

User manual of HEPS CT Reconstruction stand-alone software

(Version of HEPSCT_MOCUPY : V1.0)

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1 Introduction

MOCUPY is a stand-alone CT reconstruction software of HEPSCCT (web), which based CUDA for GPU-accelerated and written by Python. MOCUPY contains modules such as Image import, Preprocessing, Shift align, Phase retrieval, Reconstruction and data analysis modules, which can realize the fast reconstruction of offline data. So as to meet the data processing requirements of synchrotron radiation users for "massive" X-ray CT.

1.1 Features

- The core algorithms achieve 100% GPU acceleration. Based on multi-threading to achieve fast reading of data and data processing with IO, CPU and GPU as the same time.
- Rotation axis correction automatically for multi-scale and ring artifacts removal based on wavelet transform.
- Provide manual and auto alignment modes for nano-CT images jitter correct, and the image correction accuracy can reach sub-pixel.
- Realize the phase retrieval of propagation-based phase imaging in single distance and multiple distances acquisition modes. The main algorithms include tie, ctf, tiehom_Rytov, tiehom_Paganin, hioer, etc. It takes only 3 minutes for phase retrieval of 1022 projections.
- A variety of reconstruction algorithms such as FBP, Grid and EM are provided. It only takes several seconds for tomographic datasets with image size of 2k*2k to reconstruct based on grid algorithm.

1.2 System Requirements

The algorithm of MOCUPY is based on CUDA Libraries, which requires Turing/Ampere cores or newer NVIDIA graphics/computing cards (<https://www.techpowerup.com/gpu-specs/?mfgr=NVIDIA&sort=name>). In addition, in order to achieve higher reconstruction speed, please use the NVMe SSD (such as WD:SN770/SN570、KBG40ZNS) to data read and write.

1.3 Download and Installation

- 1) The software package can be downloaded from the following link:
<http://www.ihep.cas.cn/dkxzz/HEPS/download/software/>
- 2) Unzip the files without installation;
- 3) How to open the software: in the folder, find the startCTRecon.bat file and double-click it.

1.4 Software update log

➤ V1.0 — 2023.04.28 (First update)

Functionality Added: Added jitter correction for nano-CT (automatic and manual modes).

Functionality Added: Added phase retrieval module for propagation-based phase imaging.

Functionality Added: Add data format conversion (support txrm to tiff,etc)

Interface optimization: The pop-up prompts information for the memory is not enough.

Function optimization: Image preview can fix the enlarged area

➤ V0 — 2022.09.21 (Original version)

System: The modules were tested and integrated to realize the CT reconstruction function.

2 Support data types and information

2.1 Support data types

MOCUPY support TIFF (uncompressed Tiff, 8bit uint, 16bit uint, and 32bit float) format images. The output is a dataset of 32bit float type TIFF format images. In addition, MOCUPY provides a solution to convert TIFF format of 12bit uint (compressed or uncompressed) to 16bit uint (details seen in section 3.1)

To ensure that the data is read in the right order, therefore, all images should have the same number of data bits for the index number, which can be achieved by prefixing the small index number with 0. For example: tomo_0001, tomo_0002... tomo_0180; flat_0001, dark_0001.

2.2 Information

- **Functions:**

- 1) Image preview and convert.
- 2) Micro-CT reconstruction.
- 3) Nano-CT reconstruction, which contains shift alignment.
- 4) Phase Retrieval for propagation-based X-ray phase-contrast imaging.

- **Definition:**

- 1) Projections: detector collected image with sample in the beam at a CT rotation angle.
- 2) Background: detector collected image without sample in the beam.
- 3) Dark: detector collected image without beam.

3 GUI of MOCUPY

The main GUI of the MOCUPY is shown in Figure 1, which contains three drop-down menus and five tabs. The specific function of each button is as follows:

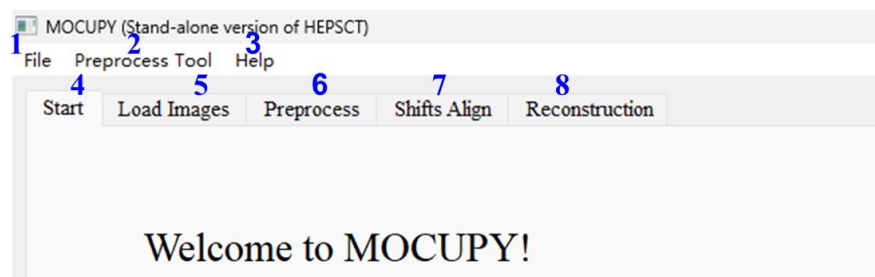


Figure 1 The main GUI of MOCUPY

- ① **Drop-down menus (3)**

- 1) File: preview and conversion;

2) Preprocess Tool: Phase Retrieval for propagation-based X-ray phase-contrast imaging

3) Help

② Tab (5)

4) Start: preview, conversion and save;

5) Load Images: Image import, including projection, background and dark field image import and preview;

6) Preprocess: The reconstruction preprocessing includes denoise, background remove, negative value remove, region of interest, background normalization and line profile preview of projections.

7) Shifts Align: Provide manual and auto alignment modes for nano-CT images jitter correct

8) Reconstruction: A variety of reconstruction algorithms such as FBP, Grid and EM ring artifacts removal, rotation axis correction and slice preview are provided.

The MOCUPY data processing mode and flow chart are shown in Figure 2. The data processing process mainly includes three parts: image format conversion, micro-CT reconstruction and nano-CT reconstruction. See 3.1~3.3 for details.

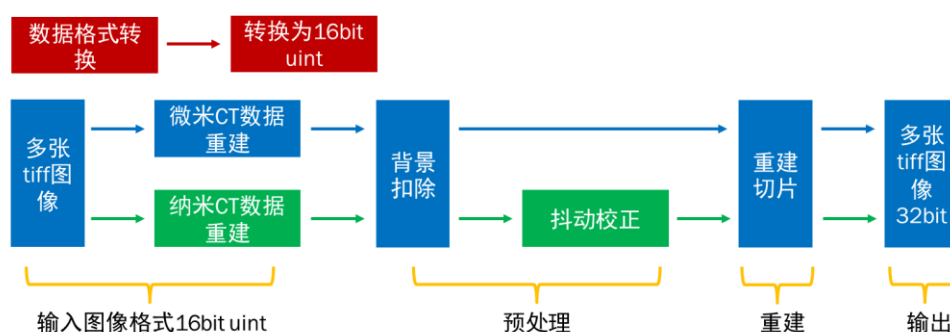


Figure 2 Schematic diagram of the data processing flow

3.1 Data format conversion and preview

3.1.1 Data format conversion

MOCUPY currently only supports the input of uncompressed 16bit/32bit Tiff format images for reading and calculation. Therefore, for the image with format of 12-bit Tiff, txrm, and xrm, it is necessary to convert the image format and convert it into 16-bit Tiff format images for output before subsequent reading and reconstruction. (Note: If the data format meets the data format of 2.1, you can skip this step directly.)

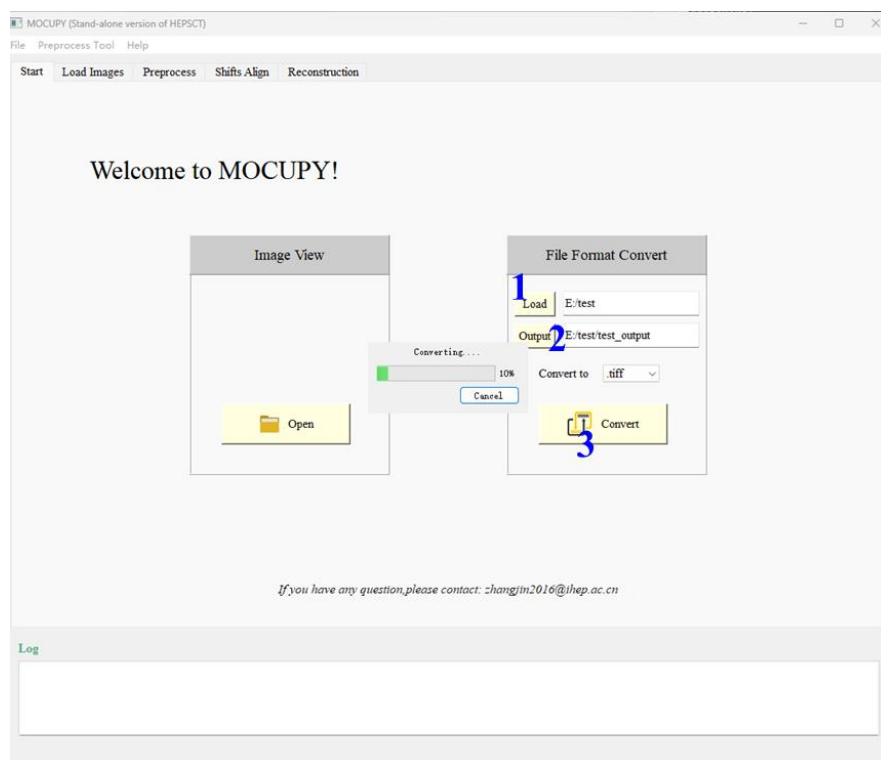


Figure 3 Start tab-image format conversion

The specific operation of file conversion is as follows:

- 1) Click the Load button and select the Tiff, txrm or xrm format that needs to be converted ;
- 2) Click the Output button to select the save path after the file format conversion;
- 3) Click the Convert button, and the conversion will end after the Converting window disappears.

