XRE reconstruction software

Manual Q1 2017

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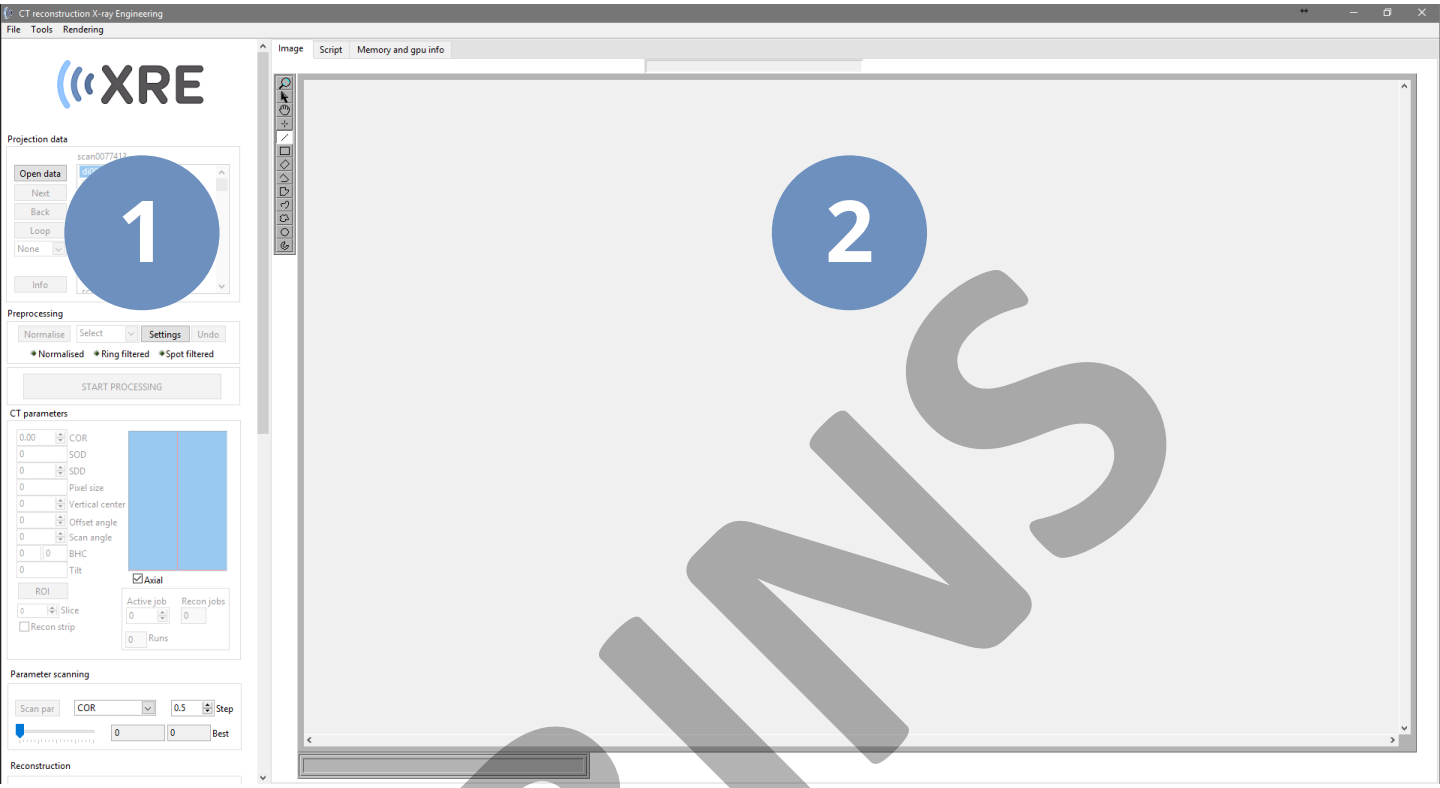
1. Software overview



Main software window

The main software window is divided into 2 parts: the workflow and the imaging section.

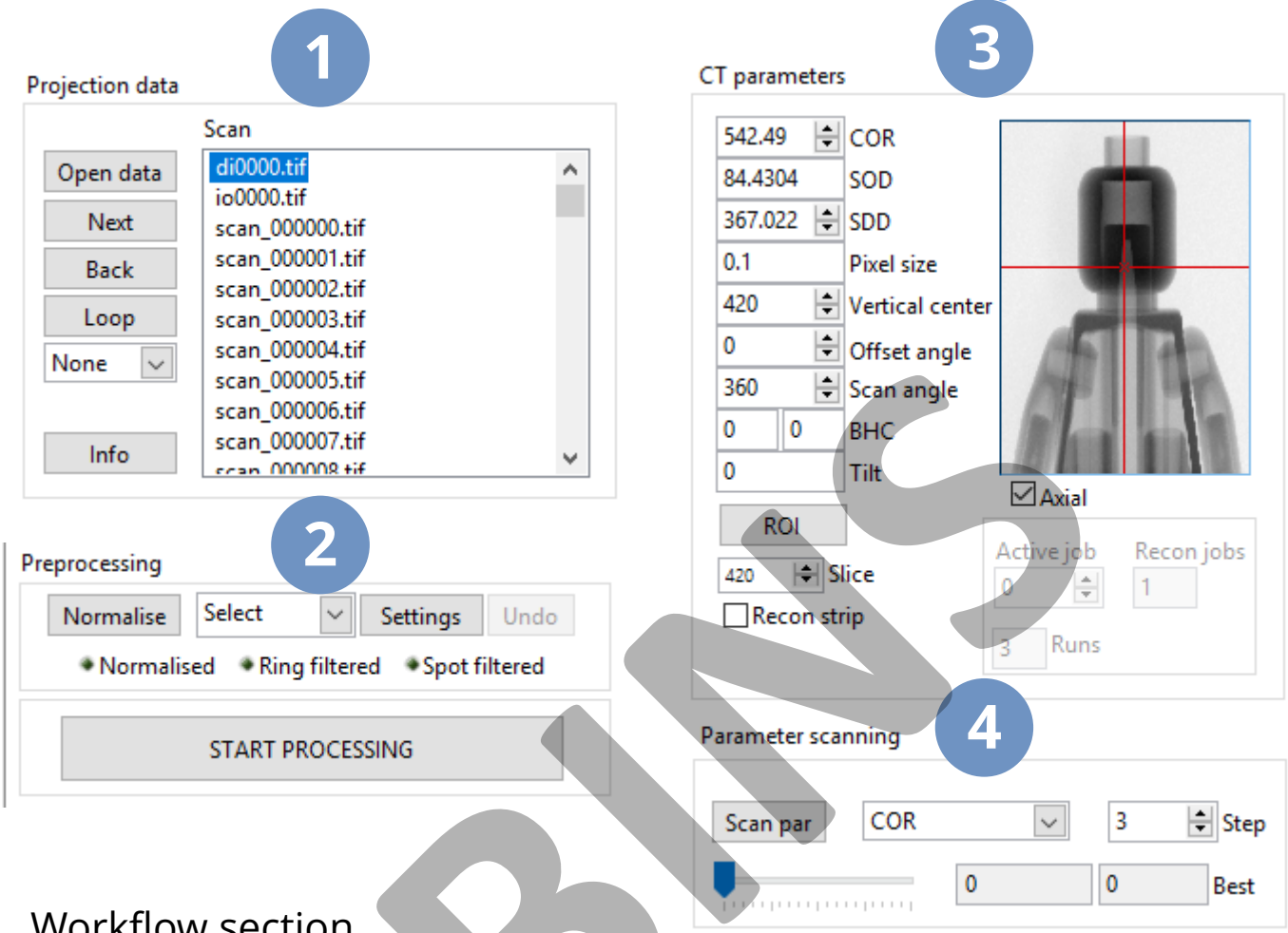
1 The workflow section

In the workflow section all steps of the reconstruction are listed starting with an overview of the projection data, followed by preprocessing steps and finetuning CT parameters and ending with reconstruction.

2 The imaging section

The image section consists of 3 tabs. The main *Image* tab provides a visual representation of the projection and reconstructed images, the *Script* tab enables scripting and automated reconstruction and the *Memory and gpu info* tab provides an overview of the available RAM and GPU memory.

1. Software overview



Workflow section

1 Projection data

In this section the projection data can be loaded using the *Open data* button and each projection can be viewed by selecting the image in the list or using the *Next*, *Back* and *Loop* buttons .

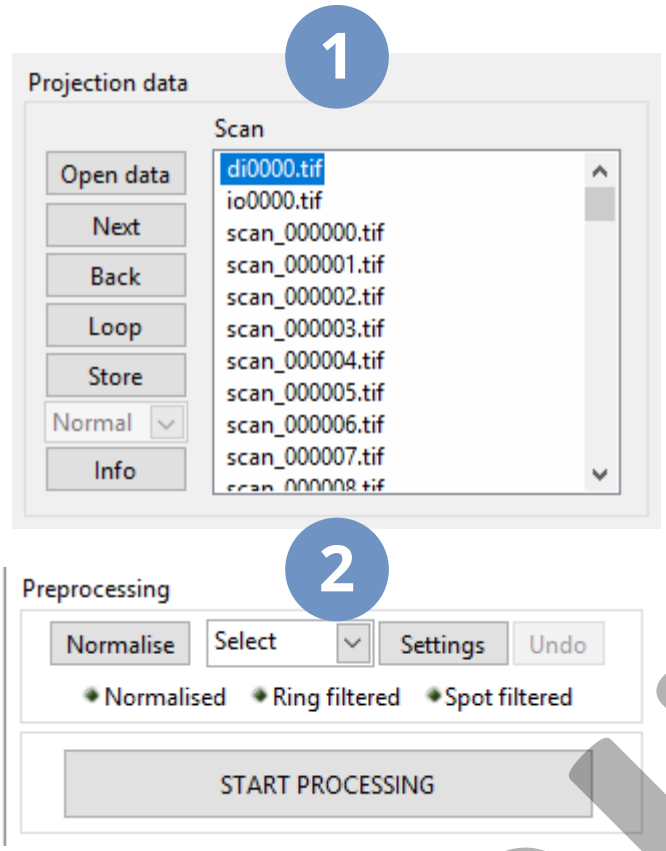
Basic arithmic operations can be performed on the projection images using the drop down menu.

Detailed information about each projection imaged can be displayed using the *Info* button.

2 Preprocessing

In this section the projection data can be normalized and image corrections like ring and spot filters can be evaluated and applied. More advanced corrections are available using the *Settings* button.

1. Software overview



Workflow section

3 CT parameters

Finetuning of different parameters of the CT scan can be performed in this section. Small changes in these parameters enables the user to obtain the best possible reconstructed image.

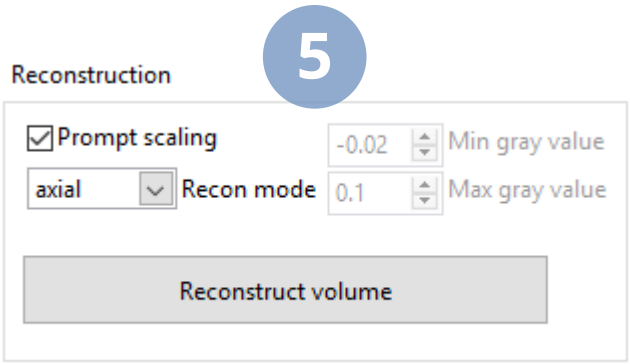
Using the *ROI* button a region of interest can be selected to limit the reconstruction to a certain volume.

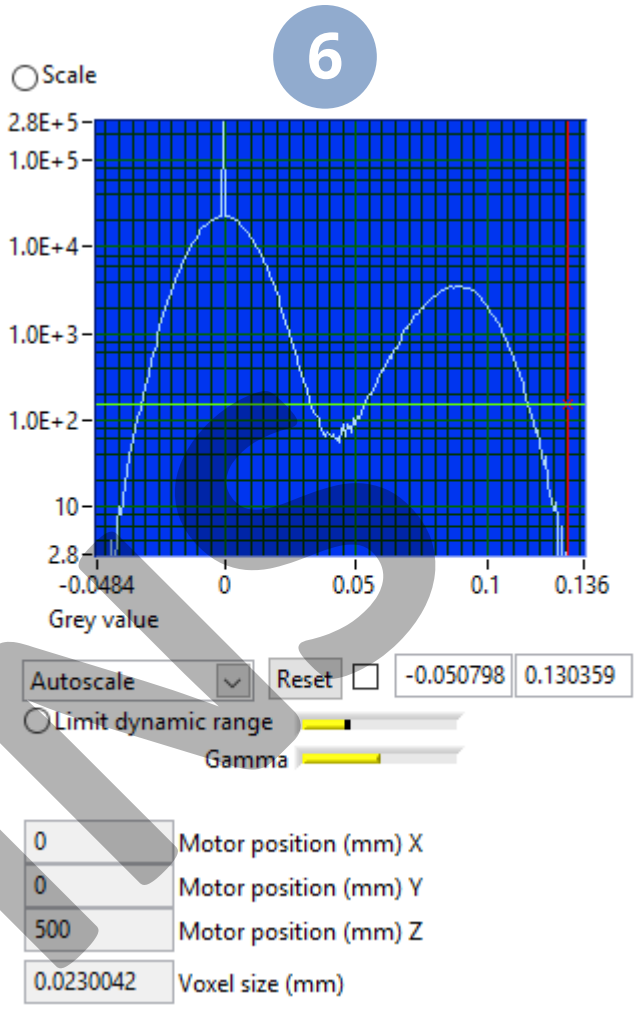
Different slices, both axial and frontal, can be selected using the navigator on the projection image or using by entering a number near the *Slice* indicator.

4 Parameter scanning

Manually determining the CT parameter can sometimes be a tedious undertaking. Parameter scanning runs through a series of different values of a chosen parameter and automatically selects the best value for that parameter.

1. Software overview





Workflow section

5 Reconstruction

Once the right CT parameters are determined the grey value scale of the images can be set using *Prompt scaling* and the values can be determined automatically or set manually.

The *Recon mode* can also be selected, which results in a stack of axial or vertical slices through the object.

6 Histogram and Line Profile indicator

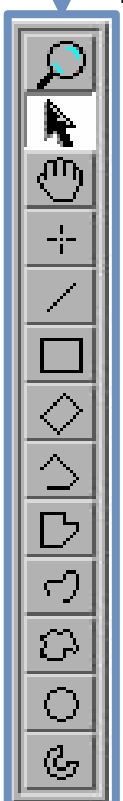
Below the *Reconstruct Volume* button the indicator for the histogram or line profile (depending on what is selected on the image) is located and below that the absolute position of the scan and voxel size are shown.

1. Software overview

Imaging section

In the image section either the radiographs or reconstructed slices can be displayed.

The toolbar on the left lets you obtain more info on the image.



Zoom tool: *click* to zoom in – *Shift+click* to zoom out

Pointer tool

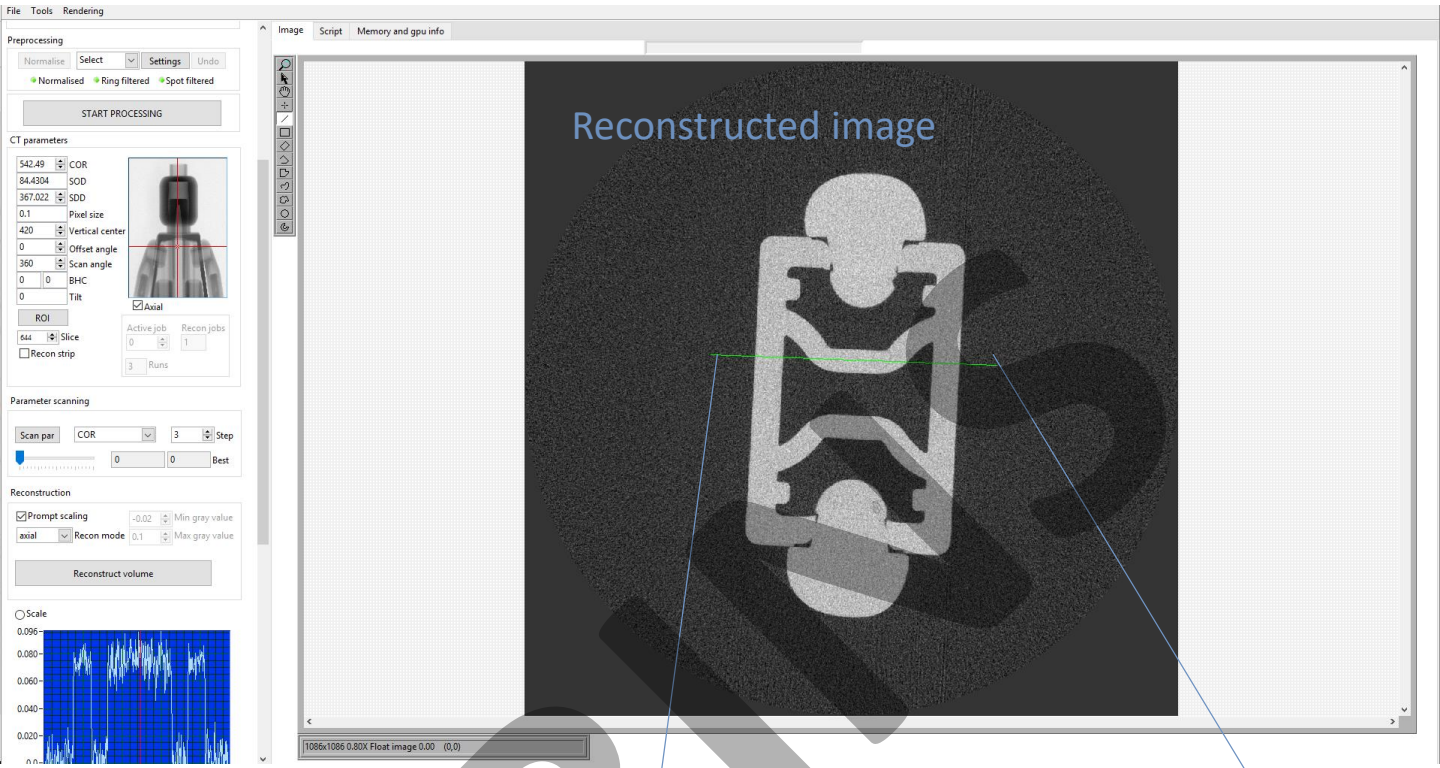
Pan tool

Pinpoint tool

Line profile tool

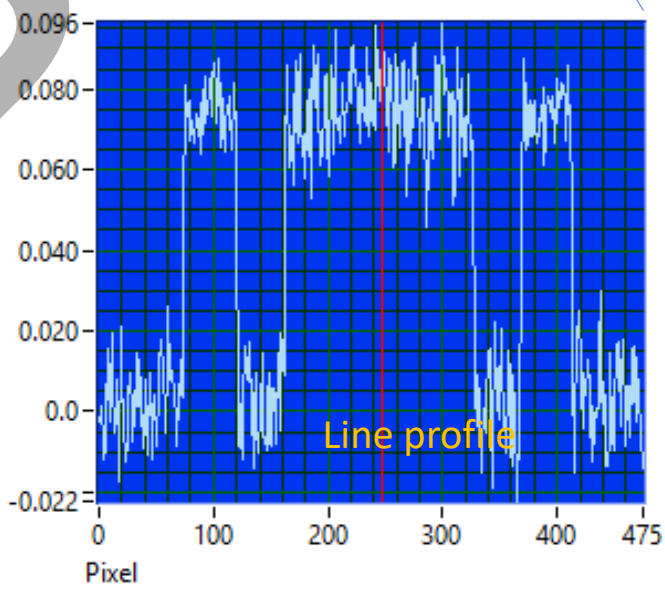
Selection tools

1. Software overview

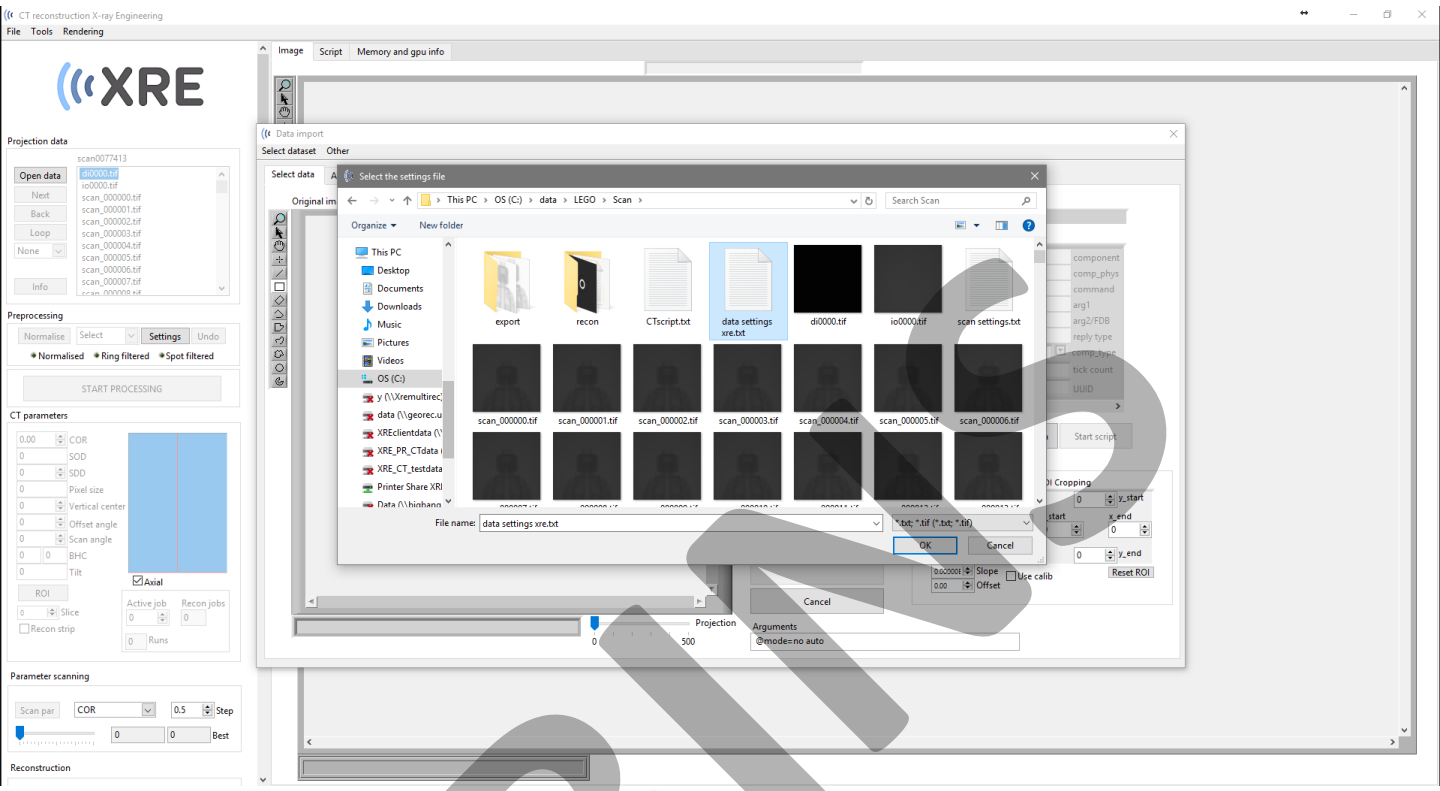


Line profile tool

Using the line profile tool a line can be drawn on the radiograph or reconstructed image and this grey value profile along this line is shown in the workflow selection.



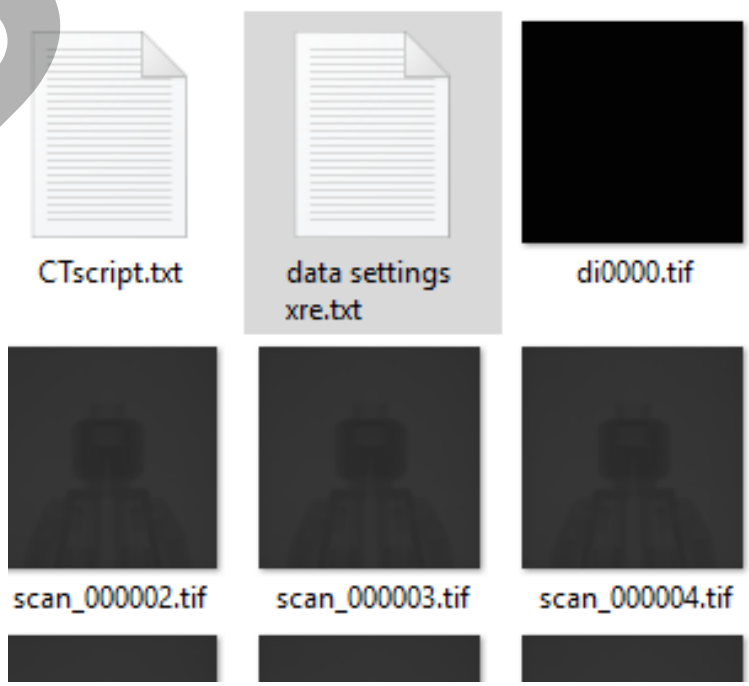
2. General reconstruction workflow



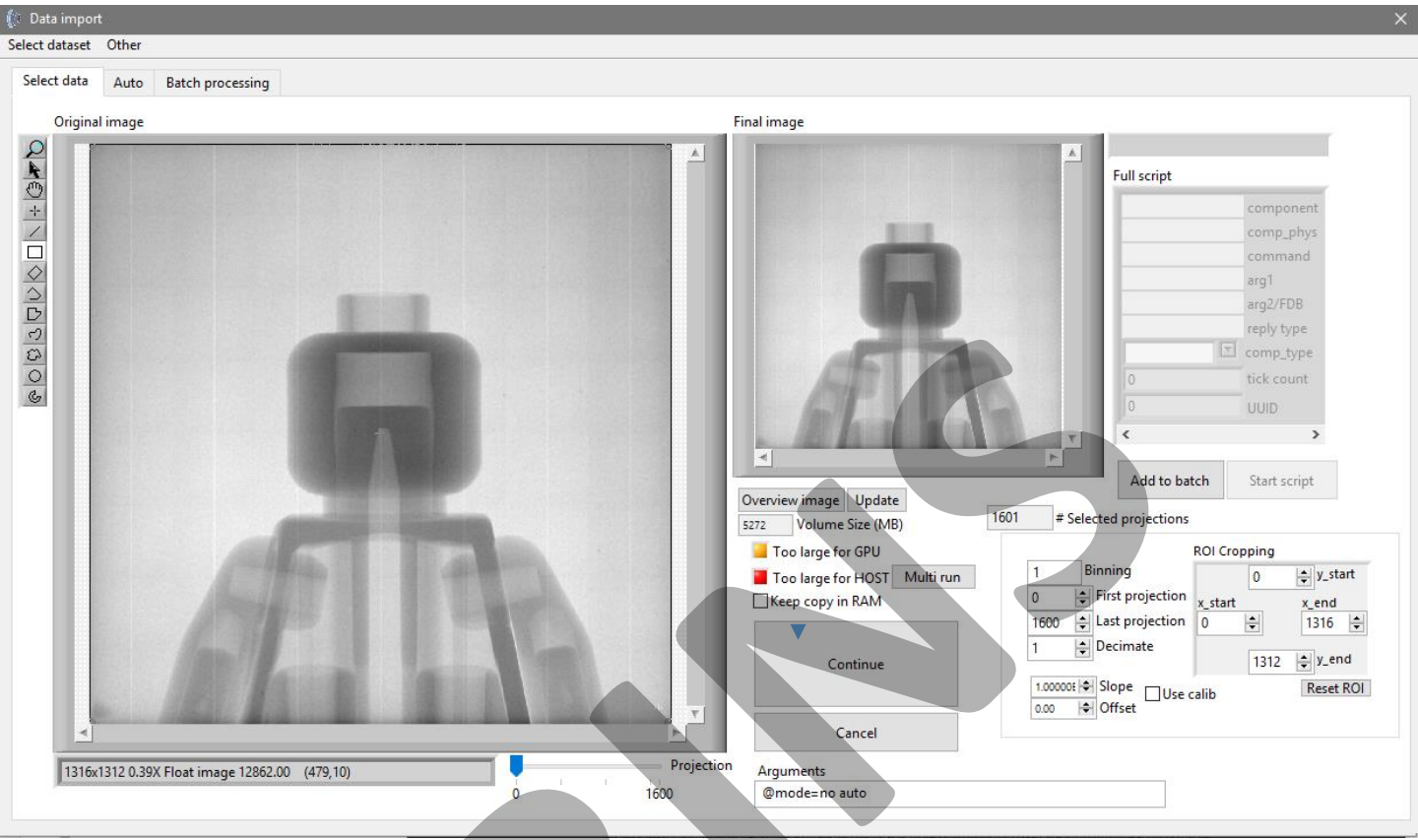
Selecting data

After clicking the *Open data* button on the workflow section of the main window, you will be prompted with an explorer window in which you can navigate to the folder with the raw data. In the raw data select the *data setting xre.txt* file and click *OK*.

If the *data setting xre.txt* file is not available, select a projection image and the file will be automatically generated, in which the scan parameters can manually added.



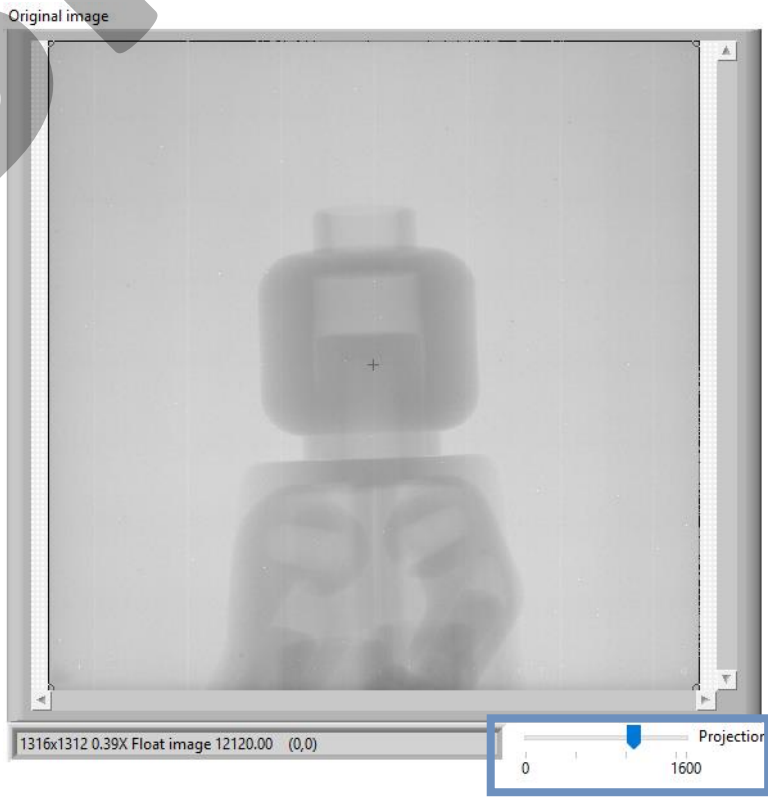
2. General reconstruction workflow



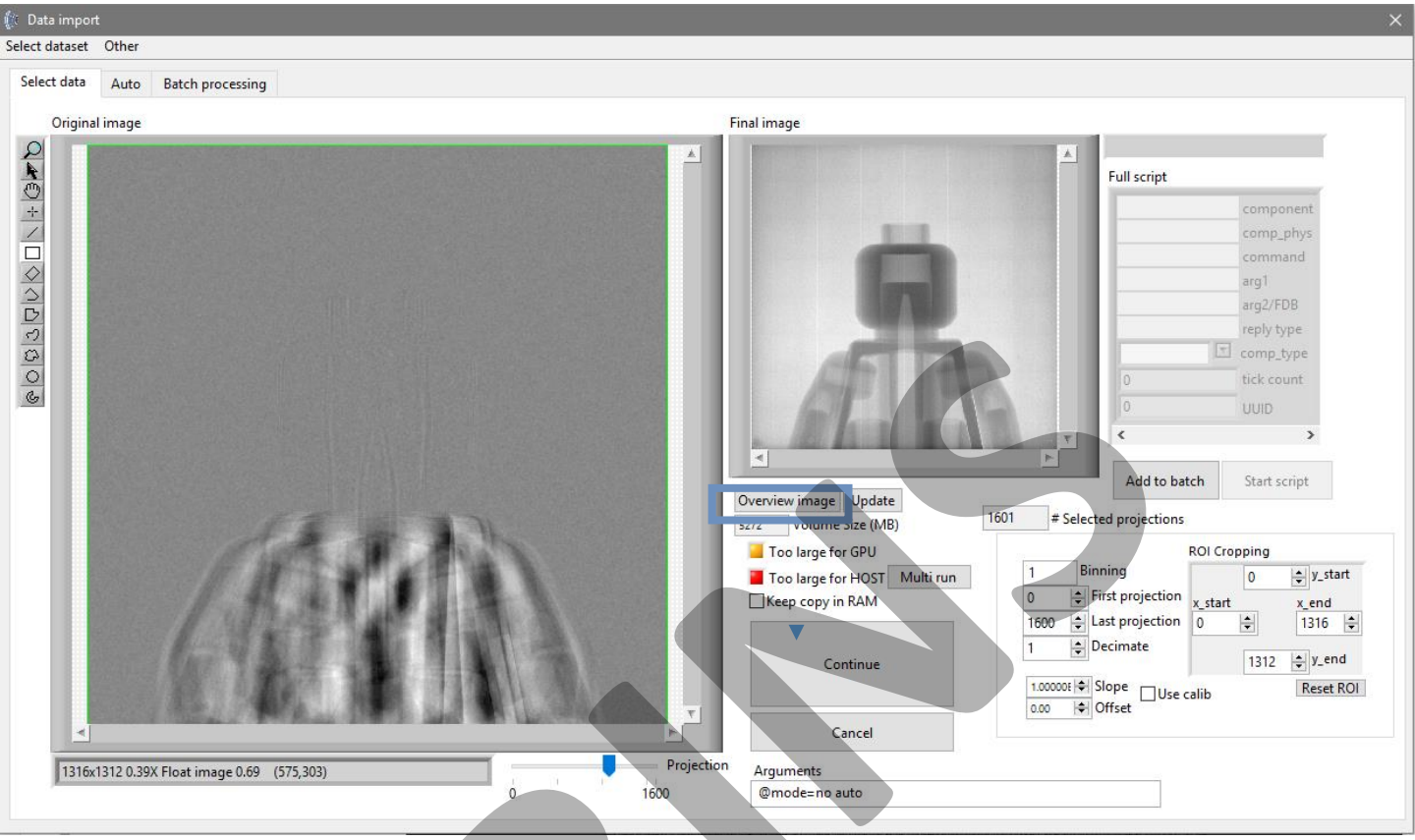
Selecting data

After selecting the *data setting xre.txt* file, the *Data import* window will give you an overview of the raw data.

The slider at the bottom allows to quickly scroll through all projections to see the extent of the object in the projections while rotating.



2. General reconstruction workflow

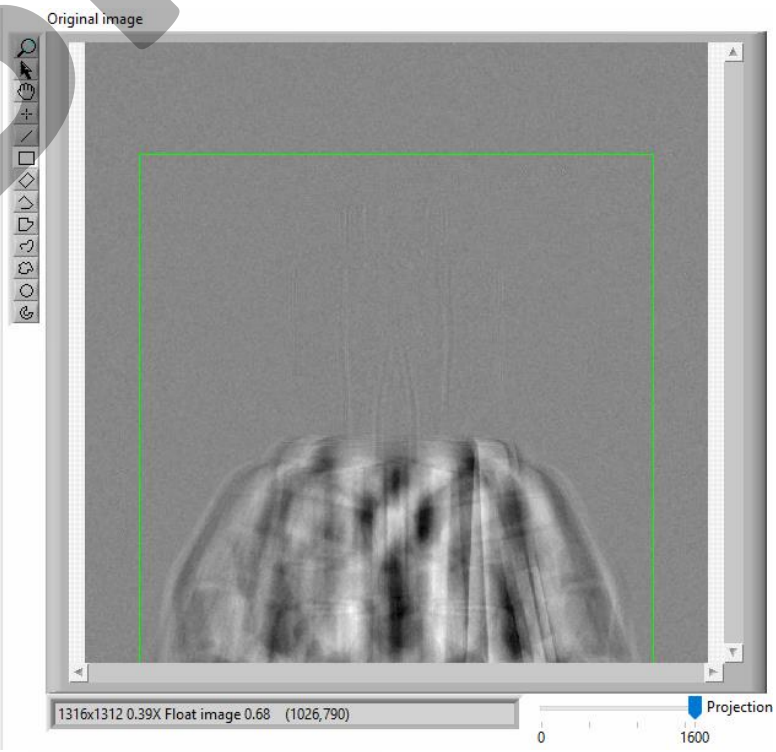


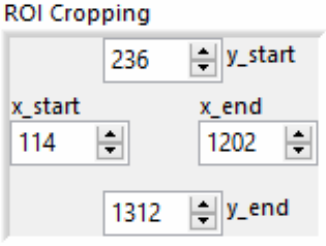
Selecting data

The extent of the object in the projections can also be checked by clicking the *Overview image* button. This function averages all projections in one image which is displayed.

