Phase-sensitive x-ray Image processing and Tomography REconstruction

Manual

(2012.05)

Main reference: R. C. Chen, D. Dreossi, L. Mancini, R. Menk, L. Rigon, T. Q. Xiao, and R. Longo, "PITRE: software for phase-sensitive X-ray image processing and tomography reconstruction," *Journal of Synchrotron Radiation* **19** (5), 836-845 (2012).

Contents

I. Configuration

1. Install 32/64 bit IDL (version 7.1 or higher), which can be downloaded from Exelis website (http://www.exelisvis.com/language/en-us/productsservices/idl.aspx) after a simple registration, on windows XP (or newer version). The IDL Virtual Machine is included in the IDL installation file and does not require a license to run.
2. Download the PITRE installer (32/64 bit) and run it as Administrator;
   The installer will process the following actions to your PC:
   a. Extract PITRE files to default directory 'C:\PITRE\';
   b. Add 'C:\PITRE\lib\' to Windows system environment variable "Path". In this way, PITRE will locate and call automatically the external libraries, such as Gridrec and GraphicsMagick. All the needed external libraries for PITRE are included in the installer and will be installed automatically;
   c. Request to reboot the PC, which is essential to let step (b) take effect.
3. **Reboot the PC;**
4. Double click `PITRE.sav` (or use IDL Virtual Machine to open it) to run the software;
5. Have fun.

System requirement:

Nowadays PC can run the PITRE without any problem. One suggestion is to installed large RAM size due to the sinogram generation method. Moreover, it is recommended to use 64-bit version operation system and PITRE rather than 32-bit ones in case of PC RAM size is larger than 4 Gigabytes.

II. Supported data types

- **Format**

PITRE accepts TIFF (Tagged Image File Format, 8-bit unsigned integer, 16-bit unsigned integer and 32-bit single-precision float format), PNG (8-bit unsigned integer) and BMP (8-bit unsigned integer) format images. The output is a dataset of 32-bit single-precision float TIFF images. Moreover, PITRE provides a solution to convert 12-bit unsigned integer TIFF (compressed or uncompressed) into 16-bit unsigned integer TIFF by using GraphicsMagick as plugin [1]. PITRE also provides specific features to elaborate data acquired by the PICASSO detector [2, 3].

- **Naming**

The name of projection, flatfield and darkfield images is a combination of prefix and index number. The prefix of projection, flatfield and darkfield must be ‘tomo_’, ‘flat_’ and ‘dark_’. All projection, flatfield and darkfield images must be named progressively, and saved in the same folder. In order to meet the alphabetical sorting rule in IDL, the digit number of all images index number must be the same. One can accomplish this by adding zero in the small index number.

One correct numbering sample is ‘tomo_0001, tomo_0002, tomo_0003, … , tomo_0010, …,tomo_0100’.

III. Information

Functions:

1. phase retrieval for propagation-based X-ray phase-contrast imaging/tomography (PPCT)
2. extraction of apparent absorption, refraction and ultra-small-angle scattering images for analyzer-based X-ray phase-contrast imaging/tomography (DEI-CT)
3. parallel beam extended view CT data handling
4. tomography reconstruction: parallel beam CT, PPCT and DEI-CT, employing filter back-projection and GRIDREC algorithms
5. images format conversion or cropping
6. and lots more

Abbreviations:

PPCI: X-ray propagation-based phase contrast imaging
PPCT: X-ray propagation-based phase contrast computed tomography
DEI: Diffraction enhanced imaging
SDD: sample-to-detector distance
PITRE: Phase-sensitive x-ray Image processing and Tomography REconstruction
PITRE_BM: Phase-sensitive x-ray Image processing and Tomography REconstruction Batch Manager

Definition:

Projection: detector collected image with sample in the beam at a CT rotation angle.
Flatfield: detector collected image without sample in the beam.
Darkfield: detector collected image without beam.

IMPORTANT NOTE:

1. In case someone want to copy PITRE processed data to another folder, please DO NOT forget to copy the PITRE generated text file, otherwise strange/error result can be happened in the further PITRE processing since the information in text file will be used.

IV. PITRE data processing

The data processing flow of PITRE is shown in Figure 1, in which the red, blue and green boxes represent input data, PITRE processing functions and output data respectively, and the arrows denotes the data flow direction. The output can also be input for the further processing in PITRE, such as the phase retrieval result is input for sinogram creation. Figure 2 shows the PITRE data processing functions in GUI. More in detail, the blue boxes represent PITRE processing functions and the orange boxes denote the place to perform the processing in the GUI.