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3.1.2 Image Preview

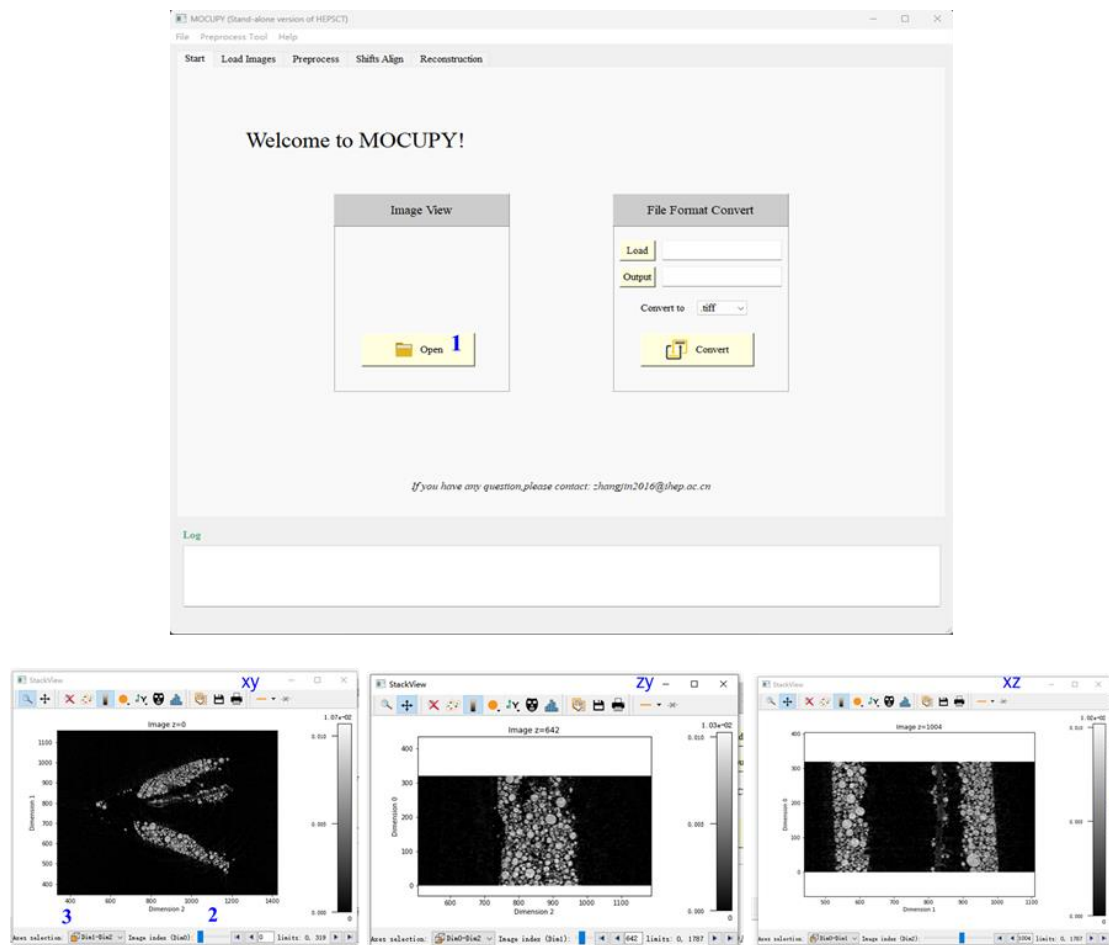


Figure 4 Start page- image preview example

The image preview mainly includes the projection and the reconstruction slice (multi-directions). The specific operations are as follows:

- 1) Click open button to select the file (the file format must meet the requirements of 2.1);
- 2) Adjust slices of different layers by dragging the slider;
- 3) Through the drop-down menu, select slice display in different directions.

3.2 Micro-CT reconstruction process

The micro-CT reconstruction process mainly includes three parts: image import, background removal (preprocessing) and reconstruction as shown in Figure 2. The specific reconstruction process and operations are as follows:

3.2.1 Image import

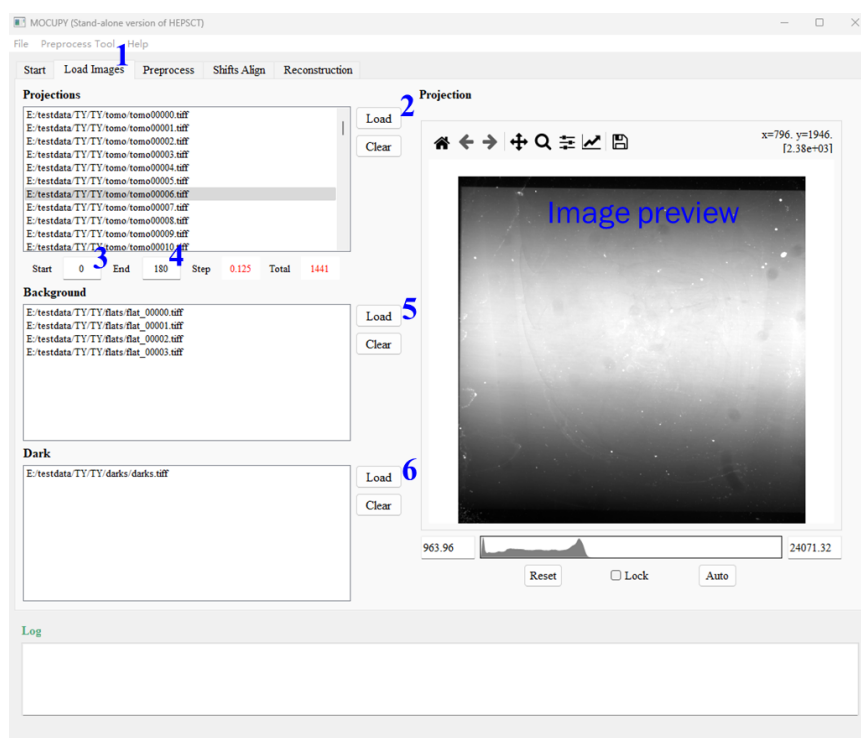


Figure 5 Load image tab and operation

- 1) Click Load Image to switch to the image import tab;
- 2) Click Load button (No.2) to import projection images;
- 3) Check whether the values of the start angle (default 0°, No.3) and end angle (default 180°, No.4) are consistent with the actual experimental collection. If not, enter the correct angle value in boxes No.3 and No.4;
- 4) Click Load button (No.5) to import the background images;
- 5) Click Load button (No.6) to import the dark filed images;

Note: If the background or dark field images are not collected during the experiment, the step can be skipped.

3.2.2 Background removal (preprocessing)

Click the Preprocess Tab to enter the preprocessing page (as shown in Figure 6).

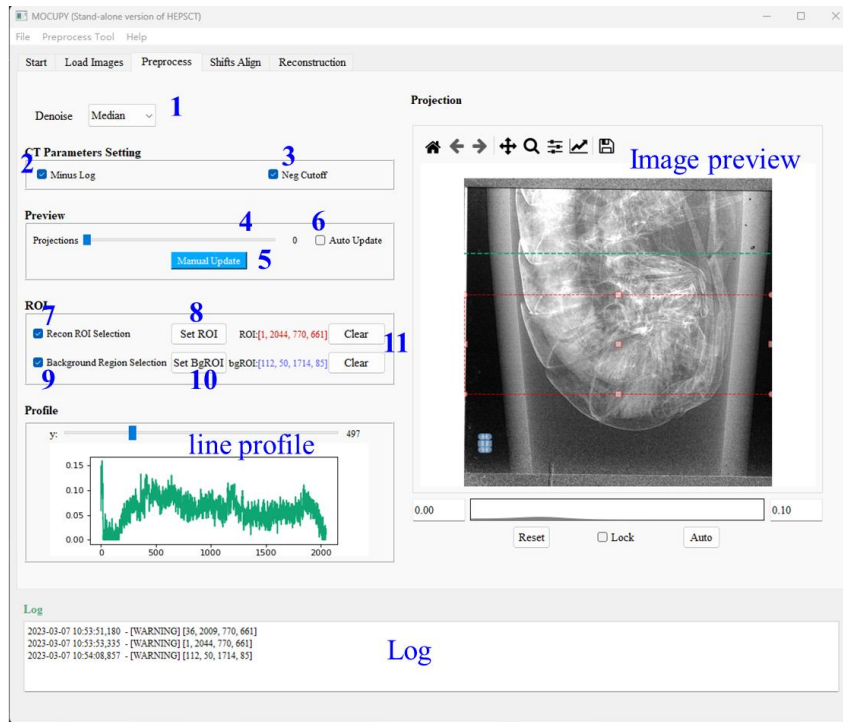


Figure 6 Preprocess tab and operation

- 1) Image denoising algorithm (Note: The algorithm can be selected according to the actual data, the default is None);
- 2) Background removal, the calculation formula is as follows:

$$I_{out} = -\log \frac{I_{prj} - I_{dark}}{I_{bg} - I_{dark}}$$

(Note: Check by default, if there is no background images import, you need to uncheck)