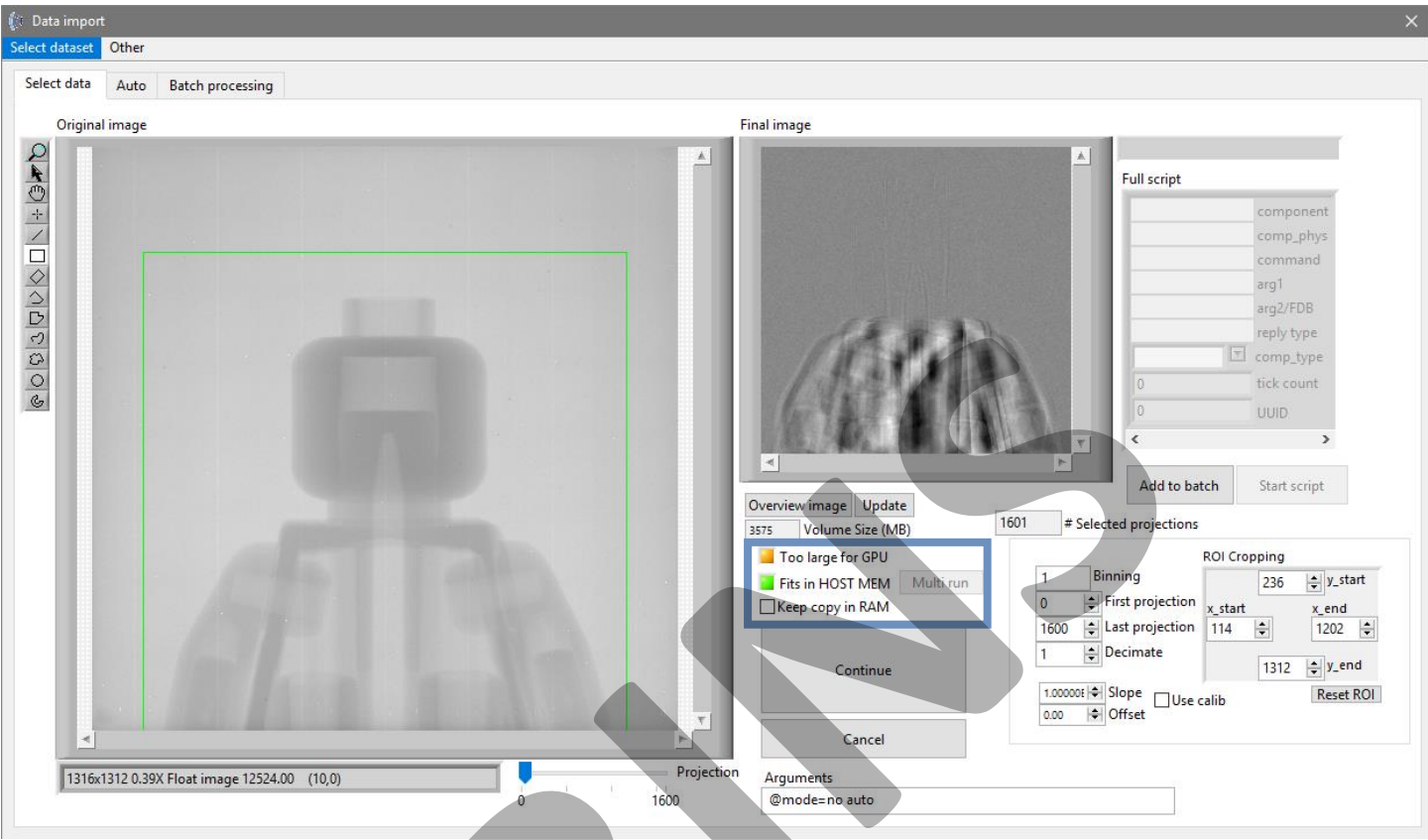
A region of interest or *ROI* for all projections can be selected using the rectangular selection tool on the image or by using the numerical indicators in the *ROI Cropping* interface on the lower right of the *Data import* window.

The selected region can be reset using the *Reset ROI* button.





2. General reconstruction workflow

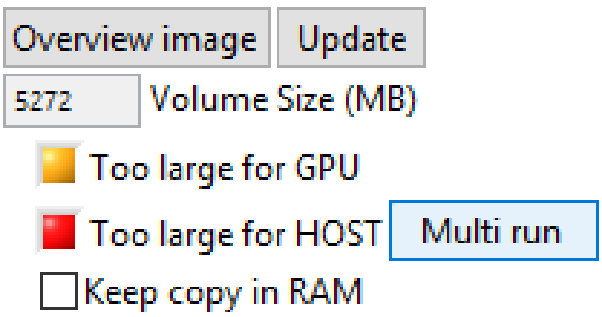


Selecting data

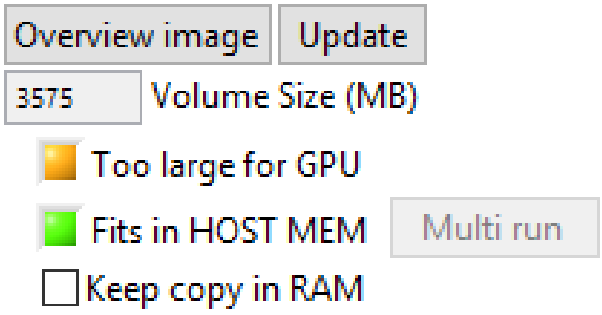
When importing the data the projection images can be stored in either the RAM memory of the computer or directly on the RAM memory of the GPU. Storage directly on the GPU is preferred as this reduces reconstruction time. The green indicator shows which RAM memory options are available.

If no options are available (red indicator) the reconstruction can be split up in different runs using the *Multi run* button or the required RAM memory can be reduced using *ROI Cropping*, *Binning* or *Decimating*.

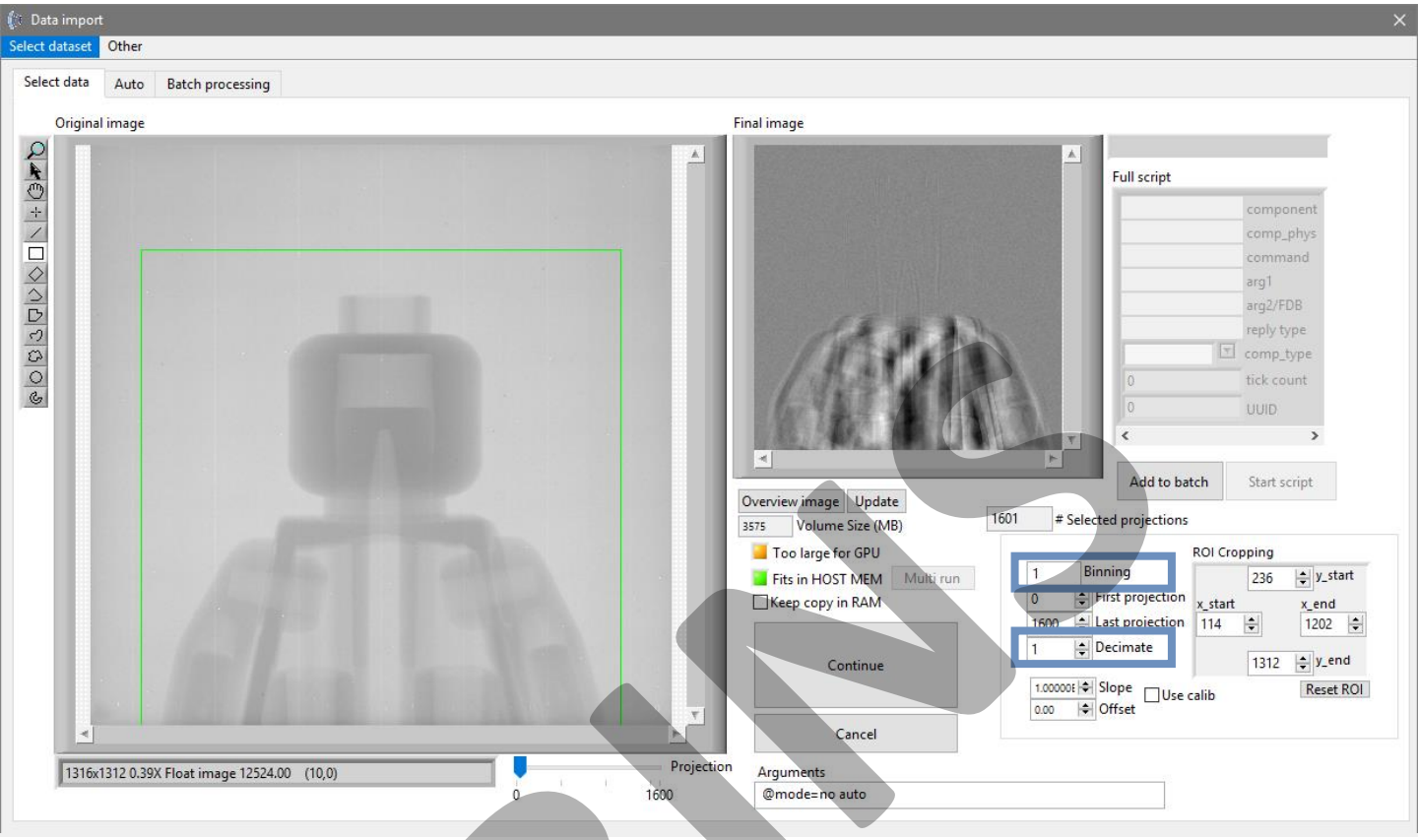
Without ROI cropping



With ROI cropping

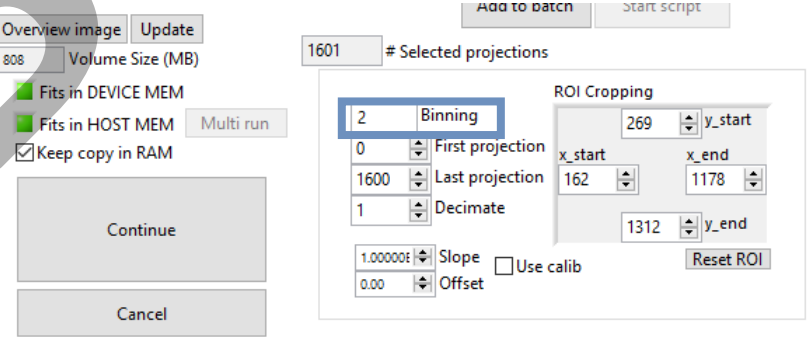


2. General reconstruction workflow

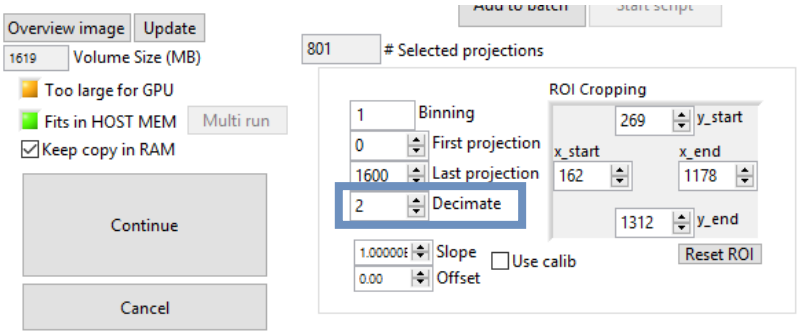


Selecting data

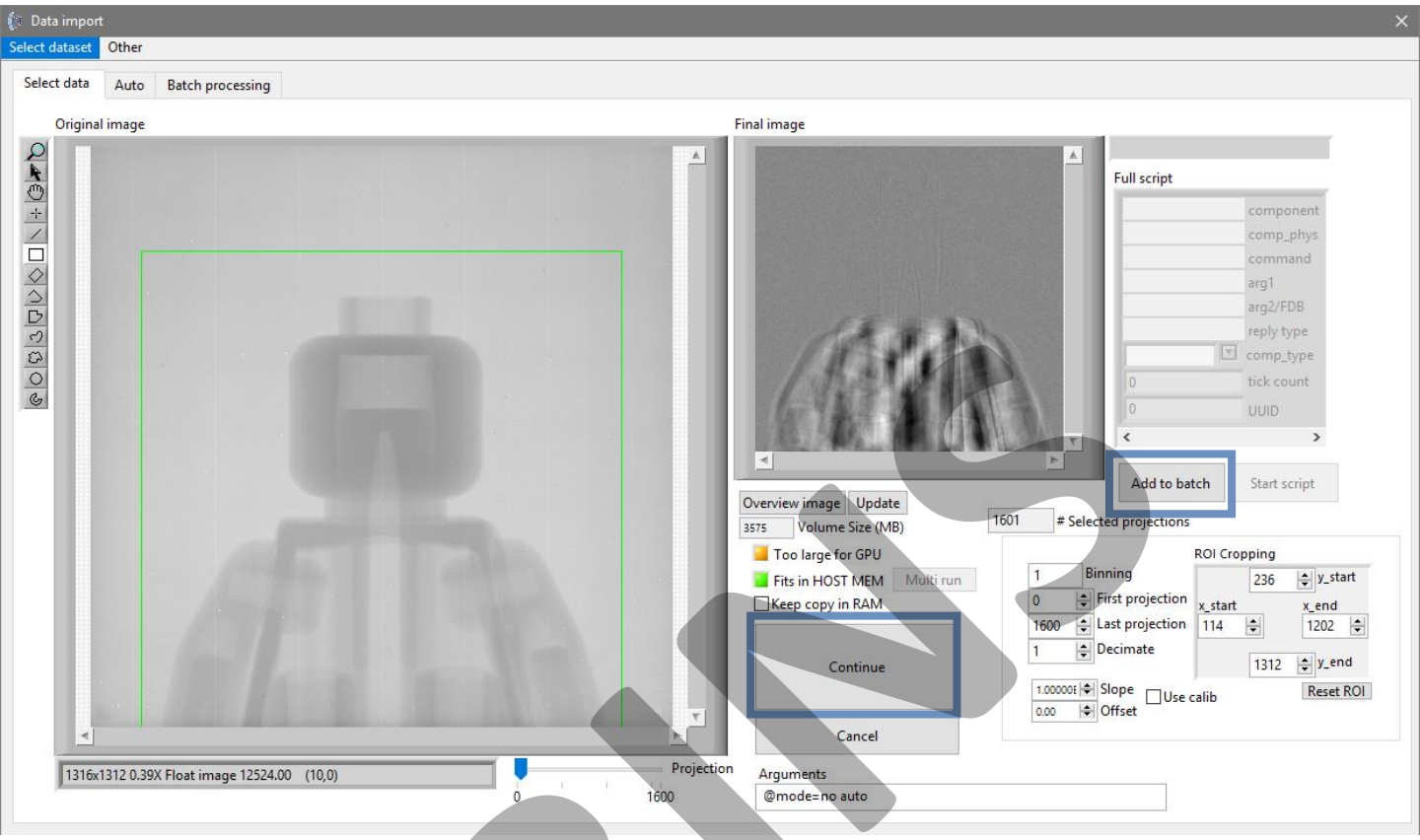
Binning averages a number of pixels in the projection image into 1 pixel, reducing the overall size of the image and improving signal to noise.



Decimate allows to reduce the total amount of projections by skipping one or more projections.



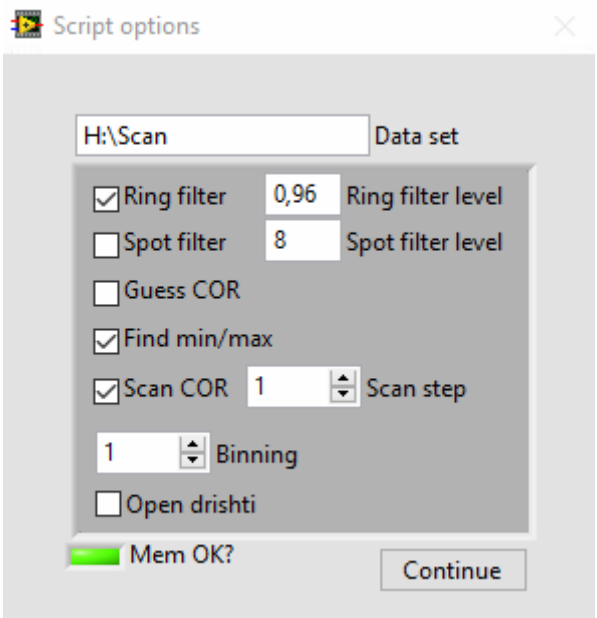
2. General reconstruction workflow



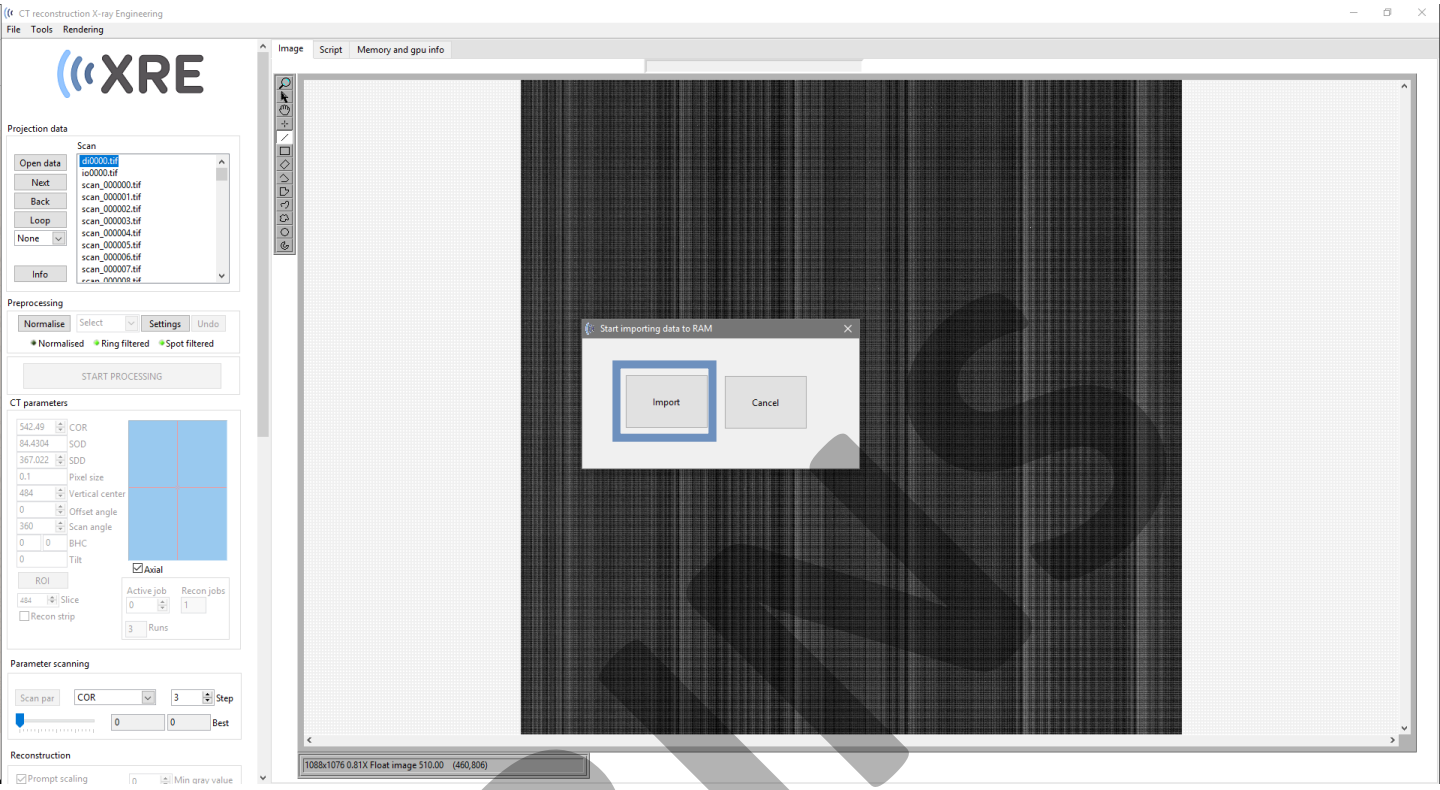
Selecting data

After selecting and adjusting the projection data you can click either *Continue* or *Add to batch*. *Continue* can be used to manually finetune the reconstruction parameters.

Add to batch can be used to automatically reconstruct multiple scans using a script. After clicking *Add to batch* you will we be prompted with a *Scripting options* window in which the desired reconstruction steps can be chosen, after which a new dataset can be chosen to add to the script.

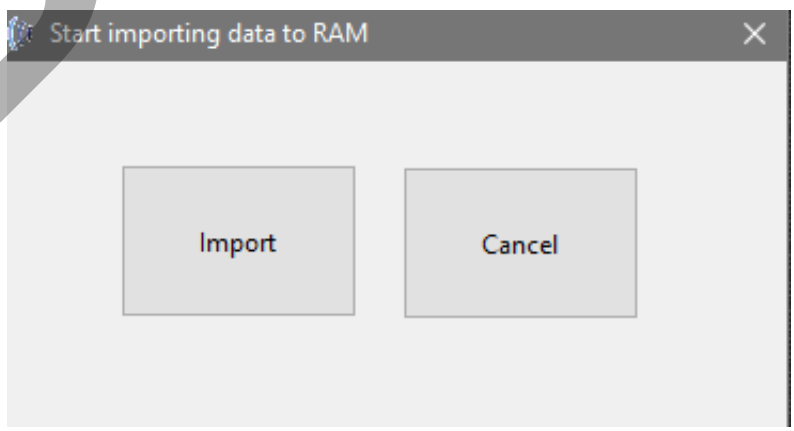


2. General reconstruction workflow



Selecting data

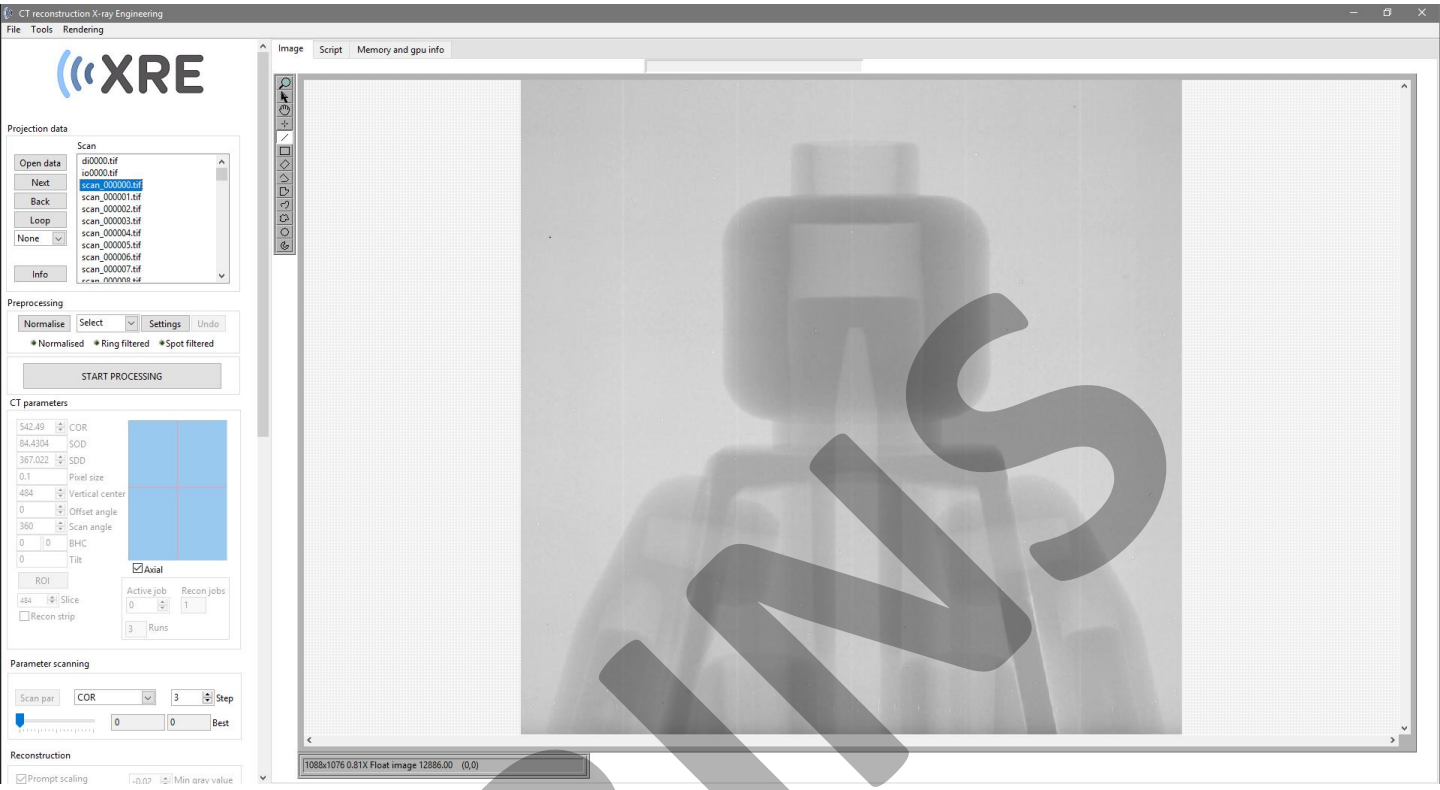
After clicking Continue in the Data import window, you return to the main window where you will be prompted with to import the projection data.



Depending on the size of the projection data and your hardware configuration, importing data into the RAM memory can take some time.

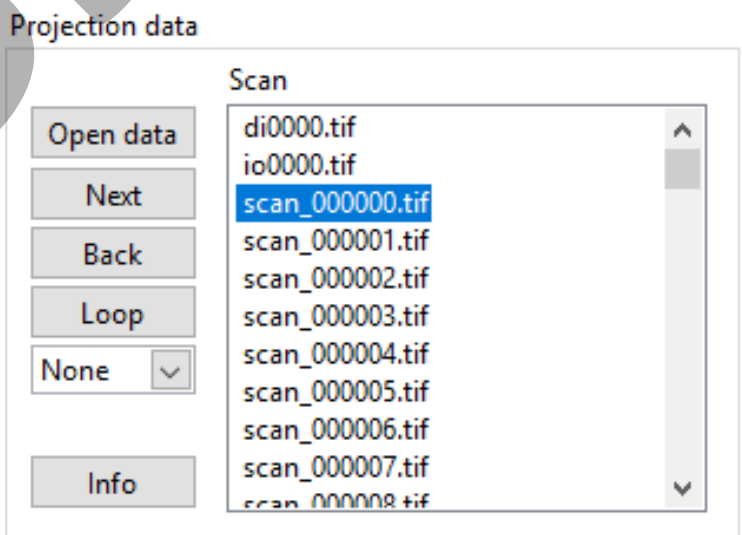
If *Cancel* is selected, you postpone this step to a later point in the reconstruction process.

2. General reconstruction workflow



Projection Data

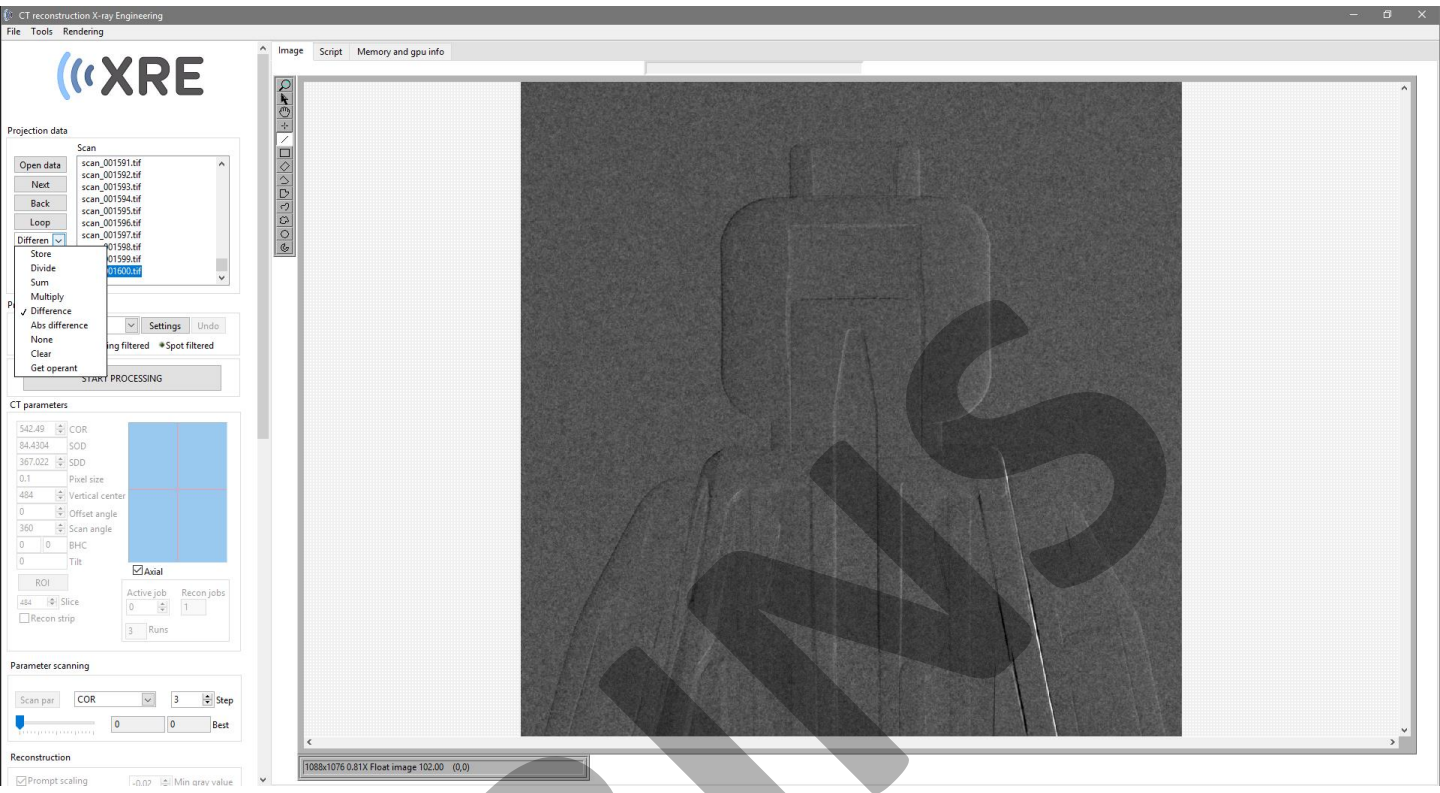
After selecting the data a list of projection images is generated and each image can be visualized in the *Imaging section* by double clicking a projection in the list.



The *Next* and *Back* buttons allow to navigate through the different projections in the list.

The *Loop* button automatically cycles through all the images in the list and these images are displayed as an animation in the *Imaging section*.

2. General reconstruction workflow

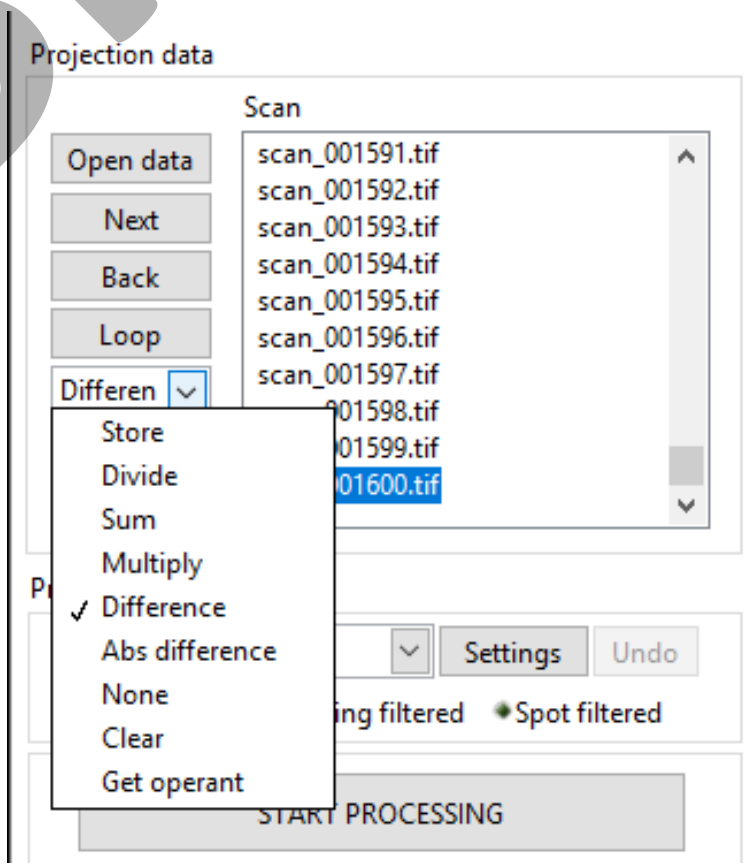


Projection Data

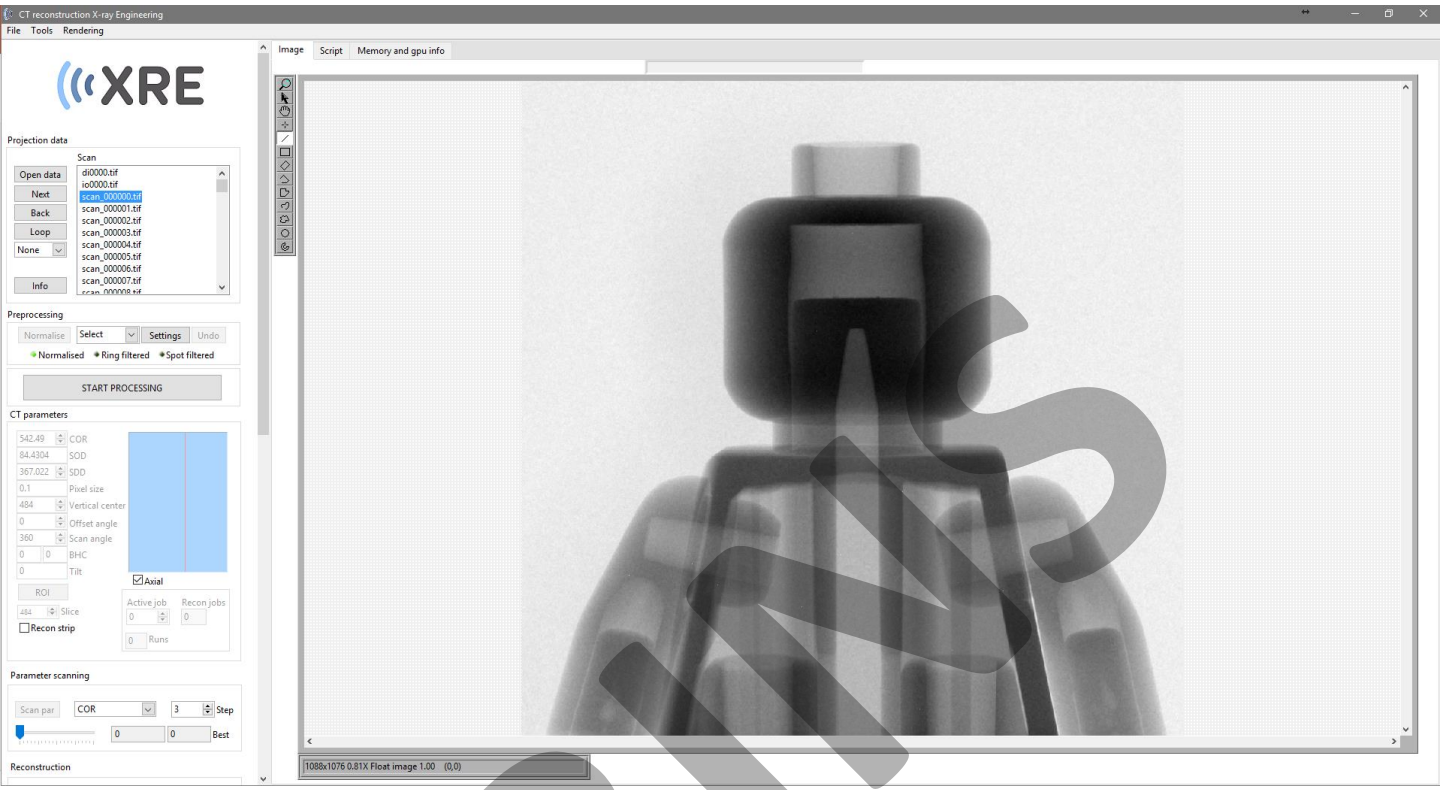
The drop down list allows to *Store* the a displayed projection image in the memory and use this image for simple image arithmetic operations.

