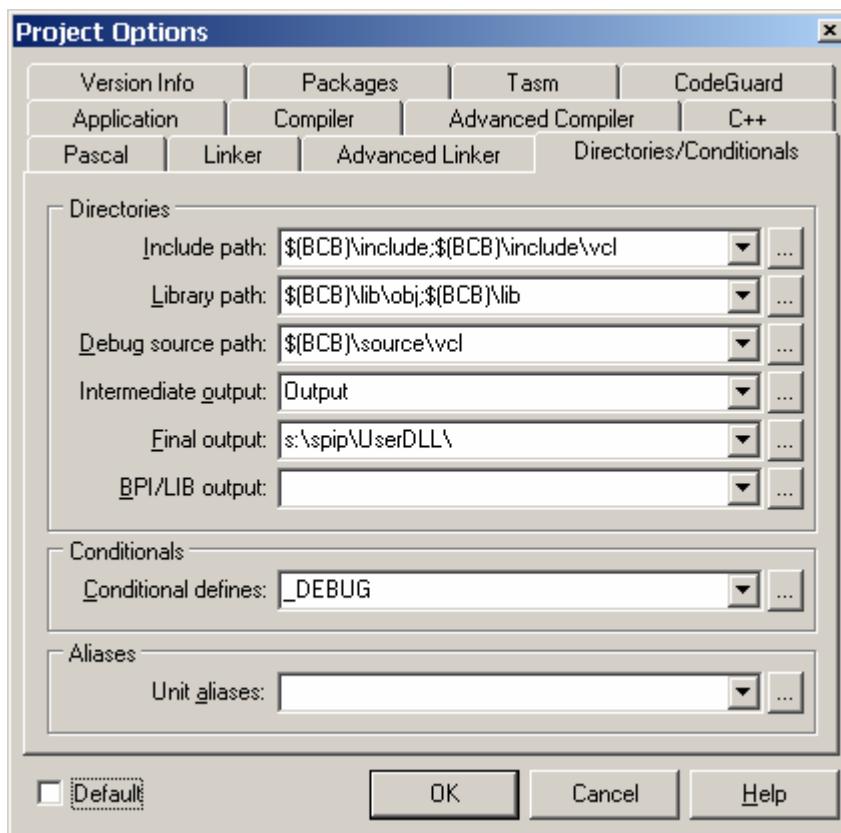
## SPIP Plug-in for Borland C++ Builder

To create a Borland C++ Builder project click **User Prog→Programming Tools→Project Creator...** as shown above and select C++ Builder as the Developer Tool:



The generated project contains code similar to the VC++ 6.0 code shown above and you can refer to that section on how to modify the code.

The SPIP package has been tested for Borland C++Builder version 5 and 6.  
After creation of the project open the project BorlandPlugIn.bpr now found in your project folder.  
Click **Project→Options** and select the Directories/Conditionals tab and set the Final output to the SPIP\UserDLL folder.



Define also where you want the Intermediate output files and remember to create this folder if it does not already exist.

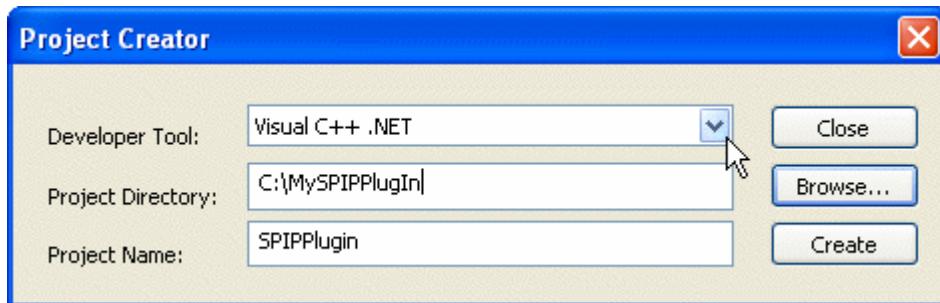
To build the project select **Project→Build BorlandPlugIn** or the associated shortcut key.

You should now have a BorlandPlugIn.dll file installed in the SPIP\UserDLL directory containing three Plug-in functions, which SPIP automatically will recognize next time you start SPIP.

To start and debug your dll from inside Borland Builder define first the Host Application; select **Run→Run Parameters** and enter the path for the spip.exe host program.

## SPIP Plug-in for Microsoft Visual Basic 6.0

To create a Microsoft Visual Studio Basic plug-in project click **User Prog→Programming Tools→Project Creator** and select **Visual Basic 6.0** as the Developer Tool:



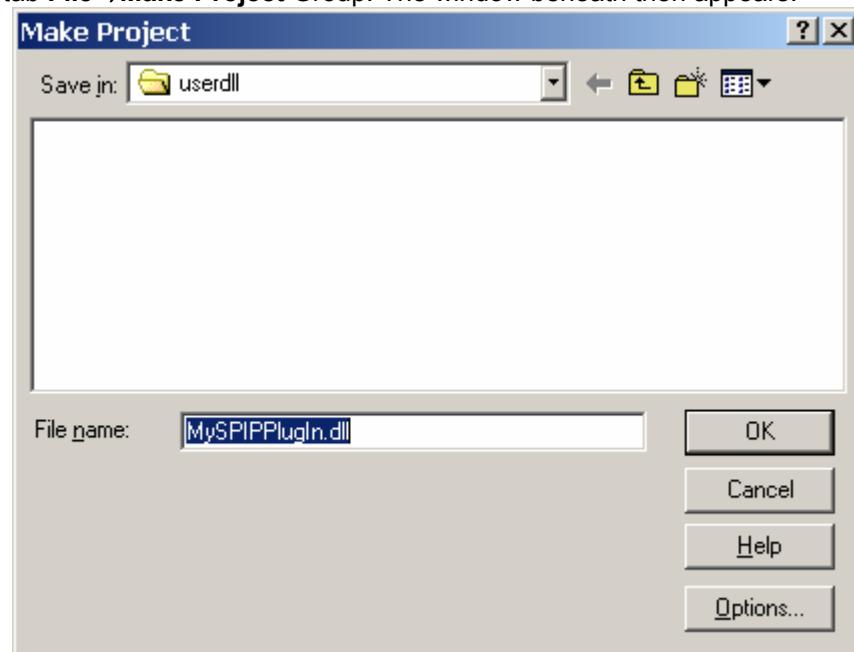
The following procedure requires that Microsoft Visual Basic 6.0 is installed on your computer. If so, the SPIP Visual Basic Plug-in Wizard will automatically be installed the first time you click on the "**User Prog**" in the SPIP menu bar.

To create and run a project, do the following

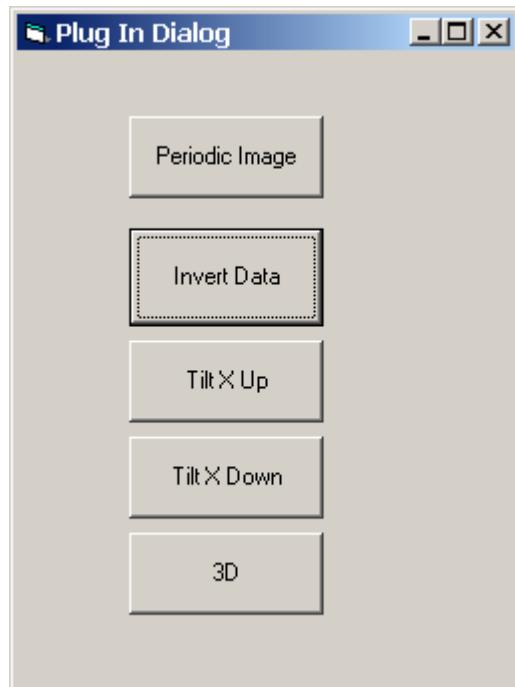
Define the project folder and name and click Create

Open the Generated project in Visual Studio. If the Project Explore window is not open, you may open it by the menu item **View→Project Explorer**.

To build the DLL, which will be recognized by SPIP next time SPIP is started, choose the menu tab **File→Make Project**. The window beneath then appears.



Simply click **Build**, and the DLL will be created and placed in the SPIP UserDLL directory. Now, you only need to restart SPIP and click the **User Prog** menu. The first time SPIP finds a new DLL you will shortly see a status bar indicating that SPIP is retrieving information from the new DLL. After the update you can choose among the new menu-items under User Prog. Try to click on **User Prog→Group MySIPPlugin→Start Dialog** or the corresponding if you have given the project a different name:

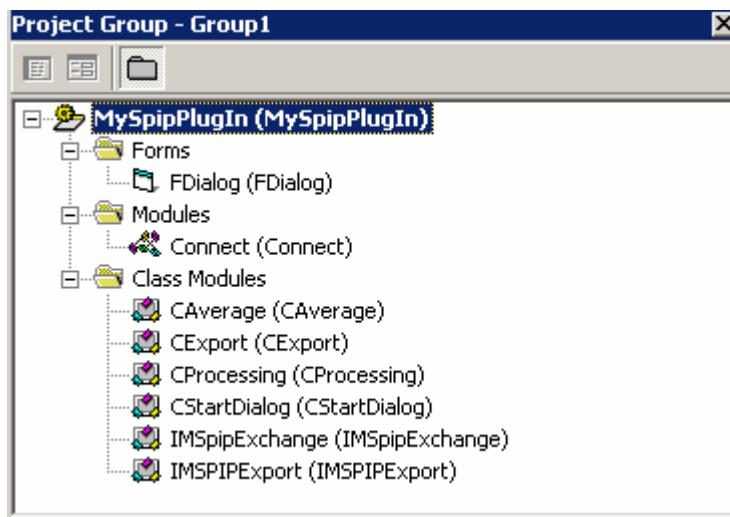


Note that some of the functions require an open image as input to perform meaningful. Try for instance the periodic image button first. Then you have an image to work on.