- 3) Remove the negative values, and select whether to check according the data;
- 4) Drag the Projection slider to change projection index, and click the Manual Preview (No.5) button to update the image manually; Or check the Auto Update (No. 6) option to automatically update the image;
- 5) If need to reconstruct the part of the projection, check the ROI option (No. 7), click the left mouse button in the image display area and drag to draw the region of interest (ROI). After determining the area, click the Set ROI button (No. 8) to

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complete the selection (as shown in the red dashed line); To cancel the selection, click the Clear button (No. 11);

- 6) If the projections need to be normalized by the background, check the Background ROI option (No.9). In the image display area, where there is no sample, click the left mouse button and drag to draw the bgROI. After determining the area, click the Set BgROI button (No.10) to complete the selection (as shown in the blue dashed line); (Note: This area can't be more than 300*300, if the sample full fill the whole area, this step can be skipped).

3.2.3 Reconstruction

Click the Reconstruction Tab to enter the reconstruction page (as shown in Figure 7)

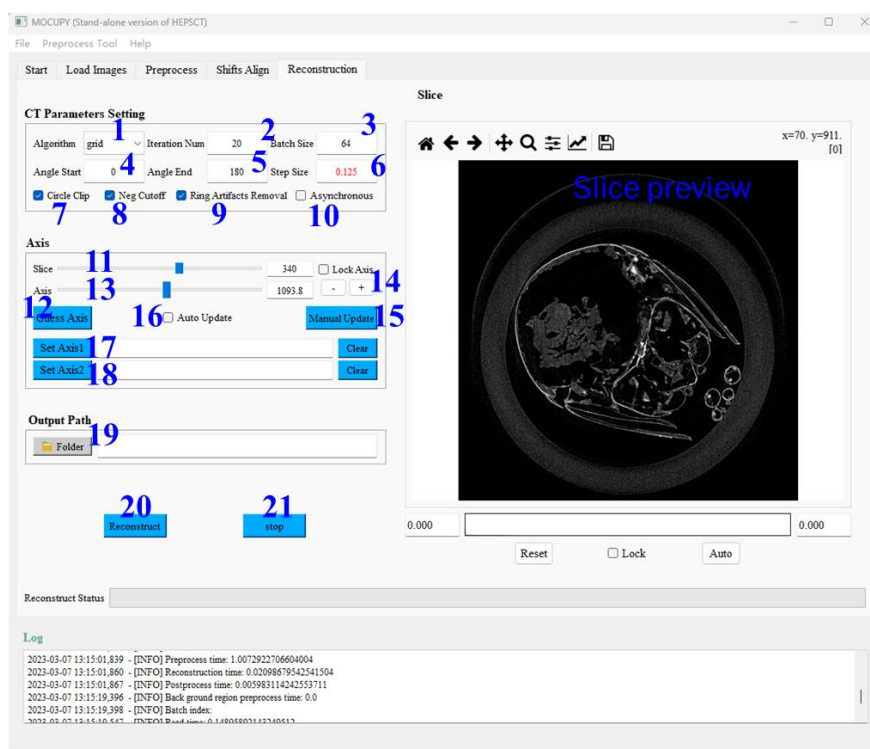


Figure 7 Reconstruction page and operations

- 1) Selection of reconstruction algorithms: FBP, grid (fast), EM and other algorithms (default grid);
- 2) Iteration number, default 20;

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- 3) The number of slices for each reconstruction batch, which is related to computer performance (memory), the default is 64 (which can be appropriately reduced or increased according to computer performance);
- 4) Starting Angle: according to the actual experiment to input, the default is 0;
- 5) End Angle: according to the actual experiment to input, the default is 180;
- 6) The obtained value is calculated based on the number of imported projections and the value of No.4 and No.5. Check that the step size is correct before reconstruction;
- 7) Mask the reconstruction area: the values outside the mask circle are 0 in slice. You can select whether to check according to the actual situation;
- 8) Remove the negative value in the slice, and select whether to check according to the actual situation;
- 9) Remove the ring artifacts from the slices, and it is recommended to check;
- 10) Whether the final reconstruction is asynchronous, you can choose according to the computer configuration. The is unchecked by default.
- 11) Drag the Slice slider to change the index of the current reconstructed slice;
- 12) Click the Guess Axis button (No. 12) to calculate the value of the rotating axis by the algorithm;
- 13) If the value of the rotation axis calculated in 12) is not accurate, drag the Axis slider to find the accurate value of the rotation axis;
- 14) The "+/-" button (No.14) is the fine adjustment of the slider in 13), and the rotation axis value changes by 0.5 per click;
- 15) Manually preview the reconstructed slice. After changing the parameters each time, click the Manual Update button (No. 15) for preview;
- 16) If checked, the reconstructed slice will be automatically previewed when the parameter is changed;

If the sample is large, there is a large difference between the rotating axis values of the upper and lower layers. The rotating axis values of the upper and lower layers

are determined respectively, and then interpolation by the algorithm is used in the middle to obtain the rotating axis value. See (17,18) for details.

- 17) Drag the Slice slider (No.11) to the left, select the upper Slice, repeat steps 12) to 14), find the most suitable axis value, click set Axis1; (After this step, the rotation axis value of the upper can be determined);
- 18) Similar to the 17), drag the Slice slider (No.11) to the right, select the lower Slice, repeat steps 12) to 14), find the most suitable axis value, and click set Axis2; (After this step, the rotation axis value of the lower layer can be determined);
- 19) Click the Folder button (No.19) and select the path to save the reconstruction results;
- 20) Click the Reconstruction button (No. 20) to start;
- 21) Click the Stop button (No. 21) if you need to stop the collection.

3.3 Nano-CT reconstruction process

The nano-CT reconstruction process mainly includes: image import, background removal (preprocessing), image jitter correction and reconstruction as shown in Figure 2. The specific reconstruction process and operations are as follows:

3.3.1 Image import

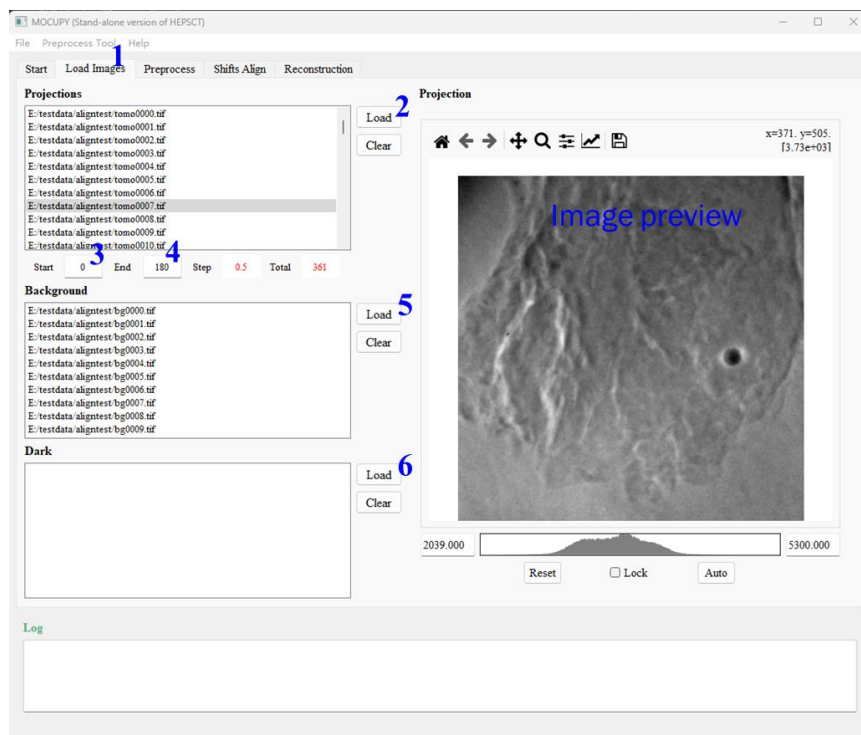


Figure 8 Load image tab and operation

- 1) Click Load Image to switch to the image import tab;
- 2) Click Load button (No.2) to import projection images;
- 3) Check whether the values of the start angle (default 0°, No.3) and end angle (default 180°, No.4) are consistent with the actual experimental collection. If not, enter the correct angle value in boxes No.3 and No.4;
- 4) Click Load button (No.5) to import the background images;
- 5) Click Load button (No.6) to import the dark filed images;

Note: If the background or dark field images are not collected during the experiment, the step can be skipped.