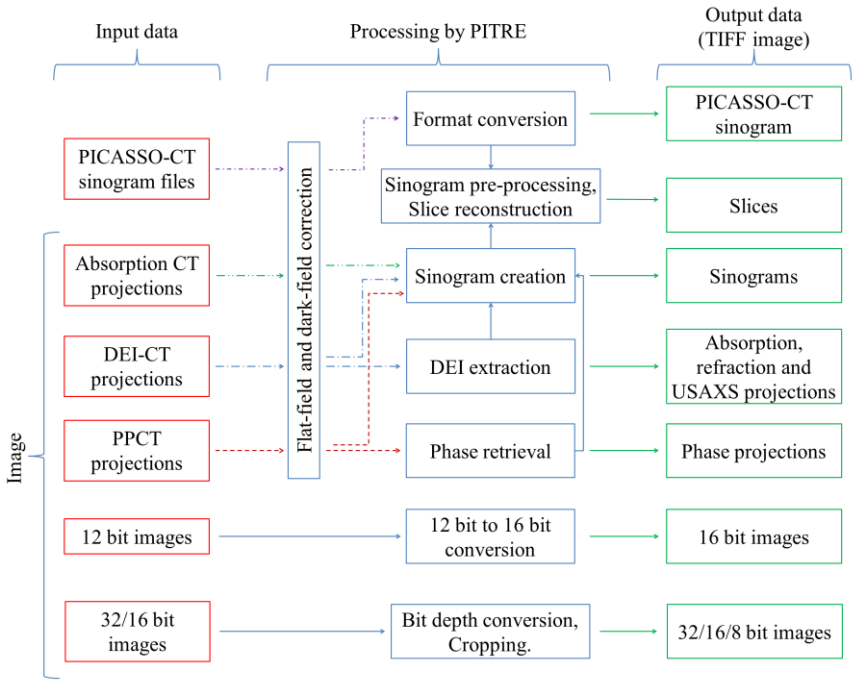


Figure 1 PITRE data processing flow

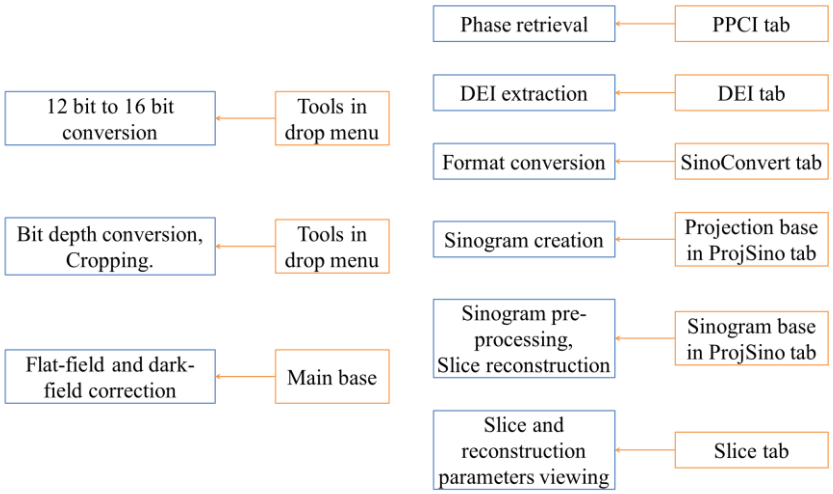


Figure 2 PITRE data processing functions in GUI

V. PITRE GUI

As shown in Figure 3, the GUI of PITRE is subdivided into five tab panels that correspond to PPCI, DEI, SinoConvert, ProjSino and Slice. These subpanels are accommodated in one global panel or base, which is effective for all tab panels. Each tab is associated with a specific task: the PPCI tab handles phase retrieval of PPCT projections; the DEI tab extracts apparent absorption, refraction and scattering from DEI-CT projections; the SinoConvert tab converts the PICASSO-CT data into a readable image format; the ProjSino tab processes sinogram creation, sinogram pre-processing and slice reconstruction; the Slice tab is used to display the reconstructed slice and corresponding reconstruction parameters.

IMPORTANT NOTE: in the GUI, editing of the processing parameters will be automatically enabled or disabled according to the specific processing function and data type. User should check all editable parameters before click the ‘Single’ or ‘All’ button to trigger the processing.

A. Main base

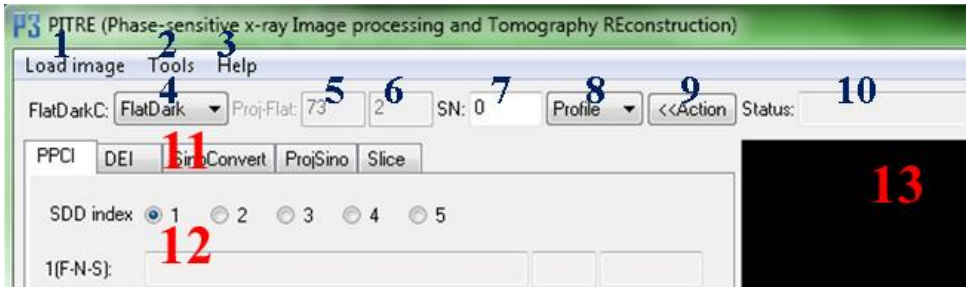
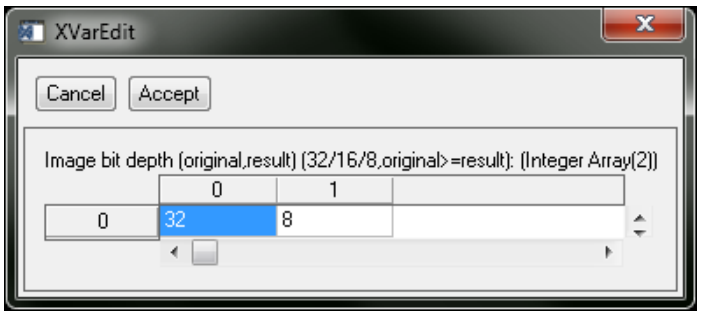


Figure 3 Main base

Main base: It contains a few drop-down menus on the top: 'Load image' contains buttons for loading image for each tab, 'Tools' has buttons for triggering image convert and cropping and 'Help' provides information about PITRE. The first row of PITRE is **global panel** that is *effective for all the tab panels*.