### Modifying the Code.

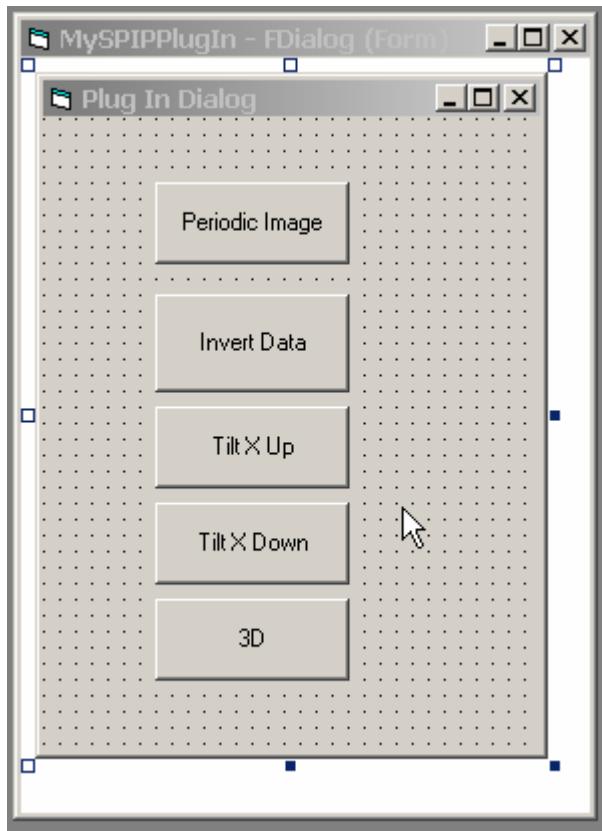
The files generated by the wizard can be viewed in the Project Group window, if not active press **View→Project Explorer**.

You need only to concentrate on the CProcessing, CExport and FDialog files, - and the latter is only generated if you decided to include a dialog in the project. You may also view the CAverage class to learn how averaging of multiple images or curves can be performed.

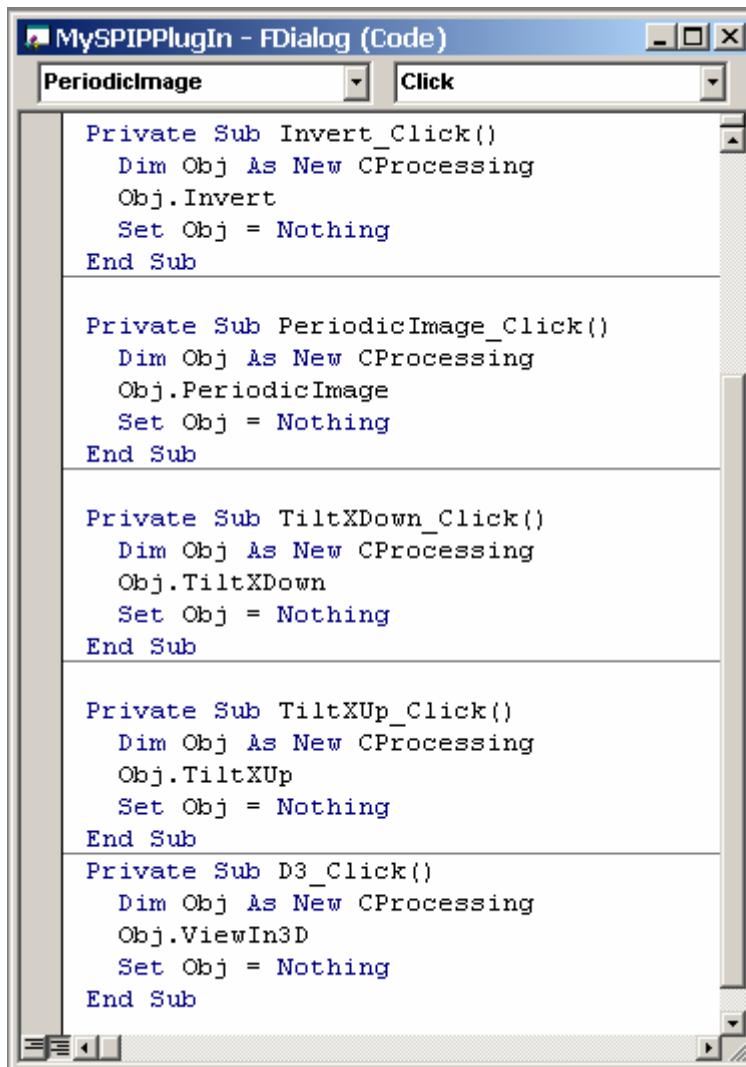


### Modifying the Dialog

To enter new buttons in the dialog double click on **FDialog**, and use the Form editor to design the dialog:



The event handlers of the individual buttons can be viewed and modified after double clicking the buttons:



The screenshot shows a Microsoft Visual Studio code editor window titled "MySPIPPlugIn - FDialog (Code)". The window has two tabs at the top: "PeriodicImage" and "Click". The "Click" tab is selected, displaying the following VBA code:

```
Private Sub Invert_Click()
    Dim Obj As New CProcessing
    Obj.Invert
    Set Obj = Nothing
End Sub

Private Sub PeriodicImage_Click()
    Dim Obj As New CProcessing
    Obj.PeriodicImage
    Set Obj = Nothing
End Sub

Private Sub TiltXDown_Click()
    Dim Obj As New CProcessing
    Obj.TiltXDown
    Set Obj = Nothing
End Sub

Private Sub TiltXUp_Click()
    Dim Obj As New CProcessing
    Obj.TiltXUp
    Set Obj = Nothing
End Sub

Private Sub D3_Click()
    Dim Obj As New CProcessing
    Obj.ViewIn3D
    Set Obj = Nothing
End Sub
```

You will see that the code in Fdialog module is very short because it makes use of the functions defined in CProcessing, which includes all the data processing, see for example the code for inverting an image:

```

Public Function Invert()
    Dim SPIPObj As New IMSpipExchange
    Dim i As Long

    SPIPObj.GetDataFromSPIP
    If Not ValidateData(SPIPObj) Then
        Exit Function
    End If

    For i = 0 To SPIPObj.SizeTypeTotal - 1
        Call SPIPObj.SetData(i, -SPIPObj.GetData(i))
    Next

    SPIPObj.Filename = SPIPObj.Orgfilename & ".inv"
    SPIPObj.ShowData SrcWindow, "Invert Same", SPIPObj.ShowInSourceWindow
    'SPIPObj.ShowData NewWindow, "Invert New", SPIPObj.ShowInNewWindow
    'SPIPObj.ShowData D3Window, "Invert 3D", SPIPObj.ShowIn3DWindow

    Set SPIPObj = Nothing
End Function

```

---

This code retrieves an image (or curve) from SPIP, changes the sign of all points, modifies the file name and shows the result in the source window. As indicated in the passive code the image could also have been shown in independent SPIP windows for example in the 3D window.

### Creating new functions

When creating your own functions it can be an advantage to use the above code as a template, simply use copy & paste modify the code to suit the task and change the function name.

### Adding new menu items

To give SPIP knowledge and access to your functions they need to be published in the SPIPExport module by a function called SpipExport (do not change this name):

```

Public Function SpipExport(ByRef pVar As Variant)
' *****
' D E F I N E   M E N U   I T E M S   H E R E   !!
' *****

'Define the menu items to appear in the User Proc menu below
'PROTOTYPE FUNCTION
'Call AddToSpip(pVar, "FunctionClass.FunctionName", "Viewable Name", "Group Name",ICON)
Dim IM As New IMSPIPExport
Call IM.AddToSpip(pVar, "CStartDialog.ShowDialog", "Start Dialog", "Group Start", 0)
Call IM.AddToSpip(pVar, "CProcessing.PeriodicImage", "Periodic Image", "Group Start", 0)
Call IM.AddToSpip(pVar, "CProcessing.Invert", "Invert", "Group Start", 0)
Call IM.AddToSpip(pVar, "CProcessing.TiltXUp", "Tilt X Up", "Group Start", 0)
Call IM.AddToSpip(pVar, "CProcessing.TiltXDown", "Tilt X Down", "Group Start", 0)
Call IM.AddToSpip(pVar, "CProcessing.ViewIn3D", "View In 3D", "Group Start", 0)
Call IM.AddToSpip(pVar, "CAverage.Average", "C Average", "Group Start", 0)
Set IM = Nothing
End Function

```

There is one **AddToSpip** call for each function that will appear in the **User Prog** menu. The second parameter is the exact name of the function, the third parameter defines the name of the function as it will appear in the menu and the last parameter specifies the name of the menu group in which this item will be put. Just by using other names other menu groups will be created.

For further information about the available functions refer to SPIP Plug-in Functions For Visual Basic in the reference guide





## Reference Guide

## Fourier analysis

The Fourier transform is a powerful tool for image analysis. This is true in particular for analysis of repeated patterns such as pitch standards and molecular or atomic structures. Fourier images reflect repeated patterns as narrow peaks, the co-ordinates of which describe their periodicity and direction. Such peaks are easy to detect by image processing without any pre-knowledge of the features form or periodicity. Furthermore, the repeat distances can be measured very accurately by determining the Fourier peak co-ordinates at sub-pixel level.