3.3.2 Background removal (preprocessing)

Click the Preprocess Tab to enter the preprocessing page (as shown in Figure 9).

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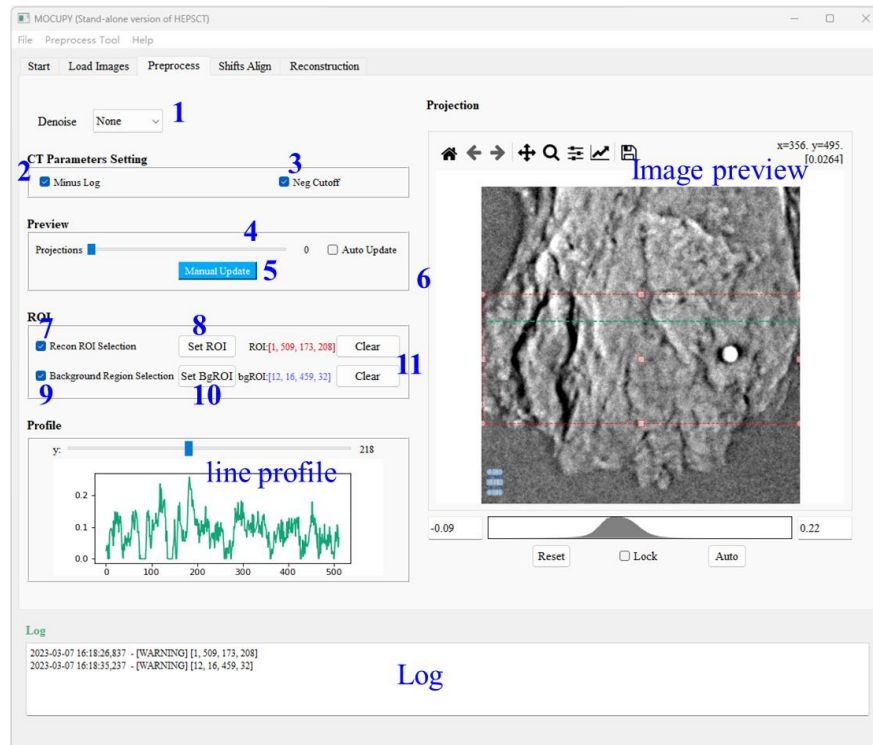


Figure 9 Preprocess tab and operation

- 1) Image denoising algorithm (Note: The algorithm can be selected according to the actual data, the default is None);
- 2) Background removal, the calculation formula is as follows:

$$I_{out} = -\log \frac{I_{prj} - I_{dark}}{I_{bg} - I_{dark}}$$

(Note: Check by default, if there is no background images import, you need to uncheck)

- 3) Remove the negative values, and select whether to check according the data;
- 4) Drag the Projection slider to change projection index, and click the Manual Preview (No.5) button to update the image manually; Or check the Auto Update (No. 6) option to automatically update the image;
- 5) If need to reconstruct the part of the projection, check the ROI option (No. 7), click the left mouse button in the image display area and drag to draw the region of interest (ROI). After determining the area, click the Set ROI button (No. 8) to complete the selection (as shown in the red dashed line); To cancel the selection, click the Clear button (No. 11);

- 6) If the projections need to be normalized by the background, check the Background ROI option (No.9). In the image display area, where there is no sample, click the left mouse button and drag to draw the bgROI. After determining the area, click the Set BgROI button (No.10) to complete the selection (as shown in the blue dashed line); (Note: This area can't be more than 300*300, if the sample full fill the whole area, this step can be skipped).

3.3.3 Image jitter correction

Due to the limitation of the mechanical stability of the sample stage, the random jitter of the sample stage will produce during the process of sample rotation in nano-CT experiment, which will affect the direct reconstruction results. It is necessary to correct the jitter of the projections. Therefore, MOCUPY provides two jitter correction modes: manual correction and automatic correction.

Manual correction mode requires label the markers on each projection manually, which has good applicability but requires a large amount of work. Automatic correction mode recognizes the markers and calculate the offset by the algorithm. For projections with good contrast, even if there is no marker, the automatic correction algorithm can be directly used to recognize and calculate offset. This method takes less time and requires less work. According to the actual experimental data, choose one of the methods to correct the projections jitter. The specific interface and operations are as follows.

◆ Manual correction

Click the Shift Align Tab to enter the image jitter correction tab seen in Figure 10.

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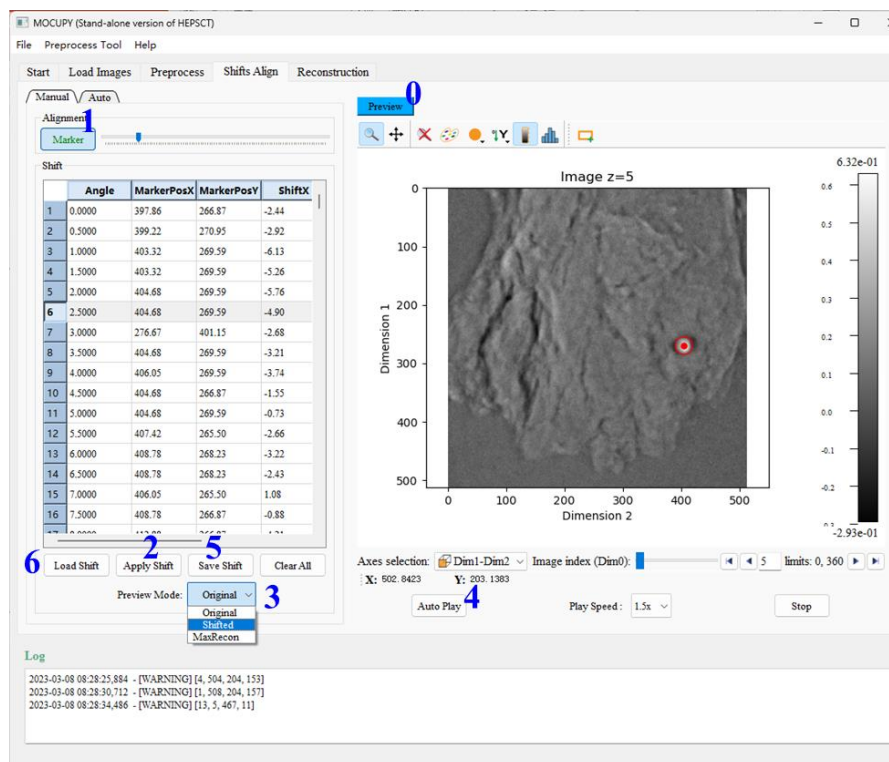


Figure 10 Operations of image jitter correction (manual mode)

- 0) Click the Preview button (No. 0) to import the images;
- 1) Click the Marker button (No.1), move the mouse to the image preview area, and drag slider on the right of Marker button to adjust the mouse pointer size to the same size of marker; Move the mouse pointer to the marker (as shown in Figure 10) and double-click. Every click will automatically move the image to the next angle. Click the same marker on each projection until all projections are completed, and the shift table will record the position of the marker.
- 2) Click the Apply Shift button (No.2), and it will automatically calculate the offset;
- 3) Click the drop-down menu to select Shifted mode;
- 4) Click the Auto Play button (No. 4). You can see that the marker is moved to the center of the field of view, and the marker is basically not move during playing, then the shift correction is completed.
- 5) Click Save Shift (No.5) to save the Shift parameter of the image;
- 6) If there is a shift value file, you can directly click the Load shift button (No.6) and import. Then click Apply Shift (No.2) to complete Align.

◆ Automatic correction

The automatic correction mainly contains two modes: Marker recognition (in the case of gold particle markers) and marker-free mode (in the case of sample image with high contrast).

➤ Marker recognition

Automatic correction process of marker recognition: ROI, parameter setting and correction. The details are as follows:

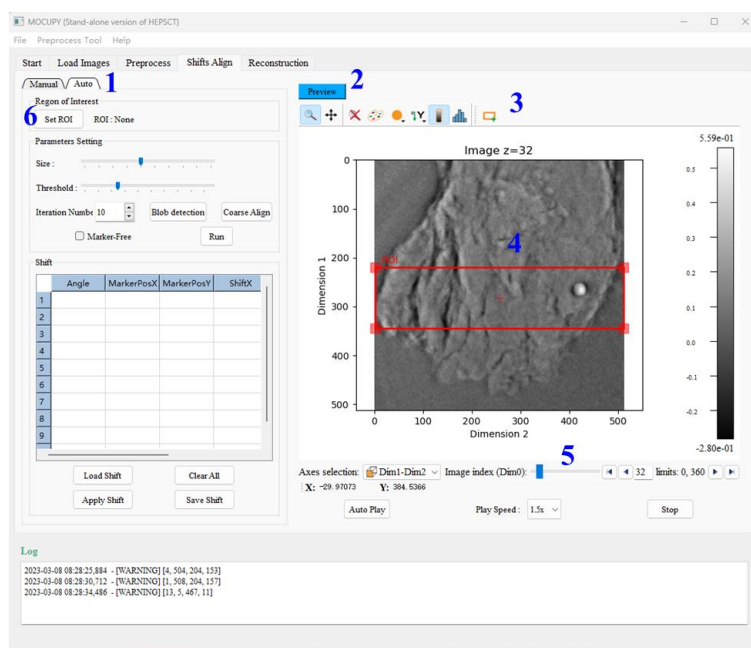


Figure 11 Operations of automatic image jitter correction (ROI)

① ROI

- 1) Click Auto Tab (No.1) to switch to the automatic correction tab as shown in the Figure 11.
- 2) Click the Preview button (No.2) to import;
- 3) Click the ROI icon ;
- 4) Click the left mouse button and drag to draw a red box;
- 5) Drag the slider to check whether the gold particles are always in the red box. If the gold particles are out of the red box, adjust the size of the red box so that all the gold particles in the projection are in the red box;

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6) Click the Set ROI button (No.6).