.After storing a projection and selecting an operation the resulting image can be generated by selecting another image in the list.

The *Info* button provides more detailed information about the selected scan.

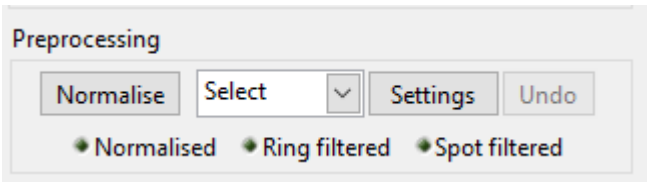


2. General reconstruction workflow

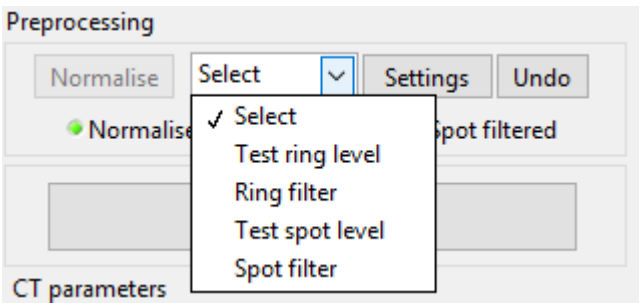


Preprocessing

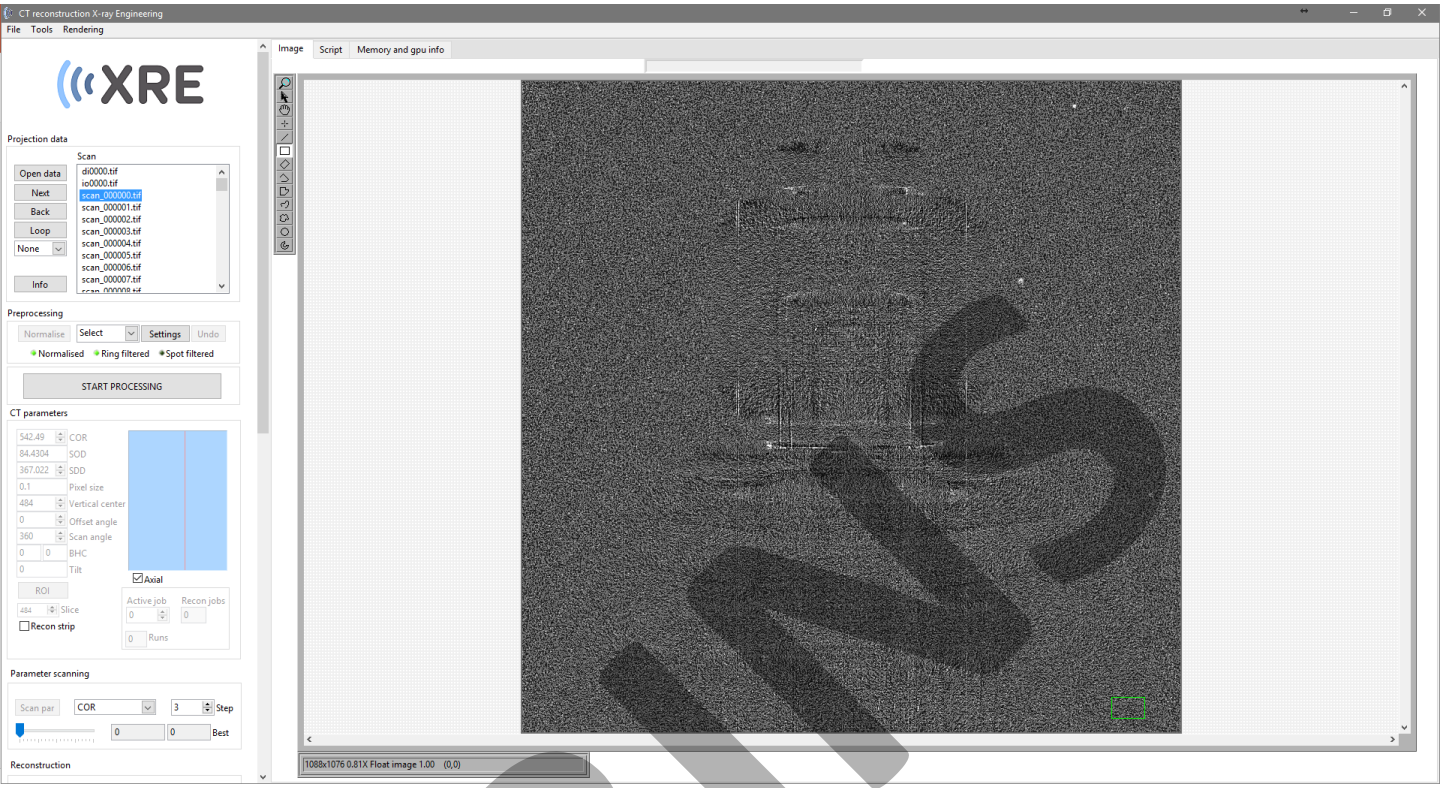
Prior to the reconstruction, an optimization of the projection images is required.



Normalise is the first step in the Preprocessing and in this step the projections are normalized with flat field and offset images. After this step the images in the list are normalized images.

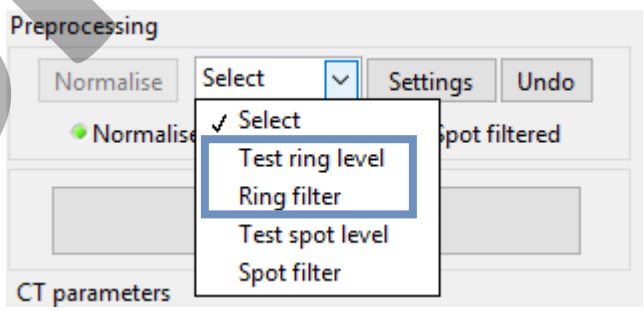


2. General reconstruction workflow



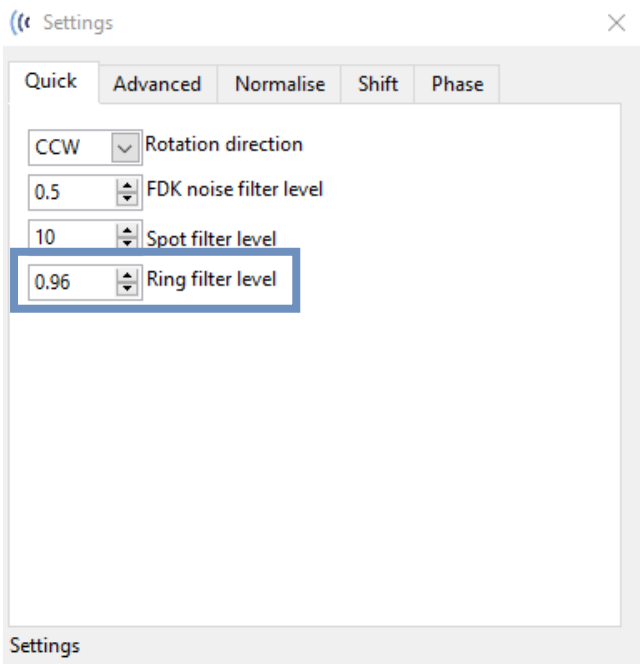
Preprocessing

Ring Filter is the next step in the preprocessing and this removes systematic pixel deviations in the detector. The standard value is usually detector specific, but this value can be adapted in using the *Settings* button and changing the *Ring filter level* value.

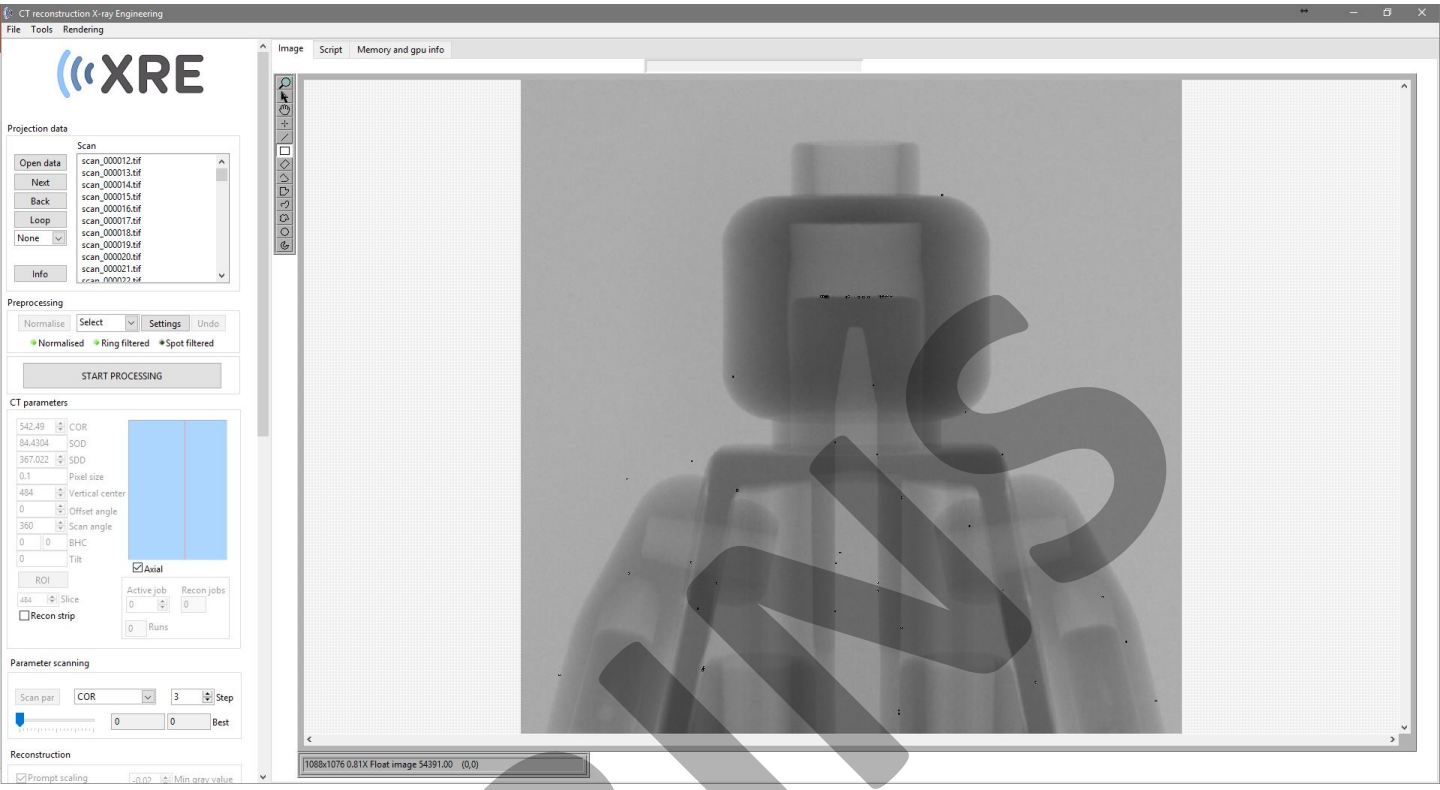


To test this value select *Test ring level* from the drop down menu.

To perform the operation on the entire dataset select *Ring filter* from the drop down menu.

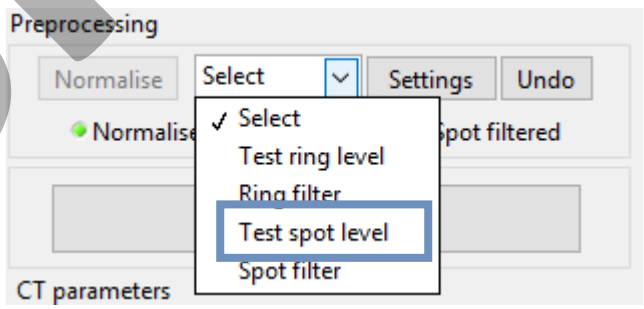


2. General reconstruction workflow

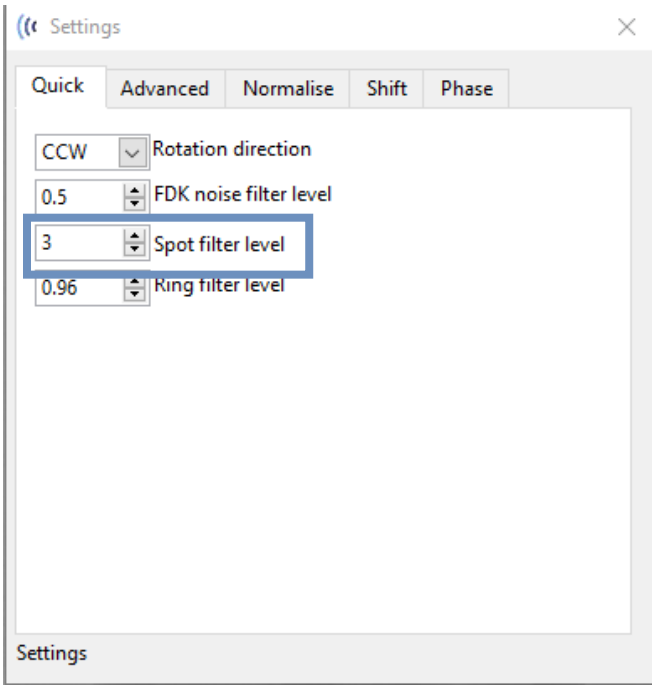


Preprocessing

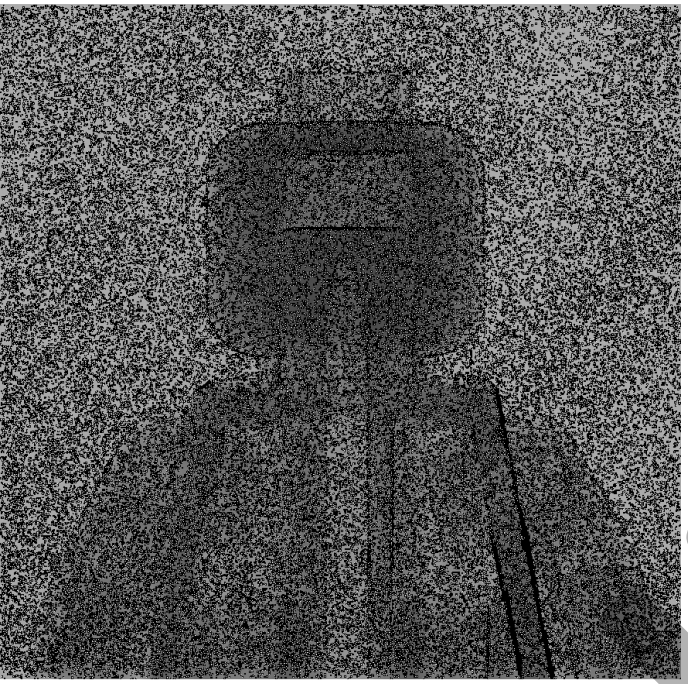
Spot filter is the final step in the preprocessing and this removes dark and bright spots in the projection images.



This value can be adapted in using the *Settings* button and changing the *Spot filter level* value and the effect of the value can be evaluated by selecting the *Test spot level* from the drop down menu.



2. General reconstruction workflow



Spot filter level: 1

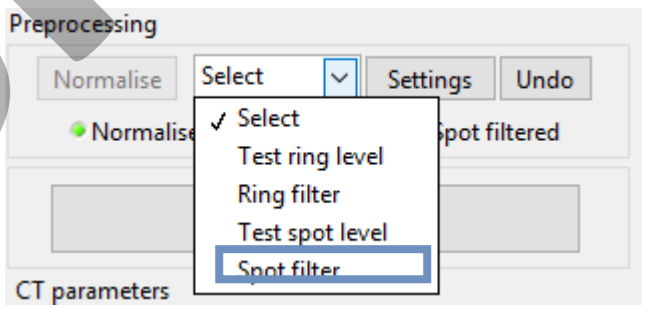
Spot filter level: 10

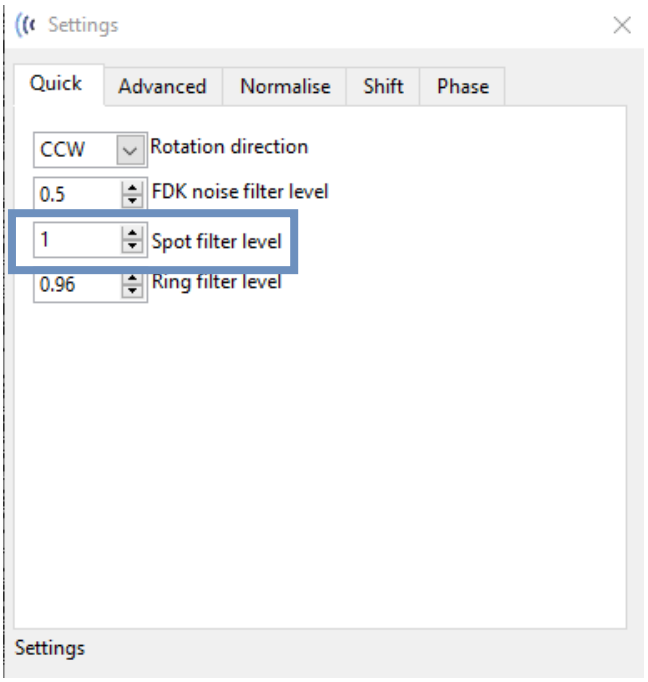
Preprocessing

The result of the *Test spot level* are displayed in the *Image section*, where the pixels that will be removed are highlighted on the image.

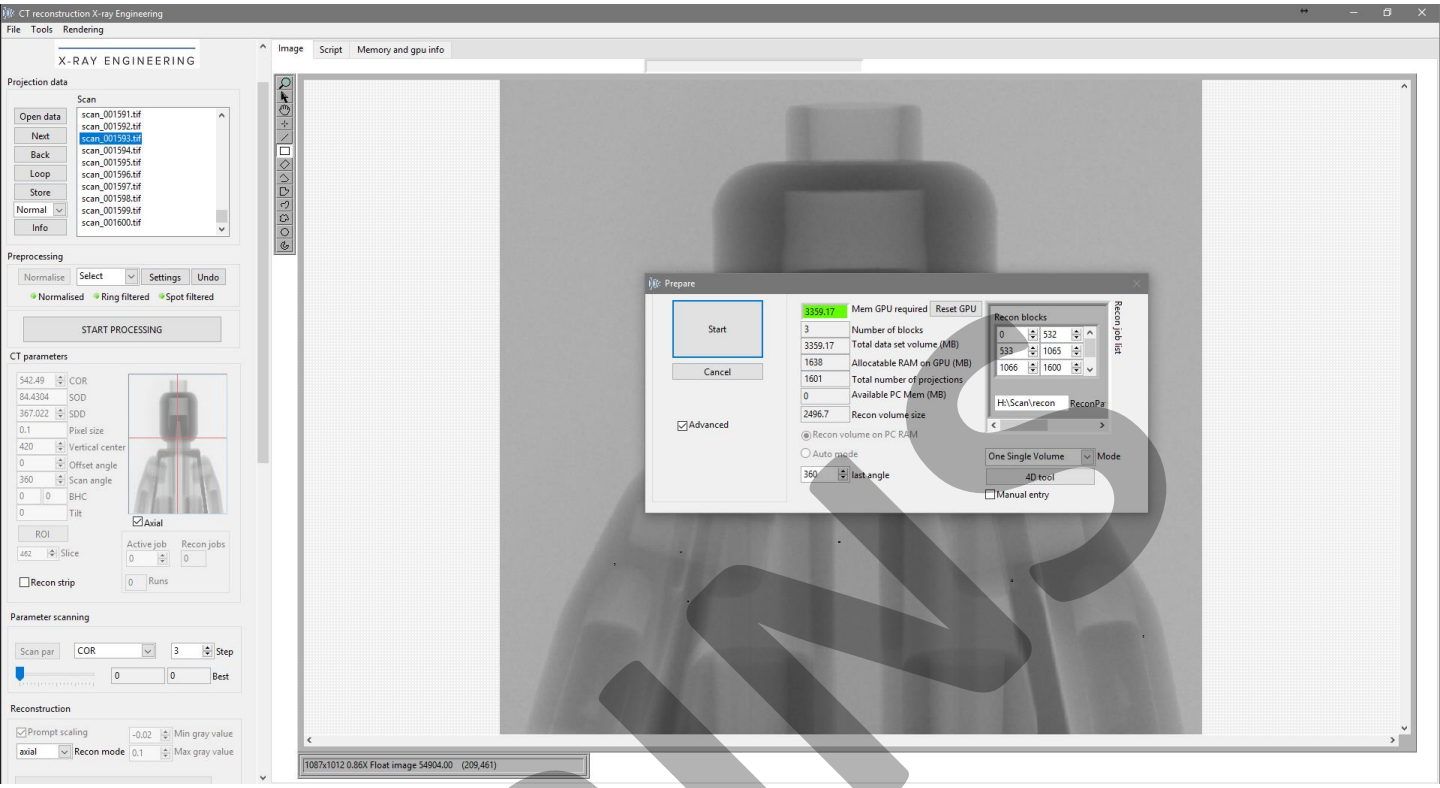
If the spot filter level is too high, parts of the scanned object are removed from the projection images, which will result in loss of information in the reconstructed image

If the desired spot filter level is found, select *Spot filter* from the drop down menu to perform the operation on the entire dataset.



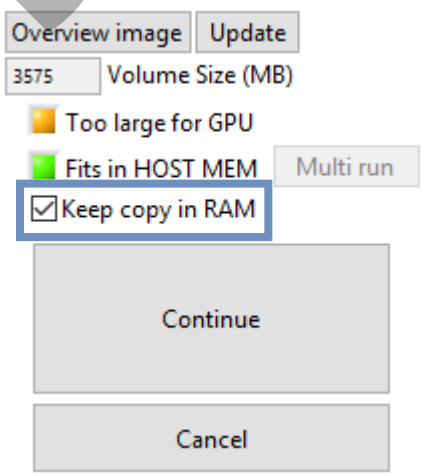


2. General reconstruction workflow

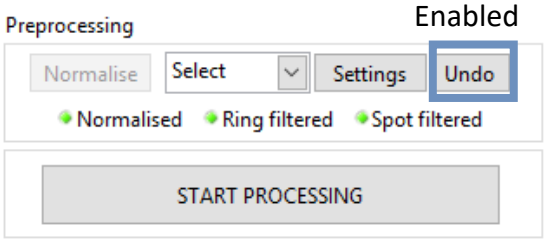


Preprocessing

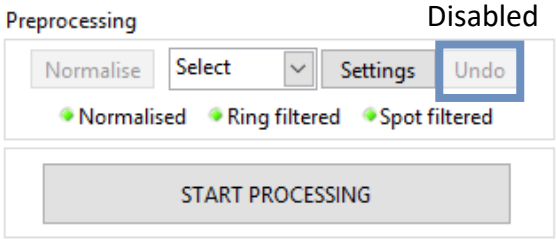
Depending on the *Keep copy in RAM* checkbox, which can be checked during the data selection depending on the available RAM memory, the *Undo* button can be enabled. This button allows to reset the performed preprocessing steps.



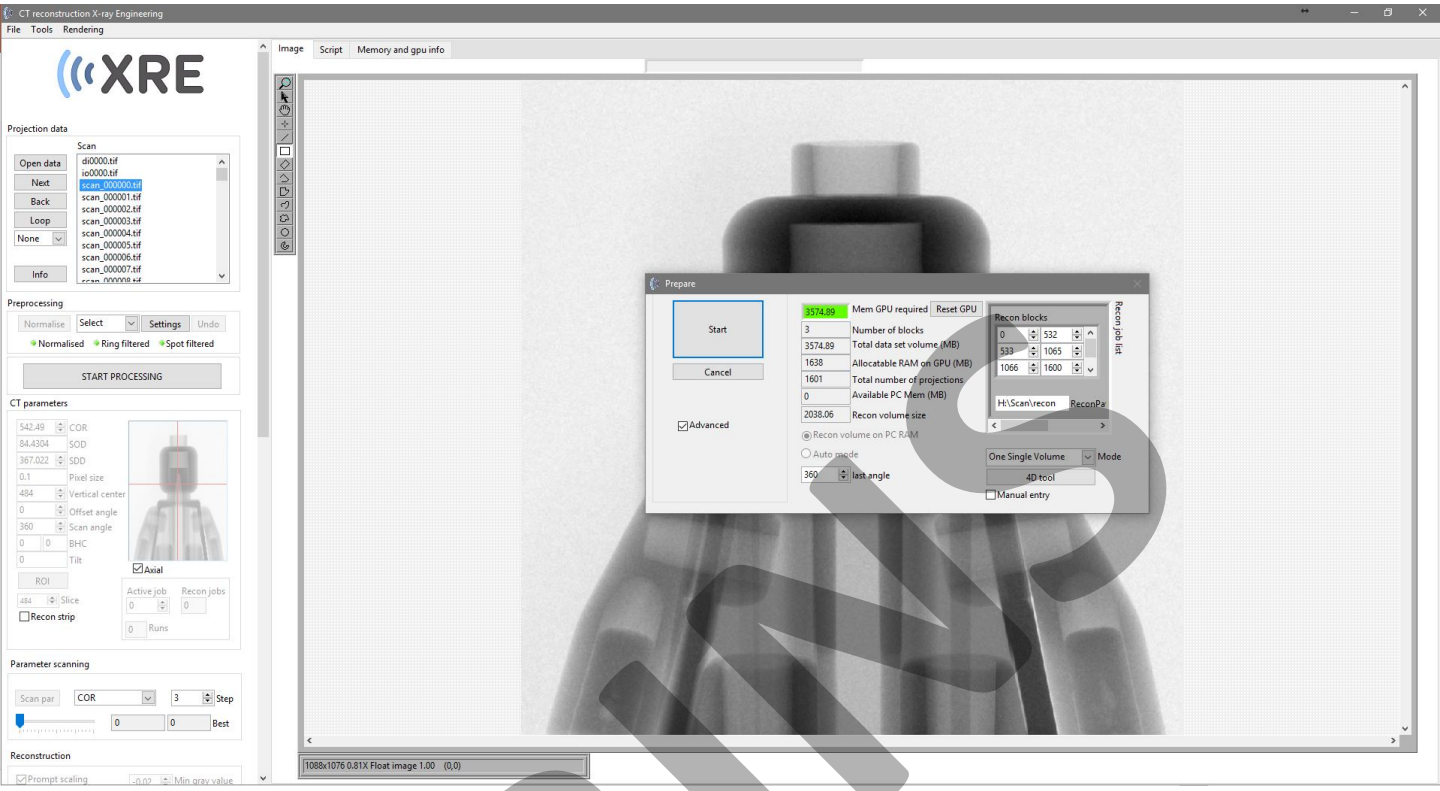
Enabled



Disabled

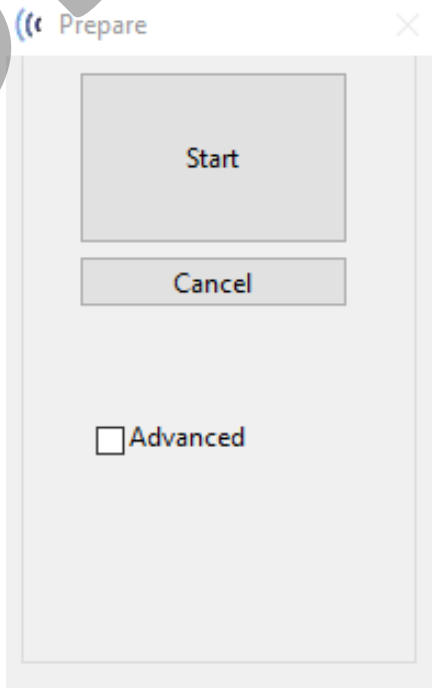


2. General reconstruction workflow



Reconstruction

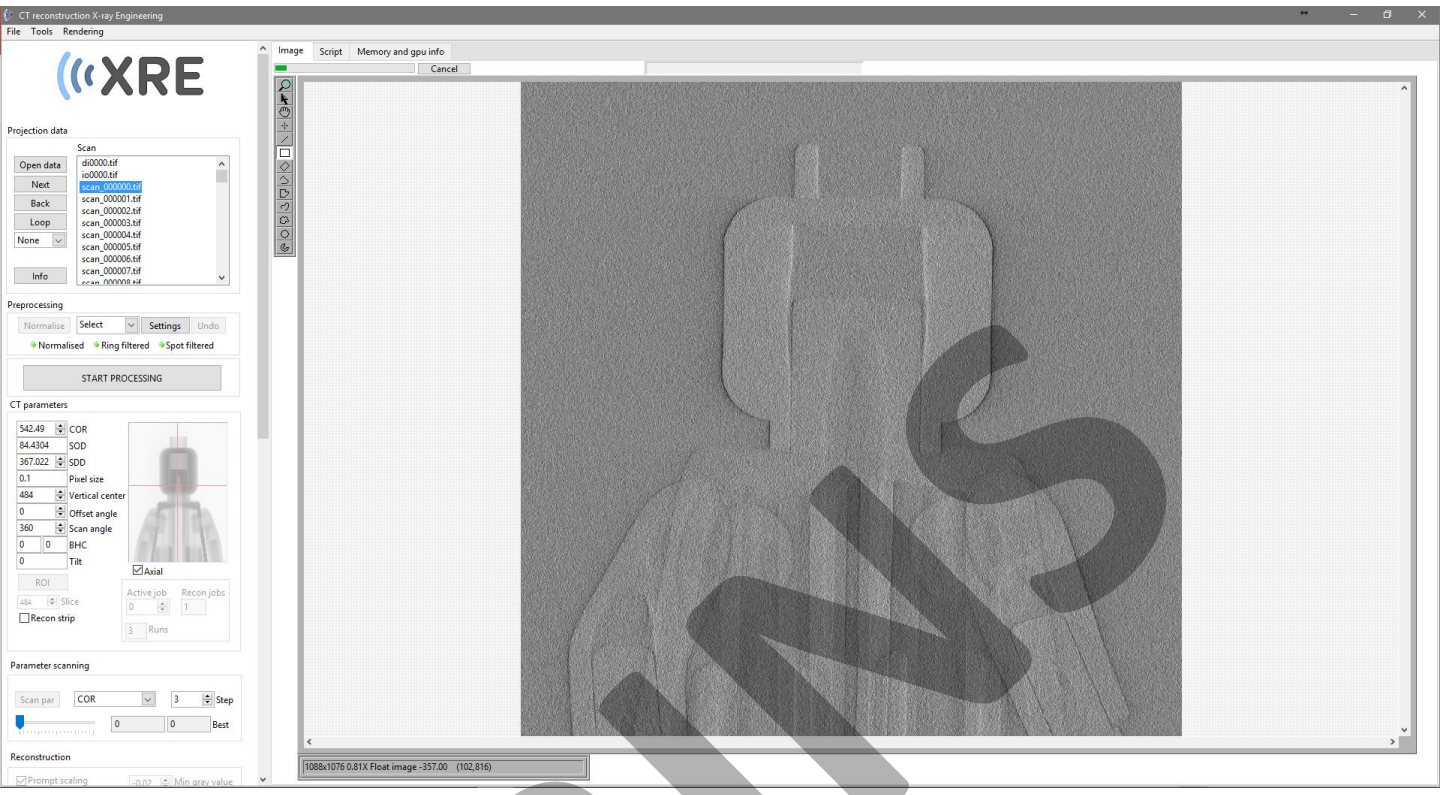
Once the preprocessing of the projection images is executed the data can be reconstructed by clicking *START PROCESSING.*



This displays a popup window on which you can choose to *Start* or *Cancel* the installation.

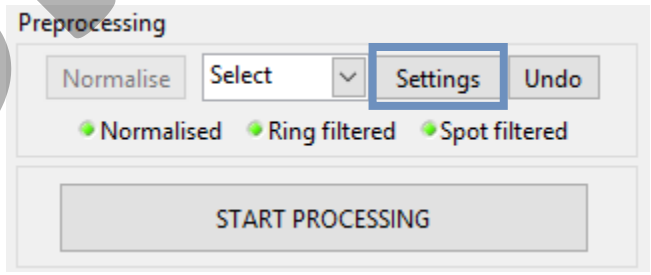
The *Advanced* checkbox can be used to obtain more details about the GPU memory and how the data will be sent to the GPU.

2. General reconstruction workflow

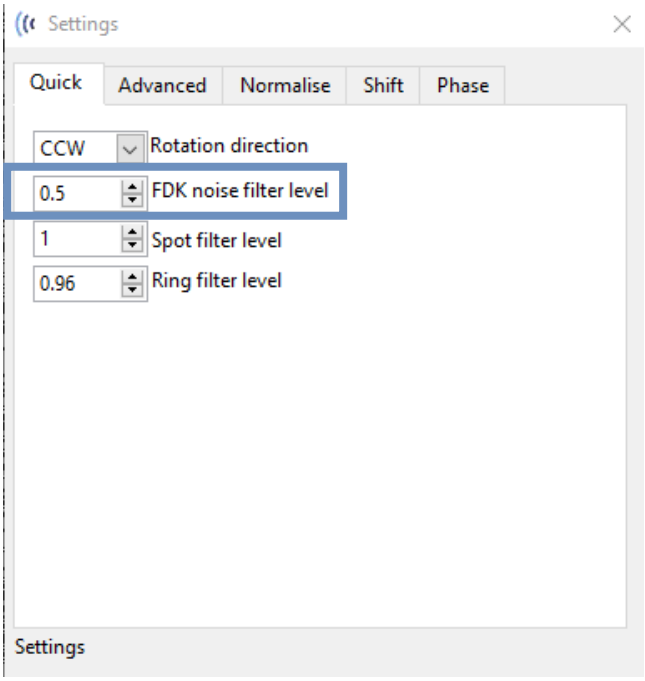


Reconstruction

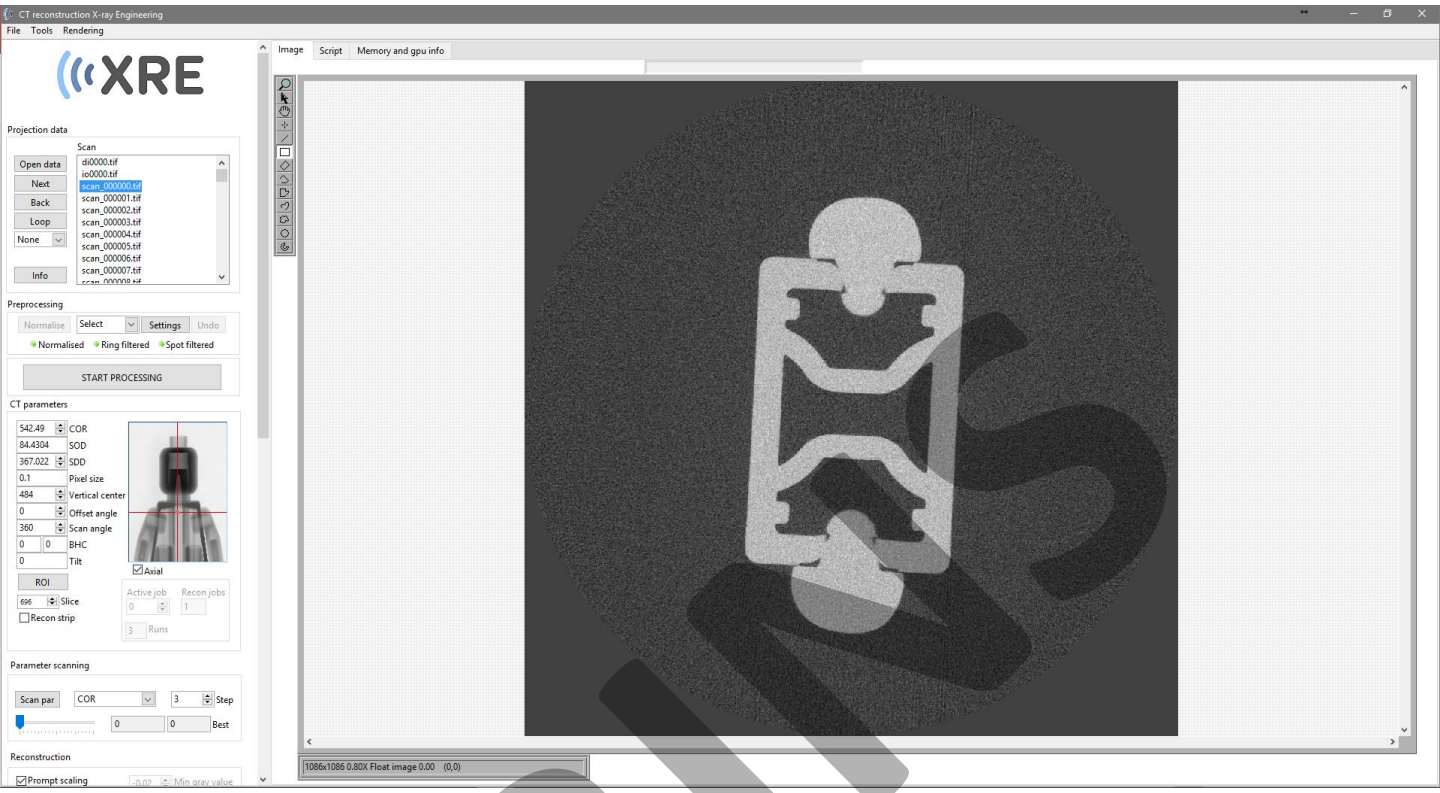
After clicking the *Start* button, the data is transferred from the computers RAM memory to the GPU.