The discrete Fourier transform is calculated by the formula:

$$F(u, v) = \frac{1}{N_x N_y} \sum_{x=0}^{N_x-1} \sum_{y=0}^{N_y-1} z(x, y) e^{-i2\pi(ux/N_x + vy/N_y)}, \quad (1)$$

Where  $N_x, N_y$  are the number of pixels in the  $x, y$  directions and  $u, v$  the discrete Fourier indexes  $= 0, 1, 2, \dots, N_x-1$  and  $v = 0, 1, 2, \dots, N_y-1$ . The Fourier transform can also be regarded as a sum of sinusoidal functions, each described by a frequency, amplitude and a phase. The inverse transform, which, for example, may be applied after filtration where, for example, unwanted Fourier components are set to zero, has a similar form:

$$f(x, y) = \sum_{u=0}^{N_x-1} \sum_{v=0}^{N_y-1} F(u, v) e^{i2\pi(ux/N_x + vy/N_y)}, \quad (2)$$

The number of computational operations can be reduced dramatically by Fast Fourier Transform (FFT) algorithms that break the calculation down to a sequence of smaller Fourier transforms. The highest efficiency is obtained when the side lengths  $N_x$  and  $N_y$  are powers of 2. Thus, typical images are  $256 \times 256$  or  $512 \times 512$  pixels. The chosen size is a compromise between a high pixel density and the costs in form of extra acquisition time, storage demands and calculation time.

The Fourier transform can be visualized by its amplitude spectrum, which contains the absolute values of the complex Fourier components:

$$|F(u, v)| = \sqrt{R^2(u, v) + I^2(u, v)}, \quad (3)$$

Where  $R$  and  $I$  denotes the real and imaginary parts respectively.

The phase information is rarely used but preserved in case inverse transformations have to be applied after exclusion of some Fourier components. To enhance the contrast of weaker components a square root function or logarithmic function may be applied to the amplitude values. Likewise, more dominant components may appear with even higher contrast when the amplitude values are squared. Contrast changes by color manipulation may also be a valuable technique to reveal weak Fourier components.

## Detecting Line Profiles

Periodic surface features will exhibit peaks corresponding to the periodicity in the Fourier amplitude image. For a spatial image of  $k$  line profiles parallel to the y-axis we will in the Fourier image have a peak at  $(u,v) = (k,0)$ . For profiles not aligned parallel to one of the axes, but where  $k$  periods can be counted along the x-axis and  $l$  periods along the y-axis a Fourier peak can be found for  $(u,v) = (k,l)$ . The corresponding wavelength  $\lambda$  is easily calculated:

$$\lambda = \sqrt{\left(\frac{w_x}{l}\right)^2 + \left(\frac{w_y}{k}\right)^2}, \quad (4)$$

where  $w_x$  and  $w_y$  are the physical x, y ranges of the image.

When the number of periods differs from an exact integer the real Fourier peak is not part of the discrete components of equation (1) and therefore is not calculated. However, due to the *picket fence effect* the neighboring Fourier elements will exhibit higher values from which the real frequency can be estimated by inverse interpolation or by an iterative sub-pixel Fourier algorithm. The sub-pixel Fourier algorithm makes it possible to calculate Fourier components also for non-integer  $u,v$  co-ordinates just by entering those values directly into equation (1) and thereby get sub-pixel resolution. To obtain a good computation efficiency the  $u,v$  co-ordinates are only calculated within a pixel distance from the peaks found at pixel level. Within these areas, a steepest ascent algorithm can locate the peaks.

For regular patterns, which are not of sinusoidal form the structure can not be described by a single Fourier component only. The Fourier transform will then consist of a fundamental peak at  $(u_0,v_0)$  associated with the main periodicity and by higher harmonics, i.e. components for which the  $(u,v)$  co-ordinates are  $n$  times higher than the fundamental Fourier component:

$$(u_n, v_n) = n (u_0, v_0). \quad (5)$$

This can be an advantage because we can obtain from each harmonic an estimate of the fundamental component by dividing co-ordinates by the harmonic number:

$$(u'_0, v'_0) = (u_n, v_n) / n. \quad (6)$$

Thus, it is possible to obtain a statistical mean value for the fundamental Fourier component. The advantage of this use of the higher harmonics is also that the uncertainty of the  $(u,v)$  co-ordinates are divided by the harmonic number. However, higher Fourier harmonics are usually weaker and are therefore harder to estimate accurately. It is therefore impossible to predict from which harmonic components we get the most accurate estimate of the fundamental component, as it will depend on the measurement object as well as the measurement conditions. The accuracy may also be influenced by false detection, for example electrical noise might mistakenly be regarded as a harmonic component associated with the repeated surface structure. To make statistical estimation of the fundamental periodicity based on higher harmonics more robust it is an advantage to use the median value instead of the mean value.

# Detecting Unit Cells

## The oblique unit cell

The arrangement of repeated units of periodic patterns can be described by a Bravais lattice. The units may be individual atoms, molecules or, for example, artificially created calibration structures. The two dimensional Bravais lattice summarizes the geometry of the periodic structure, and consists of all points with position vectors  $\mathbf{S}$  of the form:

$$\mathbf{S}=k \mathbf{a} + l \mathbf{b}, \quad (7)$$

where  $\mathbf{a}$  and  $\mathbf{b}$  are any two dimensional vectors of different and  $k$ , and  $l$  range through all integer values. An area on the surface that, when translated through all the vectors in a Bravais lattice just fills all of the surface without either overlapping itself or leaving voids, is called a primitive unit cell of the lattice, and the  $\mathbf{a}$  and  $\mathbf{b}$  vectors are then called primitive vectors. There is no unique way of choosing a primitive unit cell for a Bravais lattice and they can have different forms: square, hexagonal (rhombus), rectangular or oblique.

The oblique unit cell is general and we will use this in the following. Note also that even though the calibration structure is quadratic the distortions are most likely to create images with oblique unit cells. By Fourier transform of a Bravais lattice a reciprocal lattice  $\mathbf{K}$  is created with Fourier peaks that can be described by the reciprocal unit cell vectors  $\mathbf{A}$  and  $\mathbf{B}$ :

$$\mathbf{K}=k \mathbf{A} + l \mathbf{B}, \quad (8)$$

where  $k$ , and  $l$  range through all integer values. The important property of the Fourier transform is that the reciprocal unit cell vectors can be found directly from the positions of the peaks. Having found the  $\mathbf{A}$  and  $\mathbf{B}$  reciprocal unit cell vectors the spatial unit cell vectors  $\mathbf{a}$  and  $\mathbf{b}$  can be found as

$$\mathbf{a} = \frac{\bar{\mathbf{B}}}{\bar{\mathbf{A}} \cdot \bar{\mathbf{B}}}; \quad \mathbf{b} = \frac{-\bar{\mathbf{A}}}{\bar{\mathbf{A}} \cdot \bar{\mathbf{B}}} \quad (9)$$

## Lateral Calibration by Quadratic Unit Cells

To describe the correspondence between the observed surface lattice and the real physical lattice, we use the transformation matrix. Here we will ignore non-linearity and the influence from the z-axis. We arrange the co-ordinate system of the uncorrected and the correct co-ordinate systems so that their x-axes are parallel.

$$\begin{pmatrix} x \\ y \end{pmatrix} = \begin{pmatrix} C_x & C_{xy} \\ 0 & C_y \end{pmatrix} \begin{pmatrix} x' \\ y' \end{pmatrix}, \quad (10)$$

Where  $C_x$ ,  $C_y$  and  $C_{xy}$  are the unknown correction parameters to be estimated. If the scanned x- and y-axes are perpendicular, then  $C_{xy}$  equals zero and  $C_x, C_y$  are the scale factors for the x- and the y-directions respectively, i.e.,  
 $x = C_x x'$  and  $y = C_y y'$ .

$C_{xy}$  describes the coupling between the x and y axes, i.e. how much the scanner moves in the x-direction when stepping in the y-direction. The angle  $\gamma$  between the scanned x-axis and the scanned y-axis is given by

$$\gamma = \cot^{-1}(C_{xy}/C_y) \text{ and the angular distortion } \gamma_e = 90^\circ - \gamma.$$

When using a calibration standard with square unit cells described by a repeat distance,  $L$ , then based on the observed unit cell vectors

$$\mathbf{a}' = \begin{pmatrix} a_x \\ a_y \end{pmatrix}, \mathbf{b}' = \begin{pmatrix} b_x \\ b_y \end{pmatrix}$$

and the reference value  $l$  we can find an analytical solution for the three unknown correction parameters:

$$C_x = \frac{L\sqrt{a_y^2 + b_y^2}}{a_x b_y - a_y b_x}, \quad C_y = \frac{L}{\sqrt{a_y^2 + b_y^2}}, \quad C_{xy} = \frac{(b_y b_x + a_x a_y)L}{(a_x b_y - a_y b_x)\sqrt{a_y^2 + b_y^2}} \quad (11)$$

Off-line correction of images can be performed by re-sampling at equidistant ( $x', y'$ ) positions.

$$x'(x, y) = \frac{C_y x - C_{xy} y}{C_x C_y}, \quad y'(x, y) = y / C_y \quad (12)$$