Note: Since the size of the ROI determines the memory occupied by the subsequent calculation, the performance of the computer should be considered. If the memory is exceeded, the subsequent calculation cannot be performed.

② Parameter setting

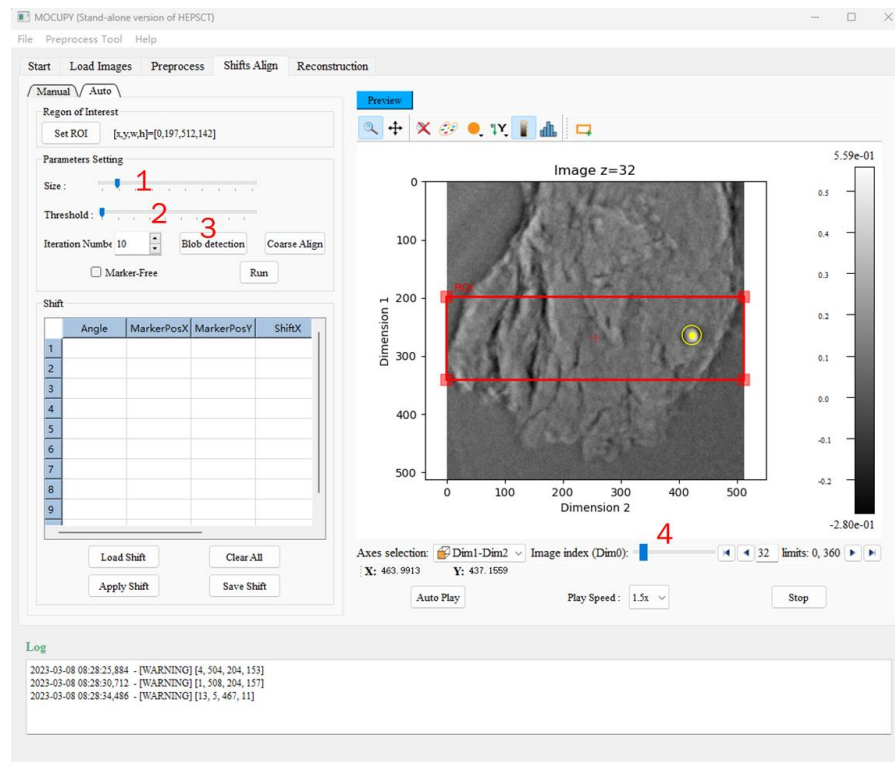


Figure 12 Operations of automatic image jitter correction (parameter setting)

- 1) Drag the Size slider so that the size of yellow circle in the image is close to the size of the gold particle in the red box;
- 2) Drag Threshold slider to the left (the detection is strongest);
- 3) Click the Blob detection button, then the gold particles should be circled in yellow; If not, adjust the slider corresponding to the Size and Threshold, and click the Blob detection button for every adjusting. If other noise or impurities are also detected, the Threshold slider is appropriately adjusted to the right;
- 4) Drag the Image index slider and click the Blob detection button at each position to ensure that gold particles can be detected at most positions.

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③ Correction

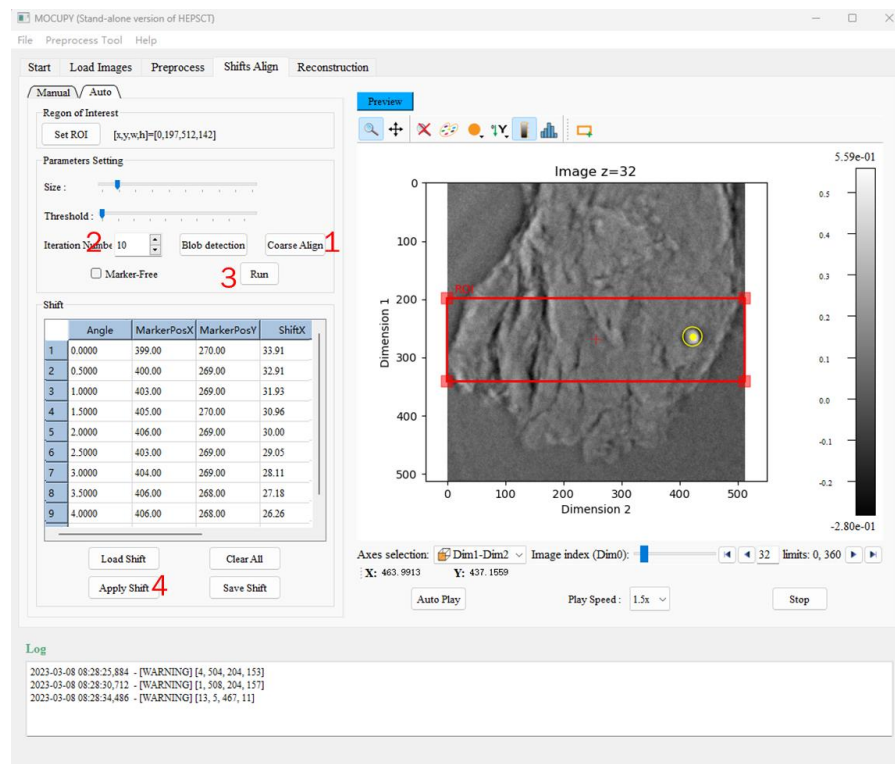


Figure 13 Operations of automatic jitter correction (correction)

- 1) Click the Coarse align button;
- 2) Adjust Iterations Num (0-100), the recommended value is 10;
- 3) Click Run button, and the program will automatically calculate the offset;
- 4) After the correction is completed, the shift value will be updated in the shift table, and the offset can be used after clicking Apply Shift.

➤ **Marker-Free Mode**

For the experimental data with good contrast, after the ROI (see ① selection for details), the following operations can be directly performed:

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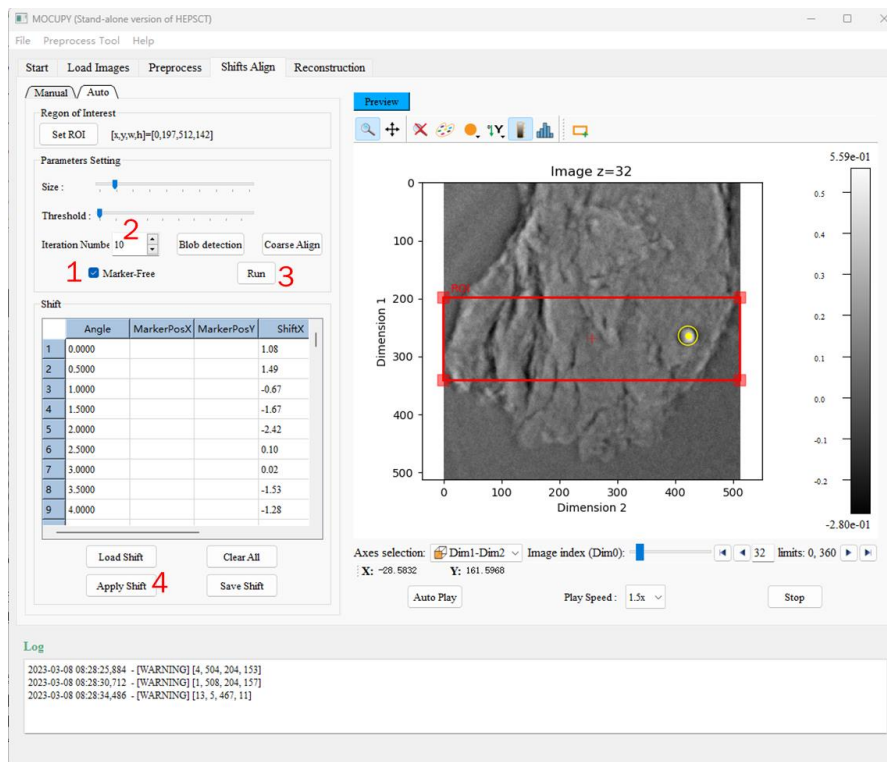


Figure 14 Operations of automatic jitter correction (Marker-Free)

- 1) Check Marker-Free;
- 2) Adjust Iterations Num (0-100), the recommended value is 10;
- 3) Click Run button, and the program will automatically calculate the offset;
- 4) After the correction is completed, the shift value will be updated in the shift table, and the offset can be used after clicking Apply Shift.