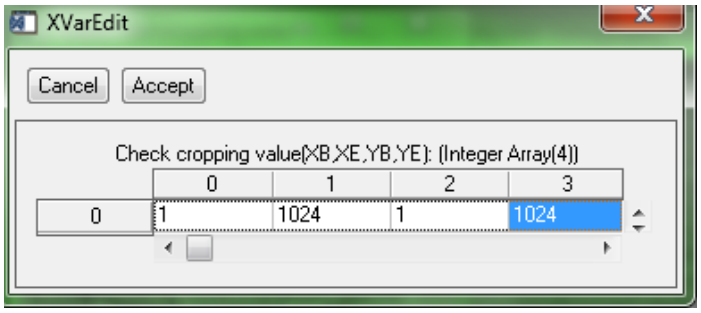
1. Load image for different tabs. When it is triggered, PITRE will pop-up a window to select image and then load it to the tab according. It provides following options
   a. PPCI: load PPCT projection to PPCI tab
   b. DEI: load DEI projection to DEI tab
   c. SinoConvert: load data to SinoConvert tab
   d. Projection: load projection to projection base in ProjSino tab
   e. Sinogram: load image to sinogram base in ProjSino tab
   f. Slice: load image to Slice tab
2. Tools.
   a. Convert/crop/.. images: it provides image bit depth conversion, cropping, contrast scaling and sampling to all images in the selected folder. Last three functions are optional; user can make combine processing according to their needs.
      i. Image bit depth conversion: grayscale images only. PITRE will pop-up an editable dialog box asking the bit depth of original and convert result images. After editing the value, "ENTER" to confirm.



      ii. Cropping ('Cropping the image?'): PITRE will pop-up a windows to select the cropping area. The cropping area is indicated via a white retangle on the image, its manipulation method is:
      Hold down the left mouse button to move the box by dragging.
      Hold down the middle mouse button to resize the box by dragging.

Press the right mouse button to exit the procedure and return the current box parameters.

Then the PITRE will pop-up a editable dialog box to confirm the cropping area. (XB,XE,YB,YE) are Beging and Ending pixel in the X or Y direction.



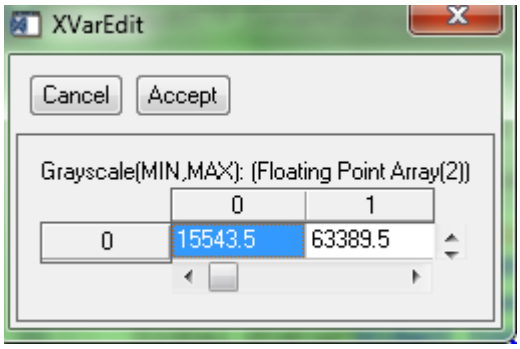
iii. Contrast scaling (‘Image contrast scaling?’): provided only when the bit depth of convert result is 8. PITRE will pop-up the image and its histogram, user can change the scaling contrast range via clicking on the histogram ‘curve’, the image will change according to the contrast range in real-time. Histogram ‘curve’ manipulate method is:

press left button to move lower histogram level.

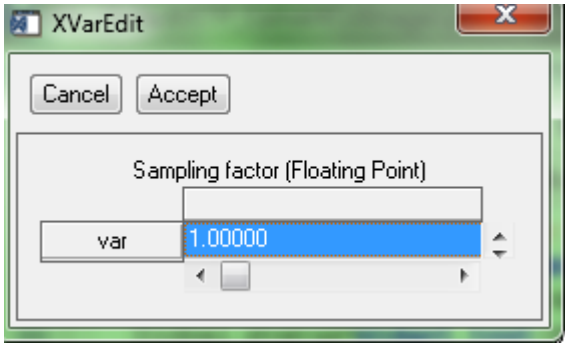
press middle button to move upper histogram level.

press right button to comfirm/exit.

Then the PITRE will pop-up a editable dialog box to confirm scaling contrast range.



iv. Sampling (‘Re-sampling?’): PITRE will pop-up an editable dialog box asking the sampling value (factor). One pixel in the original image will be ‘value (factor)’ pixel(s) in the result image.



b. 12Bit to 16Bit: convert 12-bit unsigned integer TIFF to 16-bit unsigned integer TIFF [1].

c. 12Bit to 16Bit task: create '12Bit to 16Bit' task that can be handled by PITRE_BM.

d. **Enable ALL**: this is to enable the 'ALL' button in PPCI, DEI and ProjSino tabs. The name and the function will change between 'Enable ALL' and 'Disable ALL' according the current status of 'ALL' buttons. It is highly recommended to create the task and use the PITRE_BM to handle it instead of using 'ALL' button in the tabs.

3. Help: help file and information about PITRE.

4. Flat-field and dark-field correction option. The corrected projection I_{PC} is

$$I_{PC} = \frac{I_P - I_D}{I_F - I_D} \tag{1}$$

where I_P, I_F and I_D are the recorded projection, flat-field and dark-field image, respectively.

During this procedure, the dark current subtraction ($I_P - I_D$ and $I_F - I_D$) may create zeros or even negative values, this is problematic when performing the natural logarithm during the reconstruction, and thus corrupts the result. In PITRE, these zeros or even negative values in $I_P - I_D$ and $I_F - I_D$, if they have, will be replaced by $mean(I_P - I_D)/1000$ and $mean(I_F - I_D)/1000$ respectively, where the $mean()$ represents the mean value. In this case, this problem will be corrected and the substitute value is small so it does not affect the quantitative nature of the reconstruction. It provides following options

a. FlatDark: correct flatfield and darkfield, it will load projection, average the flatfield and darkfield file in the folder, perform flatfield and darkfield correction to projection and then show it in the panel. In this case, the flatfield are collected at the beginning and the end of the CT scan.

b. FlatDark+: correct flatfield and darkfield with interval flatfield collection with values in '*step 5, 6'*. In this case, the flat-field images are taken not only at the beginning and the end of a scan but in between as well, the interval number of flatfield and projection must be provided in '*step 5, 6'*.

c. Flat：only correct flatfield. In this case, the flatfield are collected at the beginning and the end of the CT scan.

d. No：not flatfield and darkfield corrected, it will load and show projection without any processing.

5. The interval projection number for 'FlatDark+' option.

6. The interval flatfield number for 'FlatDark+' option.

7. Show different image in the selected folder for current effective tab, such as PPCI is the current effective tab in Figure 3. If images are already loaded in this tab, enter different number to show the corresponding image.