## Lateral Calibration by Hexagonal Unit Cells

Calibration by hexagonal lattices can be done very similarly to the calibration by square lattices. However, the equations to calculate the linear correction parameters are different:

$$\begin{aligned} C_x &= \frac{L\sqrt{a_y^2 + b_y^2 - a_y b_y}}{a_x b_y - a_y b_x}, \\ C_y &= \frac{\sqrt{3}L}{2\sqrt{a_y^2 + b_y^2 - a_y b_y}}, \\ C_{xy} &= \frac{(2a_x a_y + 2b_x b_y - a_y b_x - a_x b_y)L}{2(a_x b_y - a_y b_x)\sqrt{a_y^2 + b_y^2 - a_y b_y}} \end{aligned} \quad (13)$$

It is not possible to calibrate the  $C_x$ ,  $C_y$  and  $C_{xy}$  parameters by a single image of line structures. Only by careful alignment of the structure along the X or Y-axis, it is possible to deduce the  $C_x$  or the  $C_y$  parameters. However, by acquiring three images of a line structure rotated at three different angles is possible to setup an equation system from which the three correction parameters can be deduced:

In a Fourier transformation of an image with a line pattern, a wave vector  $\mathbf{K}$  with a high intensity will be observed. It can be shown that the wave vector  $\mathbf{K}=(u, v)^T$  of the corrected image is related to the wave vector  $\mathbf{K}'=(u', v')^T$  of the uncorrected image through the transformation  $\mathbf{K}=(\mathbf{C}^{-1})^T \mathbf{K}'$ , or

$$\begin{pmatrix} u \\ v \end{pmatrix} = \frac{1}{C_x C_y} \begin{pmatrix} C_y & 0 \\ -C_{xy} & C_x \end{pmatrix} \begin{pmatrix} u' \\ v' \end{pmatrix} \quad (14)$$

Furthermore the reciprocal length  $|\mathbf{K}|^{-1}$  of the wave vector  $\mathbf{K}=(u, v)^T$  is equal to the known periodicity  $1/\lambda$  of the. That is:

$$|\mathbf{K}|^2 = (u w_x)^2 + (v w_y)^2 = 1/\lambda^2 \quad (15)$$

By combining the equations a restraint between  $C_x$ ,  $C_y$  and  $C_{xy}$  and the known period  $r$  is obtained. Thus, for three images with different orientation of the lines, an analytical solution for  $C_x$ ,  $C_y$  and  $C_{xy}$  is found. For more than three images the restraint forms an over-determined system of equations in the unknowns  $C_x$ ,  $C_y$ , and  $C_{xy}$ . A least squares sum solution of this equation system can then be found.

## Lateral Linearity Analysis

This advanced process can be started directly by pushing the associated key: 

From the detected lattice structure, we can predict the position of repeated features by knowing the position of a single feature belonging to the lattice.  
We therefore select a single feature (template) representative of the lattice and by cross correlation we find the position of the other matching features.  
If the zoom image is active it will define the template which has to be recognized otherwise SPIP automatically finds a suitable template based on a detected unit cell.

The positions are identical to the peaks in the cross correlation function, which we estimate at sub-pixel level by parabolic fits. These positions are compared with the predictions based on the unit cell vectors and we calculate a prediction error vector  $\mathbf{e}_{k,l}$ :

$$\mathbf{e}_{k,l} = \mathbf{p}'_{k,l} - (\mathbf{p}'_{0,0} + k\mathbf{a}' + l\mathbf{b}'), \quad (16)$$

where  $\mathbf{p}'_{0,0}$  is the vector pointing to the highest peak in the cross correlation function and  $\mathbf{p}'_{k,l}$  the pointing vectors to the peaks in the cross correlation function that comes closest to  $(\mathbf{p}'_{0,0} + k\mathbf{a}' + l\mathbf{b}')$ .

The integers  $k, l$  are found so that  $\mathbf{e}_{k,l}$  is minimized.

The prediction error,  $\mathbf{e}_{k,l}$ , typically reflects non-equidistant sampling during scanning. However, imperfections of the sample or environmental conditions might also be reflected in the result.

Keeping  $k, l$  fixed it is possible to adjust the unit cell vectors  $\mathbf{a}', \mathbf{b}'$  by minimizing the mean position error:

$$E_u = \frac{1}{M} \sum_{k,l} |\mathbf{e}_{k,l}|, \quad (17)$$

where  $M$  is the number of peak vectors in the cross correlation image. We can thereby find an alternative calculation of the unit cell that can be compared with the one calculated from the Fourier domain.  $E_u$  also serves as a measure of the non-linearity; the smaller it is the better.

We can visualize the prediction errors for the  $x, y$  co-ordinates of  $\mathbf{e}_{k,l}$  independently as function of their  $x, y$  co-ordinates peak position co-ordinates of  $\mathbf{p}'_{k,l}$ , see d,e, and it is possible to estimate polynomial fits to the data and obtain correction functions. From the curve describing the  $x$ -co-ordinate error,  $e_x(p'_x)$  we calculate the physical scanning co-ordinate:

$$p_x(p'_x) = p'_x - e_x(p'_x) \quad (18)$$

To resample the image at equidistantly separated points a model that describes the observed co-ordinates as function of the physical co-ordinates can be applied. The observed  $p'_x$  co-ordinates can be modeled by a function of the physical positions  $p_x$  by a least mean square polynomial fit

$$\bar{p}'_x(x) = \sum_{n=0}^N a_n x^n, \quad (19)$$

where  $N$  is the polynomial degree and the  $a_n$  coefficients found by minimizing the error function  $E_x$ :

$$E_x = \sum_{n=0}^N (p'_x - \sum_{n=0}^N a_n p_x^n)^2. \quad (20)$$

Here the summation goes over all detected peaks in the cross correlation function.

## Calibration by Line Structures

It is not possible to calibrate the  $C_x$ ,  $C_y$  and  $C_{xy}$  parameters by a single image of line structures. Only by careful alignment of the structure along the X or Y-axis, it is possible to deduce the  $C_x$  or the  $C_y$  parameters. However, by acquiring three images of a line structure rotated at three different angles is possible to setup an equation system from which the three correction parameters can be deduced:

In a Fourier transformation of an image with a line pattern, a wave vector  $\mathbf{K}$  with a high intensity will be observed. It can be shown that the wave vector  $\mathbf{K}=(u, v)^T$  of the corrected image is related to the wave vector  $\mathbf{K}'=(u', v')^T$  of the uncorrected image through the transformation  $\mathbf{K}=(\mathbf{C}^{-1})^T \mathbf{K}'$ , or

$$\begin{pmatrix} u \\ v \end{pmatrix} = \frac{1}{C_x C_y} \begin{pmatrix} C_y & 0 \\ -C_{xy} & C_x \end{pmatrix} \begin{pmatrix} u' \\ v' \end{pmatrix} \quad (14)$$

Furthermore the reciprocal length  $|\mathbf{K}|^{-1}$  of the wave vector  $\mathbf{K}=(u, v)^T$  is equal to the known periodicity  $1/\lambda$  of the. That is:

$$|\mathbf{K}|^2 = (u w_x)^2 + (v w_y)^2 = 1 / \lambda^2 \quad (15)$$

By combining the equations a restraint between  $C_x$ ,  $C_y$  and  $C_{xy}$  and the known period  $r$  is obtained. Thus, for three images with different orientation of the lines, an analytical solution for  $C_x$ ,  $C_y$  and  $C_{xy}$  is found.

# Output Files

## Output File Formats

SPIP currently supports the following file output formats in which images and curve data can be saved:

*.asc	ASCII file format for import in other programs; preserves physical dimension; applies to 2D image and curves including histogram
*.bcr	The BCR-STM file format , binary 16 bit integers; preserves physical dimension data; applies to 2D image and curves including histogram.
*.bcrf	The BCR-STM file format , binary 32 bit floating points; preserves physical dimension data; applies to 2D image and curves including histogram.
*.bmp	Bitmap, for import in most DT programs; applies to all data windows.
*.jpeg	JPEG for import in most DT programs; applies to all data windows.
*.tiff	Tiff, for import in most DT programs; applies to all data windows.

To save your images in other graphics file formats you can always Copy and Paste the windows content into third party programs.

## Result files

When you are analyzing images the results can automatically be written into ASCII files. These files are useful for keeping track of the calibration history and for statistical analysis.

*.cal	Contains lateral unit cell and calibration results
*.cross	Cross correlation peak positions
*.grn	Results from grain analysis
*.lin	Lateral calibration result for 1D objects
*.linc	Linearity correction parameters
*.rgh	Roughness parameters
*.slope	Calculated slope correction parameters
*.tip	Tip characterization results
*.zcal	Vertical calibration results

You may import the files into a spreadsheet program and create your own presentations of the results. Typically the fields are tab separated and ‘.’ is used as the decimal character (Most European countries use ‘,’ as decimal character). Therefore, depending on your nationality settings you might need to replace ‘.’ in numbers with commas.

## Parameter Files

There are a number of files used for preference and correction parameters. These files are written by **Save** functions and retrieved by **Recall** functions. The default folder for these files is the -SPIP/Settings folder, which is also the location where SPIP looks for Default files.