During loading a fourier filter is applied on the projection images. The strength of this fourier filter can be adapted by changing the value of the *FDK noise filter level* using the *Settings* button. Higher levels, up to 1, will reduce the noise level in the reconstructed image.

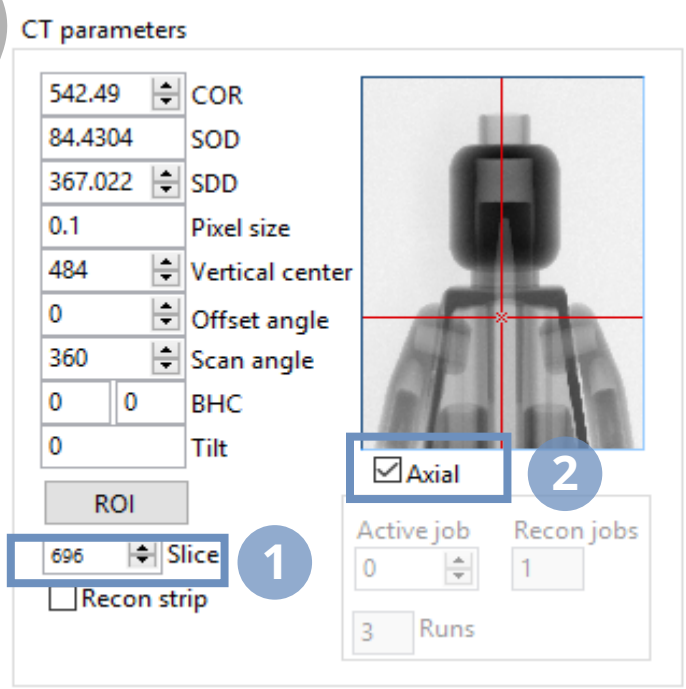


2. General reconstruction workflow



Reconstruction

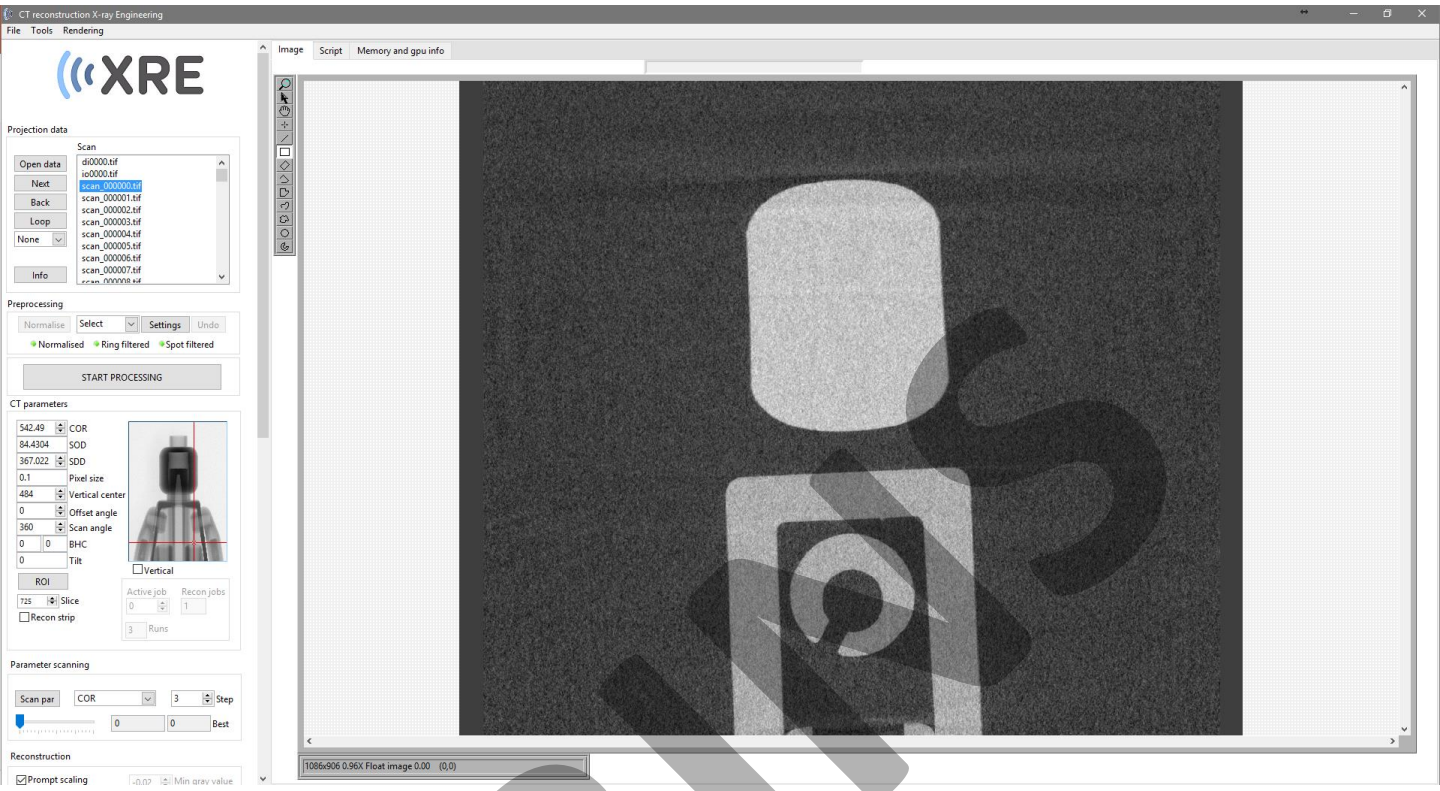
Once the data is loaded into the GPU memory, an axial slice through the center of the sample is displayed in the *Imaging section.*



1. The displayed slice can be changed by changing the slice number in the *Slice* indicator.

2. The checkbox below the overview radiography can be used to switch from *Axial* to *Vertical* slices.

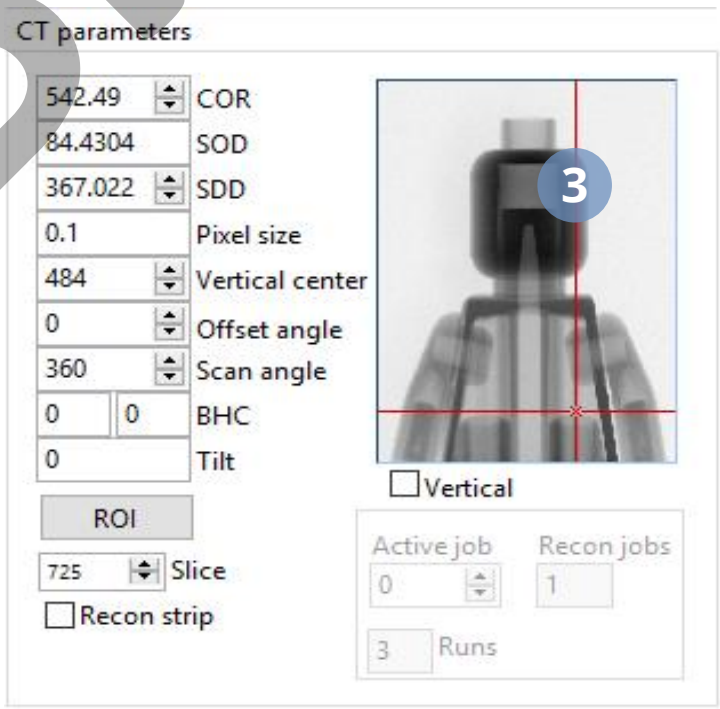
2. General reconstruction workflow



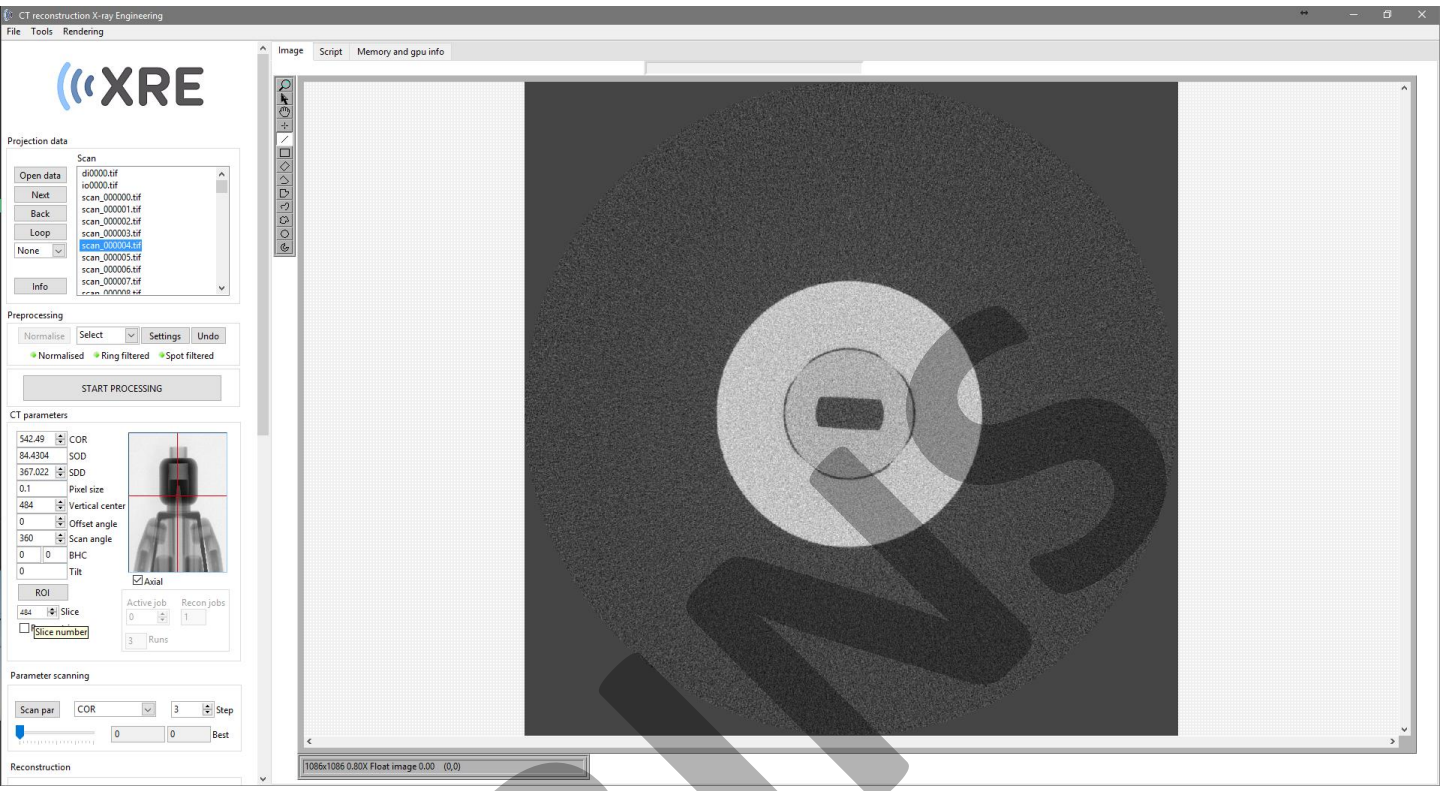
Reconstruction

3 The reconstructed slice can also be changed using the 2 red line indicators in the overview radiography. The horizontal line can be used to display an axial slice, while the vertical line can be used to display a vertical slice.

Right clicking the overview radiography enables to easily *Center cursors and* display the central axial slice.



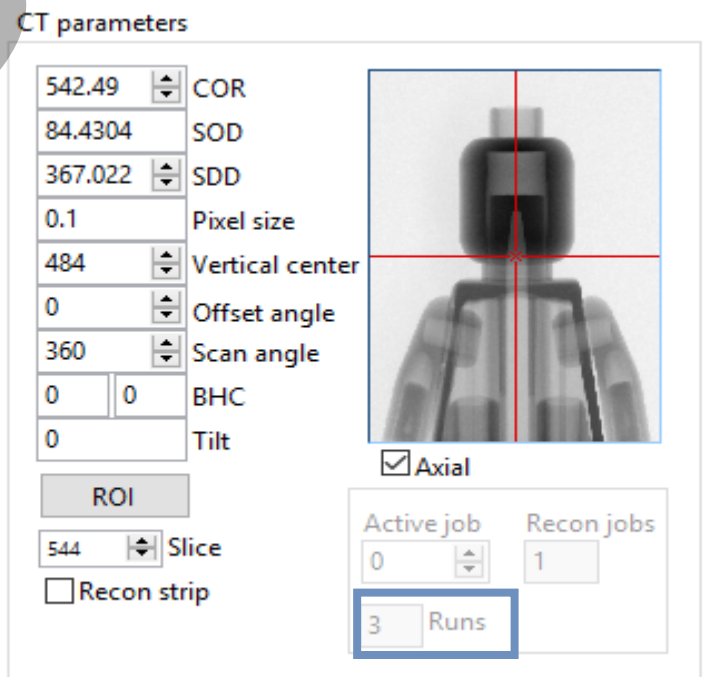
2. General reconstruction workflow



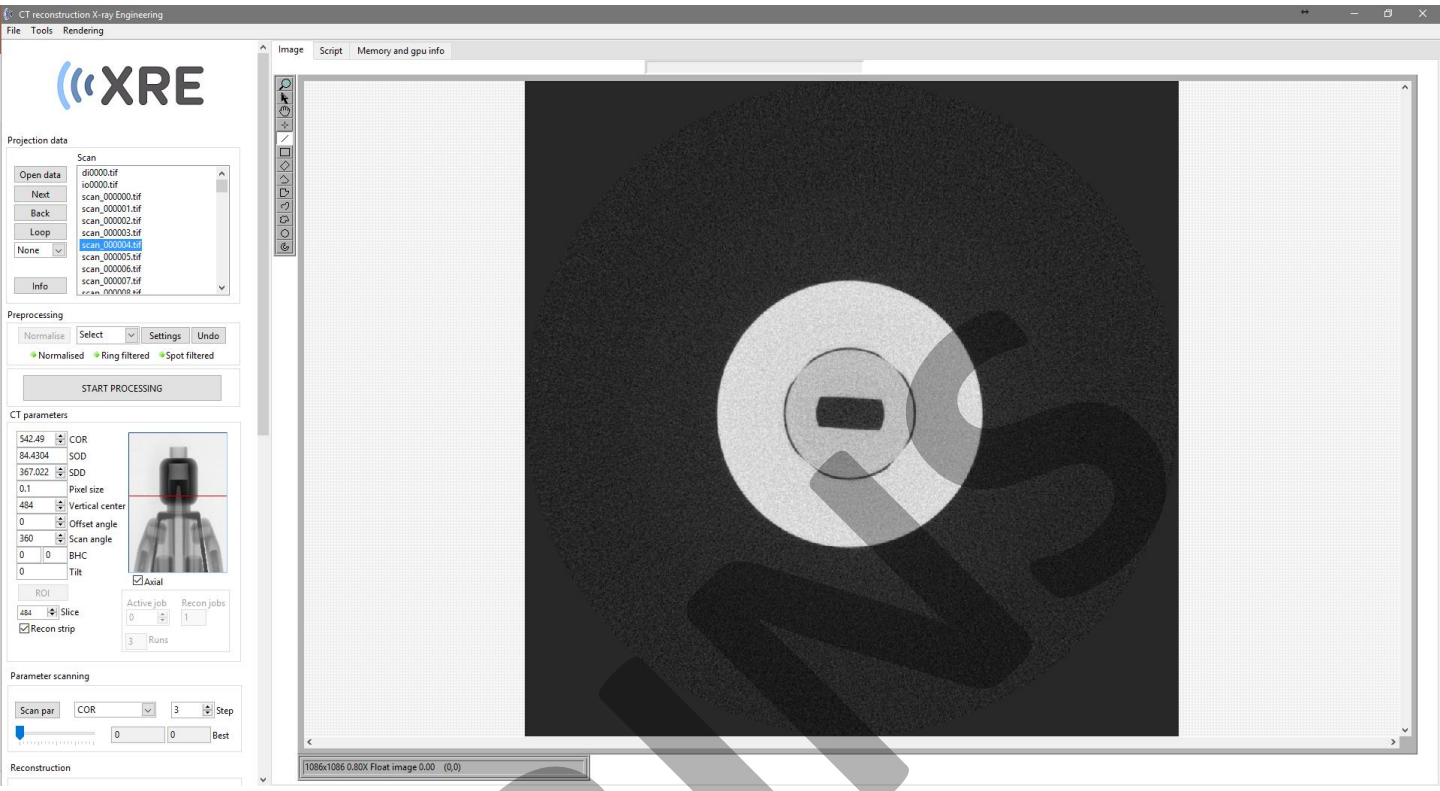
Reconstruction

Depending on the hardware configuration of the Reconstruction PC and the size of the dataset, the reconstruction can be split up in multiple *Runs.* This makes it possible to reconstruct very large datasets at full quality even if the hardware configuration of the PC is limited.

To generate a reconstructed slice in the *Image section* however, only a part of the data is sent to the GPU and the quality of the preview slice will be lower than the quality in the final reconstruction.



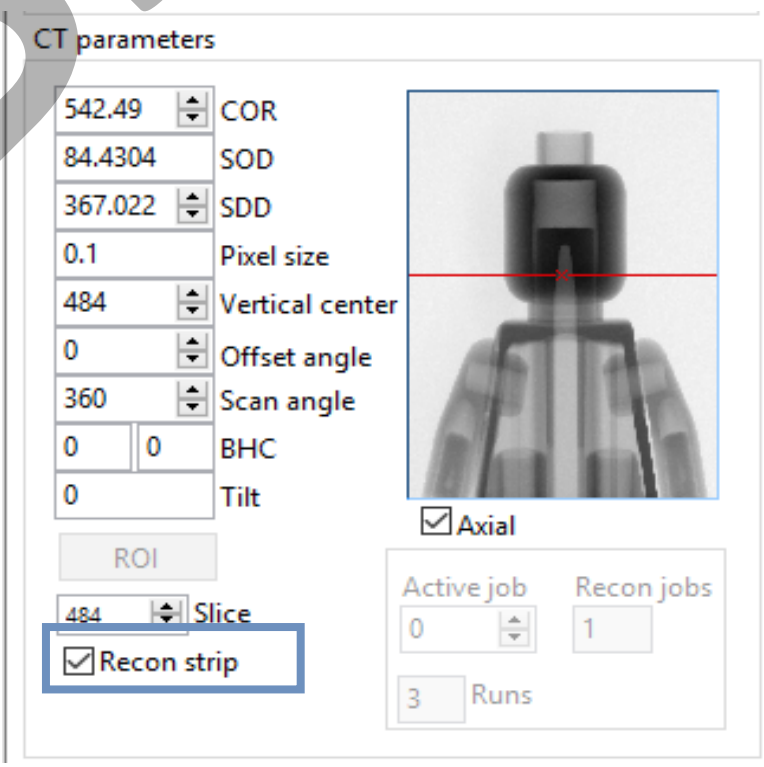
2. General reconstruction workflow



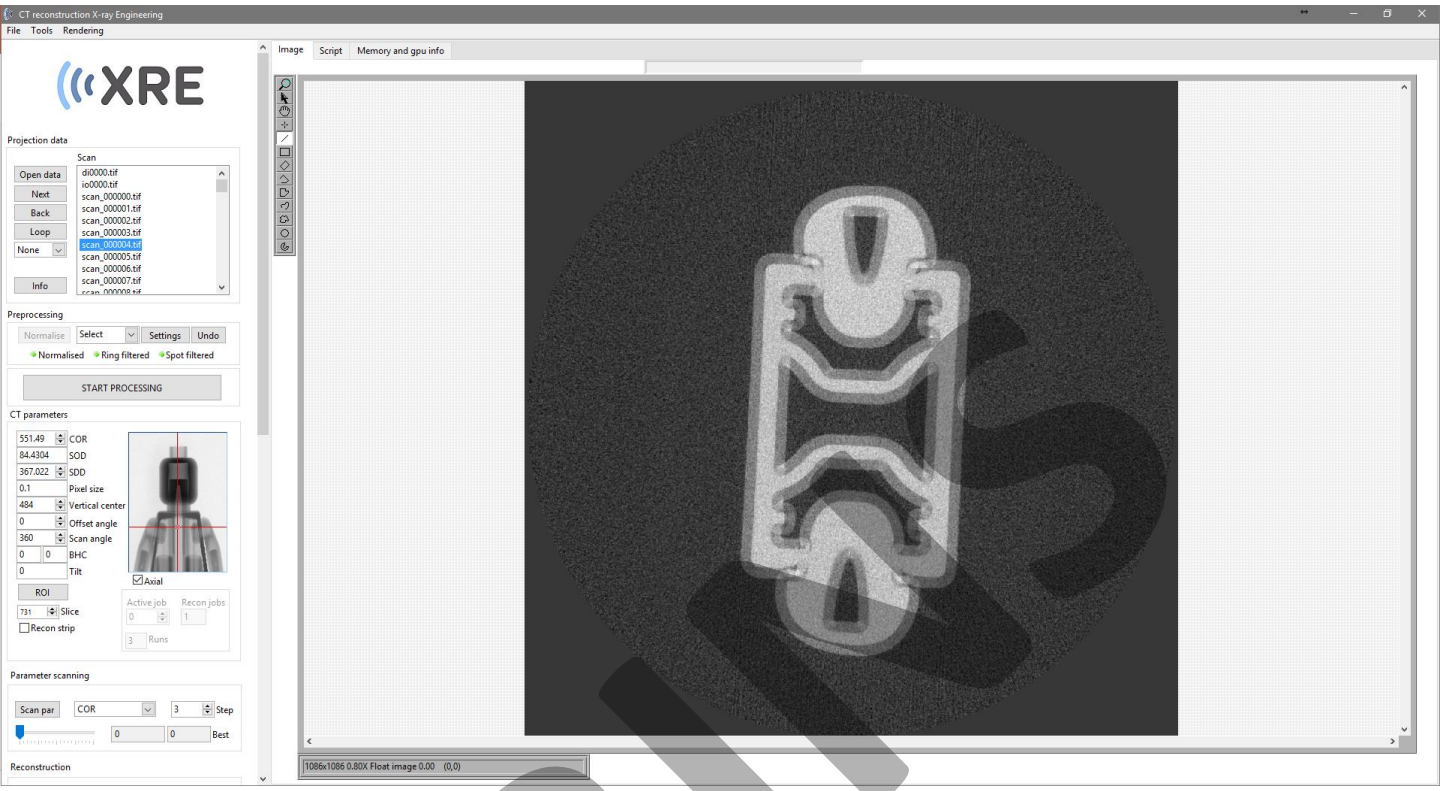
Reconstruction

In order to obtain a full quality axial reconstructed slice in the *Image section* the *Recon strip* checkbox can be clicked.

This will load a small strip of the of the projection data to the GPU and to do a high quality reconstruction of the selected slice.



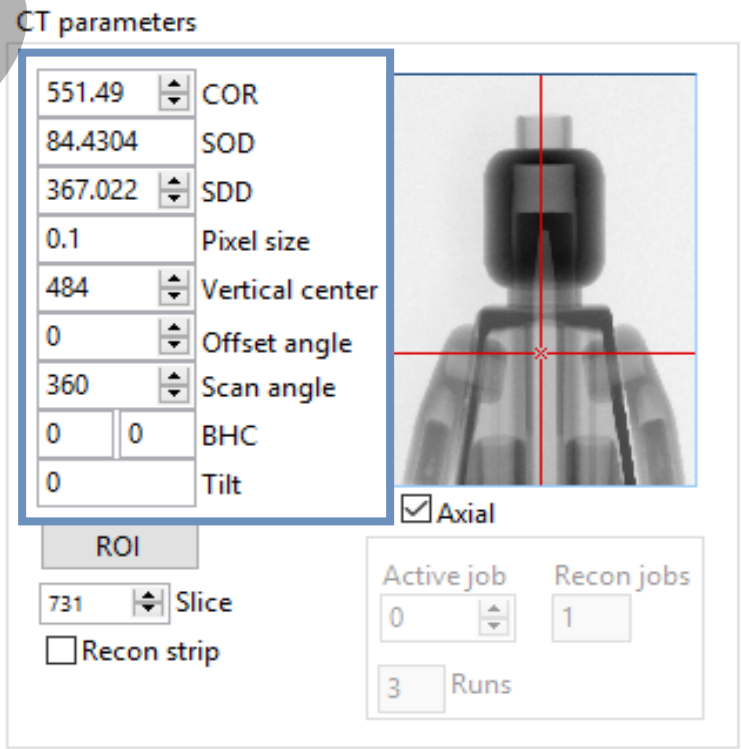
2. General reconstruction workflow



Reconstruction

Once the data is loaded, multiple *CT parameters* can be evaluated to finetune the reconstructed slices.

The parameters can be manually changed using the numerical indicator and the effect of the parameter change is directly shown in the *image section.*

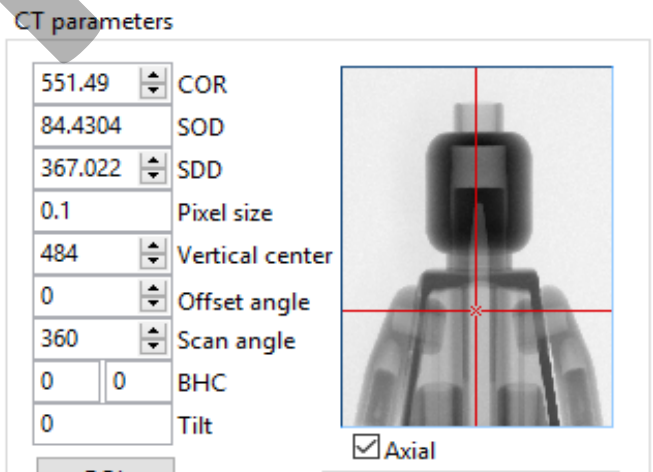


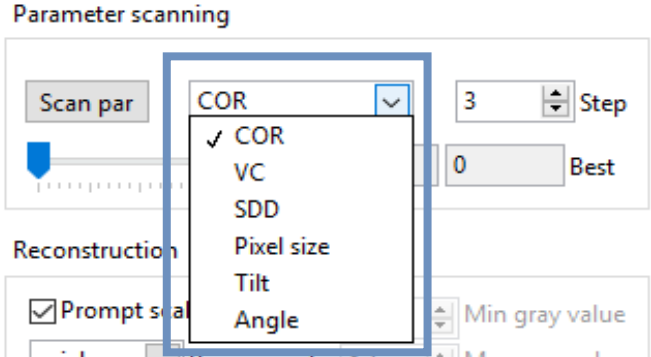
2. General reconstruction workflow

Reconstruction

The CT parameters can also be automatically evaluated using *Parameter scanning*.

A CT parameter for evaluation can be selected from the drop down menu and a *Step* needs to be defined. When the *Scan par* button is pressed, the optimal CT parameter will be detected by evaluating 17 values around the current parameter value and with the given step size.



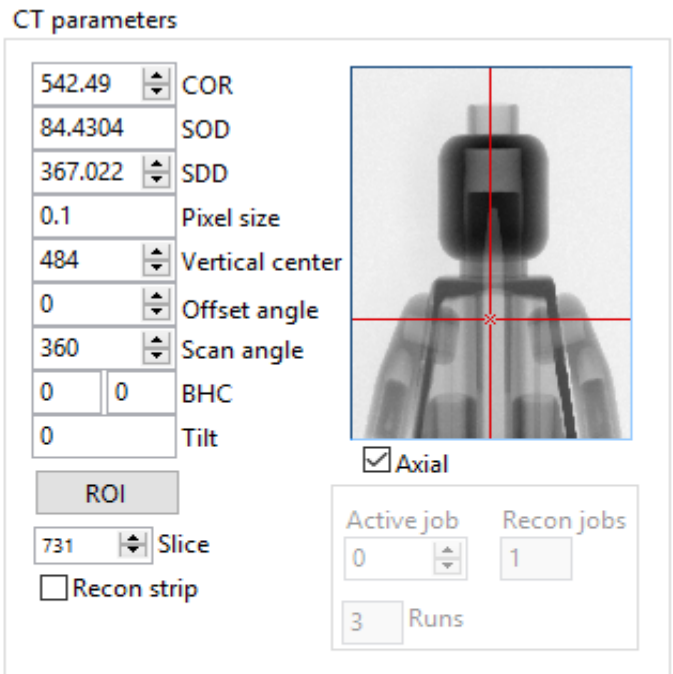


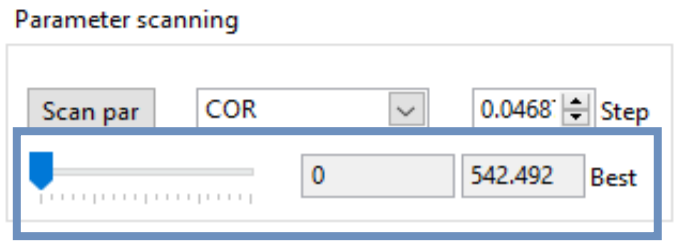
2. General reconstruction workflow

Reconstruction

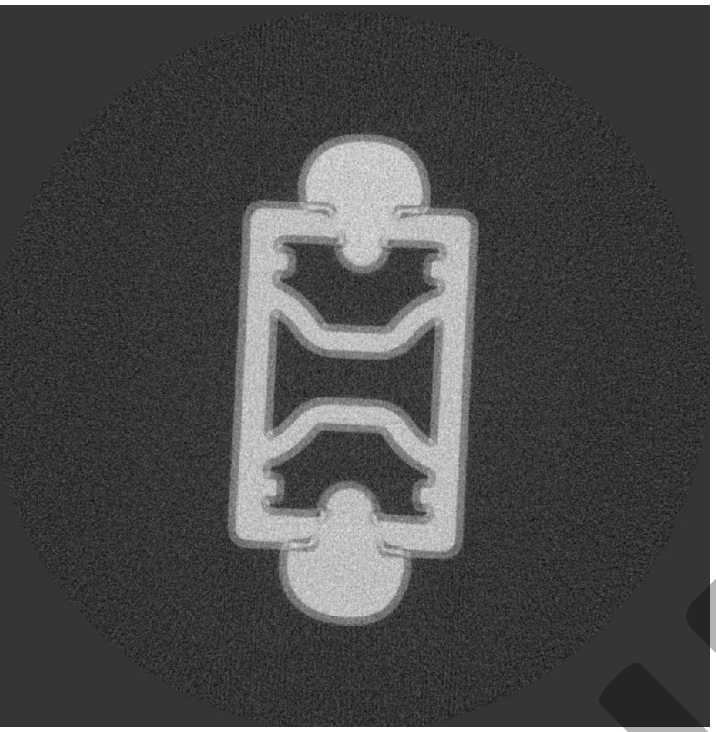
The best value of the parameter scan is automatically selected by the software. If needed however, this value can be manually altered using the slider below the *Scan par* button.

After a parameter scan the *Step* value is automatically reduced 4 times, which allows to finetune the CT parameter even further.

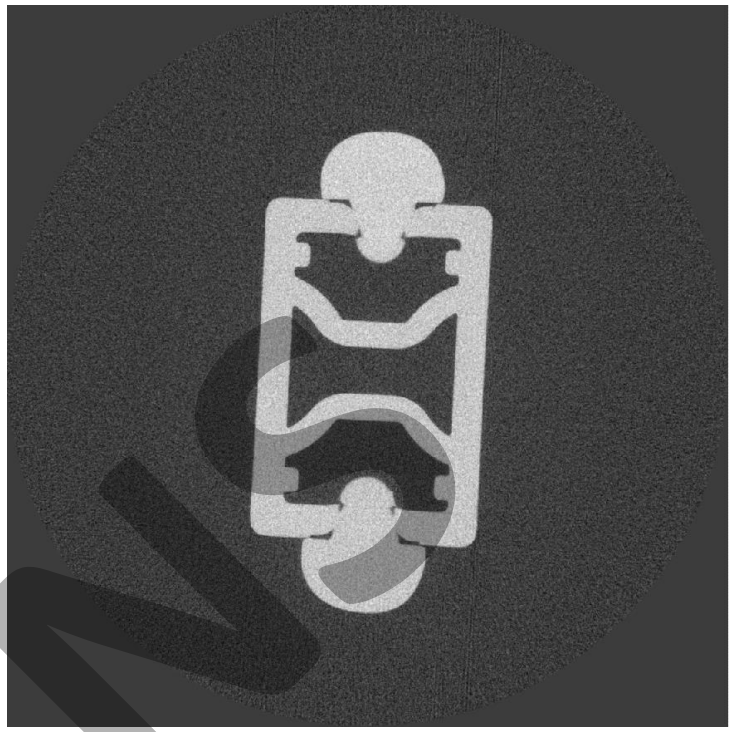




2. General reconstruction workflow



COR = 548.54



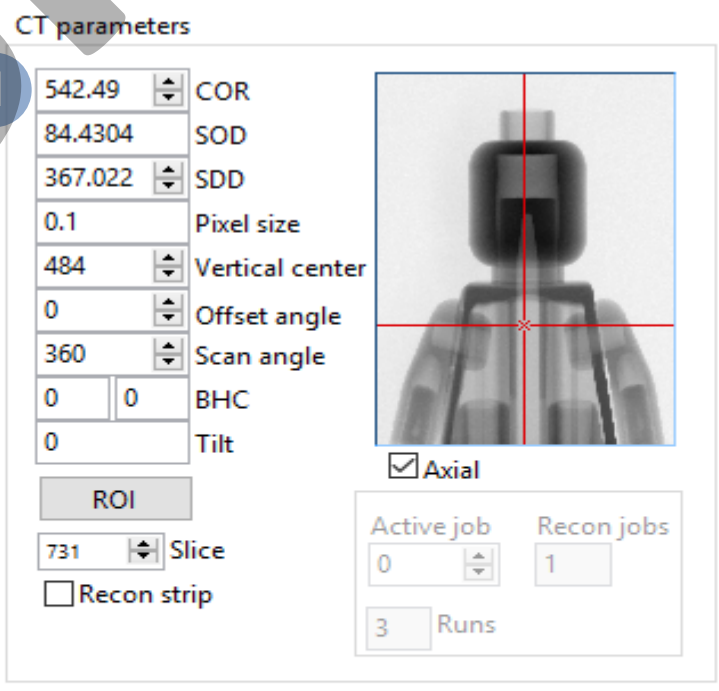
COR = 542.54

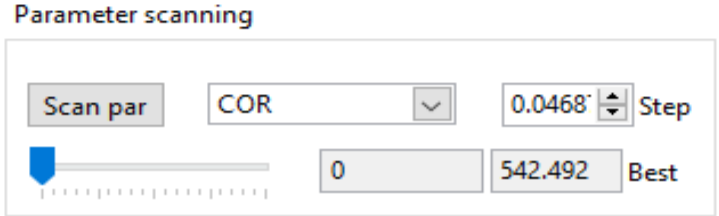
Reconstruction

1 *COR – Center of Rotation*

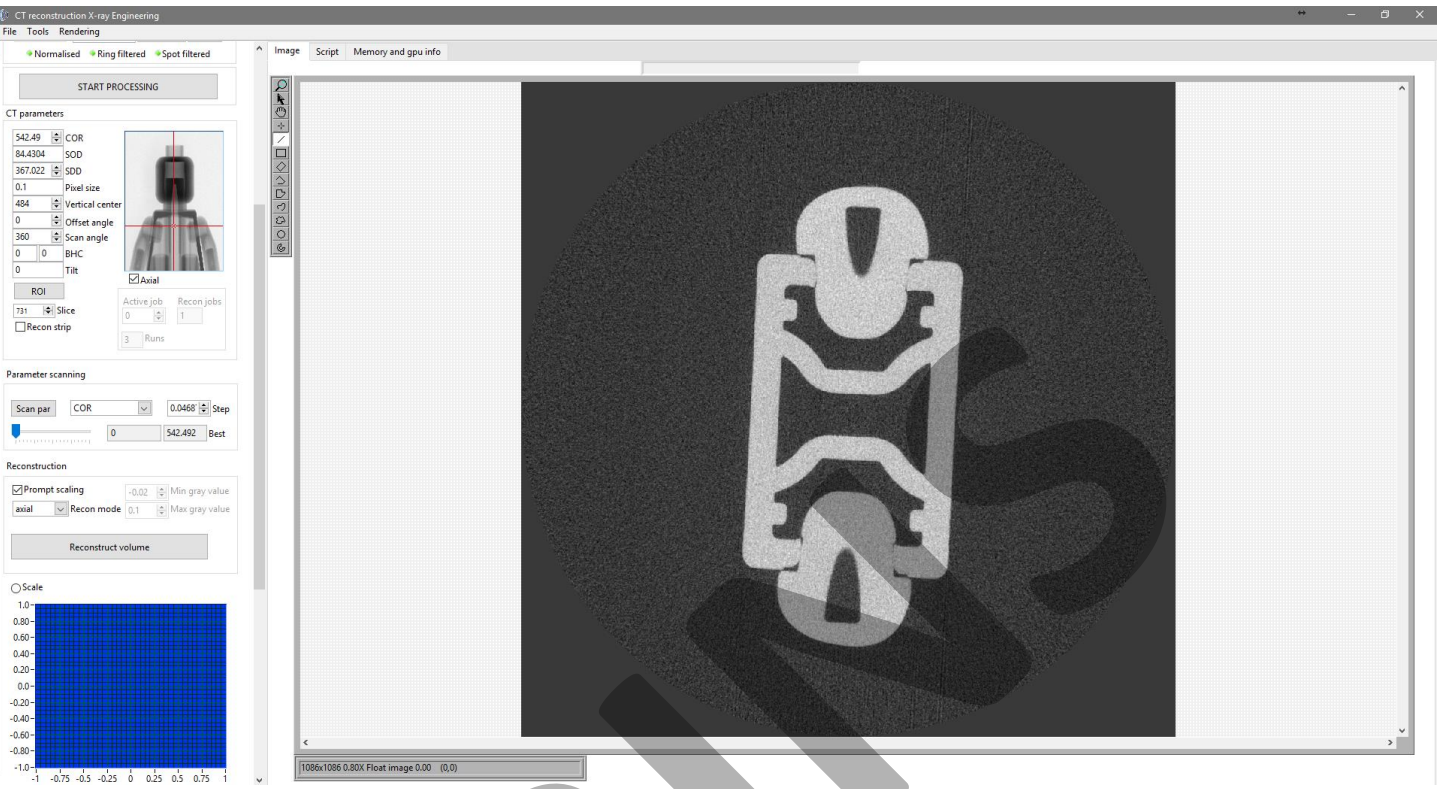
The position of the rotation axis or the centre of rotation is the horizontal position where the rotation axis is projected on the detector.