8. Option for action '*step 9*'. It provides following options

a. Profile: show the profile of the image. The manipulation method is:
Move the mouse on the image to show the profile of row and column.

Left mouse button to toggle between rows and columns.
Right mouse button to Exit.

b. IIMAGE: show the image, with the processing of '*step 4*', via IIMAGE in IDL.
c. TIFF: save the image to tiff image, with the processing of '*step 4*'.
d. HisAdj: Check image contrast range via its histogram, user can change the contrast range via clicking on the histogram 'curve', the image will change according to the contrast range in real-time. Histogram 'curve' manipulate method is:
press left button to move lower histogram level.
press middle button to move upper histogram level.
press right button to comfirm/exit.

9. Trigger the function in '*step 8*'.
10. Status bar: an indicator to show the current processing status.
11. Tabs. As Figure 3 shows, it contains five tabs.
    a. PPCI tab: handles phase retrieval of PPCT projections;
    b. DEI tab: extracts apparent absorption, refraction and USAXS from DEI-CT projections;
    c. SinoConvert tab: converts the PICASSO-CT data to image format;
    d. ProjSino tab: processes sinogram creation, sinogram pre-processing and slice reconstruction;
    e. Slice tab: shows the reconstructed slice and corresponding reconstruction parameters.
12. Tab contents. This will be shown in detail for each tab in the following text.
13. Image viewer for all tabs.

In **global panel**, user should always take care 'step 4~6' before load the image, while can skip 'step 7~10'.

B. PPCI tab

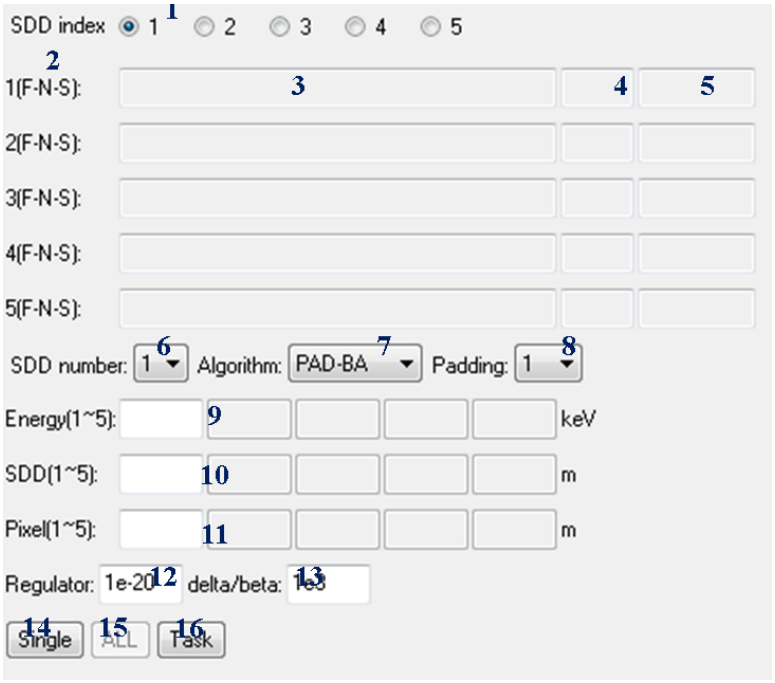


Figure 4 PPCI tab

Function: phase retrieval for PPCT projection.

1. Switch among different SDD PPCT data
   In order to load projection for different SDD, the corresponding SDD index should be checked before trigger the 'Load image' in 'main base'. After the images are loaded, this can be used for viewing different SDD PPCT projection.
2. Label of different SDD PPCT data. *(F-N-S) are short for file-number-size.*
3. Projection file which is currently loaded.
4. Number of projection file in the same folder.
5. Size of image.
6. Number of SDD to be used in the phase retrieval (PR). This is depend on the PR algorithm, so far only supports single SDD PR.
7. Phase retrieval algorithm
   a. SDD=1: phase-attenuation duality Born Algorithm (PAD-BA) [4-6], phase-attenuation duality Modified Bronnikov Algorithm (PAD-MBA) [7-11].
8. Padding option (default value 1), the padded image size will be $(\text{padding value}) * 2^{ceil(\log_2^{original\ size})}$.
   The reason of implementing the padding is during the phase retrieval the Fourier transform is done via FFT and usually the projection size is not an integer power of 2.
9. Energy for 1~5 SDD PPCT data, unit is keV.
10. SDD for 1~5 SDD PPCT data, unit is meter.
11. Effective pixel size for 1~5 SDD PPCT data, unit is meter.
    Note: for 'step 9~11', if there is 'info_PPCT.txt' file in the projections folder, then PITRE will load these parameters from 'info_PPCT.txt' file to the panel automatically. The 'info_PPCT.txt'

file is created manually. *One example is in 'C:\PITRE\Examples\'.*

12. Regulator is a small dimensionless regularization parameter to handle zeros in the denominator of PAD-BA [5].
13. δ / β value of sample (phase attenuation duality property [12]), where $n = 1 - \delta + i\beta$ is complex refractive index. This value depends on the particular sample. In PITRE, the user should manually provide this value, which can be obtained from X-ray database like CXRO [13, 14].
14. Single projection phase retrieval. When trigger this PITRE will ask where to save the result.
15. Phase retrieval of all projections.
    NOTE: *By default, this button is disabled since it is highly recommended to do this task with PITRE_BM. However, it can be enabled (or disabled) by the 'Enable ALL' option in the 'Tools' drop menu.*
16. Create phase retrieval task which can be handled by PITRE_BM. It is recommended to create task after check the phase retrieval result and the parameters via *'step 14'*.