*.3Anim	3D Animations parameters
*.animation	
*.3Dp / *.3D	Parameters defining the 3D scene (Default in Default.3Dp)
*.batch	Batch processing sequence. (Default in Default.batch)
*.col	Color parameters defining the color bar (Default in Defalt.col)
*.cp	Contains correction parameters for all dimensions.
*.crp	Calibration reference parameters (Default in Default.crp)
*.cus	Customized menus and toolbars configuration
*.flt	Filter parameters (Default in Kernels/Default.flt)
*.grs	<a href="#">Grain Analysis settings file. (Default in Default.grs)</a>
*.views	<a href="#">View Settings parameters</a>
*.pln	<a href="#">Plane Correction settings parameters</a>

## BCR-STM File Format

The BCR-STM file format has been developed by the partners, within the project ``Scanning Tunneling Microscopy (STM) methods for roughness and micro hardness measurements Contract No 3423/1/0/184/4/91-BCR-DK(30)'' for easy exchange of SPM files independent of the instruments used

The header is 2048 bytes long and written in ASCII characters, which can be edited by a text editor. The first line identifies the format and should be:

**fileformat** = bcrstm or

**fileformat** = bcrf

The "bcrstm" format identifies the data following the header to be in 16 bit integer format while the "bcrf" format identifies the data as being in 32 bit floating point.

**xpixels** and **ypixels** defines the number of pixels in the image.

**xlength** and **ylength** defines the scanning range in the given unit.

**xunit**, **yunit** and **zunit** units for the three axes. If not defined nm will be the default unit.

**current** defines the tunneling current in nA (optional)

**bias** defines the bias voltage in V (optional).

**starttime** defines the starting time of the scanning (DD MM YY hh:mm:ss:hh) (optional).

**scanspeed** is measured in nm/sec (optional).

**intelmode** = 1 indicates that the data is written in 16-bit integers used by Intel processors in PCs.

**intelmode** = 0 indicates that the data is written in 16-bit integers for, for example, UNIX workstations.

**bit2nm** is the scale factor for scaling the integer height data to nm.

**xoffset** and **yoffset** defines physical offset in nm (optional).

**voidpixels** defines the number of void pixels, if the field is not present the number is set to zero. For the 16 bit integer bcrstm format void pixels should be set equal to 32767. For the 32 bit floating point bcrf format void pixels are set to 1.7014118219281863150e+38.

**Comments** can be written by starting the line with '%' or '#'

It is possible to integrate new parameters as long the header size does not exceed 2048 bytes. SPIP do currently only recognizes the above parameters and will ignore other parameters.

If you want to extend the number of parameters and want the SPIP program to make use of them please contact support@imagemet.com.

```
Fileformat = bcrstm
xpixels = 256
ypixels = 256
xlength = 88000.0
ylength = 88000.0
xunit = nm
yunit = nm
zunit = nm
current = 10.0
bias= 0.1
starttime = 10 18 93 16:15:55:99
scanspeed = 10.1
intelmode = 1
bit2nm = 0.0592512
xoffset = 0.0
yoffset = 0.0
voidpixels = 0

# This is a comment
# the size of the header is 2048 bytes
# the size of the data is xpixels * ypixels * 2 bytes
```

```
# the size of the file is 2048 + xpixels * ypixels * 2 bytes  
% this is also a comment
```

Example of a BCR file header, 2048 bytes are reserved for the header, *xpixels* x *ypixels* 16 bit integer data follows just after the 2048 first bytes.

## SPIP Plug-in Functions

### SPIP Plug-in Functions for C++

#### Required Interface Functions:

There are two interface functions needed to establish a connection between the SPIP program and a Plug-in function **SpipExport** and **AddToSPIP**, and for cleaning up plug-ins containing dialogs an **ImCloseAllDialogs** should also exist.

```
void SpipExport()
```

To inform the SPIP program about the available Plug-in functions a **SpipExport()** function need to be defined. This function should perform one **AddToSPIP** call for each Plug-in interface function that shall appear in the SPIP User Prog menu.

```
void AddToSPIP(char* FunctionName, char* VisibleName, char* GroupName, int ICON);
```

The **AddToSPIP** function defines the individual Plug-ins that can be called from the SPIP menu.

The first parameter should be identical to the name of the function to be associated with a menu item (except for Borland compilers where you need to include an underscore in front of the name, e.g., `_TiltXUp`).

The second parameter is the friendly name that will appear as the menu item text.

The third parameter is the Group Name, which enables you to group the Plug-in functions to different submenus.

The last parameter is reserved for future application of icons.

The user functions which **AddToSPIP** refers to should be declared with an

```
extern "C" __declspec(dllexport)
```

 compiler directive to make them available for the SPIP program.

for example: `extern "C" __declspec(dllexport) int TiltXUp()`

The return parameter should be true for success and false for failure.

```
extern "C" __declspec(dllexport) int ImCloseAllDialogs()
```

The **ImCloseAllDialogs** is only required for Plug-ins containing Plug-ins and should contain the necessary code for cleaning up and destroying dialogs.

#### The CSpipExchange Class:

Exchange of data between the SPIP program and the Plug-in functions are performed through the **CSpipExchange** class with the methods and variables described below:

#### CSpipExchange Class Primary Methods:

```
CSpipExchange::CSpipExchange()
```

The constructor that will establish a connection to the SPIP program.

```
float* Get_ImageData();
```

Retrieve Data from the active SPIP client window (1D or 2D) into a floating-point array. If no active window exists a NULL pointer is returned.

```
float* Create_ImageData(int sizeX, int sizeY);
```

Use this function to create your own data independent on existing SPIP windows. A floating-point array of `sizeX × sizeY` elements will be returned if successful otherwise a NULL pointer is returned.

```
void Show_ImageData(IM_PWIN* Window, char* pVal, int iFlag);
```

Shows the data in the SPIP client window defined by the Window parameter. If Window is set to NULL a new SPIP window is created and the Window parameter is set to refer to the new window so next time Show\_ImageData is called with the same Window parameter the data is shown in that same window.

iFlag can be set to `IMF_3D` indicating that the data should be shown in a 3D view or `IMF_SOURCE` to show the image in the SPIP source window. These flags will overwrite the function of the Window parameter.

### CSpipExchange Class Primary Data Elements:

`float *Data;`

Floating point pointer to the image or curve data array of the object.

`int SizeX; int SizeY;`

The number of x pixels and y pixels in the Data array.

`int SizeTotal;`

The total number of elements in the Data array, equals SizeX x SizeY.

`IM_PWIN *pWin;`

The SPIP window defined when the data was shown using the Show\_ImageData() method.

### CSpipExchange Class Get Methods:

<code>char* Get_Filename();</code>	Get the current filename
<code>char* Get_Orgfilename();</code>	Get Original filename
<code>float Get_CantileverSensitivity();</code>	Get the Cantilever sensitivity
<code>char* Get_Desc();</code>	Get the Description
<code>char Get_FrameDir();</code>	Get the Direction of the image scan (Upwards or Downwards ~ 'u' or 'd')
<code>char Get_LineDir();</code>	Get the Direction of the line scans (left right ~ 'l' or 'r')
<code>float Get_Max( );</code>	Get the Maximum from the value of the Data array
<code>float Get_Min( );</code>	Get the Minimum from the value of the Data array
<code>float Get_RetraceTime();</code>	Get the Retrace time = time between the end of a line scan and the beginning of the next
<code>float Get_RotationAngle();</code>	Get angle of rotation while scanning the image
<code>float Get_SpringConstant();</code>	Get the Spring Constant of the Cantilever
<code>float Get_TimePerImage();</code>	Get time used for scanning the Image
<code>float Get_TraceTime();</code>	Get Trace time = time for scanning one line
<code>int Get_WordSize();</code>	Get Word size of the Data Array = 4
<code>float Get_XOffset();</code>	Get the X offset for of the physical coordinates used when scanning the image
<code>float Get_XRange();</code>	Get the X Range in the current Xunit
<code>char* Get_Xunit();</code>	Get the X axis unit
<code>float Get_XYRatio();</code>	Get the XY ratio = SizeX/SizeY
<code>float Get_YOffset();</code>	Get the Y offset for of the physical coordinates used when scanning the image
<code>char* Get_Yunit();</code>	Get the X axis unit
<code>float Get_YRange();</code>	Get the X Range in the current Yunit
<code>float Get_ZScale();</code>	Get the scaling Z scaling factor to convert to nanometers, normally 1.0
<code>char* Get_Zunit();</code>	Get the Z axis unit

**CSpipExchange Class Put Methods:**

void Put_CantileverSensitivity( float newVal)	Put the Cantilever sensitivity
void Put_Desc(char* cBuf);	Put the description to the object
void Put_Filename(char* cBuf);	Put filename
void Put_FrameDir( char newVal);	Put the Direction of the image scan (Upwards or Downwards ~ 'u' or 'd')
void Put_LineDir( char newVal);	Put the Direction of scanning a line (left right ~ 'l' or 'r')
void Put_Orgfilename(char* cBuf);	Put Original filename
void Put_RetraceTime( float newVal);	Put the Retrace time = time between the end of one line scan and the beginning of the next
void Put_RotationAngle( float newVal);	Put angle of rotation for used when scanning the image image
void Put_SpringConstant( float newVal);	Put the Spring Constant of the cantilever related
void Put_TimePerImage( float newVal);	Put the time used for scanning the Image
void Put_TraceTime( float newVal);	Put the Trace time = time for scanning one line
void Put_XOffset( float newVal);	Put X offset for the physical coordinates used when scanning
void Put_XRange( float newVal);	Put the X Range in defined in the actual XUnit
void Put_Xunit(char* cBuf);	Put the unit for the X axis
void Put_YOffset( float newVal);	Put the Y offset of the physical coordinates used when scanning
void Put_YRange( float newVal);	Put the Y Range in the actual Y Unit YUnit
void Put_Yunit(char* cBuf);	Put the unit for the Y axis
void Put_ZScale( float newVal);	Put a scaling factor for to be multiplied with the image. Should be 1.0
void Put_Zunit(char* cBuf);	Put the unit for the Z axis

**Working with void pixels**

Pixels can be defined as void by setting their value to the maximal floating point value, MAX\_FLT, and in this way be treated as invisible, see donut example in the reference guide.