When the position of the rotation axis is incorrect, an unsharp double edge is often present in the reconstructed image (image above at COR = 548.54).





2. General reconstruction workflow



Reconstruction

2 *SOD – Source Object Distance*

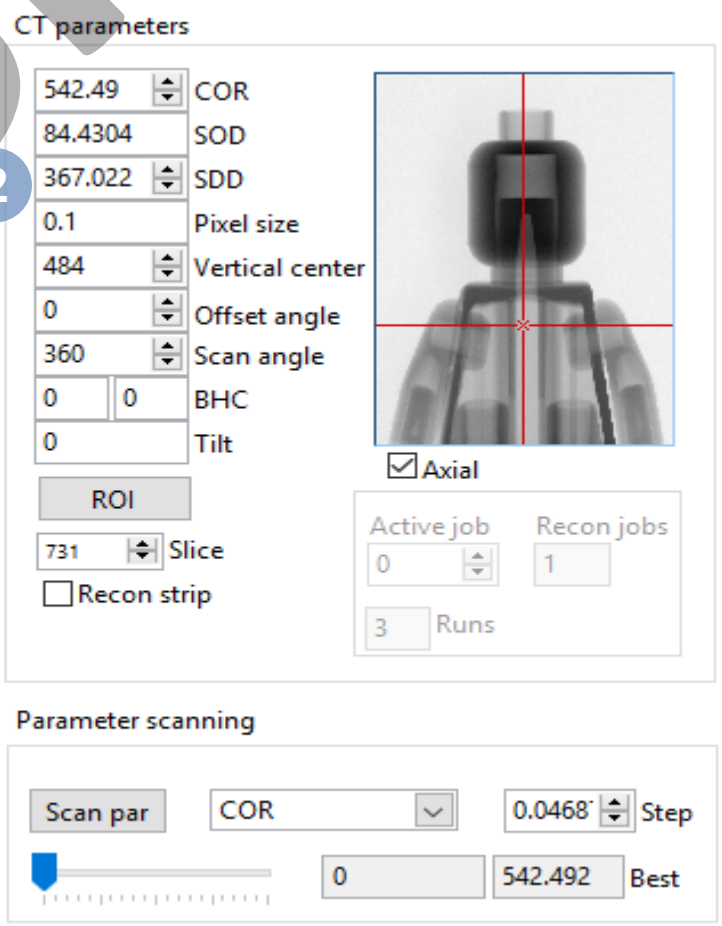
The distance between the focal spot of the X-ray source and the rotation axis of the sample.

SDD – Source Detector Distance

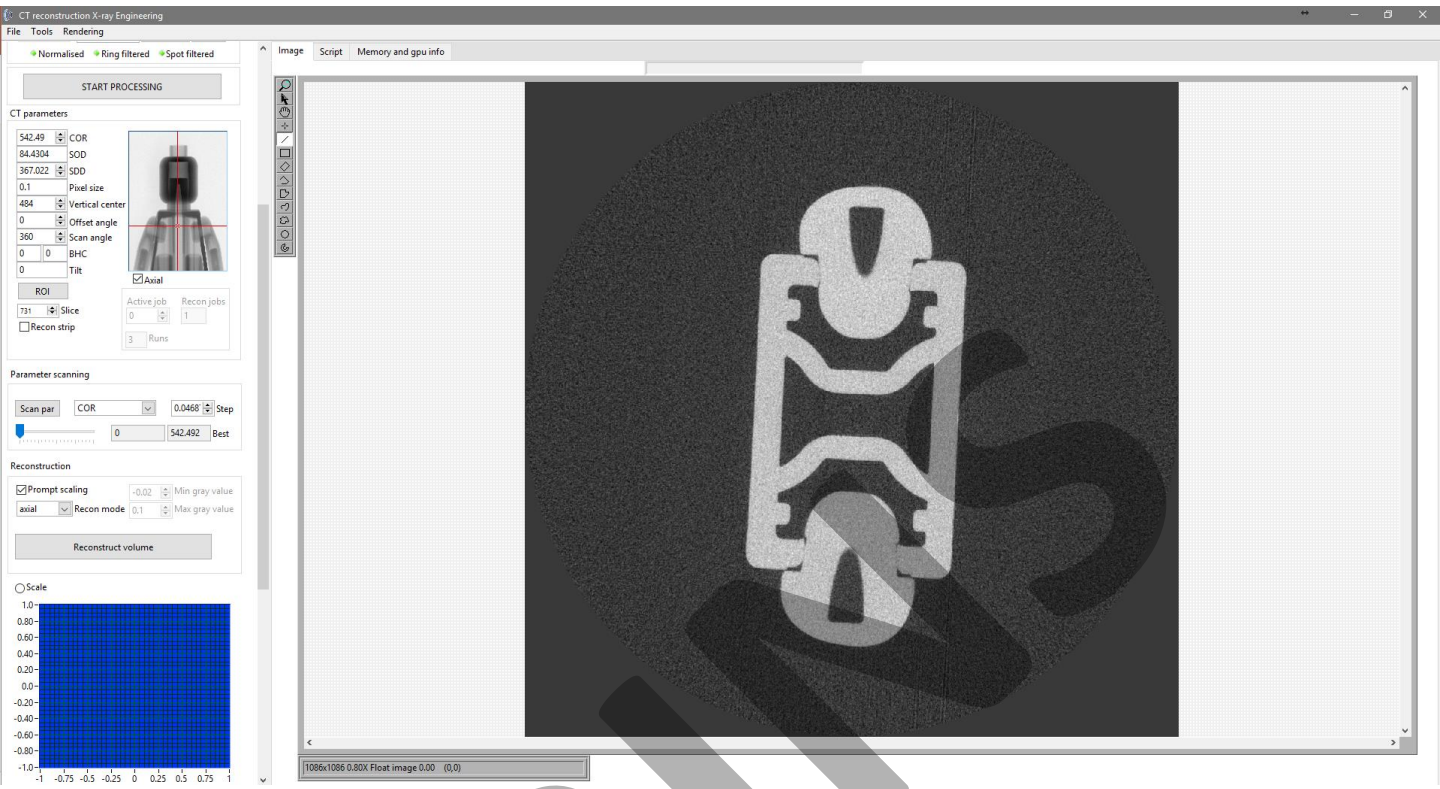
The distance between the focal spot of the X-ray source and the detector.

Pixel size - Is the size (in mm) of a single pixel in the detector and is detector specific.

The parameters above are provided by the system and should not be altered if the system is correctly calibrated.



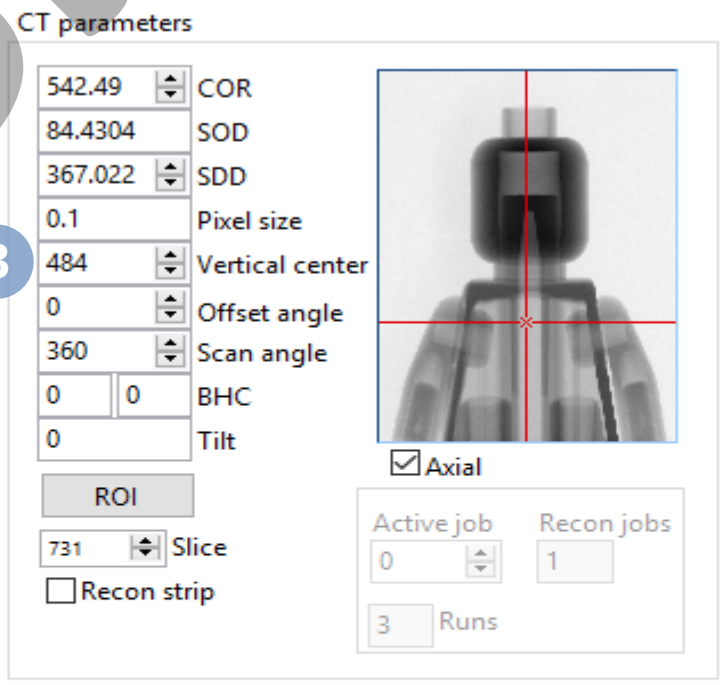
2. General reconstruction workflow

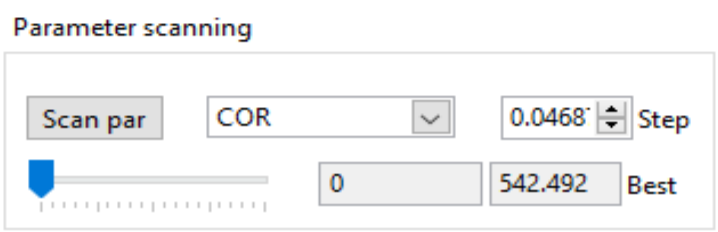


Reconstruction

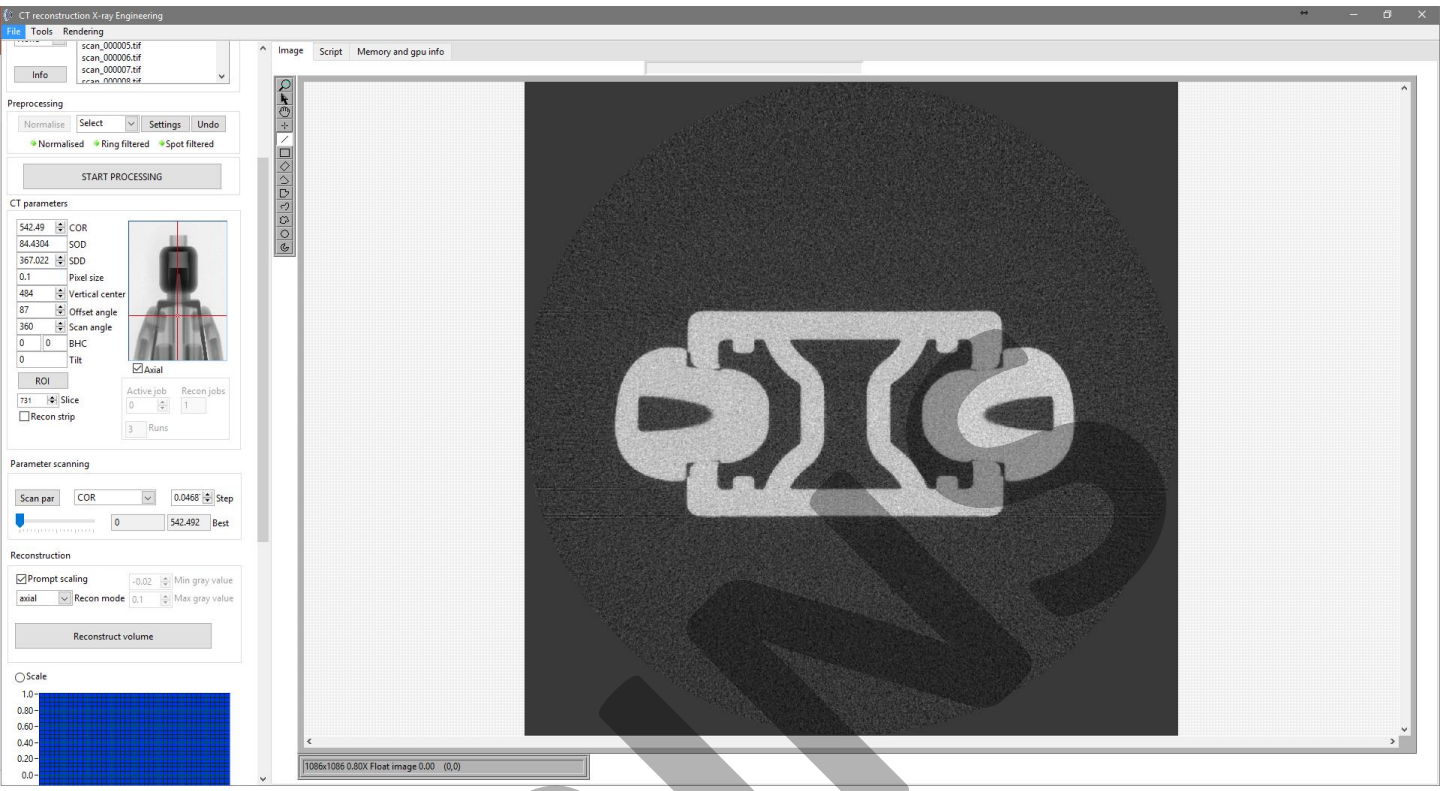
3 *Vertical center*

The vertical center is the vertical position of intersection of the optical axis and the detector. Normally the intersection is the center of the detector, but this can change if the vertical position of the detector is altered.





2. General reconstruction workflow



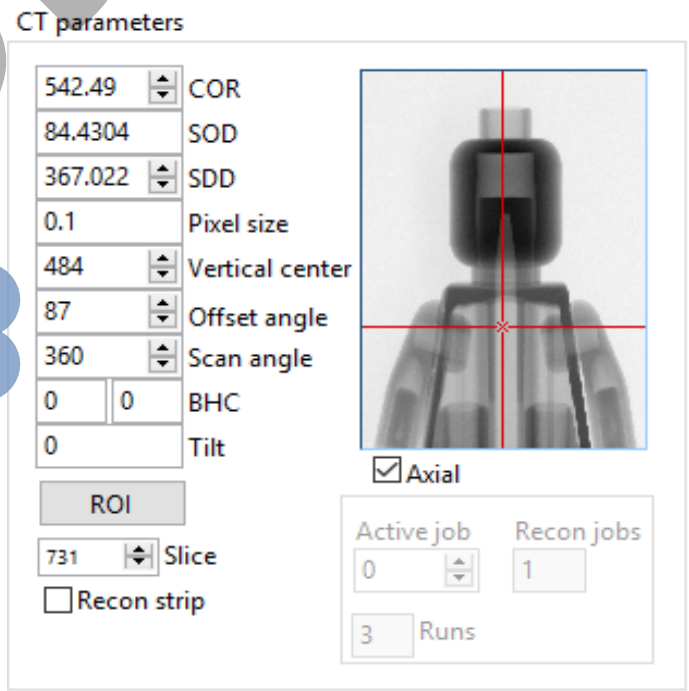
Reconstruction

4 *Offset angle*

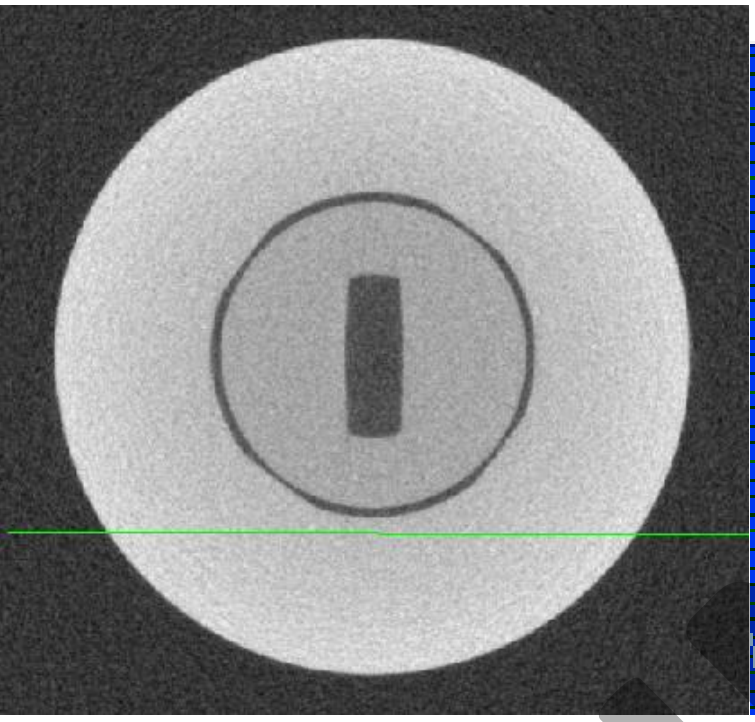
The offset makes it possible to virtually rotate the reconstructed images around the rotation axis. This can be useful for post processing the images or optimize the cropping region to reduce image size

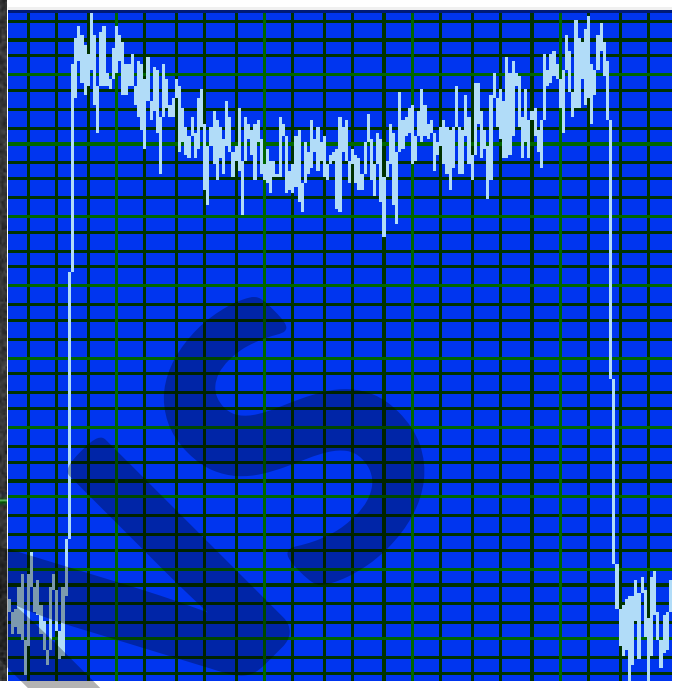
5 *Scan angle*

The scan angle is the number of degrees the sample has rotated and is usually 360 degrees.



2. General reconstruction workflow



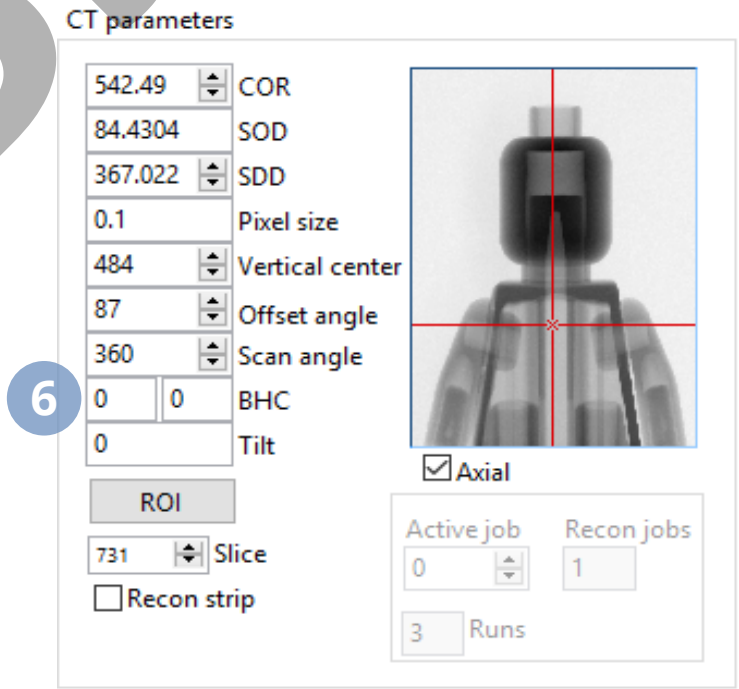


Reconstruction

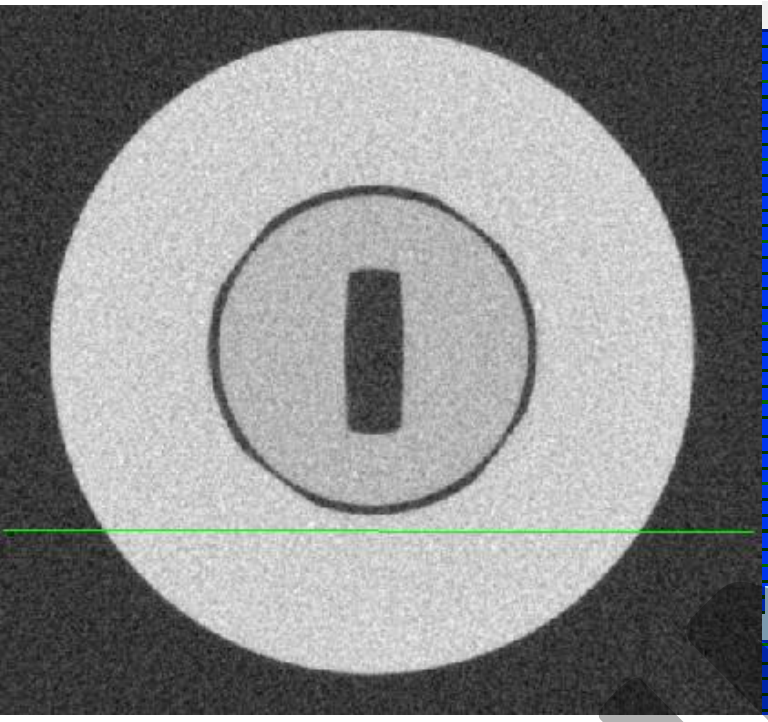
6 *BHC – beam hardening correction*

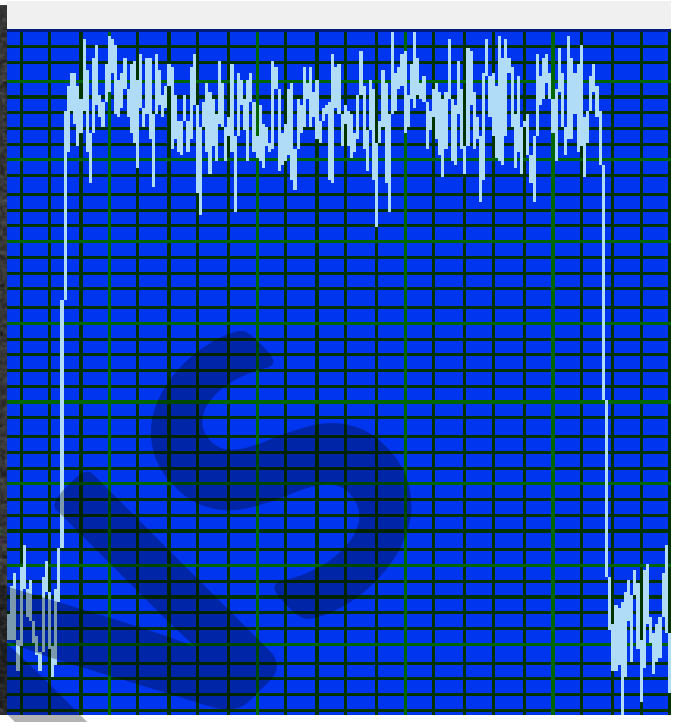
Beam hardening is an artifact caused by the polychromatic nature of the X-ray beam. In the reconstructed image this introduces non-linearities which gives the impression that an object is less dense in the center and more dense towards the edges.

This is sometimes also referred to as a cupping effect and is very noticeable when a line profile of the grey values is plotted (images above).



2. General reconstruction workflow



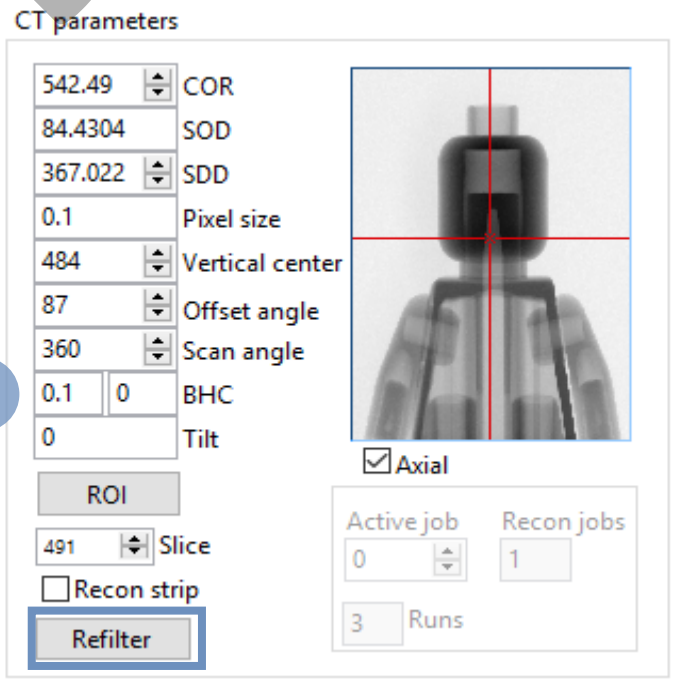


6 Reconstruction

Beam hardening can be avoided by placing a hardware filter on the X-ray source and pre-hardening the X-ray beam.

If beam hardening artefacts are present in the slices, the *BHC* parameters can be adapted to obtain a straight grey value profile through the object, reducing the cupping effect.

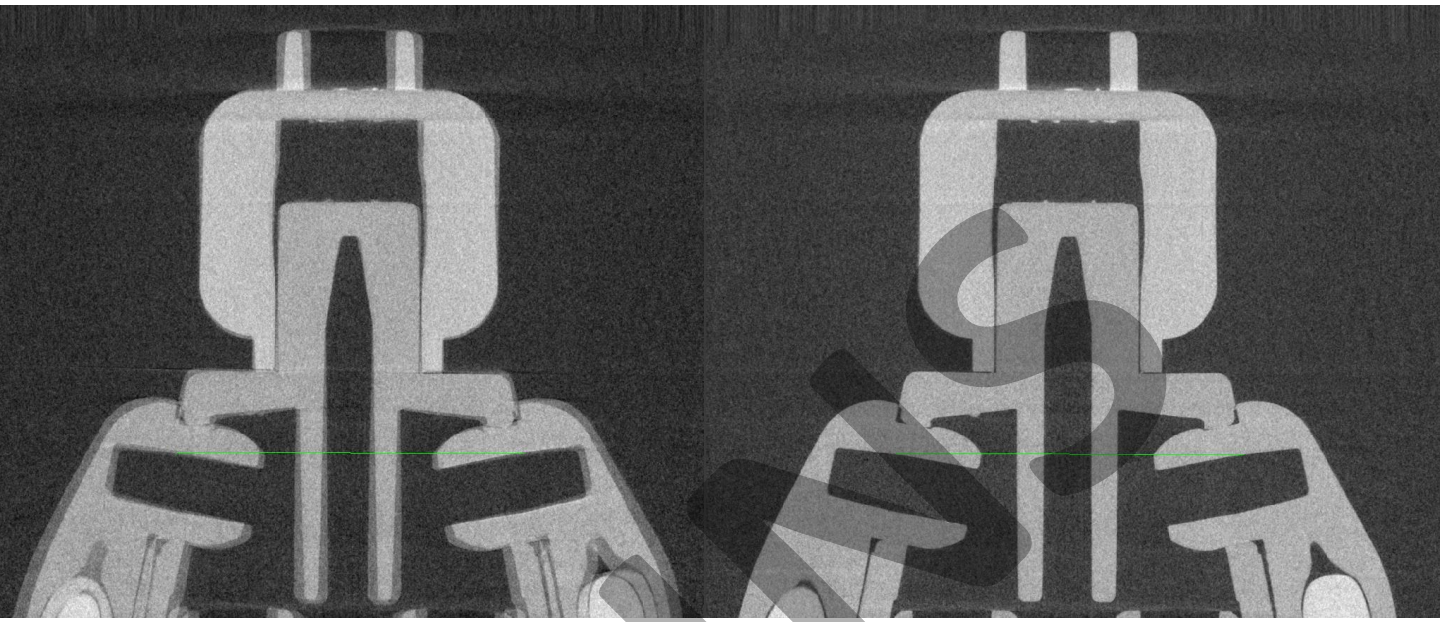
Usually the first parameter is sufficient for the correction, if this is however not sufficient the seconds parameter can be applied.



6

Once a *BHC* parameter is altered the projection data needs to be refiltered, which can be done by clicking the *Refilter* button.

2. General reconstruction workflow



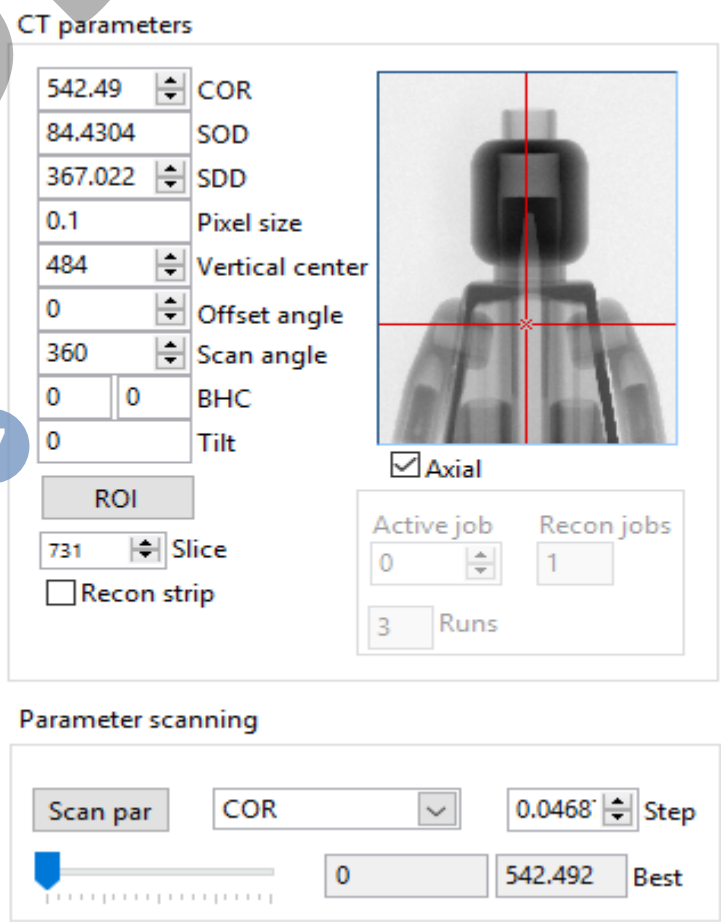
Tilt = 1 Tilt = 0

Reconstruction

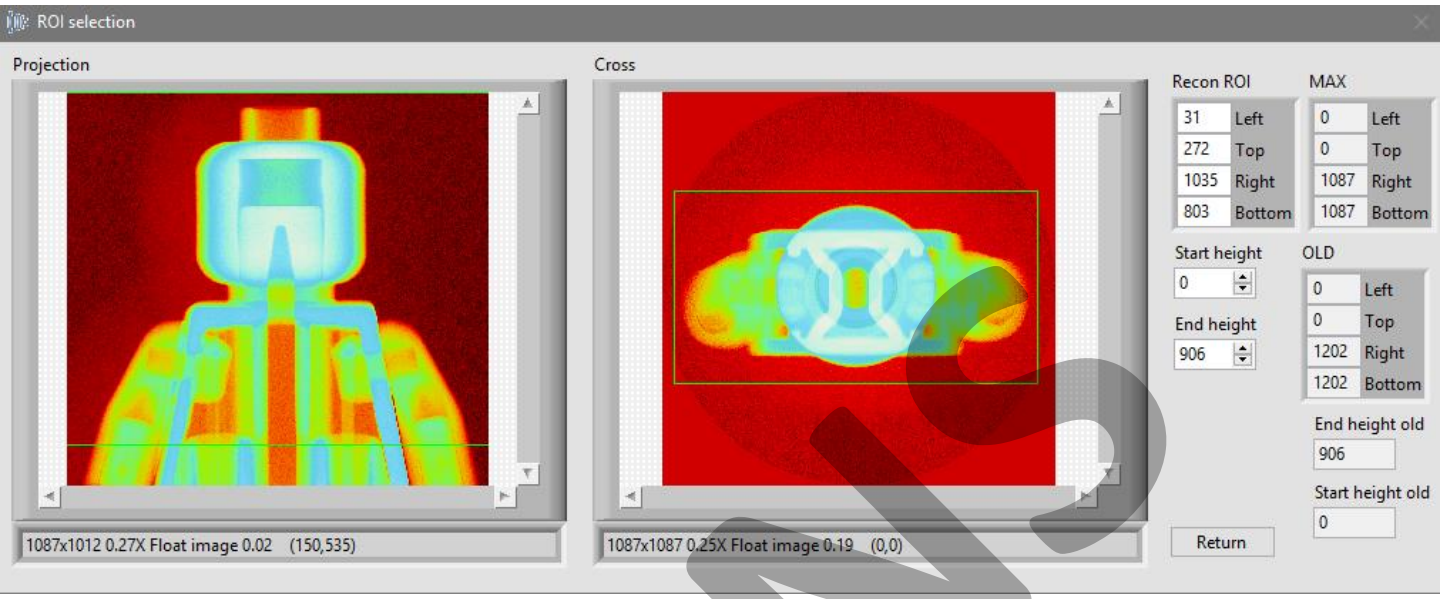
7 *Tilt*

The tilt parameter corrects misalignments of the detector, which are more prominent at the top an bottom of the scanned volume.