C. DEI tab

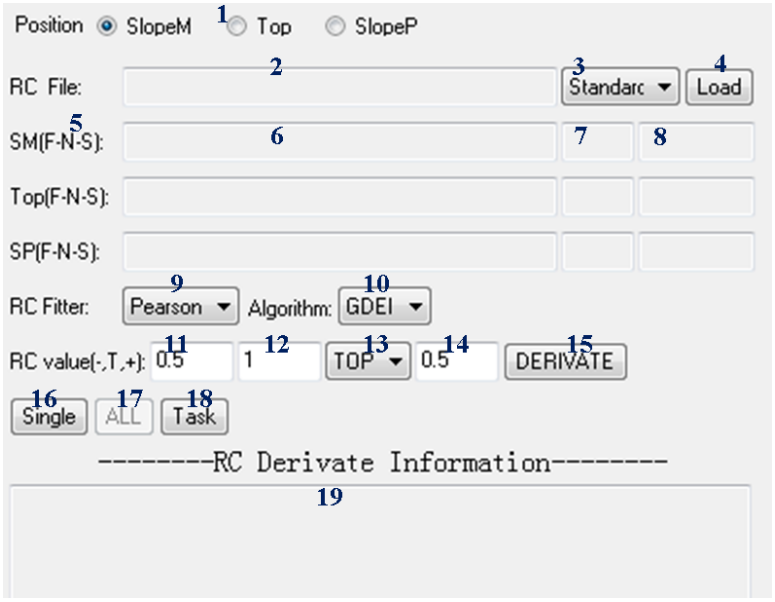


Figure 5 DEI tab

Function: Extract absorption, refractive and scattering information from DEI projection.

1. Switch among different Rocking Curve (RC) position tomography data: slop minus (on the left of the RC top position), top, slop plus.
   In order to load projection for different RC position, the corresponding RC position should be checked before trigger the 'Load image' in 'main base'. After the image is loaded, this can be used for viewing different RC position image.
2. RC file.
3. RC file saving style. The file should be a text file or file which can be open by notepad. The 'Standard' RC saving style is (*one example is in 'C:\PITRE\Examples'*):
   a. First column is the motor position.
   b. Second column is the corresponding RC values (the file can have more than two column information).
4. Load the RC file. After loaded the RC, it will poo-up a window and draw the RC for checking.
5. Label of different RC position tomography data.
6. Projection file which is currently loaded.
7. Number of projection file in same folder.
8. Size of image.
9. Rocking curve fitting function name: Pearson [15], Guass. In *'step 15'*, PITRE will first curve fitting the RC with fitting function and then obtain the first and second derivate value of RC.
10. Reconstruction algorithm: generalized DEI (GDEI) [16-19], conventional DEI (CDEI) [20].
11. RC value at slop minus position (on the left of top position) projection data.
12. RC value at top position projection data.
13. RC top position adjustment. This is because the top data could be collected not exactly at the RC top position but on the side of it.
14. RC value at slop plus position projection data.

15. Using value of `*step 2, 9, 11~14*` to obtain the first and second derivate value of RC at slpope minus, top and slope plus position, the result will be shown at `*step 19*` and use for DEI extraction.
16. Extract information for single projection.
17. Extract information for all projections.
    NOTE: *By default, this button is disabled since it is highly recommended to do this task with PITRE_BM. However, it can be enabled (or disabled) by the 'Enable ALL' option in the 'Tools' drop menu.*
18. Create DEI extraction task that can be handled by PITRE_BM. It is recommended to create task after check the result, via *'step 16'*, and the parameters.
19. Show the derivation result of RC of *'step 15'*.

D. SinoConvert tab

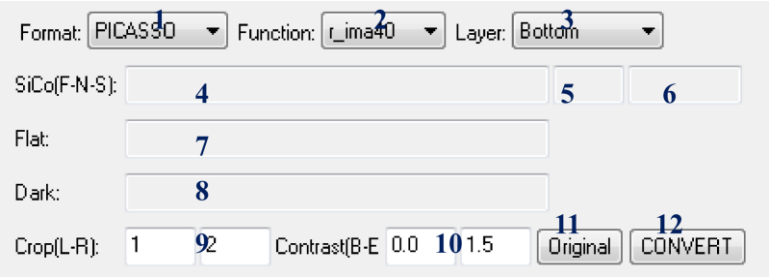


Figure 6 SinoConvert tab

Function: convert sinogram to TIFF for PICASSO and CLS.
Note: please check the value of `*step1*` before load the images.

1. Data format option.
2. PICASSO file open function name.
3. The layer of PICASSO data to be loaded.
4. Data file.
5. Number of file.
6. Size of image.
7. Flatfield file.
8. Darkfield file.
9. CropL: Begin value of crop range. Press `ENTER` show cropped image.
   CropR: End value of crop range. Press `ENTER` show cropped image.
10. Contrast range. 'ENTER' to show contrast condensed image.
11. Return to original image for `*step 9,10*`.
12. Convert image to TIFF with values of `*step 9,10*`.