**Activating a Batch Process**

A batch process can be activated for at plug-in generated or modified image by setting the file name to the name of the batch process file:

```
b.Put_Filename("Roughness.batch");
b.Put_Orgfilename("TheNameOfTheImage.bcr");
```

The name of the image will then be defined by the Put\_Orgfilename function.

If a batch process is active but you do not want a given image to be processed by the batch sequence you can put "norun" behind the filename as show below:

```
b.Put_Filename("MyFile.Bcr norun");
or
b.Put_Filename("norun");
```

**Forcing an image to be shown in the Main Image Window**

To force an image to be shown in the Main Image Window put "show\_in\_main" behind the filename as shown below:

```
b.Put_Filename("MyFile.Bcr show_in_main");
```

This might be desirable if the user want to process the image further with the extra processing utilities associated with the Main Image Window.

## SPIP Plug-in Functions for Visual Basic

### Required Interface Functions:

There only one interface function required to establish a connection between the SPIP program and a Plug-in function **SpipExport** located in the CspipExport class module.

```
Public Function SpipExport(ByRef pVar As Variant)
```

To inform the SPIP program about the available Plug-in functions a **SpipExport()** function need to be defined. This function should perform one AddToSPIP of the IMSPIPExport class call for each Plug-in interface function that shall appear in the SPIP User Prog menu.

```
Public Function AddToSpip(ByRef pVar As Variant, pName As String, pViewName As String, pGroupName As String, Icon As Integer)
```

The AddToSPIP function is part of the IMSpipExport class and defines the individual Plug-ins that can be called from the SPIP menu.

The first parameter pVar is a list pointer that keeps the individual menu items.

The second parameter should be identical to the name of the function to be associated with a menu item.

The third parameter is the friendly name that will appear as the menu item text.

The fourth parameter is the Group Name, which enables you to group the Plug-in functions to different submenus.

The last parameter is reserved for future application of icons.

The user functions, which AddToSPIP refers to should be declared as simple public functions without parameters for example:

```
Public Function Invert()
```

### The IMSpipExchange Class:

Exchange of data between the SPIP program and the Plug-in functions are performed through the **IMSpipExchange** class with the methods and variables described below:

#### IMSpipExchange Class Primary Methods:

An object of the CspipExchange class is usually created as below:

```
Dim SPIPObj As New CSpipExchange
```

Having established a CspipExchange object it is possible to operate on it with a number of methods:

```
Sub GetDataFromSPIP()
```

Retrieve Data from the active SPIP User Source Window (1D or 2D) into a floating-point array.

```
Function GetData(Index As Long) As Single
```

Retrieves the pixel value of the pixel number specified by Index as Single floating point.

```
Sub SetData(Index As Long, Value As Single)
```

Sets the pixel value of the pixel number specified by Index equal to Value.

```
Sub CreateData(Size_X As Integer, Size_Y As Integer)
```

Use this function to create your own data independent on existing SPIP windows. A floating-point array of sizeX × sizeY elements will be created and be part of the CSpipExchange object.

```
Sub ShowData(Window As String, Title As String, Style As Integer)
```

Shows the data in the SPIP client window defined by the Window parameter. If Window is set empty a new SPIP window can be created and the Window parameter will be set to refer

to the new window. So next time **ShowData** is called with the same Window parameter the data is shown in that same window. The Style parameter defines how the data will be shown and can be set to **CSpipExchange.ShowInSourceWindow**,  
**CSpipExchange.ShowInNewWindow** or **CSpipExchange.ShowIn3Dwindow**

### **CSpipExchange Class Primary Data Elements:**

**Variant \*pData;**

Floating point (single) pointer to the image or curve data array of the object.

**Long SizeX; Long SizeY;**

The number of x pixels and y pixels in the Data array.

**Long SizeTotal;**

The total number of elements in the Data array, equals SizeX x SizeY.

### **CSpipExchange Class Parameter Properties:**

The following properties can be used to get and set various parameters of a CSpipExchange object.

<b>CantileverSensitivity</b>	The Cantilever sensitivity
<b>Desc</b>	The Description of the data
<b>Filename</b>	The current filename
<b>FrameDir</b>	The Direction of the image scan (Upwards or Downwards ~ 'u' or 'd')
<b>LineDir</b>	The Direction of the line scans (left right ~ 'l' or 'r')
<b>Max</b>	The Maximum from the value of the Data array
<b>Min</b>	The Minimum from the value of the Data array
<b>Orgfilename</b>	The Original filename
<b>RetraceTime</b>	The Retrace time = time between the end of a line scan and the beginning of the next
<b>RotationAngle</b>	The angle of rotation while scanning the image
<b>SpringConstant</b>	The Spring Constant of the Cantilever
<b>TimePerImage</b>	The time used for scanning the Image
<b>TraceTime</b>	The Trace time = time for scanning one line
<b>WordSize</b>	The Word size of the Data Array = 4
<b>XOffset</b>	The X offset for of the physical coordinates used when scanning the image
<b>XRange</b>	The X Range in the current X-unit
<b>Xunit</b>	The X axis unit
<b>XYRatio</b>	The XY ratio = SizeX/SizeY
<b>YOffset</b>	The Y offset for of the physical coordinates used when scanning the image
<b>YRange</b>	The X Range in the current Y-unit
<b>Yunit</b>	The X axis unit
<b>ZScale</b>	The scaling Z scaling factor to convert to nanometers, normally 1.0
<b>Zunit</b>	The Z axis unit



## Roughness Parameters

The following describes the surface roughness parameters implemented in SPIP. All parameters recommended in the European BCR Project Scanning tunneling microscopy methods for roughness and micro hardness measurements are implemented and several other parameters applied by SPIP users is also included.

Symbol	Name	2D standard	Default Unit	3D reference
<u>Amplitude parameters:</u>				
Sa	Roughness Average	DIN 4768	[nm]	[6]
Sq	Root Mean Square	ISO 4287/1	[nm]	[6]
Ssk	Surface Skewness	ISO 4287/1		[6]
Sku	Surface Kurtosis	ANSI B.46.1		[6]
Sy	Peak-Peak	ISO 4287/1	[nm]	
Sz	Ten Point Height	ANSI B.46.1	[nm]	[6]
Smin	Min Value			
Smax	Max Value			
Smean	Mean Value			
<u>Hybrid Parameters:</u>				
Ssc	Mean Summit Curvature		[1/nm]	[6]
Sti	Texture IndexTexture_Direction_Index_S tdi			[7]
Sdq	Root Mean Square Slope		[1/nm]	[6]
Sdr	Surface Area Ratio			[6]
S2A	Projected Area		nm^2	
S3A	Surface Area		nm^2	
<u>Functional Parameters:</u>				
Sbi	Surface Bearing Index			[6]
Sci	Core Fluid Retention Index			[6]
Svi	Valley Fluid Retention Index			[6]
Spk	Reduced Summit Height	DIN 4776	[nm]	
Sk	Core Roughness Depth	DIN 4776	[nm]	
Svk	Reduced Valley Depth	DIN 4776	[nm]	
Sδcl-h	I-h% height intervals of Bearing Curve.	ISO 4287	[nm]	
<u>Spatial Parameters:</u>				
Sds	Density of Summits		[1/μm^2]	[6]
Std	Texture Direction		[deg]	[6]
StdI	Texture Direction Index			[7]
Srw	Dominant Radial Wave Length		[nm]	[7]
Srwi	Radial Wave Index			[7]
Shw	Mean Half Wavelength		[nm]	
Sfd	Fractal Dimension			
Scl20	Correlation Length at 20%			
Scl37	Correlation Length at 37%			
Str20	Texture Aspect Ratio at 20%			
Str37	Texture Aspect Ratio at 37%			

The table lists the roughness parameters by their symbol, name, corresponding 2D standard and unit.

Most parameters are general and valid for any  $M \times N$  rectangular image. However, for some parameters related to the Fourier transform we assume that the image is quadrangular ( $M=N$ ).

Before the calculation of the roughness parameters we recommend carrying out a slope correction by a 2<sup>nd</sup> or 3<sup>rd</sup> order polynomial plane fit. Note, also that roughness values depends strongly on measurement conditions especially scan range and sample density. It is therefore important to include the measurement conditions when reporting roughness data.

Some of the parameters depend on the definition of a local minimum and a local maximum. Here, a local minimum is defined as a pixel where all eight neighboring pixels are higher and a local maximum as a pixel where all eight neighboring pixels are lower.

As there are no pixels outside the borders of the STM-image there are no local minimums or local maximums on the borders. Note that parameters based on local minimums and/or local maximums may be more sensitive to noise than other parameters.

The parameters are divided into four groups as described in the following.

### **Amplitude parameters**

The amplitude properties are described by six parameters, which give information about the statistical average properties, the shape of the height distribution histogram and about extreme properties. All the parameters are based on two-dimensional standards that are extended to three dimensions.