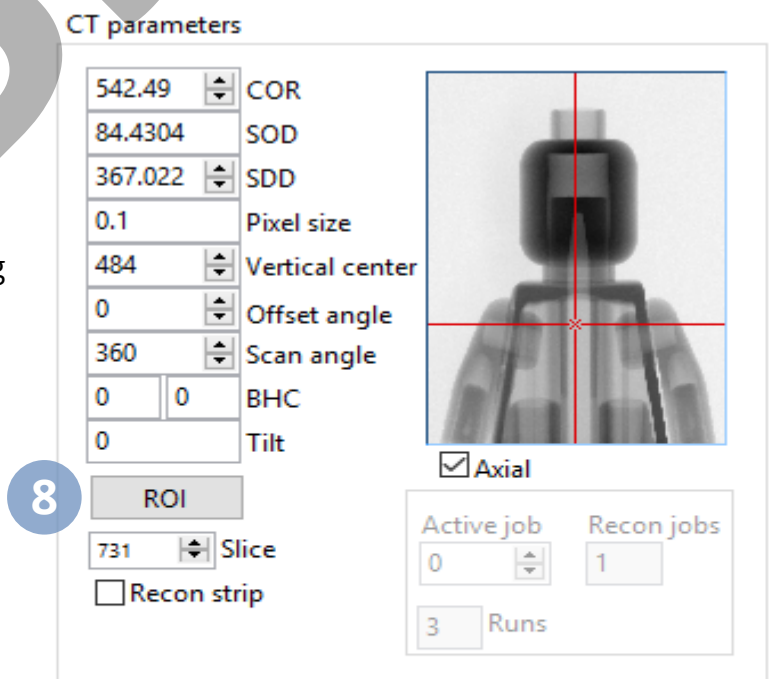
The effect of tilt is easy to detect as an unsharp double edge in the vertical slice though the volume or in an axial slice at the top or bottom.



2. General reconstruction workflow



Reconstruction



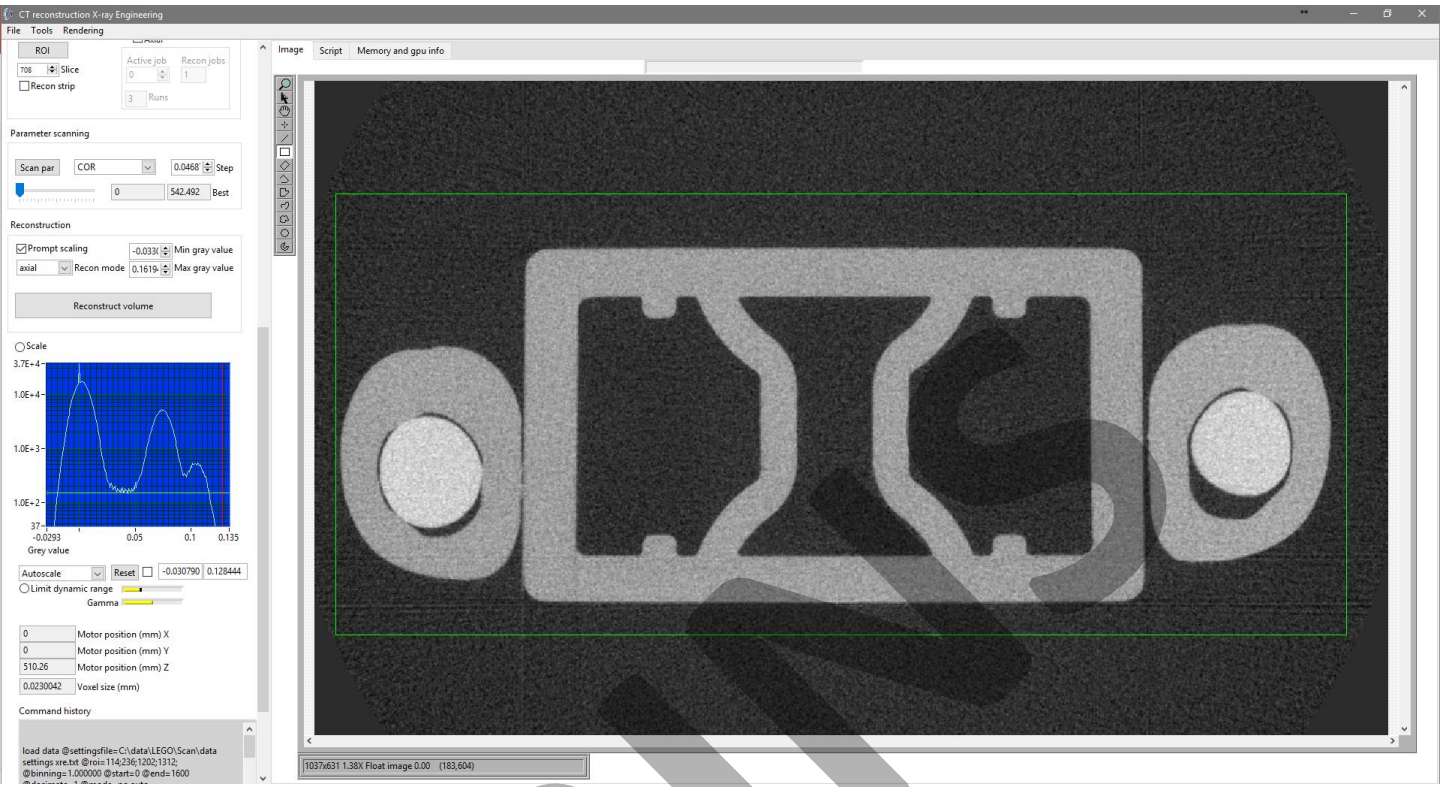
8 *ROI*

The *Region Of Interest (ROI)* button allows to reduce the size of the reconstructed volume. After clicking the *RIO* button, the software loops through all the slices, generating an average of all the images . A new window display the resulting vertical and axial image in which a region can be selected.

A part of the height is automatically cropped, as beyond this zone cone artefacts can occur.

After clicking *Return* the cropped slices are displayed in the *imaging section*

2. General reconstruction workflow

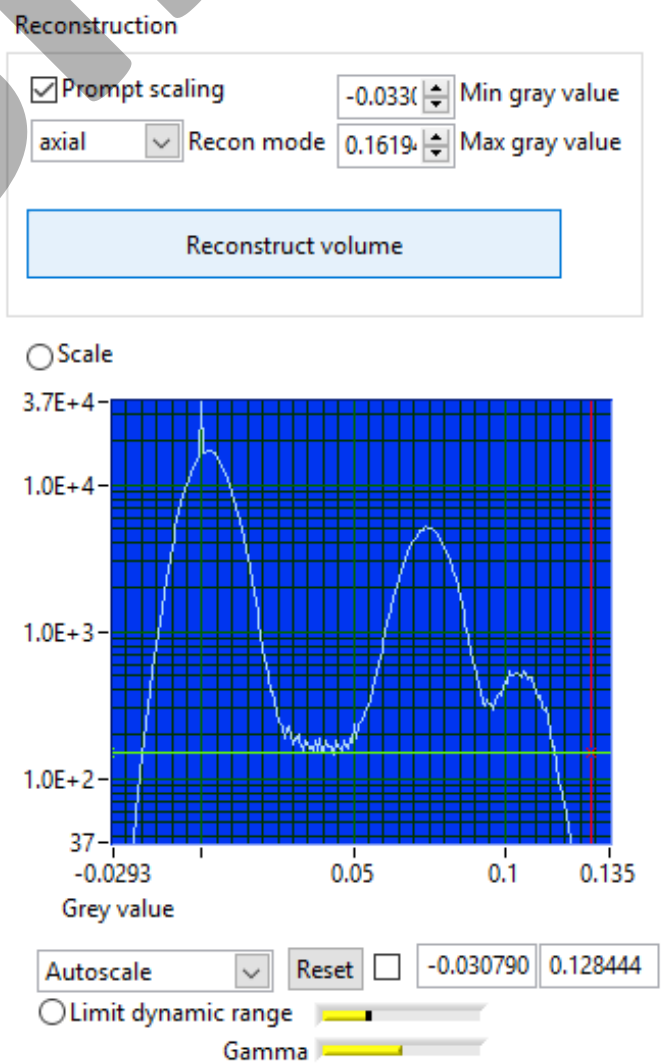


Reconstruction

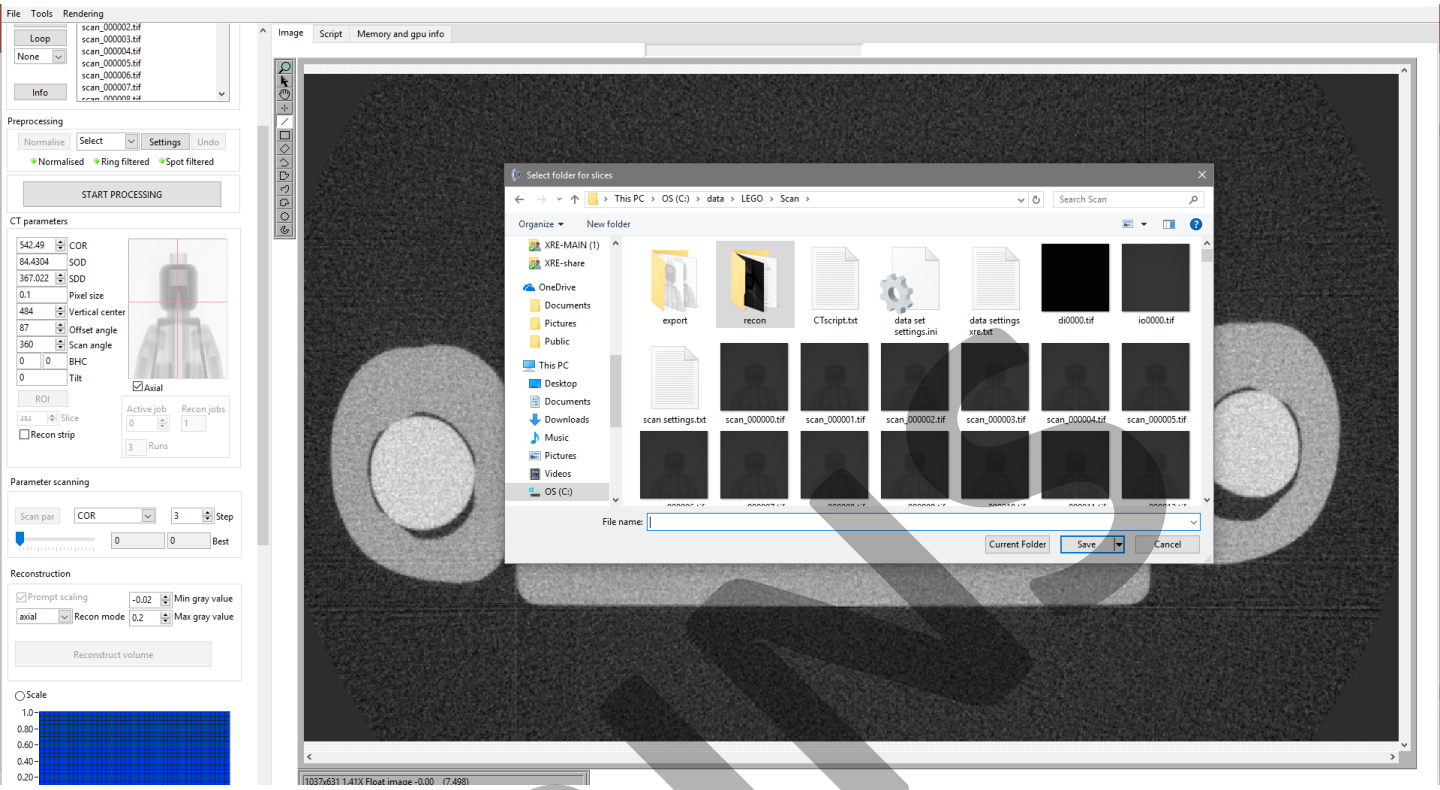
When the parameters in the *CT parameter* section are evaluated or optimized, the grey value range of the slices needs to be set.

By checking the *Prompt scaling* box, the software will loop through the slices, automatically determining the grey value range.

The grey value range can also be manually entered in the *Min & Max grey value* boxes.

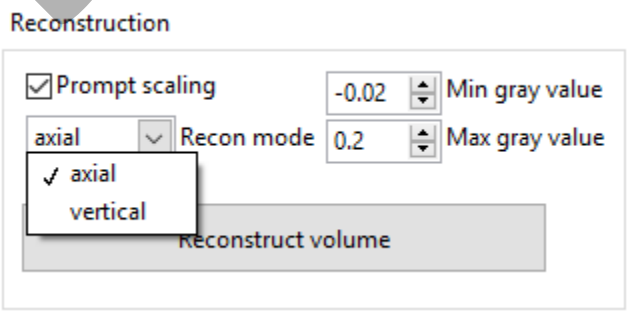


2. General reconstruction workflow

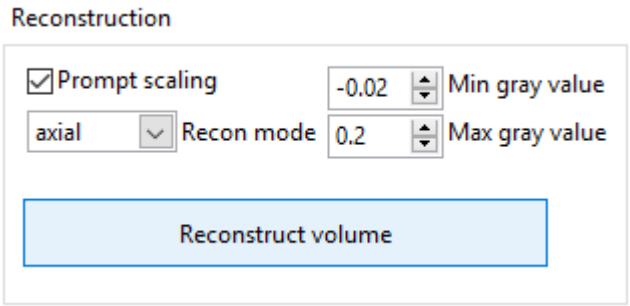


Reconstruction

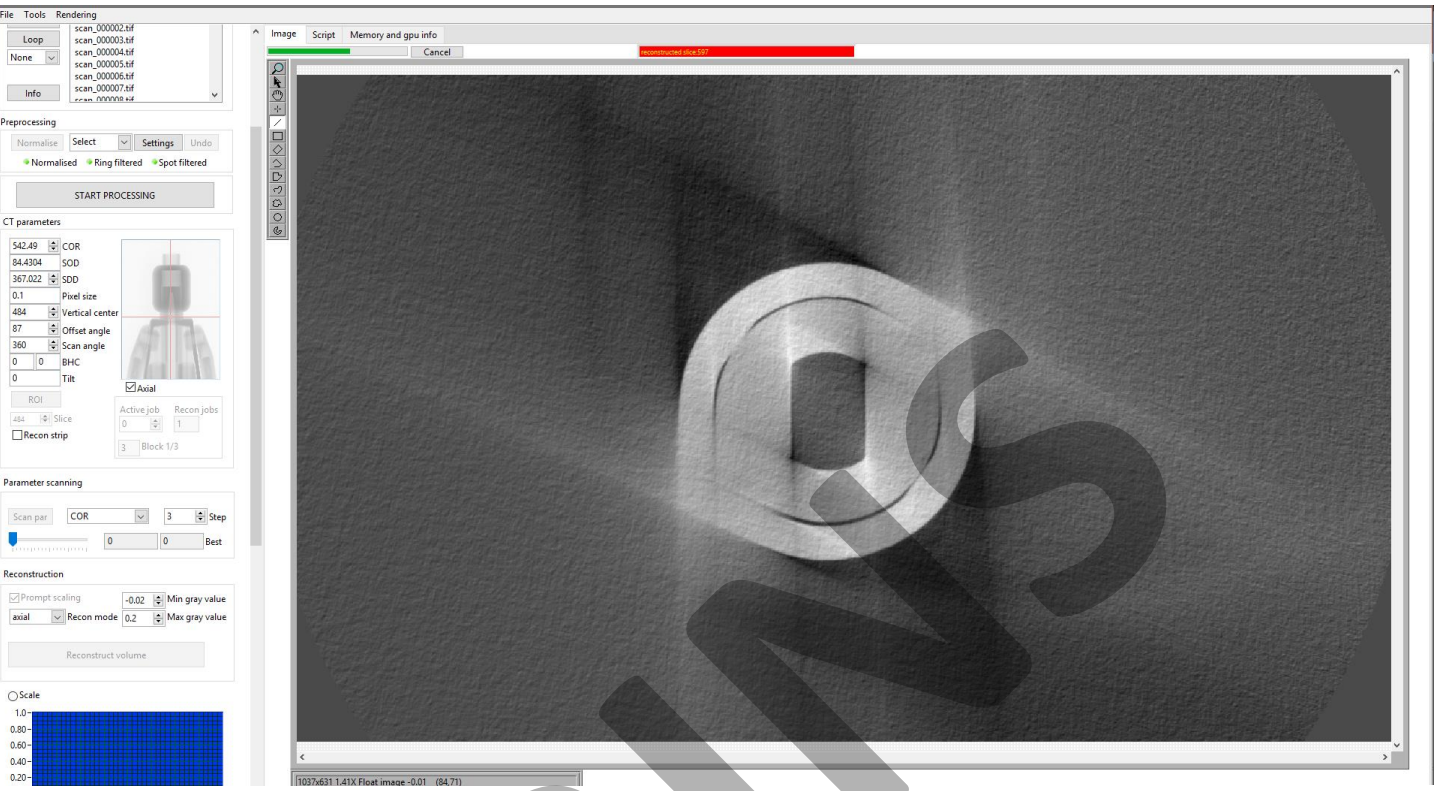
In the *reconstruction* section the direction of reconstruction can also changed between axial or vertical and the slices are exported accordingly.



By clicking *Reconstruct volume* you will be prompted with a explorer window in which you can select a folder to save the reconstructed tiff slices. After which the reconstruction starts



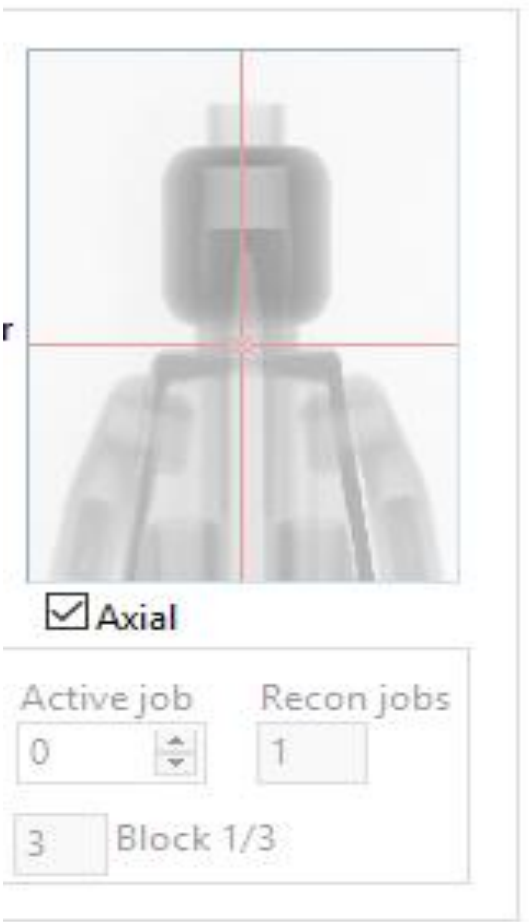
2. General reconstruction workflow



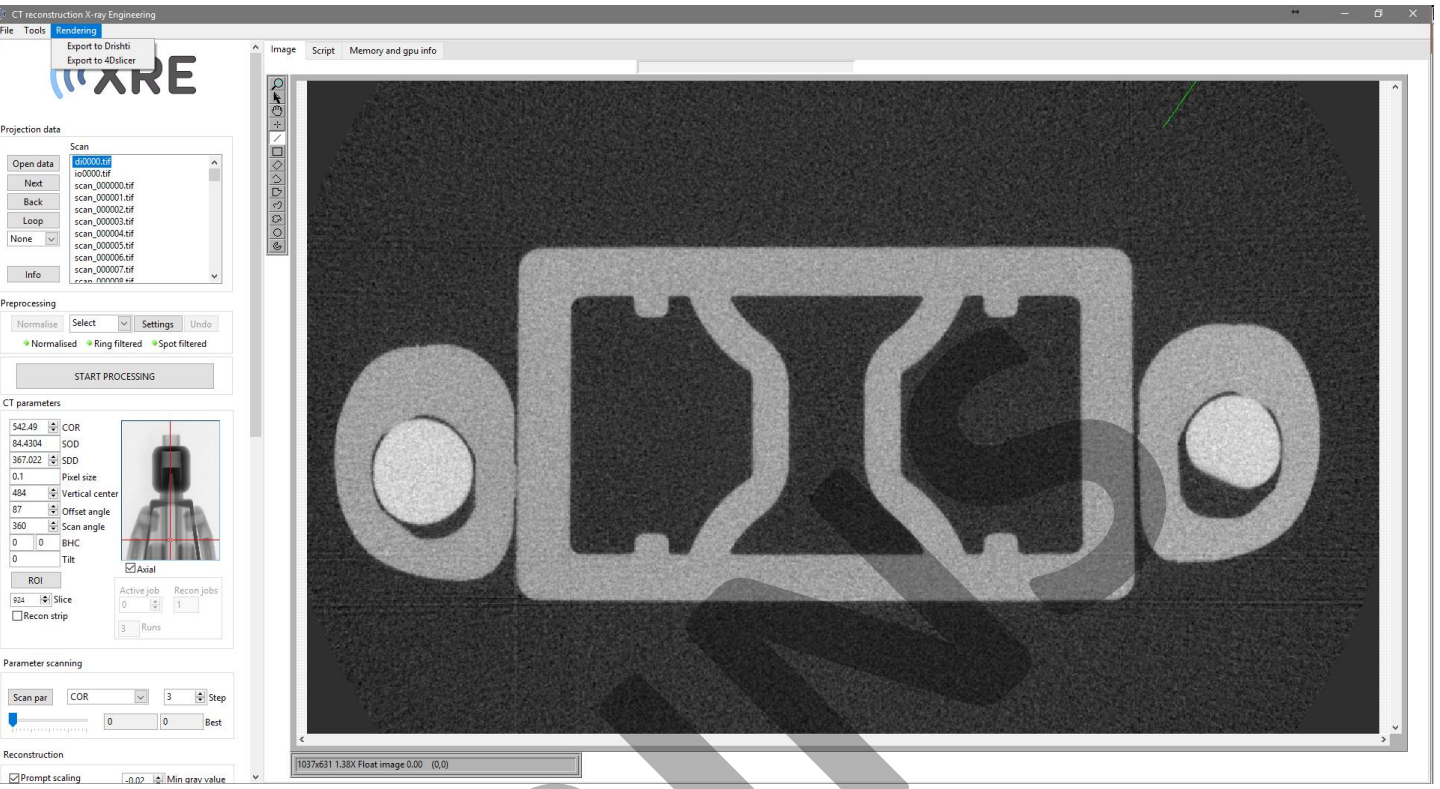
Reconstruction

During the reconstruction the projection images are filtered and loaded into the GPU and afterwards the slices are reconstructed from top to bottom.

If the data is to big for the GPU, the data is split up into different blocks which are run sequentially, gradually improving the image quality after each run.



2. General reconstruction workflow



Data visualization

After the reconstruction the data is stored as a stack of tiff slices which can be used for further analysis in practically all software packages for 3D image analysis.

The reconstruction software however offers 2 options for visualizing the reconstructed data.:

Drishti

An open source 3D renderer
https://github.com/nci/drishti

4Dslicer

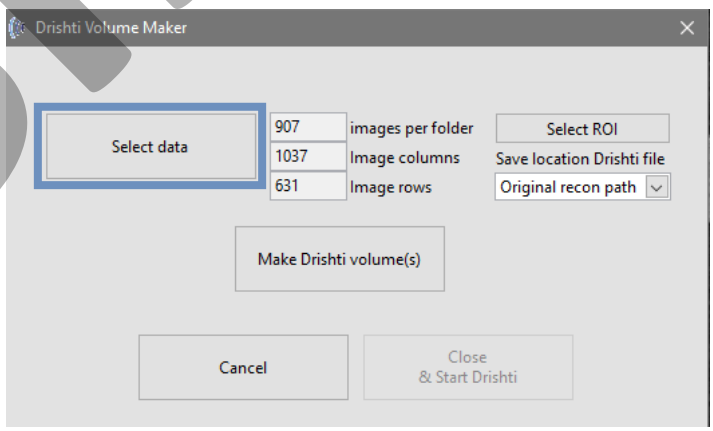
XREs proprietary data viewer

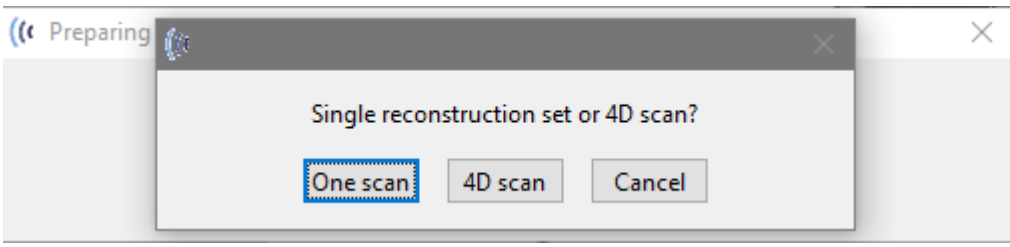
2. General reconstruction workflow

Data visualization

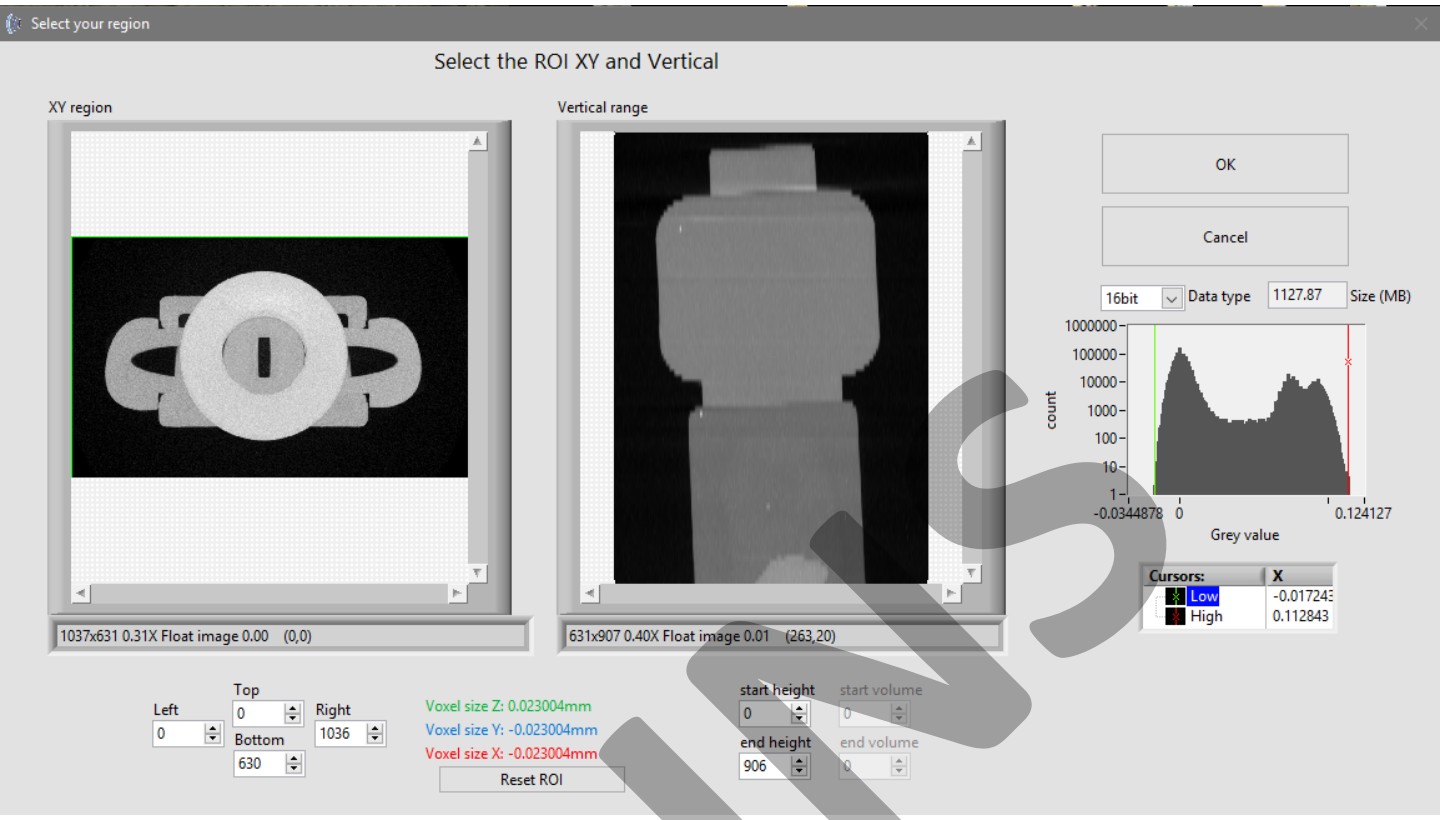
When selecting *Export to Drishti* the Drishti Volume Maker window is displayed.

Select data allows to select other reconstructed datasets. This can be *One scan* or a *4D scan* depending on the type of data.



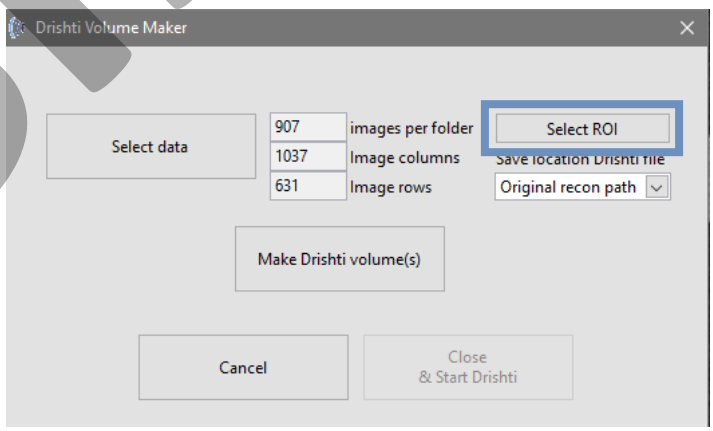


2. General reconstruction workflow

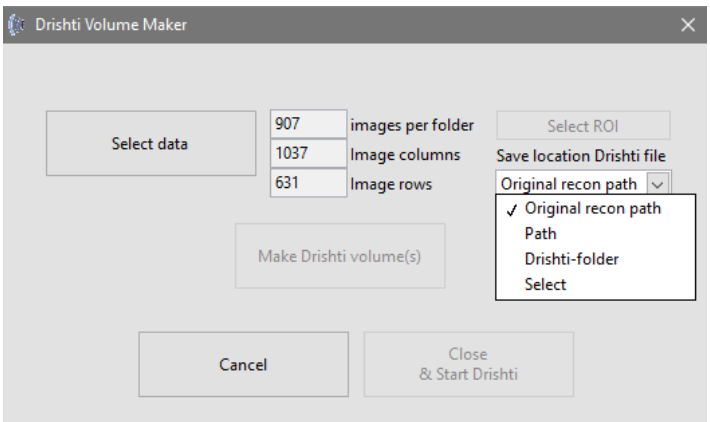


Data visualization

Select ROI allows to select a region of interest and select the amount of grey values in the image (16 bit or 8 bit) for the volume rendering, which enables you to reduce the size of the generated volume file.

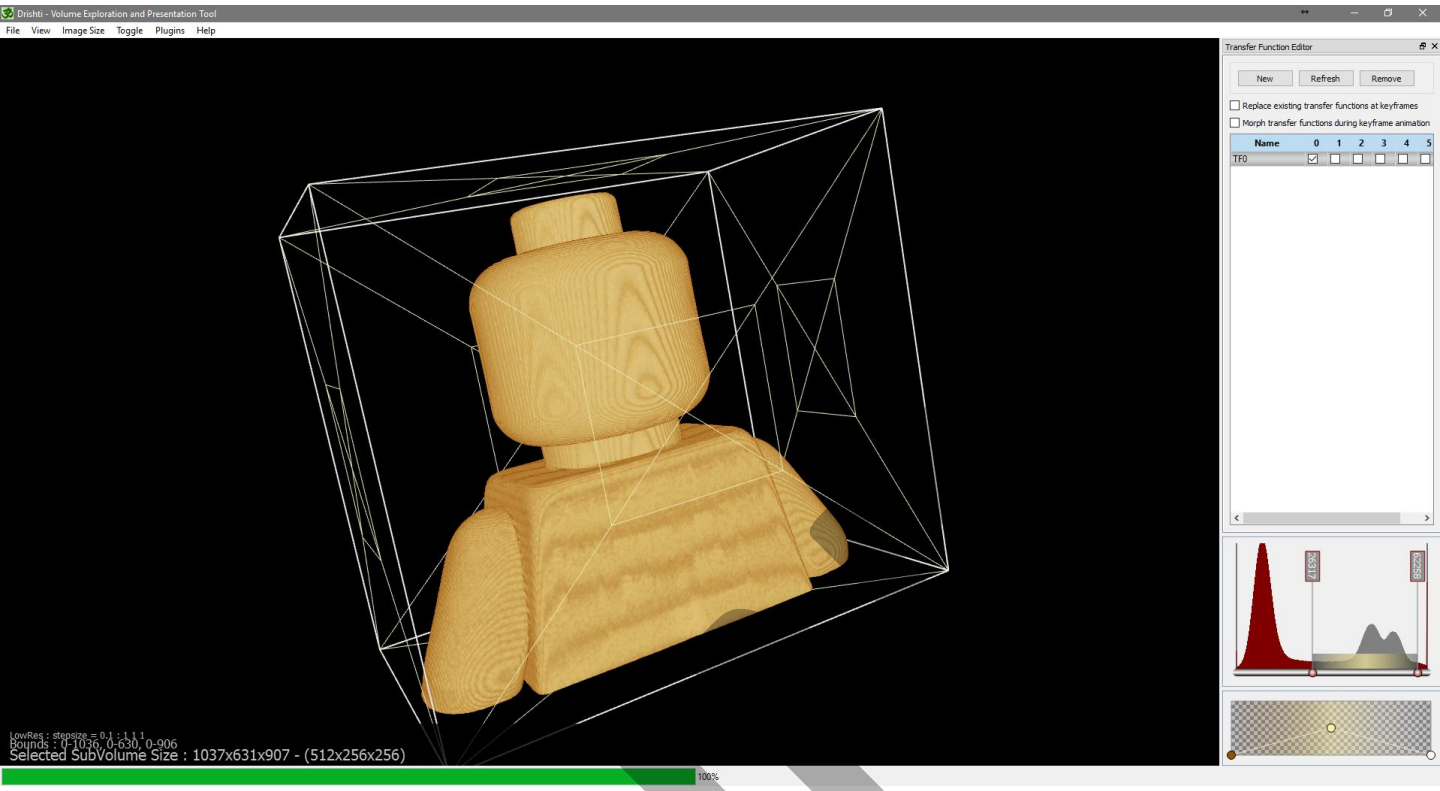


The drop down list in *Save location Drishti file* lets you choose the specific location of the volume file.



Make Drishti volume(s) generates the volume file in the selected location.

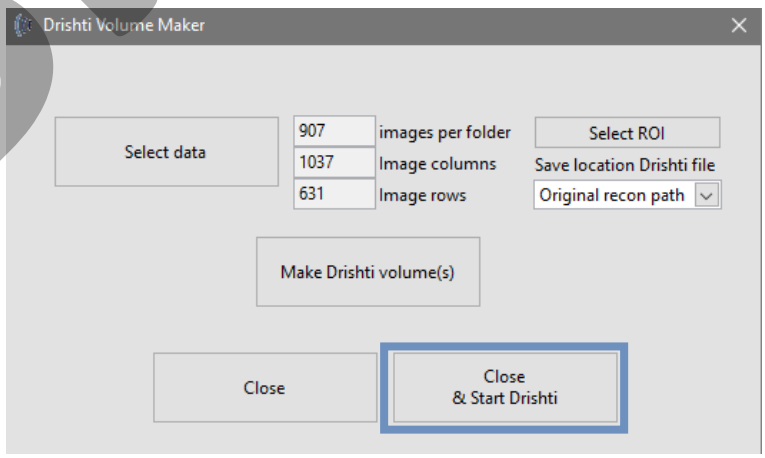
2. General reconstruction workflow



Data visualization

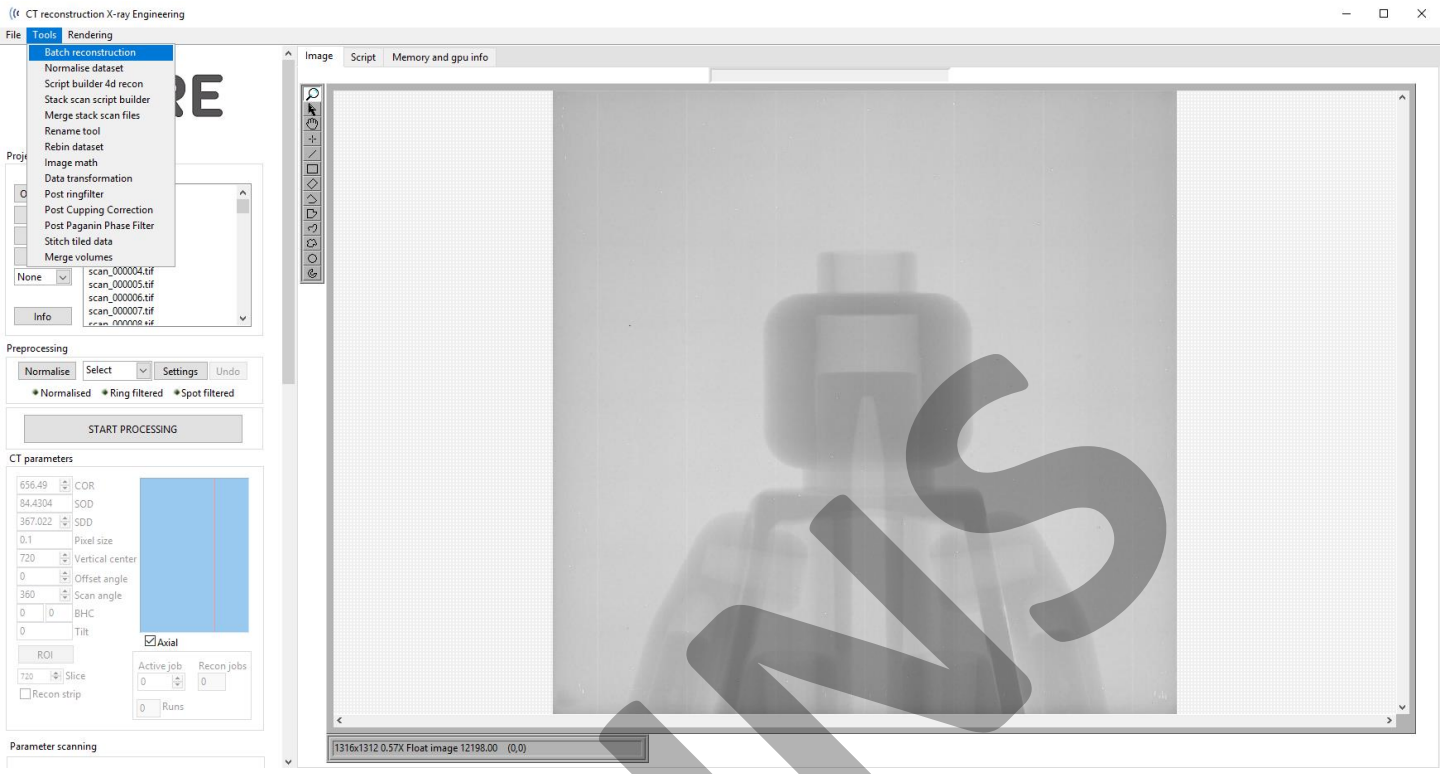
After making the Drishti volume file you can either select *Close* or *Close & Start Drishti*.