E. ProjSino tab

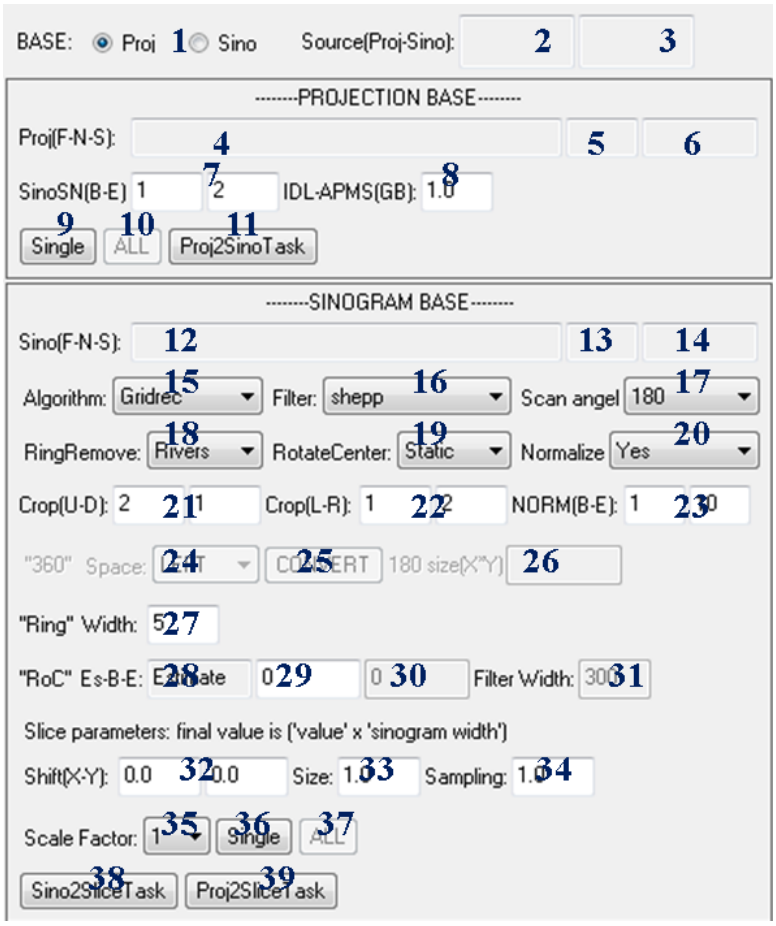


Figure 7 ProjSino tab

Function: sinogram generation, sinogram pre-processing and reconstruct slices of parallel beam CT data.

1. Switch between 'Proj' and 'Sino' base.
   This can be used for viewing projection and sinogram after they are loaded.
2. Projection source. It indicates CT data type. This will be automatically set to phase retrieval algorithm, DEI extraction information or 'raw' value (*Automatically load from PITRE generated 'info_tomo.txt' file or set to 'raw' if this file doesn't exit*). Based on the 'Source' information, PITRE will process the CT data set accordingly. This information decides the projection and sinogram processing procedure, such the phase retrieval and DEI extracted projection will not perform the flat-field and darkfield correction.
3. Sinogram source. Obtain directly from 'Projection source'.
4. Projection image file.
5. Number of projections in the folder.
6. Size of image.
7. SinoSN(B-E). 'BEGIN' and 'END' values for sinogram generation. `ENTER` shows the corresponding horizontal lines on the image. This useful because in some case the sample may not fill all the FOV (vertical), thus the empty slices are not necessary to reconstruct. With these values, user can create part or all the sinograms.

8. IDL allocated physical memory size (IDL-APMS). In parallel beam CT, the sinogram represents the signal measured along a given detector row in the imaging plane for all CT scan angles. In PITRE, this is an intermediate step of slice reconstruction from projections. The sinogram generation method in PITRE is as follows. Firstly, PITRE allocates a series of empty sinograms, whose size corresponds to the projection size and number of CT projections, in the computer memory. Thereby PITRE utilizes the IDL allocated physical memory size (IDL-APMS) that is provided by the user in the PITRE panel. The IDL-APMS is relative to the operation system (OS)-free-PMS. Designed by IDL, it is smaller than the OS-free-PMS in order to guarantee the OS running smoothly. In case the provided size is larger than IDL-APMS, PITRE returns error. Secondly, PITRE loads the projections in sequence; accomplishes the flat-field and dark-field correction, and fills the empty sinograms accordingly. Finally, PITRE saves the sinograms to the hard disk in 32-bit single-precision float TIFF format. If the IDL-APMS cannot hold all sinograms at a time, PITRE will automatically divide the sinogram creation in multiple runs, determined by the IDL-APMS and the total sinogram size.
9. Create single sinogram according SinoSN-B value.
10. Create all (part) sinogram for range between SinoSN-B and SinoSN-E value.
    NOTE: *By default, this button is disabled since it is highly recommended to do this task with PITRE_BM. However, it can be enabled (or disabled) by the 'Enable ALL' option in the Tools' drop menu.*
11. Create 'Proj2Sino' task, with SinoSN-B and SinoSN-E values, that can be handled by PITRE_BM. 'Proj2Sino' means create sinogram from projection.
12. Sino image file.
13. Number of sinogram in the same folder.
14. Size of image.
15. Slice reconstruction algorithm: Gridrec [21, 22], FBP [23].
16. CT reconstruction filters.
17. CT data scan angle range option. The 360 ($[0, 2\pi)$) option is for *extended view* data [24] while 180 ($[0, \pi)$) one is for standard CT scan.

    The extended view CT data handling deals with parallel CT data collected at $[0, 2\pi)$ range in order to artificially extend the field of view (FOV) of the CT system [24]. The FOV in SR-CT is a problematic issue especially with high resolution detector. For parallel beam CT, data are typically collected in the $[0, \pi)$ angular range and it is $[0, \pi)$ sufficient for reconstruction, since the $[\pi, 2\pi)$ projections are symmetrical with $[0, \pi)$ ones. Anyway, thanks to this symmetry, it is possible to nearly double the FOV by using $[0, 2\pi)$ CT scan data. In more detail, if the sample size is larger than but less than two times the FOV, then a complete CT data cannot be collected with $[0, \pi)$ scan. However, by placing the rotation axis near one edge

of the FOV and by using the symmetry between $[0,\pi)$ and $[\pi,2\pi)$ scan, one complete sinogram can be obtained, as if the complete sample fit the FOV in a $[0,\pi)$ data collection. Extended view CT data handling is to convert the $[0,2\pi)$ raw scan data to one complete $[0,\pi)$ sinogram. It should be noted that it is an optional pre-processing tool that is used only for this specific CT data type. In PITRE, the overlap range determination between $[0,\pi)$ and $[\pi,2\pi)$ scan mode is not automatic, instead it provides the user to manually refining this by verifying the resulting slices. This works well as long as the rotation axis is within the FOV.

