

# autoAlignMirror User Guide

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## 1. Getting started

This is a software tool for aligning X-ray mirror with speckle-based technique. The principle of the method is to measure the longitudinal ray error of the distorted focus if there was misalignment of pitch of a mirror. The detailed principle of the imaging processing can be found in Ref. [1].

The software is written in MATLAB 2016a. It has been tested on Windows 7 and RedHat Linux.

The distribution package contains the executable file for the software, test data, user guide and the original script files for running the software in MATLAB.

### 1) Input file

A screenshot of the GUI is shown in Fig. 1. All parameters are accessible in a single control window. The input image files are expected to be in one directory for each stack of speckle scan at one pitch angle setting. Images within one directory are expected to have the same dimension.

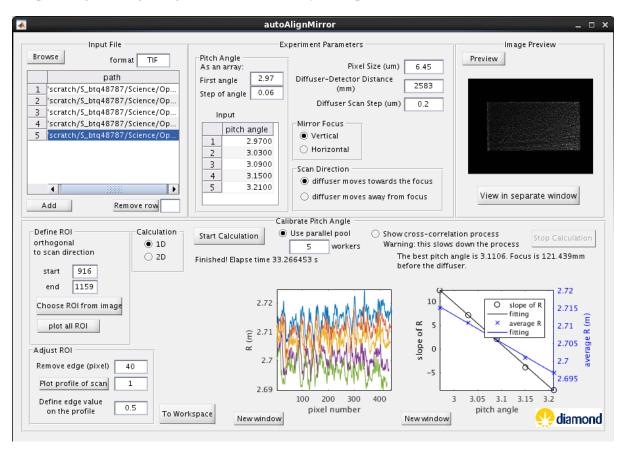


Fig. 1 A screenshot of the GUI of the software.

*Browse* button: The paths of the directories can be chosen via the file selection dialog by pressing control or shift for multiple selection. The clicked directory do not have to be the bottom level as long as each level contains only one subfolder so that the images can be found in only one subfolder in the bottom level. The chosen directories are shown in the *path* table. The directories are automatically sorted with natural order according to the last level directory such as "Scan1" "Scan2" so the clicking does not need to be in order.

*format* box: type in the extension of the image files. The software can read all the image formats that MATLAB recognizes. During the calculation the data is converted to 64-bit floating number for higher accuracy.



*path* table: showing the chosen directories. One can also type in the directories or edit them directly.

Add button: add an empty row in the bottom of path table.

*Remove row* button: remove the row specified in the text box from the *path* table.

### 2) Set experimental parameters

Pitch angle input as an array: input the start angle and the step size in the same unit. The unit is not specified in case the experimental stages have different settings for different labs. The pitch angles will be generated automatically according to the number of the file directories, and shown in *pitch angle* table in ascending order.

pitch angle table: can be edited manually if the angles are not consequentially as an array.

pixel size, diffuser-detector distance, diffuser scan step: input as specified by the names.

*Mirror Focus:* choose between vertical or horizontal focus mirror. The default assumption is that for vertical mirror the scan of the diffuser is also in vertical direction for higher spatial resolution in that direction; vice versa.

Scan Direction: the diffuser is scanned towards the focus line or away from the focus. The easy way of identifying is that if the speckle pattern is moving towards the brighter part or the darker part in the FOV, as closer to the focus the image is brighter.

### 3) Image Preview

Preview button: show the first image in the first scan directory in the GUI

View in separate window: show image in a new popup figure window for better visualization if necessary.

# 2. Calibrate pitch angle

#### 1) Define ROI

Choose ROI from image button: new figure pop up with the first image in the first scan directory shown. Use mouse to drag rectangle in the area where the speckle pattern look homogeneous. The chosen ROI will show in the title of the image as shown in Fig. 2. The numbers for the ROI in the direction that is orthogonal to the scan direction will be shown in the *start* and *end* box.



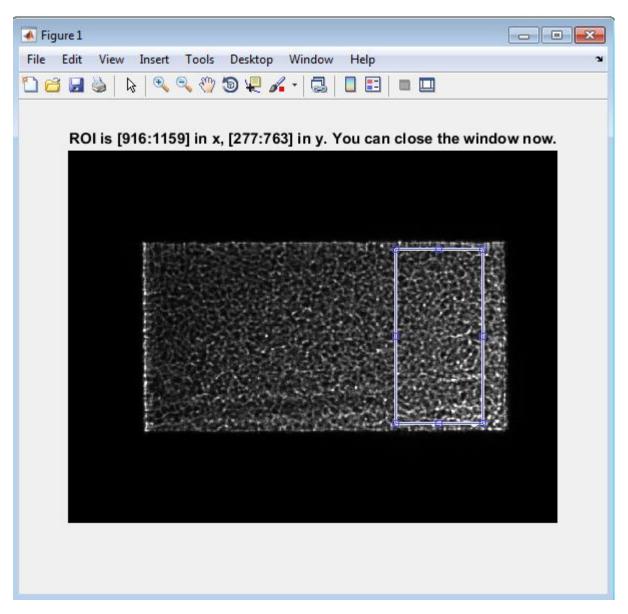


Fig. 2 Example of choosing ROI from image,

*start* box: input or edit the start pixel number of the ROI, only in the direction which is orthogonal to the scan direction.