The latter opens the visualization software and automatically opens the 3D volume.



When selecting *Export to 4Dslicer* the data is immediately loaded into the XRE 4D-CT viewer software.

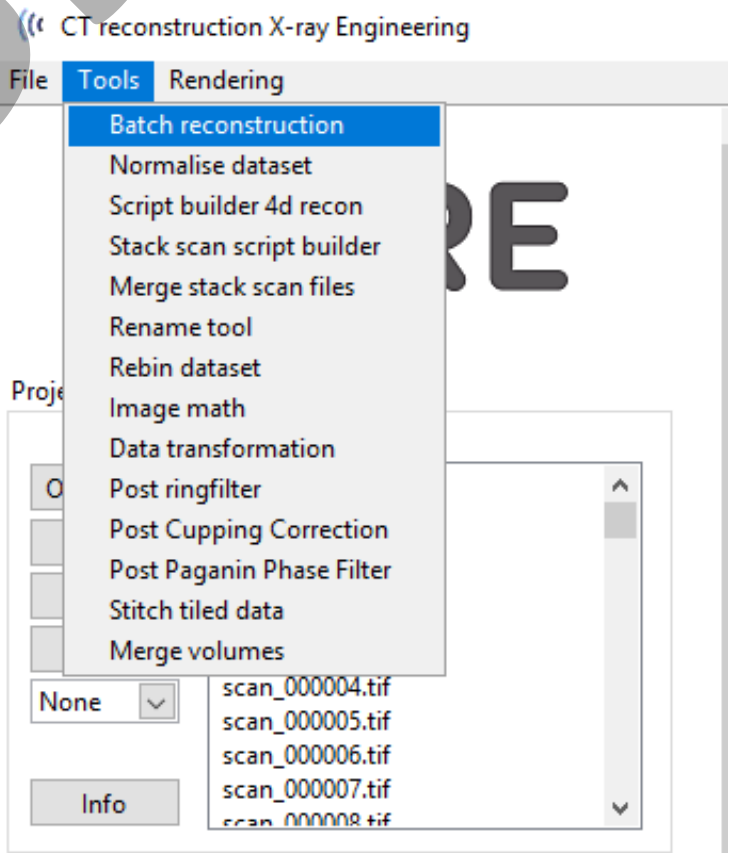
3. Batch reconstruction workflow



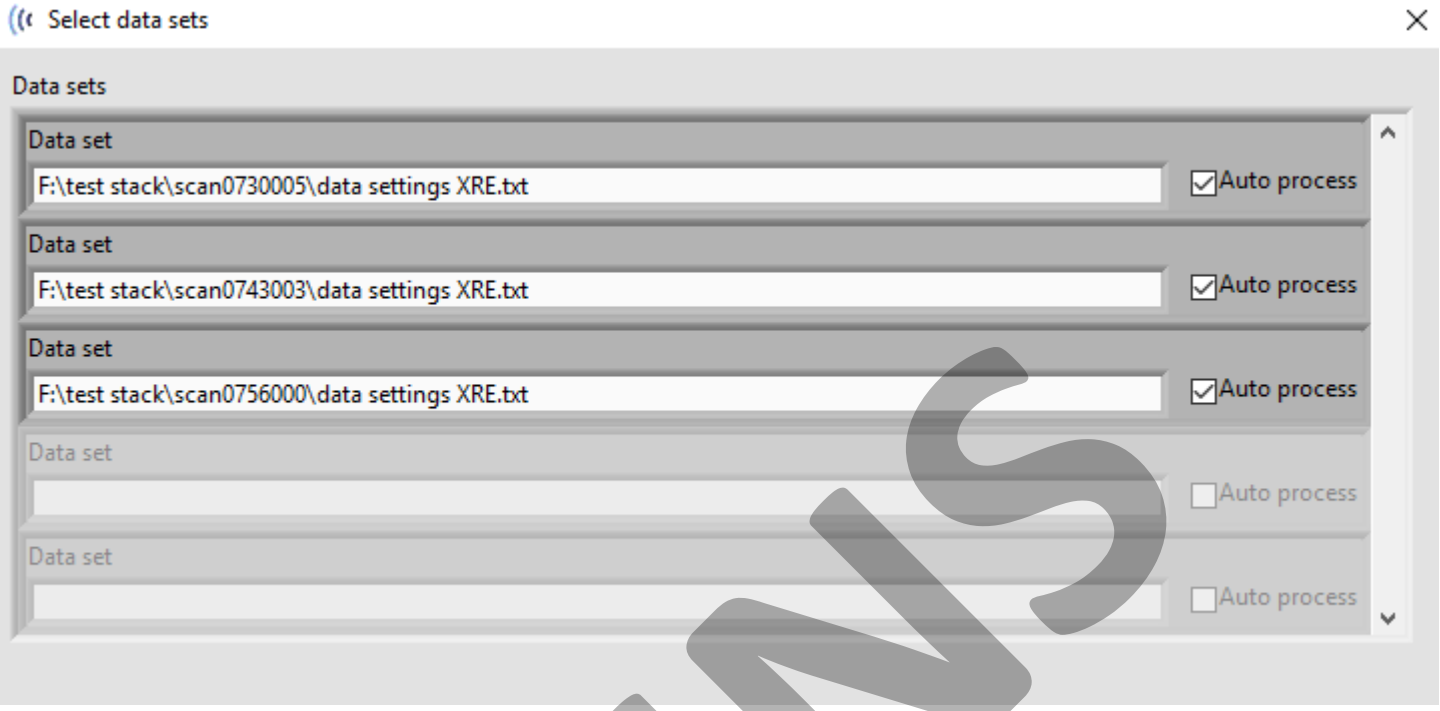
Batch reconstruction tool

If there are multiple scans (eg. Stacked scans or time lapse scans) that need to be reconstructed automatically, the *Batch reconstruction* tool can be used.

The *Batch reconstruction* tool looks for *data settings xre.txt* files in a selected folder and subfolders. Each *data settings xre.txt* file is considered as a separate reconstruction in the batch.



3. Batch reconstruction workflow

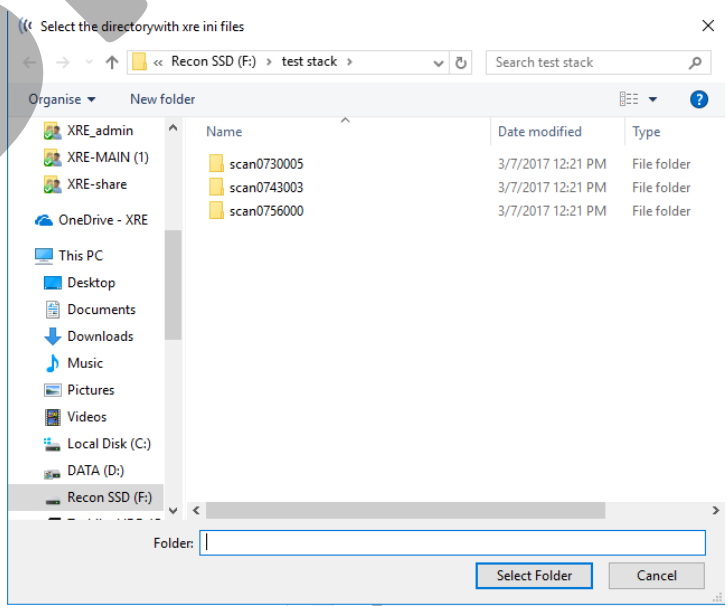


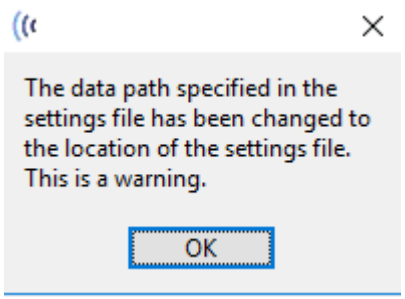
Selecting data

After selecting the main folder, a list of the *different data setting XRE.txt* files is given and the desired datasets for automatic reconstruction can be selected by checking the *Auto process* checkbox.

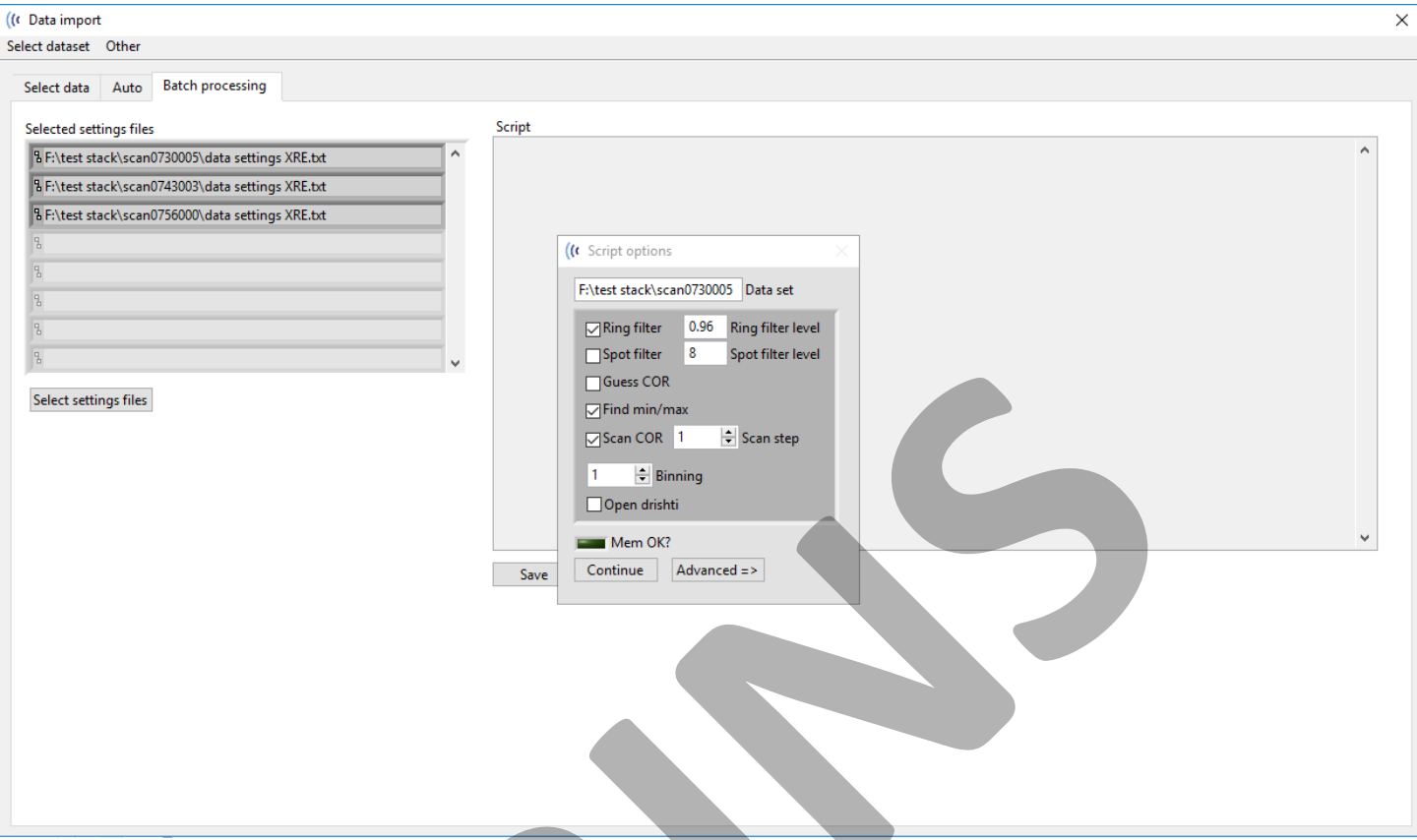
When the desired datasets are selected the *Select data sets* window can be closed

If the path in the *data settings XRE.txt* file is different from the location of the file, the reconstruction path will be updated to the location of the file.

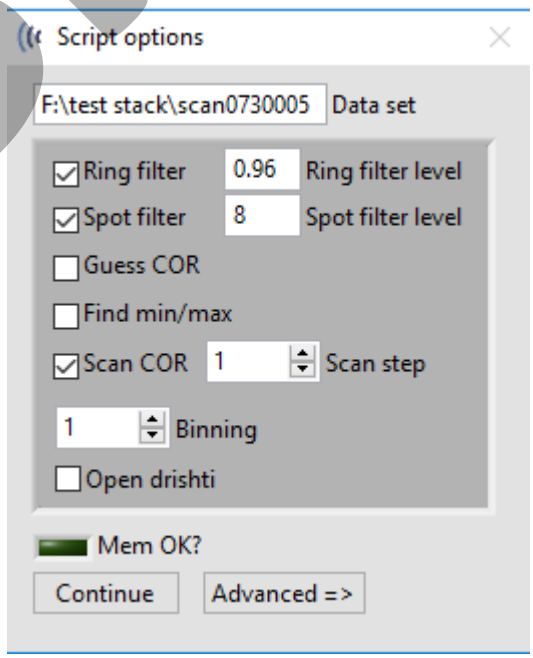




3. Batch reconstruction workflow



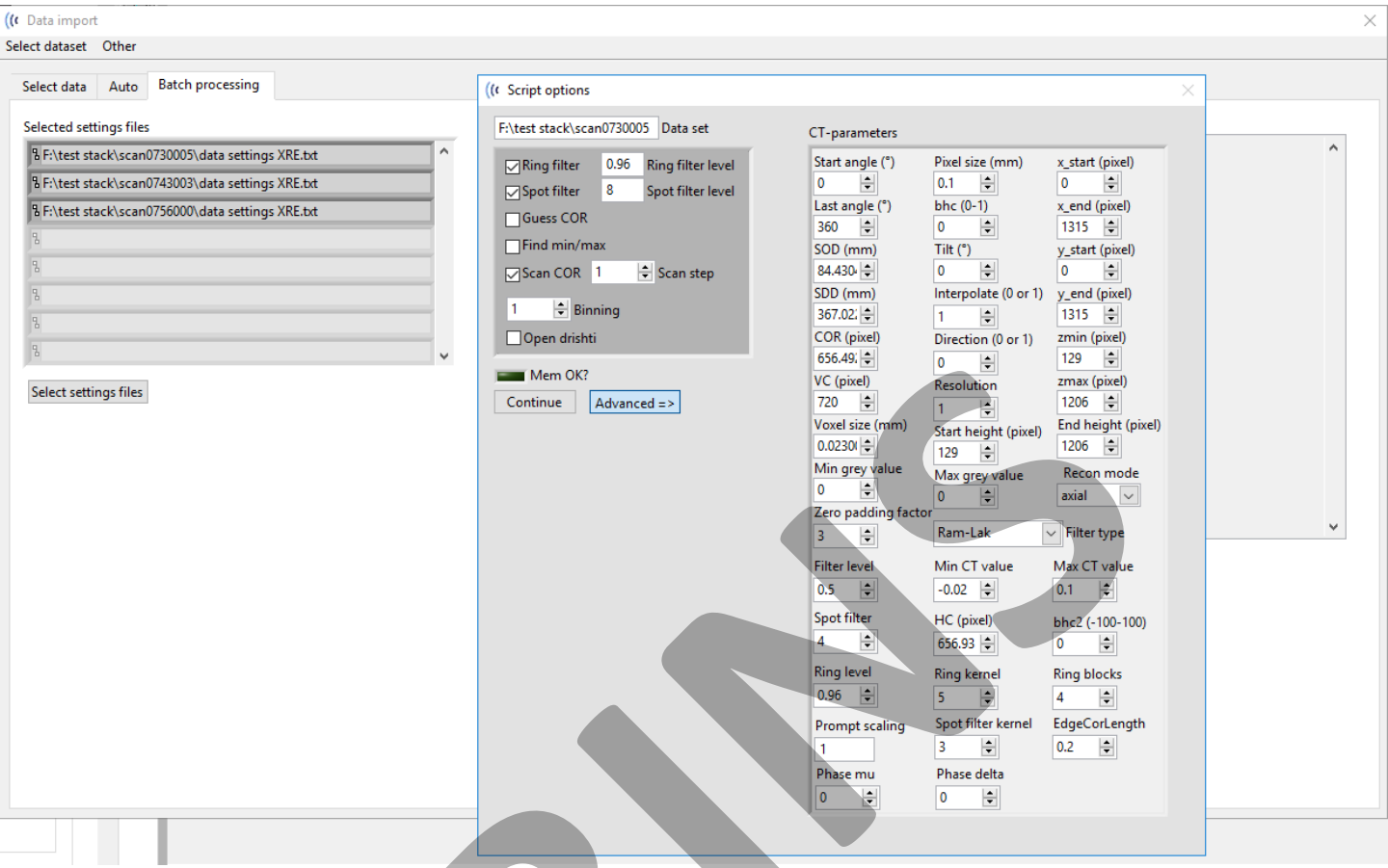
Preparing the recon script



For a selected data set a number of reconstruction options can be chosen in the *Script options* window.

The first two allow set the *Ring* and *spot filter* level. The *Guess COR* automatically guesses what the expected Centre of Rotation is. *Find min/max* automatically determines the grey value range of the dataset. *Scan COR* lets you set the step size to finetune the Centre of Rotation. *Binning* provides the option to rebin the projection images.

3. Batch reconstruction workflow

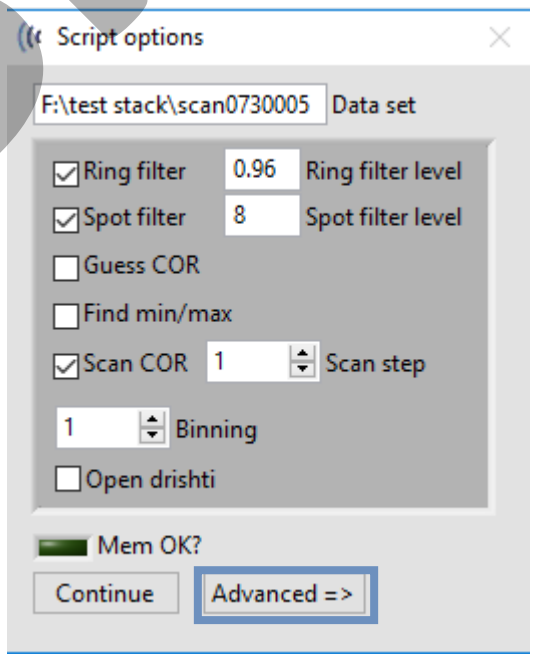


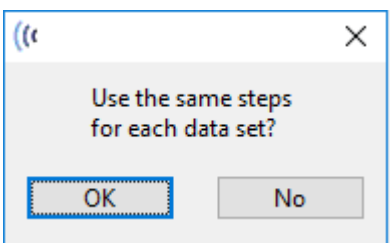
Preparing the recon script

The *Open Drishti* checkbox will automatically load the reconstructed data for rendering.

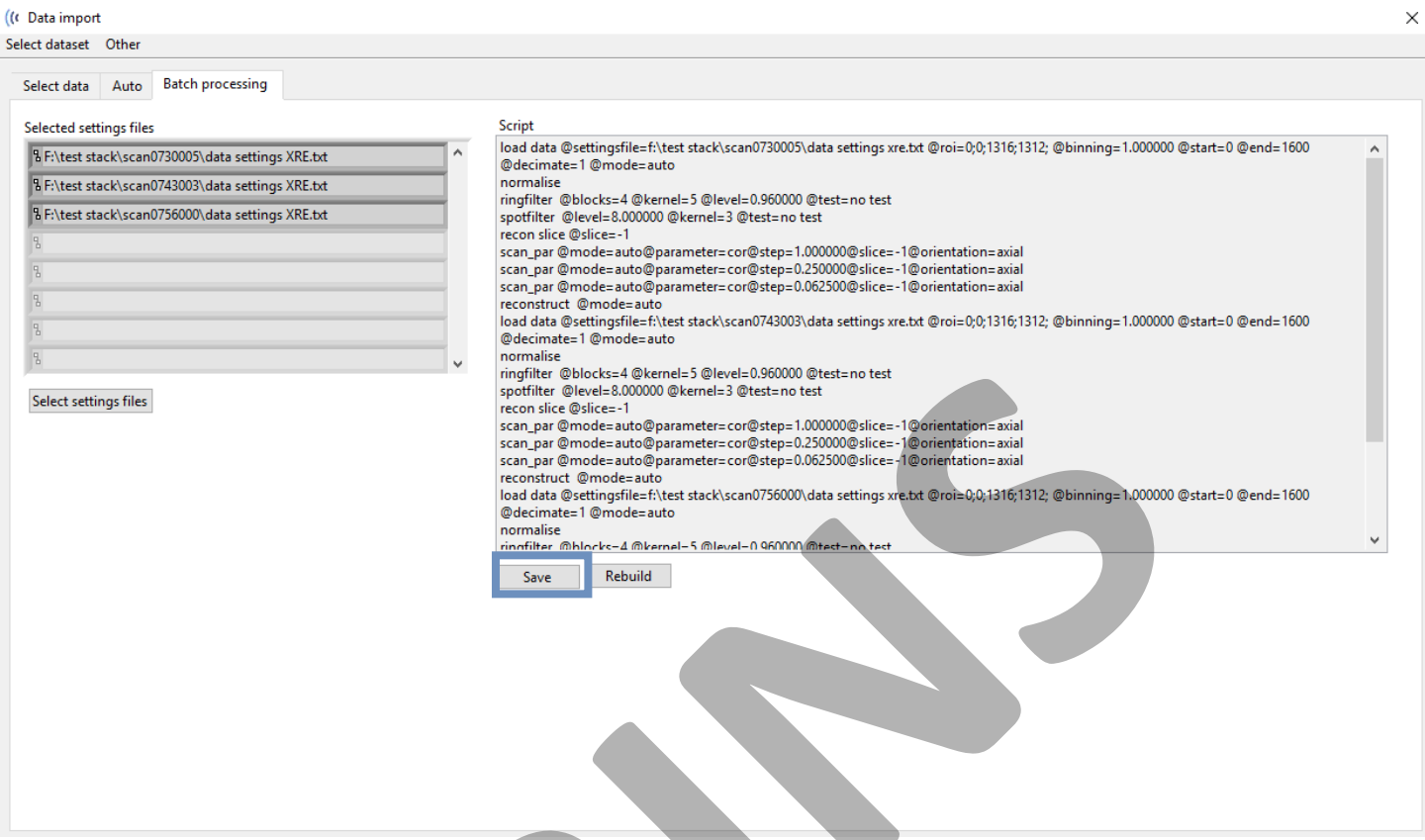
The *Advanced* button provides more options for finetuning the reconstruction parameters like additional filtering, beam hardening correction, phase correction, tilt correction and many more.

After clicking *Continue,* it can be chosen to apply the same parameters for every dataset or set the settings for each individual dataset.





3. Batch reconstruction workflow

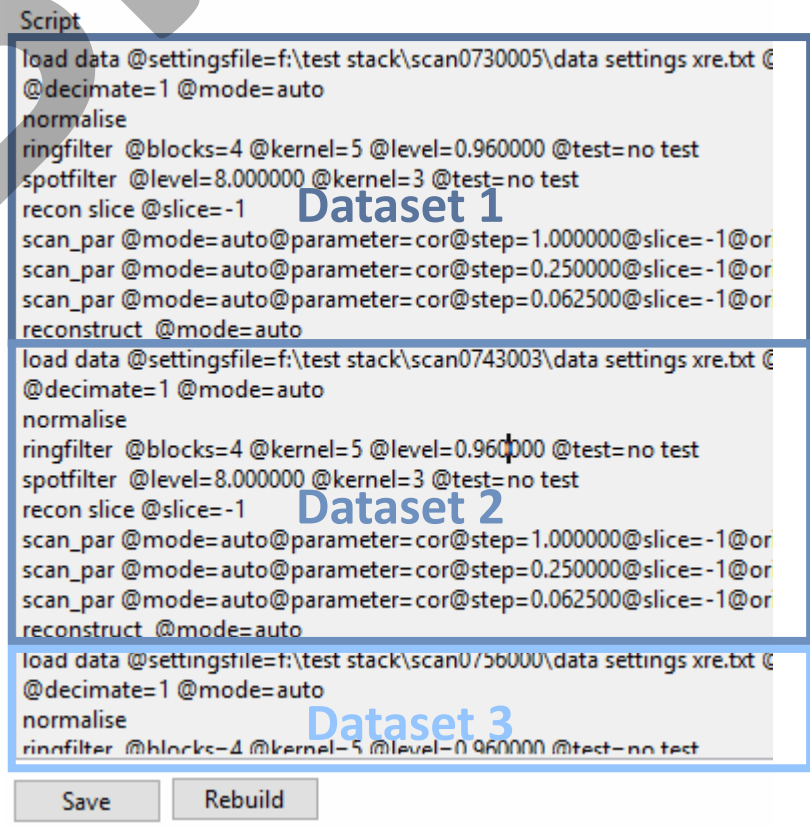


Preparing the recon script

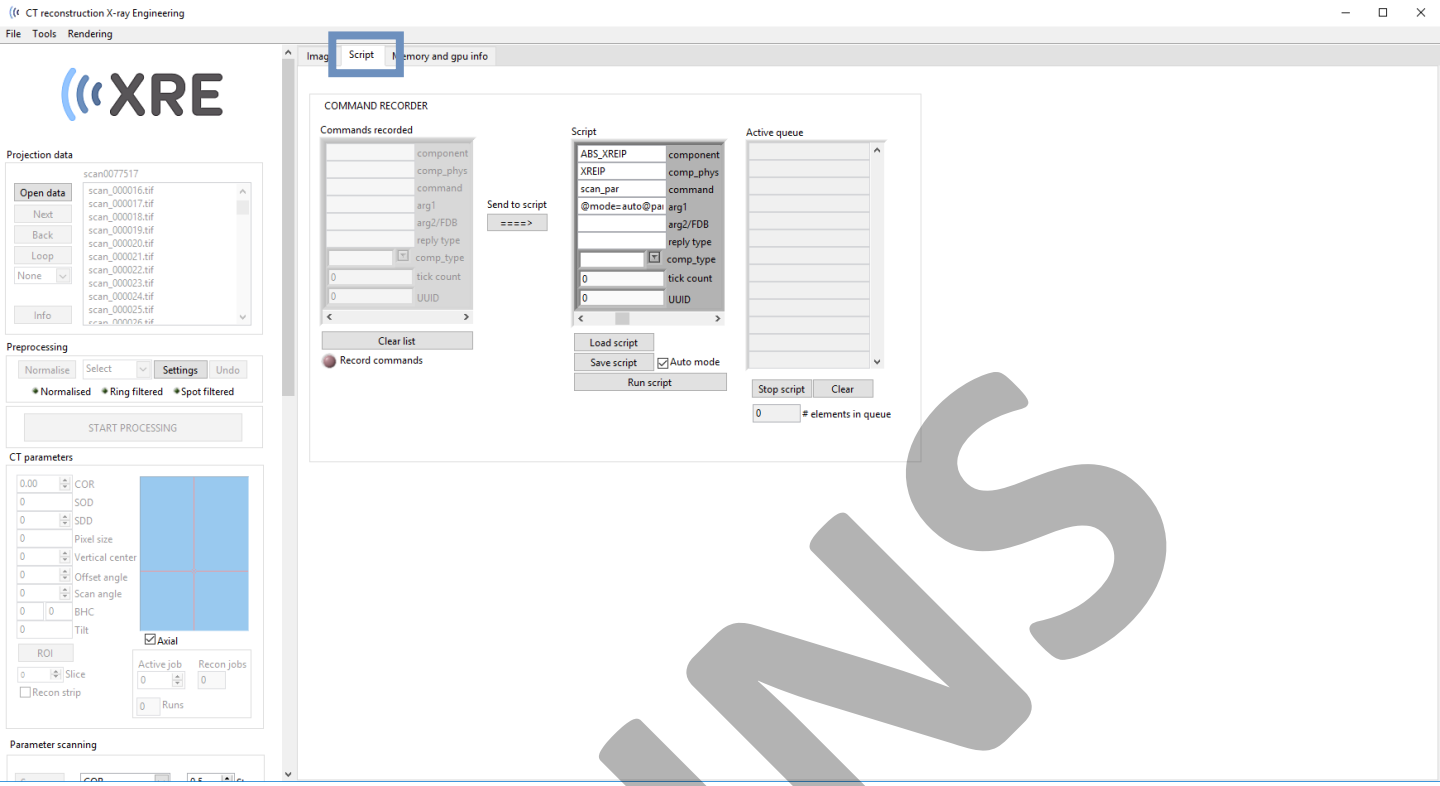
After clicking *OK* the reconstruction script for the selected datasets is generated and displayed as text file.

This text file can be saved using *Save* button and the reconstruction steps can be further edited using a text editor.

If the scrip is ready the *Data import* window can be closed.



3. Batch reconstruction workflow

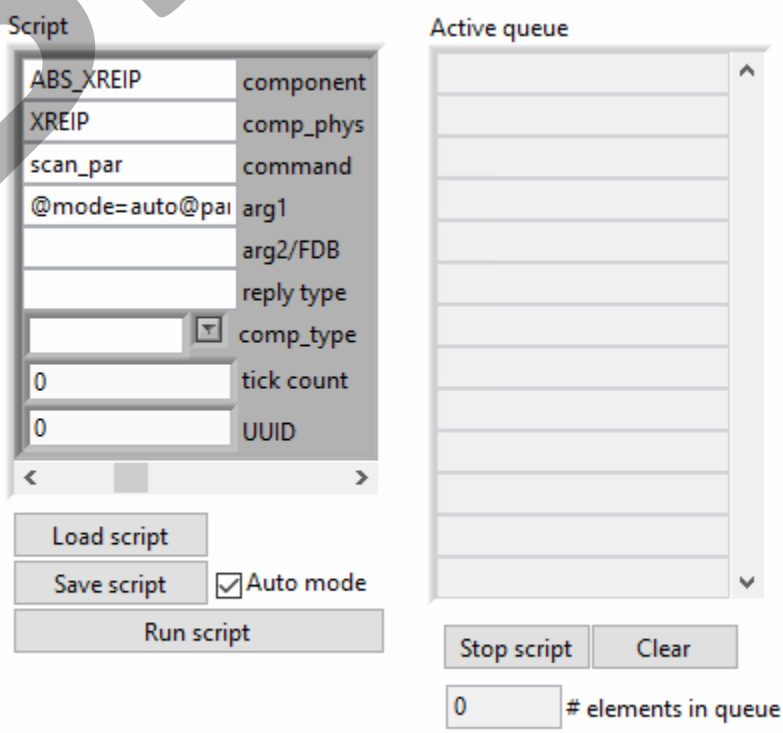


Running the script

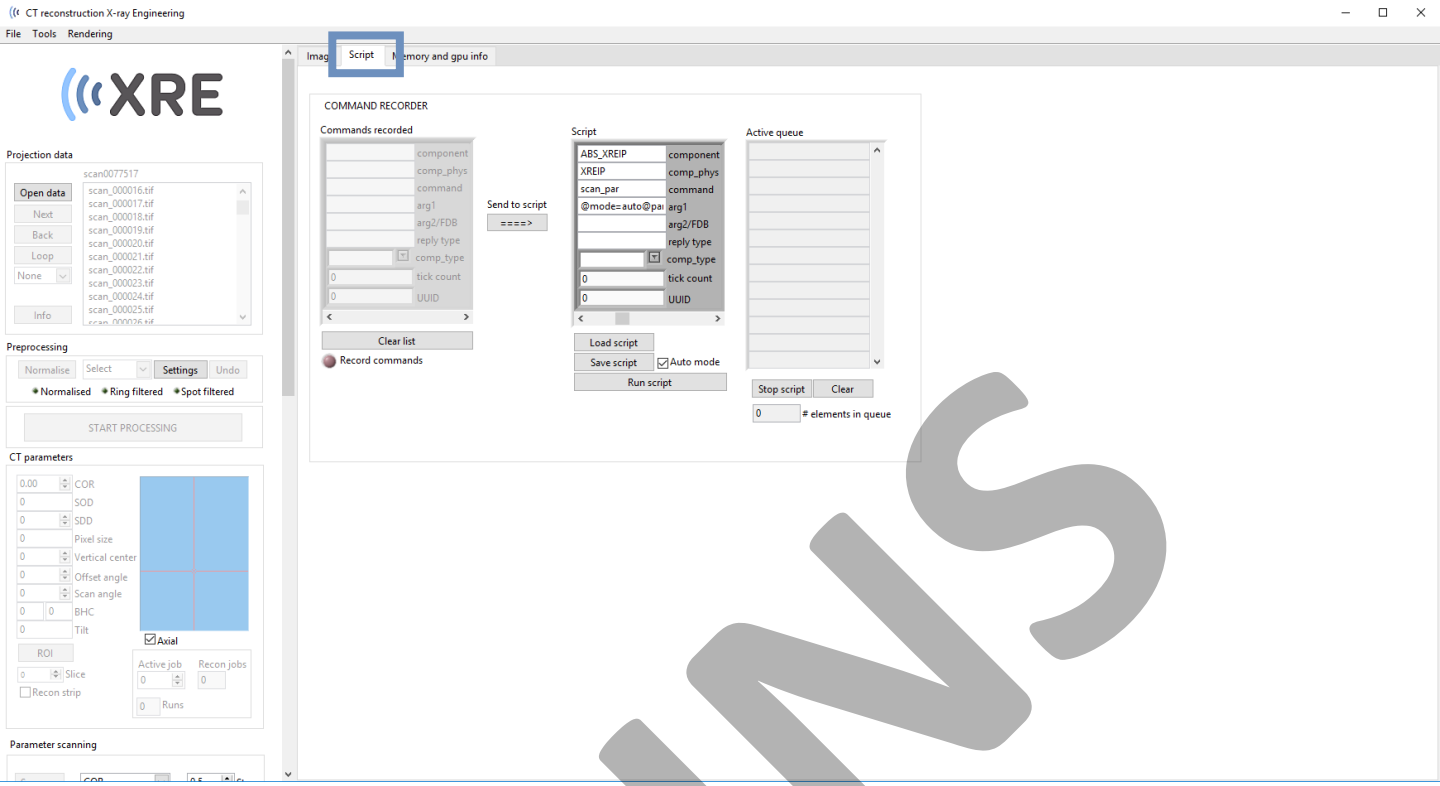
After closing the *Data import* window, the script is shown in the *Script* tab of the main window.

The script is automatically loaded and other saved reconstruction scripts can be loaded using the *load script* button.

To start the automatic reconstruction, click the *Run script* button and the progress o the reconstruction script will be displayed in the right button.