18. Ring artifact remove algorithm: Rivers [21, 25] and No.
    Ring artifacts are common features in CT imaging which are due for instance to drifts in the detector element sensitivity, non-linear detector element response, and higher energy harmonics in the incident beam. These defects will cause vertical stripes observed in the sinogram. As a result, after back-projection, the ring artifacts will superimpose on the CT slices. Reducing them is possible by using flat-field correction, but it is unlikely to completely remove them. Then a specific procedure is needed [26]. PITRE provides a simple ring artifacts removal method.
    The Rivers procedure is: firstly, compute the average row of the sinogram by summing down each column and dividing by the number of rows. This average row should have very little high-frequency content, since real objects will be blurred out when computing the average row. Secondly, compute the magnitude of these detector anomalies by subtracting a smoothed version of the average row. Finally, subtract the result of previous step, the detector anomalies, from each row in the sinogram. This result presents much less vertical striping. As mentioned above, ring artifacts on the slice are strictly related to stripe on the sinogram, thus this procedure will reduce them.
19. Rotation center mode: static and dynamic.
    The rotation center determination is to locate the CT rotation axis in the sinogram center. The CT reconstruction algorithm, by default, assumes that the rotation axis is in the center of the sinogram, which is hard to accomplish in the practical case. Therefore, the rotation center determination is an essential pre-processing step. The method is to shift the sinogram horizontally by the difference between the image center and the position of the rotation axis. PITRE will provide an estimation value of the position of the rotation axis by calculating the center of gravity of the sinogram for each row and a subsequent curve fitting with a sine wave function. The user can further refine the rotation center manually by verifying the resulting slices. When the CT scan system has some misalignment, the rotation axis could be tilted with respect to the vertical axis of the detector and in theory the collected CT data are not correct anymore. In case the misalignment is small, reasonable reconstruction result can still be obtained by adjusting the rotation center values on a slice-per-slice basis. In this case, the rotation center is different for each sinogram. PITRE provides an option to dynamically adjust it: the procedure is: once has been determined manually the rotation center for the first and the

last sinogram, then PITRE will use a linear interpolation between these two values for the other, taking into account that the rotation center values are an arithmetic progression in this case.

a. Static means use a fixed rotation center for all slices reconstruction. If the set up calibration is ok, then the rotation center is same for all slices.
b. Dynamic means use different rotation center for each slice. In this case the user provide the center of rotation center for the first and the last sinogram, then PITRE will use a linear interpolation between these two values for the other sinograms, taking into account that the rotation center values are an arithmetic progression in this case.

20. Normalize option. It corrects the beam current perturbations during the CT data collection.
    The normalization can be used to correct some beam variations during the CT data collection. In SR-CT, the X-ray beam delivered from the SR source is very intense. Owing to thermal fluctuations in the cooling system of the monochromator, intensity may change during data acquisition. In addition time-dependent instabilities of the image receptor cannot be excluded. Moreover, the current in the storage ring of the synchrotron radiation facility could change with time and so will the flux reaching the detector. Thus, a normalization procedure is needed, which will equalize the intensity of projections collected at different time, provided the intensity variations are sufficiently homogeneous. The procedure is: firstly, select some columns in the background of the sinogram, i.e. which do not contain the sample; secondly, obtain the mean value of the selected columns for each row; finally, divide all pixels in each row by this mean value.
21. Crop UP and DOWN, vertical imaging cropping, the range between UP and DOWN will be kept. `ENTER` shows the horizontal lines on the image.
    Cropping sinogram in the vertical direction to get rid of unwanted or redundant projections that are rows in the top or bottom of the sinogram. This will be useful for instance in continuous CT scan, which typically covers more than the needed angular range, or when the detector keeps acquiring projections before and after the actual CT scanning. The user can interactively refine the vertical cropping values by checking the corresponding result image.
    ***NOTE**: typically use for continuous CT scan.*
22. Crop LEFT and RIGHT, horizontal imaging cropping, the range between LEFT and RIGHT will be kept. `ENTER` show the vertical line on the image.
    Cropping the unwanted space on the left or right side of the background to speed up the reconstruction.
    ***NOTE**: `ENTER` also refresh the values of 'step28~30'.*
23. Normalize BEGIN and END. `ENTER` shows the horizontal lines on the image.
    The range between these two values will use for normalization.
24. The space position on the extended view CT data (360 scan degree ($[0, 2\pi)$) sinogram).
25. Convert $[0, 2\pi)$ sinogram to $[0, \pi)$ sinogram by using the 'Crop LEFT and RIGHT' to crop the overlap range.
    NOTE: In this case, the rotation center will be the center of the sinogram. User should refine the 'Crop LEFT and RIGHT' (instead of rotation center) to obtain the best result.
26. The size of converted 180 degree sinogram.
    ***NOTE**: 'step 24~26' for 360 projection scan mode only.*