**The Roughness Average,  $S_a$ , is defined as:**

$$S_a = \frac{1}{MN} \sum_{k=0}^{M-1} \sum_{l=0}^{N-1} |z(x_k, y_l) - \mu| \quad R\ 1$$

Where  $\mu$  is the mean height:

$$\mu = \frac{1}{MN} \sum_{k=0}^{M-1} \sum_{l=0}^{N-1} z(x_k, y_l)$$

The Root Mean Square  $S_q$ , is defined as:

$$S_q = \sqrt{\frac{1}{MN} \sum_{k=0}^{M-1} \sum_{l=0}^{N-1} [z(x_k, y_l) - \mu]^2} \quad R\ 2$$

**The Surface Skewness,  $S_{sk}$** , describes the asymmetry of the height distribution histogram, and is defined as:

$$S_{sk} = \frac{1}{MNS_q^3} \sum_{k=0}^{M-1} \sum_{l=0}^{N-1} [(z(x_k, y_l) - \mu)]^3 \quad R\ 3$$

If  $S_{sk} = 0$ , a symmetric height distributions is indicated, for example, a Gaussian like. If  $S_{sk} < 0$ , it can be a bearing surface with holes and if  $S_{sk} > 0$  it can be a flat surface with peaks. Values numerically greater than 1.0 may indicate extreme holes or peaks on the surface.

**The Surface Kurtosis,  $S_{ku}$** , describes the peaked-ness of the surface topography, and is defined as:

$$S_{ku} = \frac{1}{MNS_q^4} \sum_{k=0}^{M-1} \sum_{l=0}^{N-1} [z(x_k, y_l) - \mu]^4 \quad R\ 4$$

For Gaussian height distributions  $S_{ku}$  approaches 3.0 when increasing the number of pixels. Smaller values indicate broader height distributions and *visa versa* for values greater than 3.0.

The **Peak-Peak Height**,  $S_y$ , is defined as the height difference between the highest and lowest pixel in the image.

$$S_y = z_{\max} - z_{\min} \quad R\ 5$$

The **Ten Point Height**,  $S_z$ , is defined as the average height of the five highest local maximums plus the average height of the five lowest local minimums:

$$S_z = \frac{\sum_{i=1}^5 (z_{pi} - \mu) + \sum_{i=1}^5 (z_{vi} - \mu)}{5}, \quad R\ 6$$

where  $z_{pi}$  and  $z_{vi}$  are the height of the  $i^{\text{th}}$  highest local maximum and the  $i^{\text{th}}$  lowest local minimum respectively. Only positive maximums and negative minimums are valid. When there are less than five valid maximums or five valid minimums, the parameter is not defined.

### Hybrid parameters

There are three hybrid parameters. These parameters reflect slope gradients and their calculations are based on local z-slopes.

The **Mean Summit Curvature**,  $S_{sc}$ , is the average of the principal curvature of the local maximums on the surface, and is defined as:

$$S_{sc} = \frac{-1}{2n} \sum_{i=1}^n \left( \frac{\delta^2 z(x, y)}{\delta x^2} \right) + \left( \frac{\delta^2 z(x, y)}{\delta y^2} \right) \quad \text{for all local maximums} \quad R\ 7$$

where  $\delta x$  and  $\delta y$  are the pixel separation distances.

The **Root Mean Square Slope**,  $S_{dq}$ , is the RMS-value of the surface slope within the sampling area, and is defined as:

$$S_{dq} = \sqrt{\frac{1}{(M-1)(N-1)} \sum_{k=0}^{M-1} \sum_{l=0}^{N-1} \left( \frac{z(x_k, y_l) - z(x_{k-1}, y_l)}{\delta x} \right)^2 + \left( \frac{z(x_k, y_l) - z(x_k, y_{l-1})}{\delta y} \right)^2} \quad R\ 8$$

The **Surfaces Area Ratio**,  $S_{dr}$ , expresses the ratio between the surface area (taking the z height into account) and the area of the flat x,y plane:

$$S_{dr} = \frac{\left( \sum_{k=0}^{M-2} \sum_{l=0}^{N-2} A_{kl} \right) - (M-1)(N-1)\delta x \delta y}{(M-1)(N-1)\delta x \delta y} 100\%, \quad R\ 9$$

where

$$A_{kl} = \frac{1}{4} \left( \sqrt{\delta y^2 + (z(x_k, y_l) - z(x_k, y_{l+1}))^2} + \sqrt{\delta y^2 + (z(x_{k+1}, y_l) - z(x_{k+1}, y_{l+1}))^2} \right) \cdot \left( \sqrt{\delta x^2 + (z(x_k, y_l) - z(x_{k+1}, y_l))^2} + \sqrt{\delta x^2 + (z(x_k, y_{l+1}) - z(x_{k+1}, y_{l+1}))^2} \right) \quad R\ 10$$

For a totally flat surface, the surface area and the area of the xy plane are the same and  $S_{dr} = 0\%$ .

**The Projected Area, S2A**, expresses the area of the flat x,y plane as given in the denominator of R9.

**The Surface Area, S3A**, expresses the area of the surface area taking the z height into account as given in the numerator of R9.

#### Functional parameters for characterizing bearing and fluid retention properties

The functional parameters for characterizing bearing and fluid retention properties are described by six parameters. All six parameters are defined from the surface bearing area ratio curve shown in the figures below.

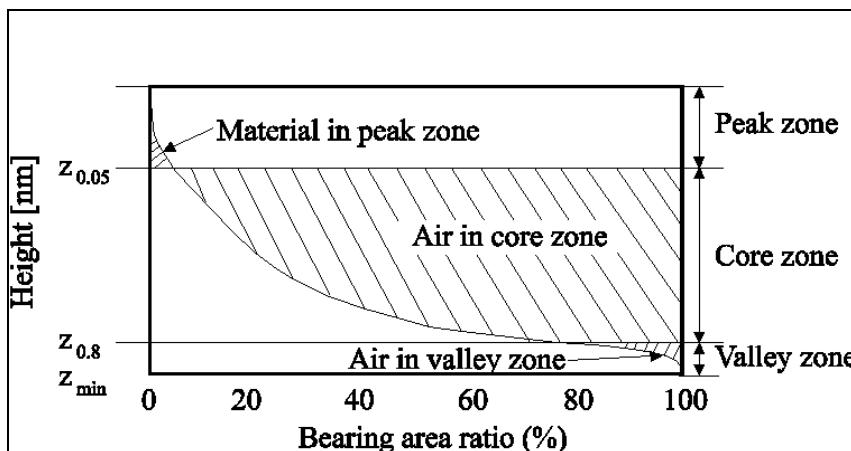


Figure 1: Bearing curve illustrating the calculation of Surface Bearing Index, Core Fluid Retention Index and Valley Fluid Retention Index

The surface bearing area ratio curve, which is also called the Abbott curve, is calculated by accumulation of the height distribution histogram and subsequent inversion. We divide both the histogram and the bearing curves into 1000 intervals except for images having less than 10000 pixels where the intervals equal 10% of the total pixels.

The hybrid parameters can be described graphically by the above figure. Horizontal lines are drawn through the bearing area ratio curve at the ratio values 5% and 80%. These lines are marked  $Z_{0.05}$  and  $Z_{0.8}$  and the three zones created are called the peak, the core and the valley zone. Three parameters are calculated based on this figure-

The Surface Bearing Index,  $S_{bi}$ , is defined as:

$$S_{bi} = \frac{S_q}{Z_{0.05}}, \quad R\ 11$$

where  $Z_{0.05}$  is the distance from the top of the surface to the height at 5% bearing area. For a Gaussian height distribution  $S_{bi}$  approaches 0.608 for increasing number of pixels. Large  $S_{bi}$  indicates a good bearing property.

The Core Fluid Retention Index,  $S_{ci}$ , is defined as:

$$S_{ci} = \frac{V_v(h_{0.05}) - V_v(h_{0.80})}{(M-1)(N-1)\delta x \delta y} / S_q, \quad R\ 12$$

where  $V_v(Z_x)$ , is the void area over the bearing area ratio curve and under the horizontal line  $Z_x$ . For a Gaussian height distribution  $S_{ci}$  approaches 1.56 for increasing number of pixels. Large values of  $S_{ci}$  indicate that the void volume in the core zone is large. For all surfaces  $S_{ci}$  is between 0 and 0.75 ( $Z_{0.05} - Z_{0.80}$ ) /  $S_q$ .

The Valley Fluid Retention Index,  $S_{vi}$ , is defined as:

$$S_{ci} = \frac{V_v(h_{0.80})}{(M-1)(N-1)\delta x \delta y} / S_q, \quad R\ 13$$

For a Gaussian height distribution  $S_{vi}$  approaches 0.11 for increasing number of pixels. Large values of  $S_{vi}$  indicate large void volumes in the valley zone. For all surfaces  $S_{vi}$  is between 0 and 0.2 ( $Z_{0.80} - Z_{min}$ ) /  $S_q$ .

Parameters associated with the two-dimensional DIN 4776 standard are also calculated based on the bearing area ratio curve. First, draw the least mean squares line fitted to the 40% segment of the curve that results in the lowest decline, see figure below. Extend this line so that it cuts the vertical axes for 0% and 100% and draw horizontal lines at the intersection points. Then draw a straight line that starts at the intersection point between the bearing area ratio curve and the upper horizontal line, and end on the 0% axis, so that the area of this triangle is the same as the area between the horizontal line and the bearing area ratio curve. Using the same principle, draw a line between the lower horizontal line and the 100% axis.