3. Batch reconstruction workflow



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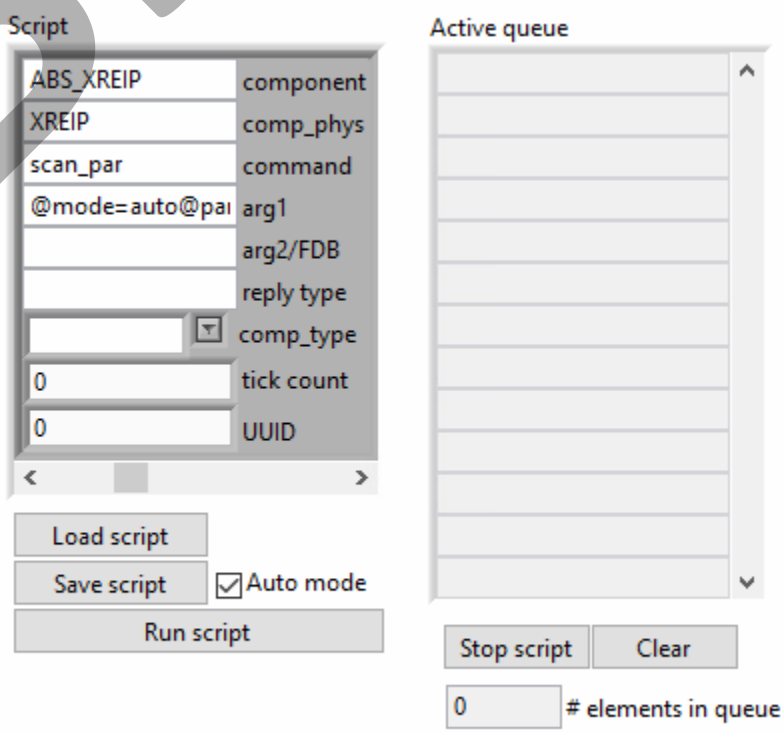
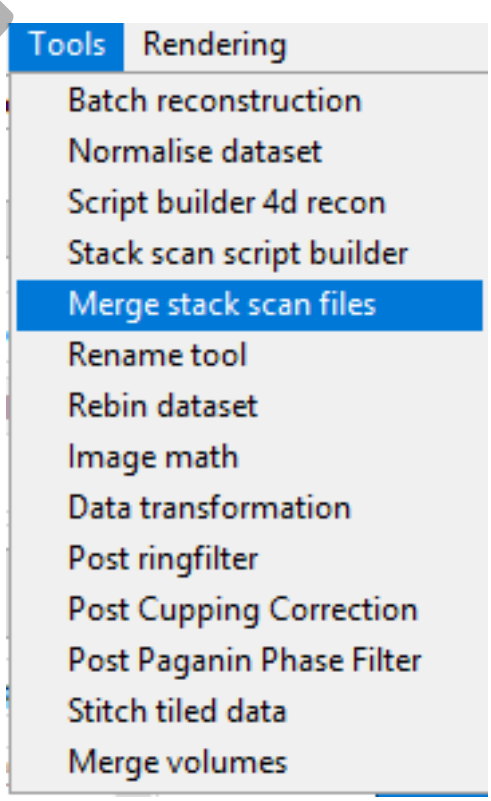


4. Merge stacked scan files

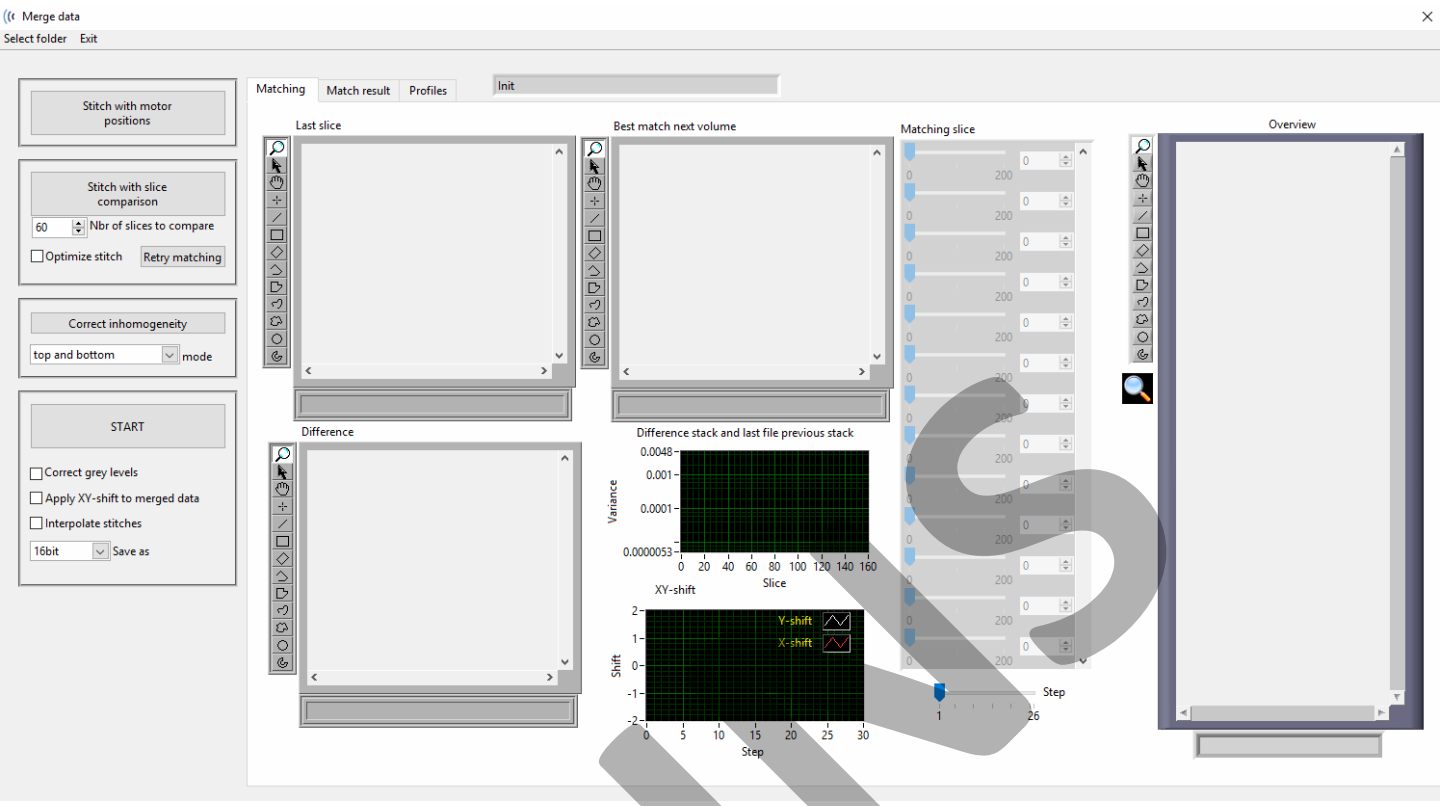
Selecting the data

If a stacked scan was acquired and the individual scans of the stack were reconstructed, the datasets can automatically be merged into one volume.

By selecting the *Merge stack scan files* from the Tools drop down list, the *Merge data* window will be displayed.



4. Merge stacked scan files

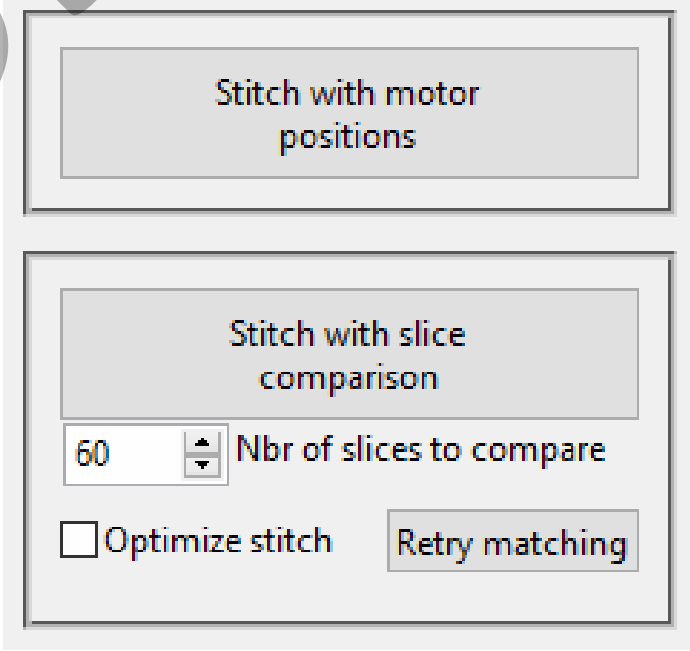


Selecting the data

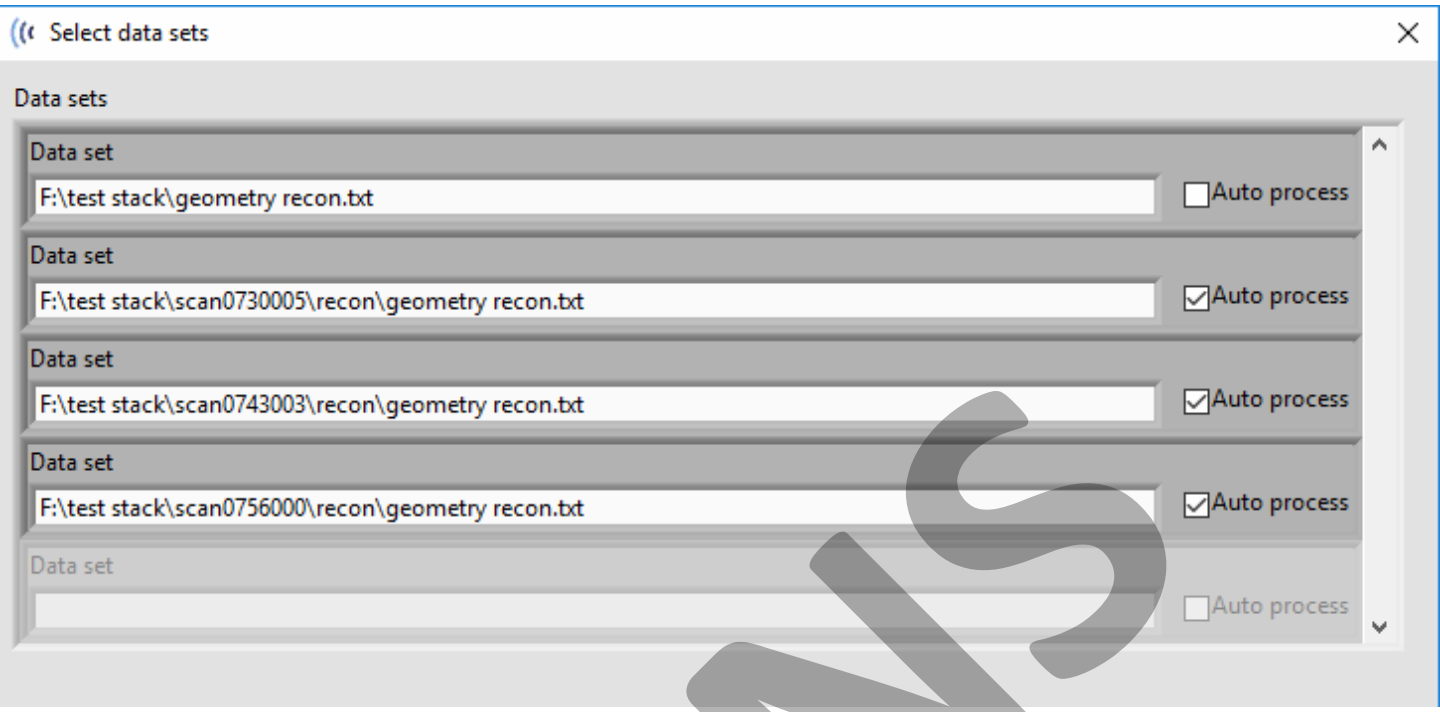
There are two main options to select the stacked scan files.

Stitch with motor positions utilizes the motor position of the vertical motor stage, if these are available. This is also the fastest option.

Stitch with slice comparison compares a number of predefined slices in the different datasets and looks for matching slices in consecutive scans.



4. Merge stacked scan files

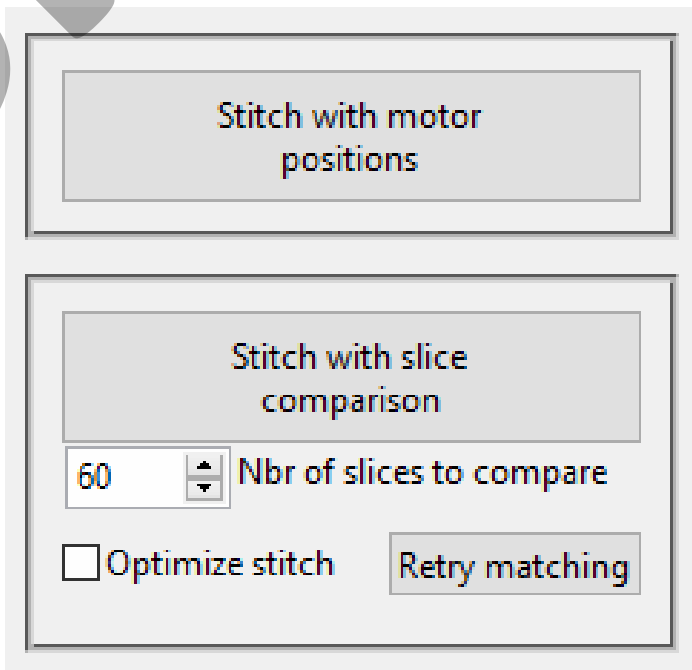


Selecting the data

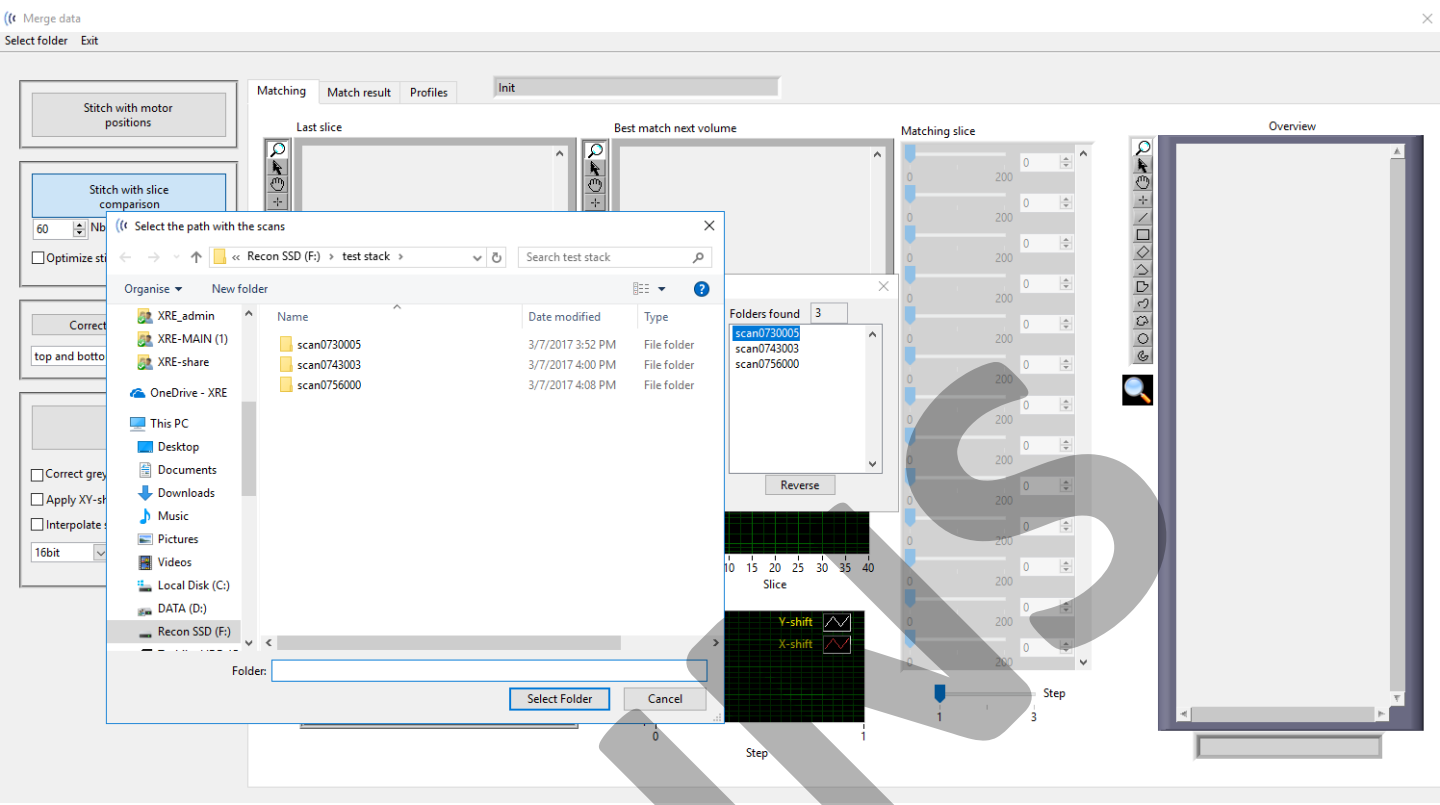
When clicking *Stitch with motor positions*, the location of the main folder with the stacked scans needs to be selected.

Inside the folder the *geometry recon.txt* files need to be selected and a merged image will be shown based on the motor positions found inside the utilizes the motor position of the vertical motor stage, if these are available. This is also the fastest option.

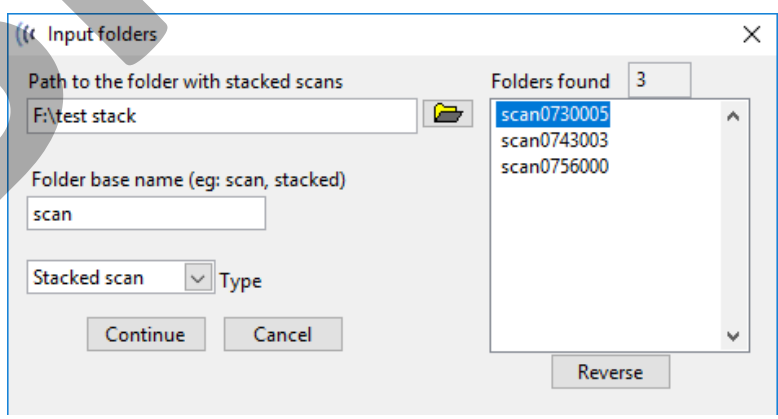
Stitch with slice comparison compares a number of predefined slices in the different datasets and looks for matching slices in consecutive scans.



4. Merge stacked scan files

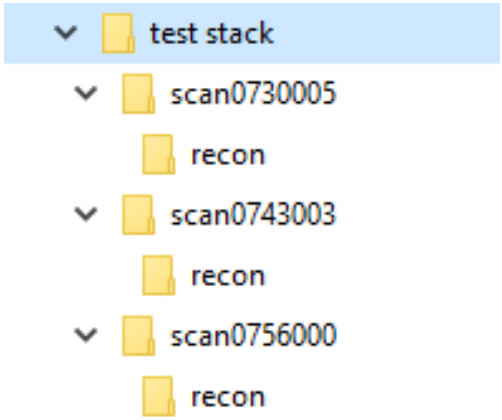


Selecting the data

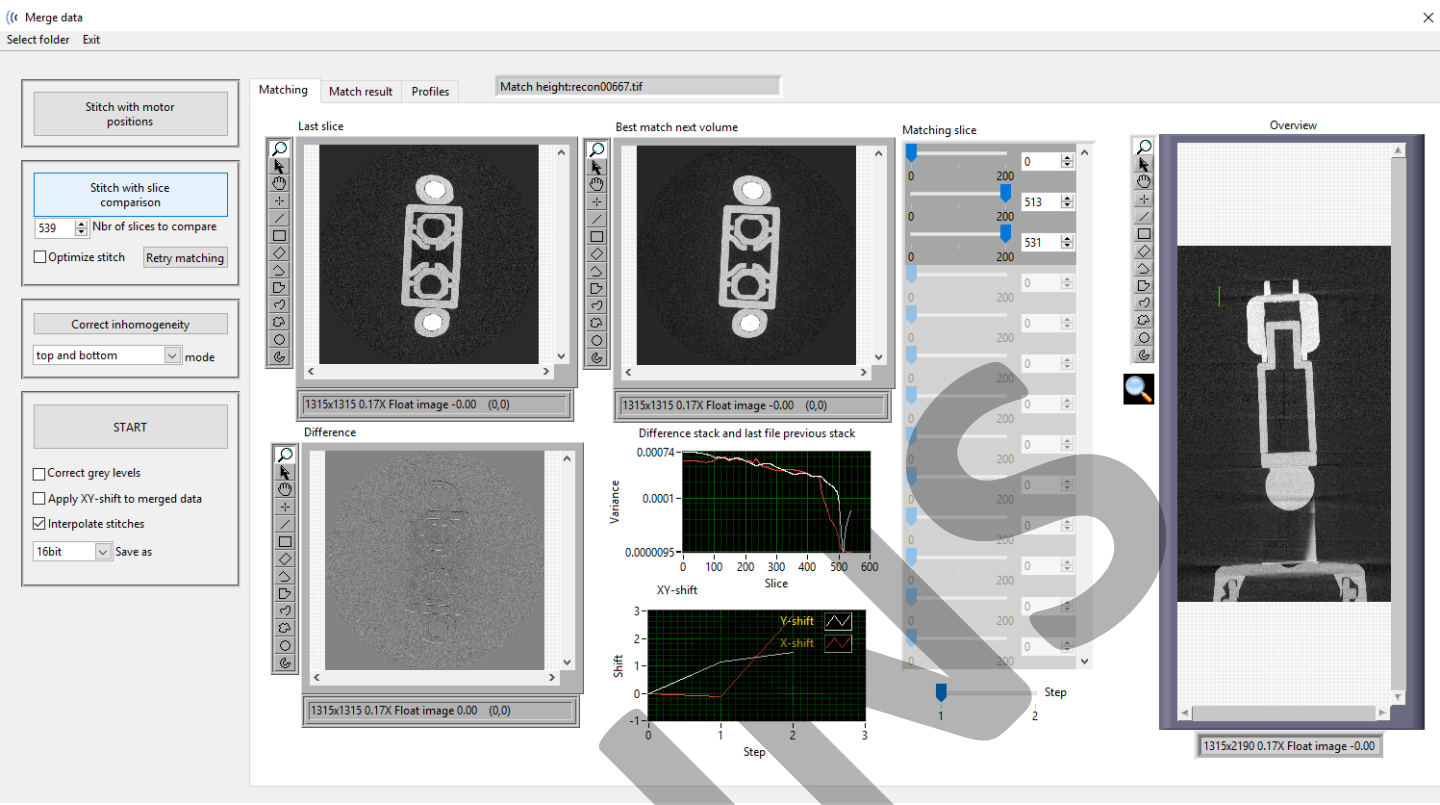


When clicking *Stitch with slice comparison*, the main folder needs to be selected and the basename of the individual dataset folders given. In these individual dataset folders a *recon* folder with the reconstructed images needs to be present.

Depending on how the data was acquired the order of the different scans can be changed by clicking the *Reverse* button

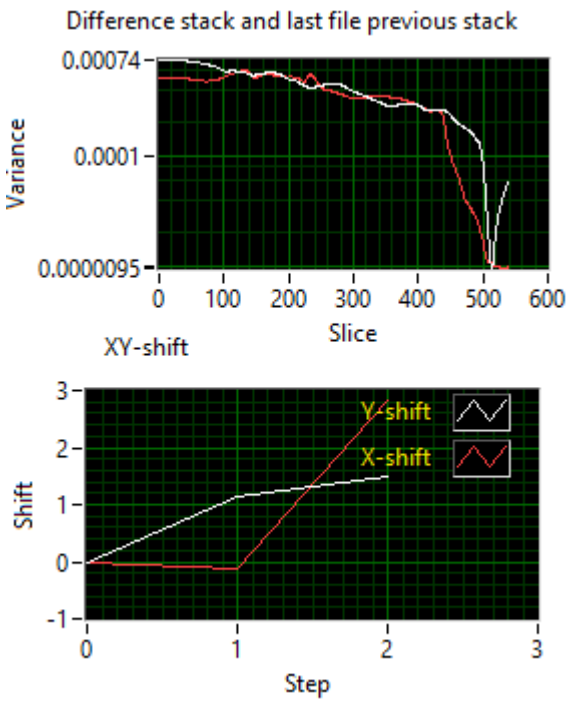


4. Merge stacked scan files



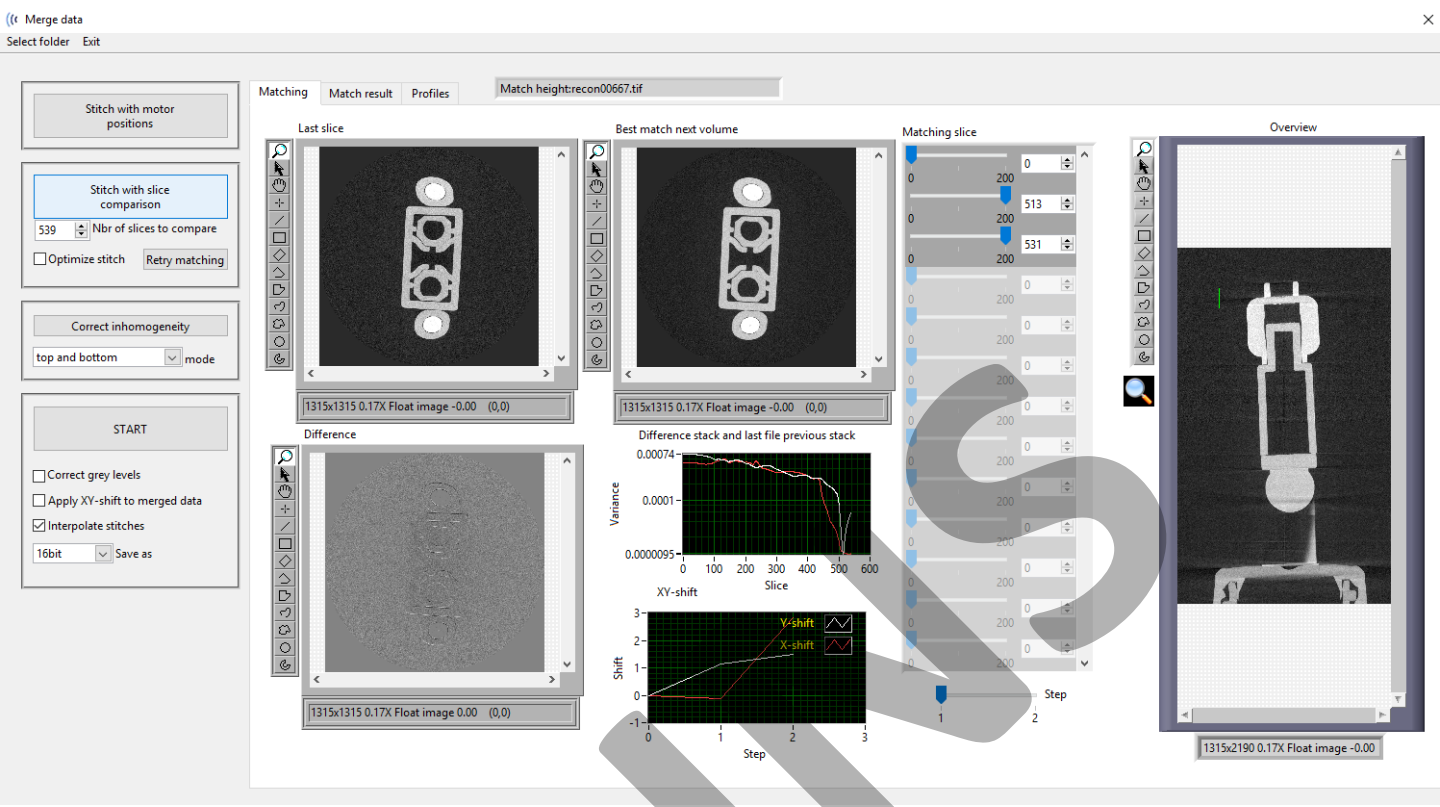
Merging data

After selecting the data a given number of slices will be compared and the variance between the slices is plotted. The points with the lowest variance are considered to be the matching slices in the different datasets.



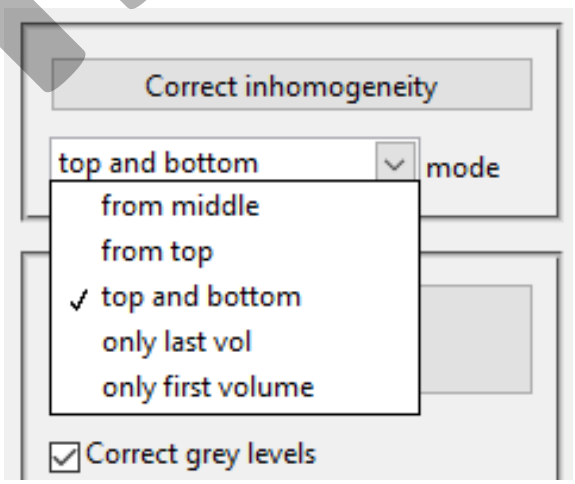
XY shifts between the matching slices are also determined and these can be corrected by checking the *Apply XY-shift to merged data* checkbox.

4. Merge stacked scan files



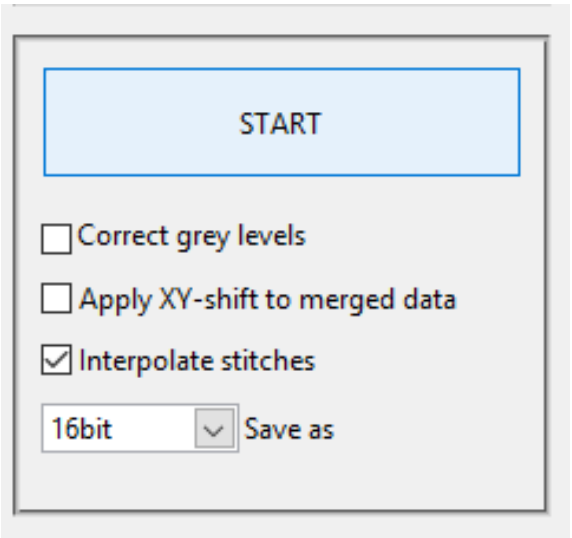
Merging data

Grey value variation between the different scans can be corrected by checking the *Correct grey levels* checkbox and selecting the mode with which dataset needs to be corrected.

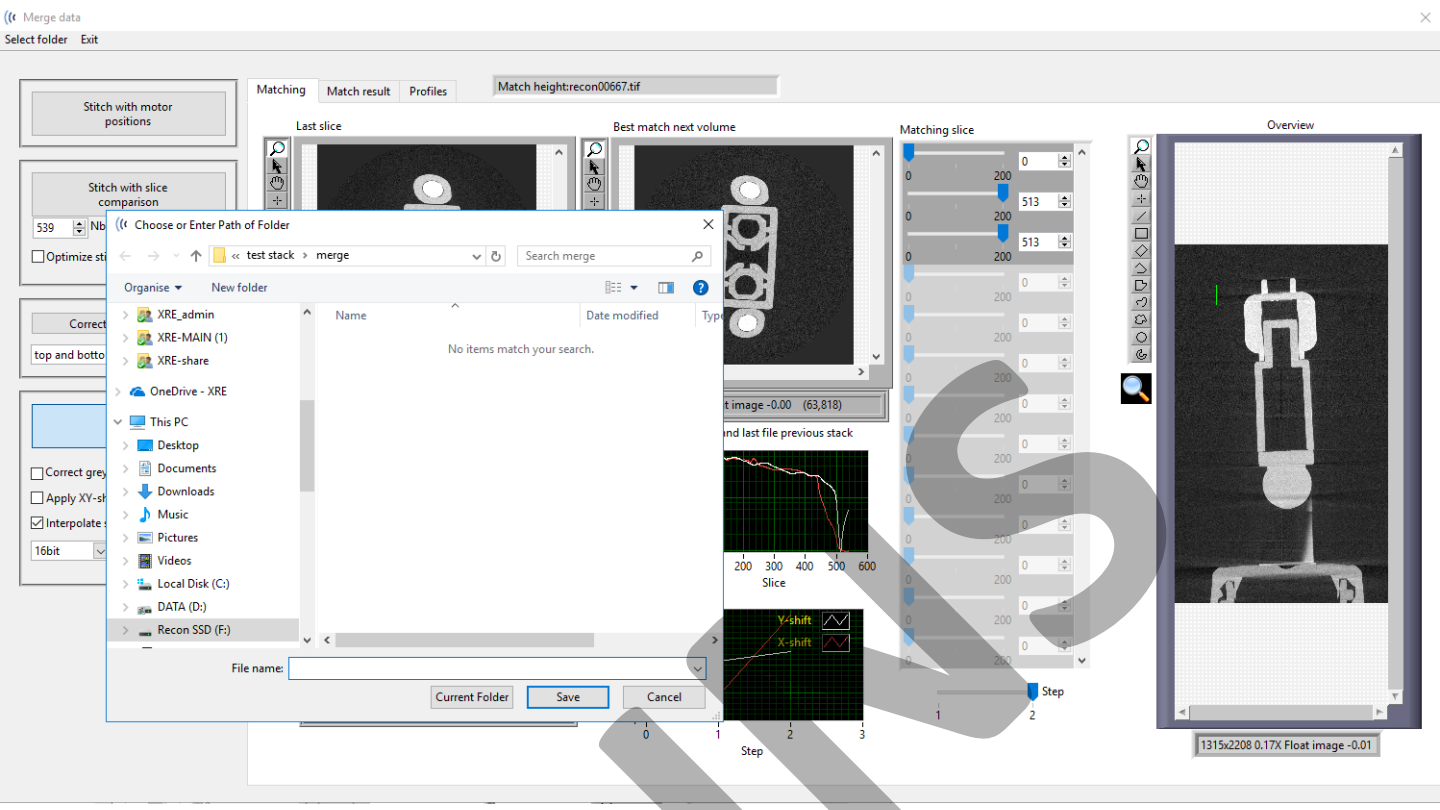


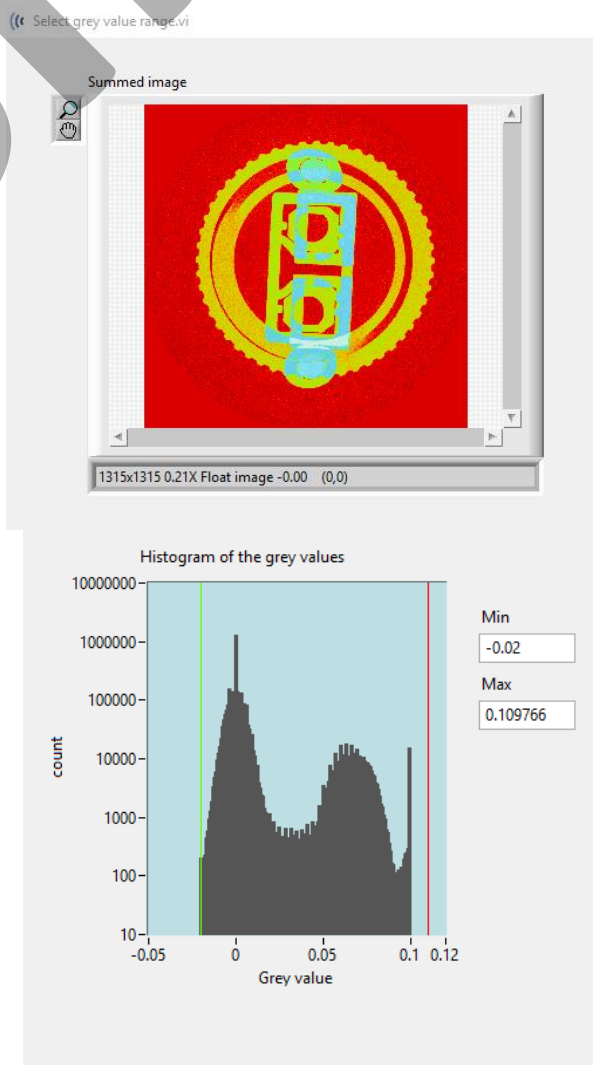
The different modes can be tested using the *Correct inhomogeneity button.*

Interpolation between the stiches can be selected and if the slices need to be saved as 16 bit or 8 bit.



4. Merge stacked scan files





Merging data

After clicking the *START* button you can select the folder in which to save the merged volume and the grey value range can also be selected for the entire core. After closing the *Slelect grey value range* window the merged slices are written to the selected folder