*end* box: input or edit the last pixel number of the ROI, only in the direction which is orthogonal to the scan direction.

plot all ROI button: new popup figure window showing the 1<sup>st</sup> image from all scan directories with ROI marked in red rectangle. It is for checking if the ROI have been corrected found for all scans in different pitch angle positions as the mirror reflection moves on the detector if the mirror's pitch angle is changed. If they don't look good, adjust the values in *remove edge* or *define edge value in the profile* box.

#### 2) Adjust ROI

*Remove edge* box: if the ROI found to be too close to the edges of the mirror, where bad polishing and interference of the beam can affect the data processing, we can increase the number to remove more pixels from the edges in the ROI. ROI will be updated later during processing.



plot profile of scan button: plot the normalized line profile of the 1<sup>st</sup> image in the scan directory specified by User in the text box. The profile is used to check if the edge is defined properly for the define edge value in the profile text box.

define edge value in the profile text box: specify the value, for example 0.5, in the normalized line profile which the software uses to define the edge of the mirror and then to define the ROI in the scan direction.

### 3) 1D process

By choosing 1D in the *calculation* panel, the calculation will be processed in 1D. The result will be an averaged result within ROI in the direction orthogonal to the scan direction. In the scan direction, the resolution is still pixel-wised.

*Use parallel pool* button: if selected, MATLAB will check if the parallel pool is opened with the User specified worker number. If not, it will open the parallel pool for parallel computing using local CPUs. When finished open the parallel pool, message will be shown with number of workers connected. If user input a number larger than the local CPU number, message will be given and the number will be automatically changed to the local CPU number and the parallel pool will be opened accordingly. With parallel pool opened, each scan is allocated to one CPU for processing. Therefore, more workers than the scan numbers will not make the process faster.

*Show cross-correlation process* button: if selected, each cross-correlation map and result will be plotted out for all the pixels. This will slow down the data processing but can be helpful for demonstrating the data processing or debugging if the result looks not reasonable. This is not compatible with parallel processing.

*Start Calculation* button: start the data processing. If selected parallel pool, wait until the pool is opened before clicking. Once clicked, software will show "Calulating..." When finished, it shows the elapse time of the process. The results will be shown in the two plots in the GUI. Text message with the best alignment angle and focus position shown in the GUI as well.

*Stop Calculation* button: stops the data processing loop. It is not compatible with parallel computing.

The two figures: Left: retrieved focus distance R with respect to the pixel number for all the scans. Right: the slope of R, and the average R with respect to the pitch angle to find the correct alignment of the pitch angle and at which the focus position.

New window buttons: popup new figure windows to see the plot.

*To workspace* button: handles of GUI is exported to MATLAB workspace for interactive manual processing for advanced Users.

### 4) 2D process

By choosing 2D in the *calculation* panel, the calculation will be processed in 2D. Extra parameters that are only useful for 2D processing show up after selecting 2D, as shown in Fig. 3.

*Scan No* box: because 2D processing takes much longer time than 1D processing, it is not recommended to be used for alignment but for characterizing the mirror surface in 2D. Only one scan of one pitch angle is chosen for processing each time as User specified.



Process every  $\Box$  pixel box: don't process every pixel in the direction orthogonal to the scan direction can save large amount of processing time. The spatial resolution in that direction is mostly limited by correlation window width so it will be larger than 1 pixel anyway. Therefore it is also not necessary to process every pixel in that direction.

*Correlation window* box: specify the 2D cross-correlation window width for the direction orthogonal to the scan direction. The window size in the scan direction will be the same as the scan steps. Therefore, with more scan steps, this window number can be smaller; with less scan steps, larger window is needed.

*Use parallel pool* button: 2D process can use parallel processing as well. The process allocates each row of image pixels to a worker, therefore, the more CPUs the better unless limited by computer memory.

The two figures: Left: retrieved focus distance *R* in 2D. Right Zernike polynomial coefficients of the first 7 terms. The classical names of the polynomials are listed above the figure.

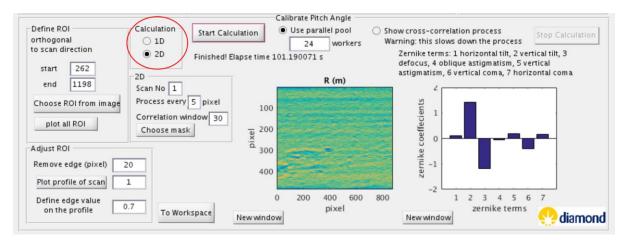


Fig. 3 Example of 2d processing.

### 3. Acknowledgment

The test data was taken at Beamline B16 Diamond Light Source with the support of Andrew Malandain, Oliver fox, Hongchang Wang. The Zernike polynomial fitting code was shared by Robert Gray and Joseph Howard. T. Z. wish to thank Sebastien Berujon and Yogesh Kashyap for early foundation of the software.

1. T. Zhou, H. Wang, O. Fox, and K. Sawhney, "Auto-alignment of X-ray focusing mirrors with speckle-based at-wavelength metrology," (submitted).