➤ Image jitter correction criteria and examples

After clicking Run, the program will automatically calculate, and it will pop up a sub-window, which can be used to evaluate the correction results according to the displayed pictures. The marker boundary is closed, the shape is clear and there are few surrounding radial artifacts (as shown in Figure 15). The radial artifacts around the sample decrease as the iterations proceed.

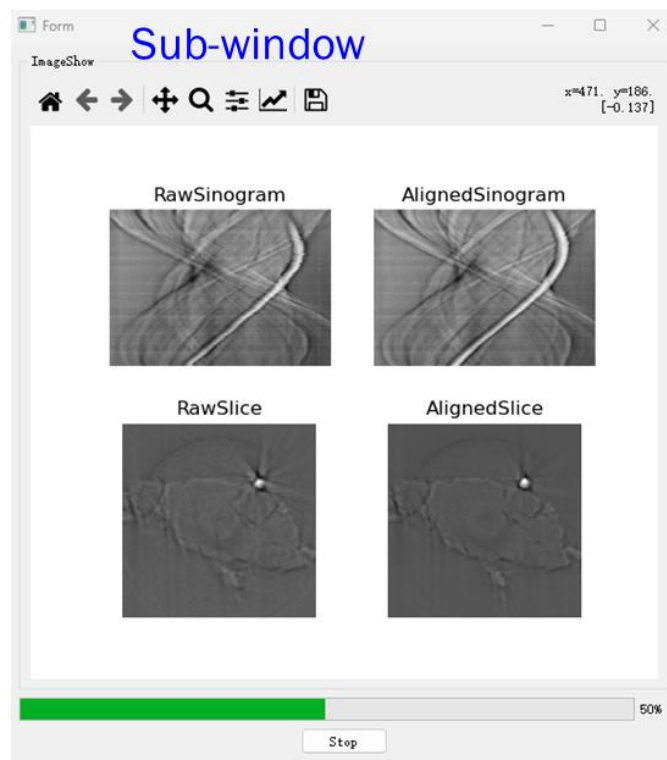


Figure 15 Example of intermediate results in jitter correction

The jitter correction and reconstruction slice for projection with and without markers are shown in Figures 16-17:

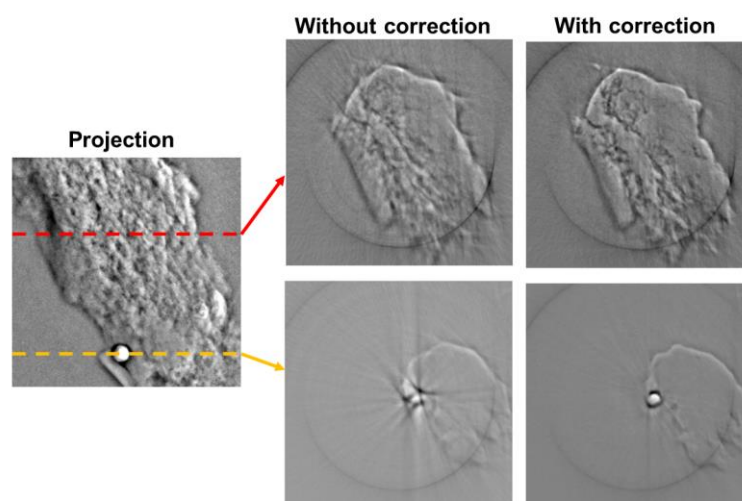


Figure 16 The reconstructed slices with and without automatic jitter correction for projections with markers

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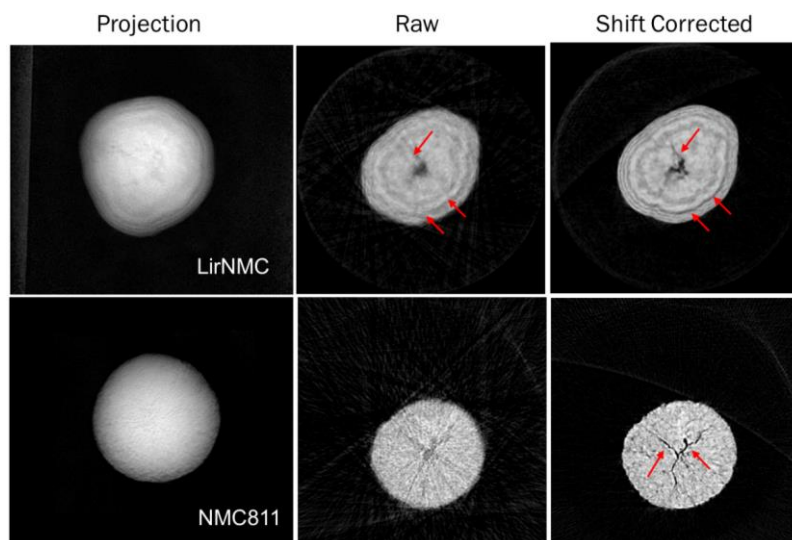


Figure 17 The reconstructed slices with and without automatic jitter correction for projections without markers

3.3.4 Reconstruction

Click the Reconstruction Tab to enter the reconstruction page (Figure 18) after finishing the shift value calculation.

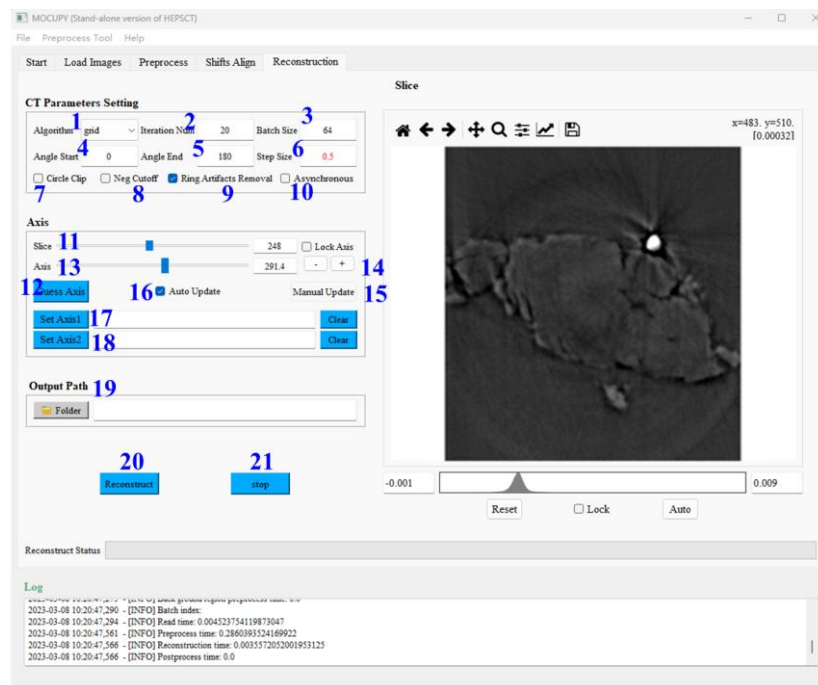


Figure 18 Reconstruction page and operations

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- 1) Selection of reconstruction algorithms: FBP, grid (fast), EM and other algorithms (default grid);
- 2) Iteration number, default 20;
- 3) The number of slices for each reconstruction batch, which is related to computer performance (memory), the default is 64 (which can be appropriately reduced or increased according to computer performance);
- 4) Starting Angle: according to the actual experiment to input, the default is 0;
- 5) End Angle: according to the actual experiment to input, the default is 180;
- 6) The obtained value is calculated based on the number of imported projections and the value of No.4 and No.5. Check that the step size is correct before reconstruction;
- 7) Mask the reconstruction area: the values outside the mask circle are 0 in slice. You can select whether to check according to the actual situation;
- 8) Remove the negative value in the slice, and select whether to check according to the actual situation;
- 9) Remove the ring artifacts from the slices, and it is recommended to check;
- 10) Whether the final reconstruction is asynchronous, you can choose according to the computer configuration. The is unchecked by default.
- 11) Drag the Slice slider to change the index of the current reconstructed slice;
- 12) Click the Guess Axis button (No. 12) to calculate the value of the rotating axis by the algorithm;
- 13) If the value of the rotation axis calculated in 12) is not accurate, drag the Axis slider to find the accurate value of the rotation axis;
- 14) The "+/-" button (No.14) is the fine adjustment of the slider in 13), and the rotation axis value changes by 0.5 per click;
- 15) Manually preview the reconstructed slice. After changing the parameters each time, click the Manual Update button (No. 15) for preview;
- 16) If checked, the reconstructed slice will be automatically previewed when the parameter is changed;

If the sample is large, there is a large difference between the rotating axis values of the upper and lower layers. The rotating axis values of the upper and lower layers are determined respectively, and then interpolation by the algorithm is used in the middle to obtain the rotating axis value. See (17,18) for details.