27. Ring artifact removes: smooth width of Rivers' method.
28. The estimate rotation center value. Act as reference.
29. Rotation center BEGIN value. It is rotation center value for static mode and for first sinogram in dynamic mode.
30. Rotation center END value for last sinogram in dynamic mode.
31. CT filters kernel width for FBP algorithm.
32. Shift (X-Y). It is used for adjust sample position in the reconstructed slice.
    Positive value shift the slice to right(X) or up(Y) direction. The shift pixels is 'value'*'sinogram width'.
33. Use for adjust the reconstructed slice size.
    The reconstructed slice size (X and Y) is ('step 33 value'*'sinogram width'/'step 34 value').
    Note: for Gridrec algorithm, this value should be one of ['0.25', '0.5', '1', '2','4', '8' …]; for FBP, it is continuous.
34. Use for sampling the reconstructed slice.
    One pixel in the sinogram will be 'value' pixel(s) in the slice.
    Note: for Gridrec algorithm, this value should be one of ['0.25', '0.5', '1', '2','4', '8' …]; for FBP, it is continuous.
35. For '*step 36*' only. This option is used when interactively refining the reconstruction parameters. A fast single-slice reconstruction can be obtained by reducing the number of projections actually utilized in the reconstruction to $(CT\ data\ projection\ number)/('Scale\ Factor'\ value)$.
36. Reconstruct single slice.
37. Reconstruct all slices.
    NOTE: *By default, this button is disabled since it is highly recommended to do this task with PITRE_BM. However, it can be enabled (or disabled) by the 'Enable ALL' option in the 'Tools' drop menu.*
38. Create 'sino2slice' task. In this case all the parameter in sinogram base should be determined before create it.
39. Create 'proj2slice' slice. In this case all the parameter in both projection and sinogram base should be determined before create it.

F. Slice tab

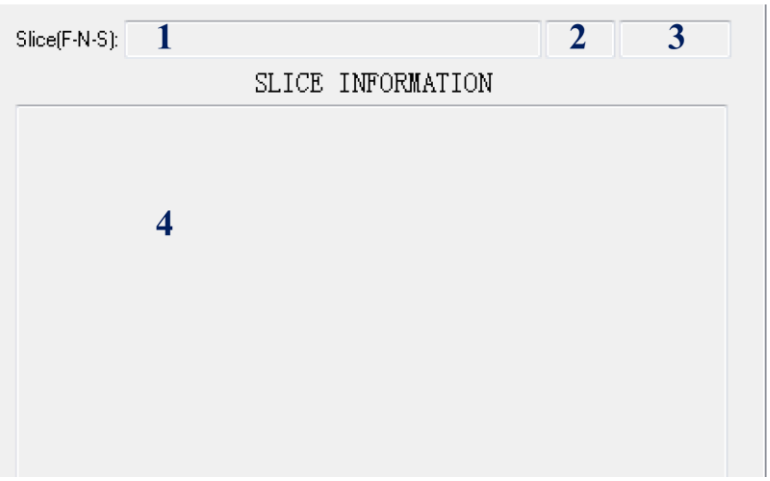


Figure 8 Slice tab

Function: show slices and reconstruction parameter.

1. Slice image file.
2. Number of images in the folder.
3. Size of image.
4. Slice reconstruction parameters.

VI. PITRE_BM GUI

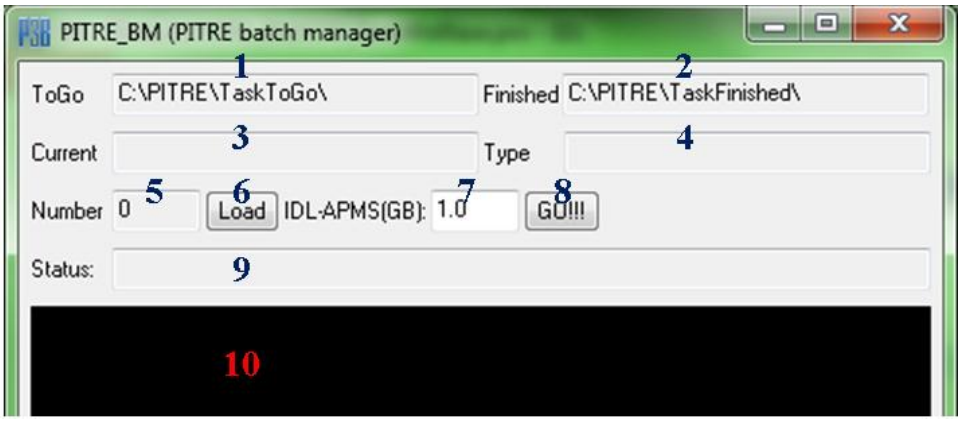


Figure 9 PITRE_BM panel

Function: it is a batch processing manager for PITRE, it executes a series of tasks ("jobs"), which is created via PITRE, on a computer without manual intervention.

1. Tasks folder to be handled by PITRE_BM.
2. Tasks folder processed by PITRE_BM.
3. Current task name.
4. Current task type.
5. Number of task in TaskToGo folder.
6. Click to load the task in PITRE_BM.
7. IDL allocated physical memory size (IDL-APMS).
   In parallel beam CT, the sinogram represents the signal measured along a given detector row in the imaging plane for all CT scan angles. In PITRE, this is an intermediate step of slice reconstruction from projections. The sinogram generation method in PITRE is as follows. Firstly, PITRE allocates a series of empty sinograms, whose size corresponds to the projection size and number of CT projections, in the computer memory. Thereby PITRE utilizes the IDL allocated physical memory size (IDL-APMS) that is provided by the user in the PITRE panel. The IDL-APMS is relative to the operation system (OS)-free-PMS. Designed by IDL, it is smaller than the OS-free-PMS in order to guarantee the OS running smoothly. In case the provided size is larger than IDL-APMS, PITRE returns error. Secondly, PITRE loads the projections in sequence; accomplishes the flat-field and dark-field correction, and fills the empty sinograms accordingly. Finally, PITRE saves the sinograms to the hard disk in 32-bit single-precision float TIFF format. If the IDL-APMS cannot hold all sinograms at a time, PITRE will automatically divide the sinogram creation in multiple runs, determined by the IDL-APMS and the total sinogram size.
8. Click to execute PITRE_BM.
9. Task processing status indicator.
10. Image viewer.

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