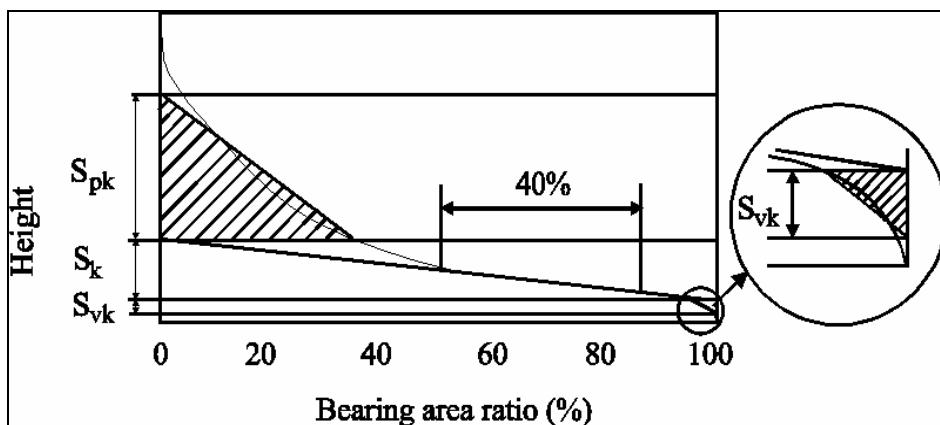


Figure 2: Bearing curve illustrating the calculation of Reduced Summit Height, Reduced Valley Height and Core Roughness Depth

**The Reduced Summit Height,  $Spk$ ,** is the height of the upper left triangle.

**The Core Roughness Depth,  $Sk$ ,** is the height difference between the intersection points of the found least mean square line.

**The Reduced Valley Depth,  $Svk$ ,** is the height of the triangle drawn at 100%.

**I-h% Height Intervals of Bearing Curve,**  $S\deltacl-h$  this is a set of parameters describing height differences between certain bearing area ratios;  $I$  and  $h$  denotes the lower and upper bearing area ratios of the interval.  $S\deltacl$  is the height value at bearing area ratio at  $I$  % and  $S\deltach$  is the bearing area ratio at  $h$  % and  $S\deltacl-h$  denotes their height difference  $S\deltacl - S\deltach$ . Currently SPIP calculates  $S\deltac0-5$ ,  $S\deltac5-10$ ,  $S\deltac10-50$ ,  $S\deltac50-95$  and  $S\deltac50-100$ .

### Spatial parameters

The spatial properties are described by five parameters. These parameters are the density of summits, the texture direction, the dominating wavelength and two index parameters. The first parameter is calculated directly from the STM-image, while the remaining are based on the Fourier spectrum. For these parameters we require the images to be quadratic.

**The Density of Summits,  $Sds$ ,** is the number of local maximums per area:

$$S_{ds} = \frac{\text{Number of local maximums}}{(M-1)(N-1)\delta x \delta y}, \quad R\ 14$$

Because, the parameter is sensitive to noisy peaks it should be interpreted carefully.

**The Texture Direction,  $Std$ ,** is defined as the angle of the dominating texture in the STM-image. For images consisting of parallel ridges, the texture direction is parallel to the direction of the ridges. If the ridges are perpendicular to the X-scan direction  $Std = 0$ . If the angle of the ridges is turned clockwise, the angle is positive and if the angle of the ridges is turned anti-clockwise, the angle becomes negative. This parameter is only meaningful if there is a dominating direction on the sample.

We calculate  $Std$  from the Fourier spectrum. The relative amplitudes for the different angles are found by summation of the amplitudes along  $M$  equiangularly separated radial lines, as shown in the figure below. The result is called the angular spectrum. Note that the Fourier spectrum is translated so that the DC component is at  $(M/2, M/2)$ . The angle,  $\alpha$ , of the  $i$ -th line is  $\alpha = \pi / M$ , where  $i=0, 1, \dots, M-1$ . The amplitude sum,  $A(\alpha)$ , at a line with the angle,  $\alpha$ , is defined as:

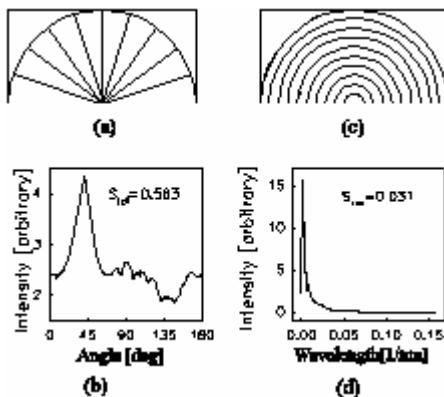


Figure 3: Fourier spectrum and the angular and radial spectra (Modified from [6]). a) Equidistant lines used for calculation of the angular spectrum shown in b). c) Equidistant semicircles used for calculation of the radial spectrum.

The angular spectrum is calculated by the following formula:

$$A(\alpha) = \sum_{i=1}^{M/2-1} | F(u(M/2 + i \cos(\alpha)), v(M/2 + i \sin(\alpha))) | \quad R\ 15$$

,

For non-integer values of  $p = M/(2 + i \cos(\alpha))$  and  $q = M/(2 + i \sin(\alpha))$ , the value of  $F(u(p), v(q))$  is found by linear interpolation between the values of  $F(u(p), v(q))$  in the 2x2 neighboring pixels. The line having the angle,  $\alpha$ , with the highest amplitude sum,  $A_{max}$ , is the dominating direction in the Fourier transformed image and is perpendicular to the texture direction on the image.

Note that due to 1/f noise often a dominating direction parallel to the x-axis is found.

**The Texture Direction Index,  $Std_i$** , is a measure of how dominant the dominating direction is, and is defined as the average amplitude sum divided by the amplitude sum of the dominating direction:

$$S_{tdi} = \frac{\sum_{i=0}^{M-1} A(i\pi/M)}{M A_{max}}, \quad R 16$$

With this definition the  $Std_i$  value is always between 0 and 1. Surfaces with very dominant directions will have  $Std_i$  values close to zero and if the amplitude sum of all direction are similar,  $Std_i$  is close to 1.

**The Radial Wavelength,  $Srw$** , is the dominating wavelength found in the radial spectrum. The radial spectrum is calculated by summation of amplitude values around  $M/(2 - 1)$  equidistantly separated semicircles as indicated in sub figure (b). The radius measured in pixels of the semicircles,  $r$ , is in the range  $r = 1, 2, \dots, M/(2 - 1)$ . The amplitude sum,  $\beta(r)$ , along a semicircle with the radius,  $r$ , is

The radial spectrum is calculated by the following formula:

$$\beta(r) = \sum_{i=1}^{M-1} |F(u(M/2 + r \cos(i\pi/M)), v(M/2 + r \sin(i\pi/M)))| \quad R 17$$

Again the amplitude for non-integer values of  $p=M/2+r \cos(i\pi/M)$  and  $q=M/2+r \sin(i\pi/M)$  is calculated by linear interpolation between the values of  $F(u(p), v(q))$  in the 2x2 neighboring pixels.

The **Dominating Radial Wavelength,  $Srw$** , corresponds to the semicircle with radius,  $r_{max}$ , having the highest amplitude sum,  $\beta_{max}$ :

$$S_{rw} = \frac{\delta x(M-1)}{r_{max}}, \quad R 18$$

The **Radial Wave Index,  $Srwi$** , is a measure of how dominant the dominating radial wavelength is, and is defined as the average amplitude sum divided by the amplitude sum of the dominating wavelength:

$$S_{rwi} = \frac{2}{M\beta_{max}} \sum_{i=1}^{M/2-1} \beta(i), \quad R 19$$

With this definition  $Srwi$  is always between 0 and 1. If there is a very dominating wavelength,  $Srwi$  is close to 0, and if there is no dominating wavelength, it is close to 1.

The **Mean Half Wavelength,  $Shw$** , is based on the integrated radial spectrum  $\beta_i(r)$ :

$$\beta_i(r) = \sum_{j=1}^r \beta(j) \quad R 20$$

*Shw* corresponds to the radius *r*0.5 where :

$$\frac{\beta_i(r_{0.5})}{\beta_i(M/2 - 1)} = 0.5 \quad R\ 21$$

Having found *r* 0.5 , *Shw* is calculated this way:

$$S_{hw} = \frac{\delta x(M - 1)}{r_{0.5}} \quad R\ 22$$

The **Fractal Dimension**, **Sfd** is calculated for the different angles by analyzing the Fourier amplitude spectrum; for different angles the Fourier profile is extracted and the logarithm of the frequency and amplitude coordinates calculated. The fractal dimension for each direction is then calculated as 2.0 minus the slope of the log - log curves. The fractal dimension can also be evaluated from 2D Fourier spectra by application of the Log Log function. If the surface is fractal the Log Log graph should be highly linear, with a negative slope.

The **Correlation Length parameters**, **ScI20** and **ScI37**, are defined as the horizontal distance of the areal autocorrelation function that has the fastest decay to 20% and 37% respectively (37% is equivalent to 1/e). For an anisotropic surface the correlation length is in the direction perpendicular to the surface lay.

The **Texture Aspect Ratio Parameters**, **Str20** and **Str37**, are used to identify texture strength (uniformity of texture aspect). It is defined as the ratio of the fastest to slowest decay to correlation 20% and 37% of the autocorrelation function respectively. In principle, the texture aspect ratio has a value between 0 and 1. For a surface with a dominant lay, the parameters will tend towards 0.00, whereas a spatially isotropic texture will result in an Str of 1.00.

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