- 17) Drag the Slice slider (No.11) to the left, select the upper Slice, repeat steps 12) to 14), find the most suitable axis value, click set Axis1; (After this step, the rotation axis value of the upper can be determined);
- 18) Similar to the 17), drag the Slice slider (No.11) to the right, select the lower Slice, repeat steps 12) to 14), find the most suitable axis value, and click set Axis2; (After this step, the rotation axis value of the lower layer can be determined);
- 19) Click the Folder button (No.19) and select the path to save the reconstruction results;
- 20) Click the Reconstruction button (No. 20) to start;
- 21) Click the Stop button (No. 21) if you need to stop the collection.

3.4 Phase retrieval flow

The phase retrieval module is a separate preprocessing module. At present, it only supports the data collected by propagation-based phase imaging, including single-distance and multi-distance phase retrieval. The specific reconstruction process and operations are as follows:

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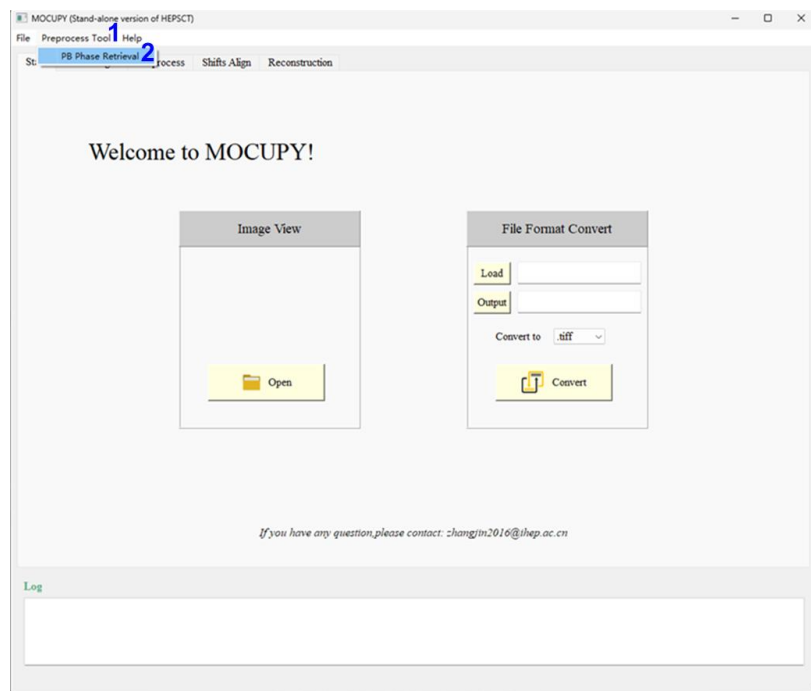


Figure 19 Main page of MOCUPY

- 1) Click Preprocess Tool (No.1) in the menu bar;
- 2) Click PB Phase Retrieval button (No.2) to open the phase retrieval window.

3.4.1 Image import

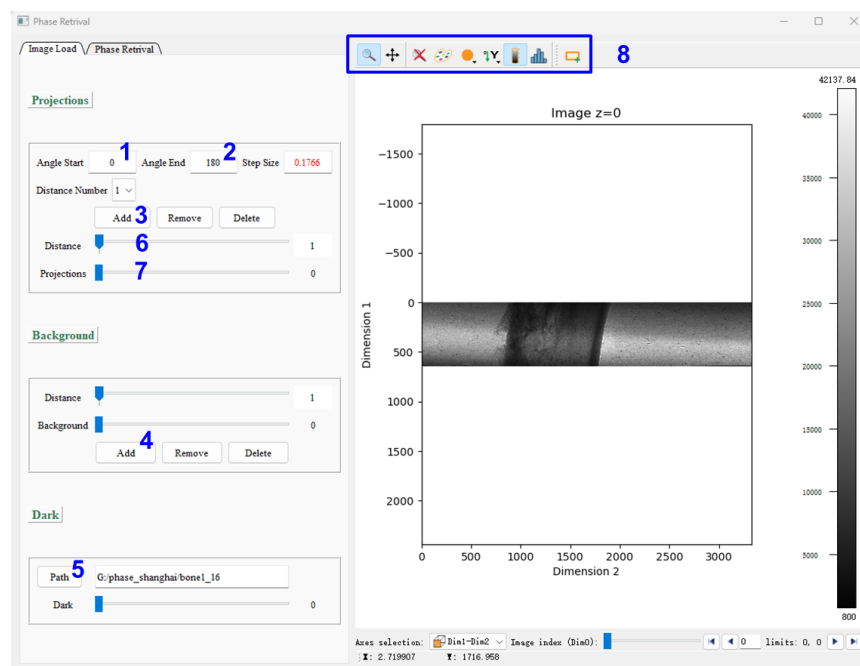


Figure 20 Main base of phase retrieval and image import tab (Separate window).

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- 1) Start Angle: If only a single angle, can be ignored;
- 2) Stop Angle: If only a single angle, can be ignored;
- 3) Click Add button (No.3) and select the projections to import; If the experimental data are collected from multiple distances, this step will be repeated. And the repeated times are same as the number of distances. The Distance Number is also incremented;
- 4) Background import: If the experimental data are collected from multiple distances, this step will be repeated. And the repeated times are same as the number of distances.
- 5) Click Path button (No.5) and select dark field data;
- 6) Drag the Projection Distance slider (No.6) to preview the projections collected at different distances; If the data is a single distance, the slider cannot be dragged;
- 7) Drag the slider to preview the projections at different angles at the same distance; If the Angle is single, the slider cannot be dragged;
- 8) Toolbars for image display, from left to right they are zoom in/out, drag, colormap, flip along Y-axis, grayscale histogram, and selection, respectively.

3.4.2 Phase Retrieval

There are multiple phase retrieval algorithms, which can be mainly divided into the following two categories:

1) **Edge Enhancement (Fresnel Number~1):**

"tie": weak absorbing materials

"tiehom_Paganin", "tiehom_Born", "tiehom_Rytov": homogeneous hypothesis, the refraction and absorption coefficients of the sample should be provided;

2) **Hologram (Fresnel Number<<1)**

"ctf": weak phase shift, weak absorption;

"ctfpurephase" : weak phase shift without absorption

"ctfhom" : homogeneous hypothesis, the refraction and absorption coefficients of the sample should be provided;

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"ctfhalf", "quasiparticle", "quasiparticlehalf", "prjctf": improved ctf algorithm, which is suitable for samples with large phase shift;

"hioer", "gd": iterative algorithm.

◆ Single-distance mode

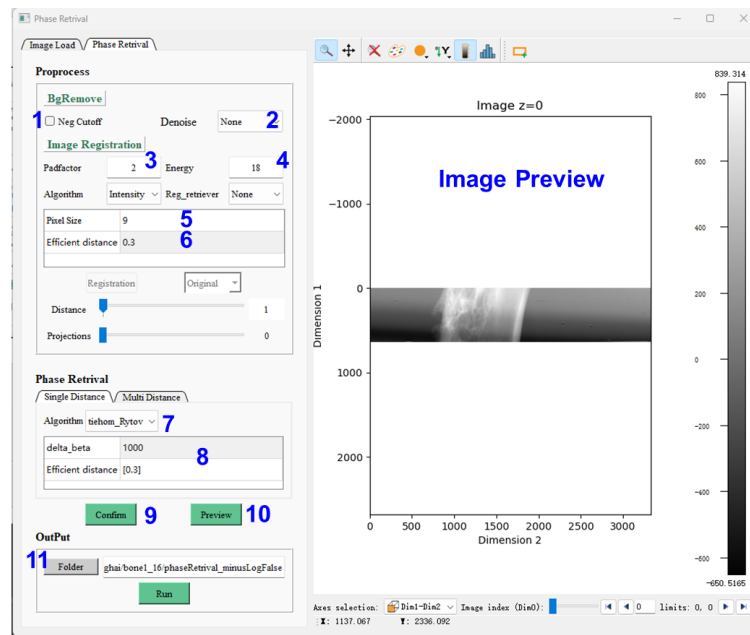


Figure 21 Phase retrieval Tab for single-distance

- 1) Remove the negative value in the image, you can choose whether to check it or not;
- 2) Image denoise (Note: The algorithm can be selected according to the actual images, the default is None);
- 3) Pad factor: default is 2;
- 4) Energy: energy parameter during the experiment, unit is keV;
- 5) Effective pixel size of the image, unit is μm ;
- 6) Effective distance from the sample to the detector, unit is m;
- 7) Choose the appropriate phase retrieval algorithm in single distance tab;
- 8) Set the parameters of phase retrieval;
- 9) Confirm whether the parameters set in 8) are correct and click Confirm button(No.9);

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- 10) Preview the phase retrieval results of the current projection;
- 11) Click Folder button to select the saving path of phase retrieval results;
- 12) Click the Run button to start phase retrieval for all projections.

◆ Multi-distance mode

For data acquisition in multi-distance mode, projection maps of different distances need to be registered before phase retrieval.

①Registration

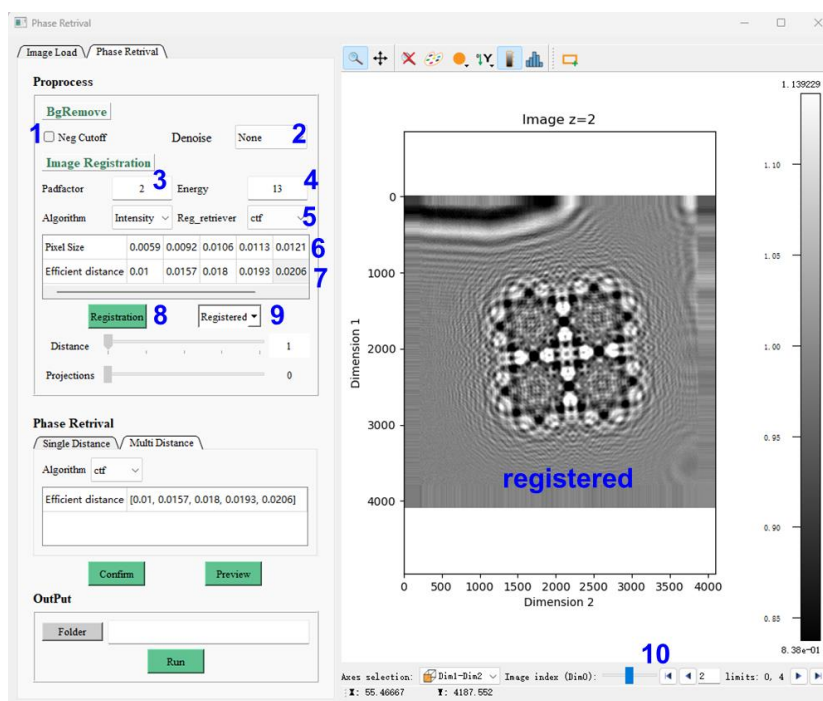


Figure 22 Phase retrieval Tab for multi-distance and registration preview

- 1) Remove the negative value in the image, you can choose whether to check it or not;
- 2) Image denoise (Note: The algorithm can be selected according to the actual images, the default is None);
- 3) Pad factor: default is 2;
- 4) Energy: energy parameter during the experiment, unit is keV;
- 5) For multi-distance registration, preprocessing parameters, “ctf” or “tie” should be selected according to the experimental data;

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- 6) Set the effective pixel size (unit: μm) of the images collected at each distance in the multi-distance mode;
- 7) Set the effective distance between the sample and the detector in the multi-distance mode, unit: m;
- 8) Click Registration button (No.8) for multi-distance images registration;
- 9) Switch to preview images before/after registration;
- 10) Drag the slider (No.10) to preview images of different distances after registration;

② Phase Retrieval

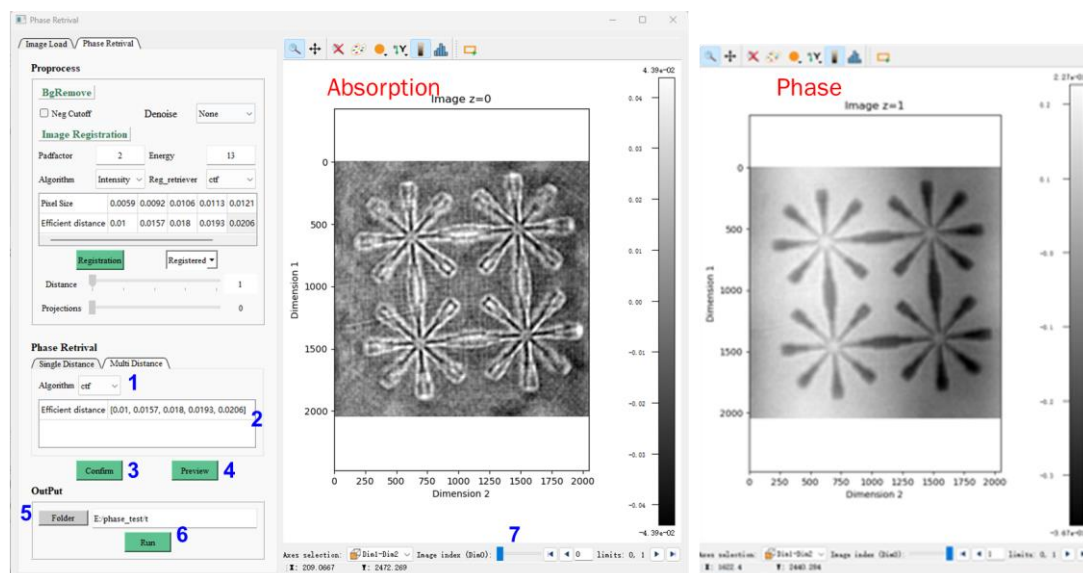


Figure 23 Phase retrieval Tab for multi-distance and preview

- 1) Choose the appropriate phase retrieval algorithm in multi-distance tab;
- 2) Set the parameters of phase retrieval;
- 3) Confirm whether the parameters set in 2) are correct and click Confirm button (No.3);
- 4) Preview the phase retrieval results of the current projection;
- 5) Click Folder button to select the saving path of phase retrieval results;
- 6) Click the Run button to start phase retrieval for all projections.

- 7) Drag the slider to preview the absorption and phase images by the phase retrieval algorithm; ($z=0$ is the image of absorbing; $z=1$ is phase image).

3.4.3 Image reconstruction and examples

For 3D propagation-based phase CT experiment, the projection of phase can be obtained after phase retrieval in 3.4.2, then the phase retrieval window can be closed and 3D reconstruction can be carried out according to the process in Section 3.2 (ignoring background and dark field import).

The results of direct reconstruction and phase retrieval slice of single-distance phase CT are shown in Figure 24 (the test data provided by SSRF). There are 1022 projections, and phase retrieval with MOCUPY takes about 3 minutes.

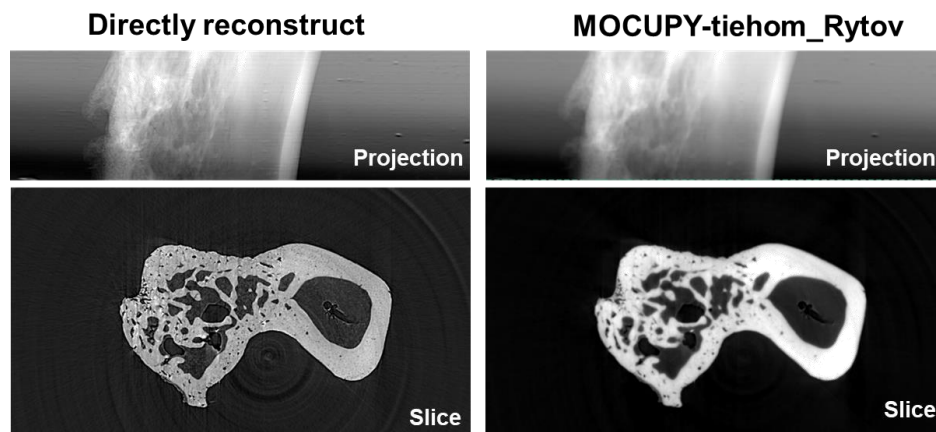


Figure 24 Phase retrieval: direct reconstruction slice and slice after phase retrieval in single distance mode of bone sample

4 Computer performance and FAQs

4.1 Computer configuration and reconstruction time

Number	Computer performance			Data size	Total Time
	Graphics Card	Hard Disc	Memory		
1	NVIDIA GeForce RTX 3060 laptop (6GB)	WD_SN570	16 GB	2k*2k*1441p(11.3GB)	49s
2	NVIDIA GeForce RTX 3090 (24GB)	Samsung 980 Pro	200 GB	2k*2k*1441p(11.3GB)	35s
3	NVIDIA GeForce RTX 3090 (24GB)	Samsung 980 Pro	200 GB	5k*4k*1441p(56.2GB)	6mins 54s
4	NVIDIA GeForce RTX 3090 (24GB)	Samsung 980 Pro	200 GB	5k*4k*5120p(200GB)	11mins 34s

Figure 25 Recommended computer performance

4.2 Common problems

- 1) MOCUPY is a fast CT reconstruction software for GPU acceleration based on CUDA. Therefore, the graphics card needs to support CUDA. When the graphics card does not support CUDA acceleration, the software may fail to run.
- 2) If the CT data missing too much angles or the sample is out of the projection field of view, guess axis may not calculate accurately. You can manually adjust the Axis value.

5 Development team and contact

5.1 Team

MOCUPY was developed by the team of HEPS TXM beamline.

5.2 Contact Us

Jin Zhang, zhangjin2016@ihep.ac.cn

The software is still in the function update, therefore, there may be some bugs. If you have any questions or suggestions during the use, please contact us. Welcome to download!