MICROCT DATA PROCESSING GUIDELINES

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ABSTRACT

Here is a brief guideline for processing microtomgraphy data collected using the microCT at SLAC/SSRL. This document can be used to reconstruct projection data into meaningful 3D datasets but it should be noted that some tweaks may need to be performed from this outline.

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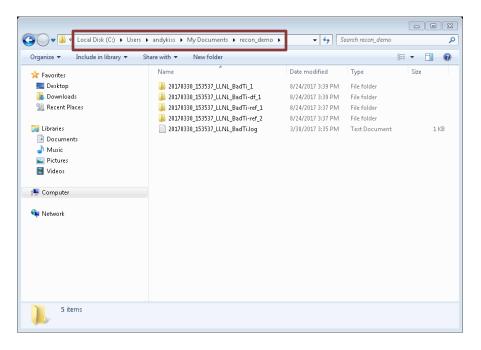
PREREQUISITES

Below is a list of software used in the following outline.

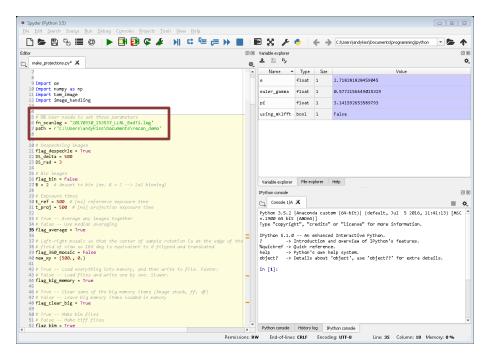
- Python 3+
 - o Anaconda distribution (recommended), using Spyder
 - Go to website https://www.continuum.io/downloads and download Anaconda installation package.
 - Packages:
 - Scipy
 - Numpy
 - Pywavelets
 - ASTRA (http://www.astra-toolbox.com)
- Py_image_processing
 - o A series of scripts on GitHub for this reconstruction
 - o These can be downloaded from https://github.com/slaclab/py image processing
- FIJI (ImageJ 2.0)
 - o Not necessary but helpful for viewing and manipulating data
 - o Go to website https://fiji.sc/#download and download FIJI zipped folder.
 - o Unzip the FIJI folder
 - o In Fiji.app folder double click ImageJ-win32 to launch the software.
- TXM Wizard
 - Necessary for mosaic imaging
 - 0

CONVERT TIFF STACKS TO REFERENCE CORRECTED PROJECTION IMAGES

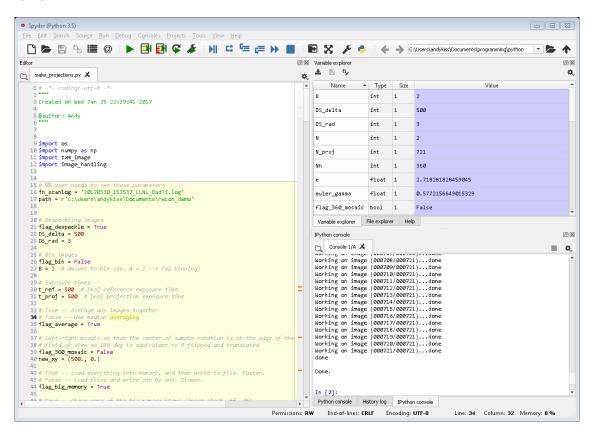
• Locate the folder where you saved your data. There should be a scan log file (*.log) as well as folders with your transmission images, dark field, and flat field image stacks.



- Open Spyder and open the *make projections.py* script.
- Locate the lines that set the scan log file name, *fn_scanlog*, and path, *path*, and set the variables to point to your data.



- Scan through the remaining settings in that block. Many of them can stay the same from
 reconstruction to reconstruction. If you are interested in modifying the binning of the images or
 removing zingers, here is where the settings are.
- Note: if you have a data processing computer with sufficient memory to perform all the analysis
 in memory (>32 GB), check that flag_big_memory is set to True. This will run the calculations
 much faster.
- Note: By default, the program will export *.bim files. These are binary image files with the metadata stored in the header. It is recommended that you perform the analysis using this file format. Check that *flag bim* is set to *True*, otherwise it will export *.tif files.
- When ready, save and run make_projections.py. This will take a while but there will be output to the console so you can track the process.
- The script will make a post-processing folder, sample-name-processing, where it will store the
 averaged dark and flat field images, and a folder where it will export the reference corrected
 projections.



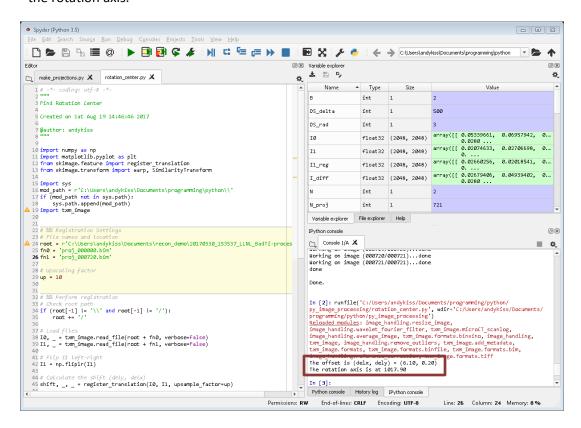
Mosaic Stitching

TXM Wizard

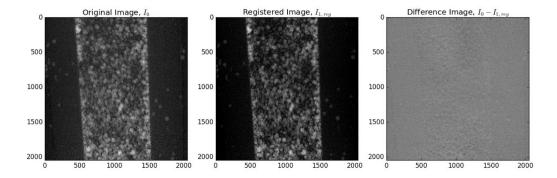
- Open Mosaic Stitcher
- Click Browse and load only the images necessary for the first mosaic image
 - All of the imaging properties should load into the fields on the right
- Start to use the options explained below to stitch together those. Click *Run Stitching* to see the stitched image.
 - Use PhCo Alignment will use phase correlation to help align the images for stage errors
 - Normalization among Tiles will normalize the edges
 - Smooth The Edge will blend the images together
- Once satisfied with the result, enable *MultipleCPU* and make sure the images are saved as *.bim
- Click Batch Stitching and select all the images

FIND THE ROTATION CENTER

- In Spyder, open *rotation_center.py*
- Find the Registration Settings cell and change
 - o root to point to the folder with the reference corrected *.bim files
 - \circ fn0 to the file name of the first image in your dataset (usually at theta = 0°)
 - o fn1 to the file name of the image in the dataset rotated 180° from the first file
- Save and run the script. The console will output the X and Y shift, as well as the pixel location of the rotation axis.

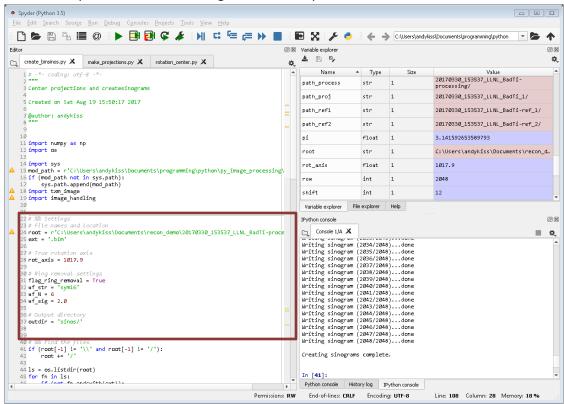


A figure will show the loaded images and the difference map after they have been aligned. The
quality of the alignment can be judged based on the difference map. If it is easy to see the
features in the original images, then the alignment is poor and will not lead to a high quality
reconstruction.



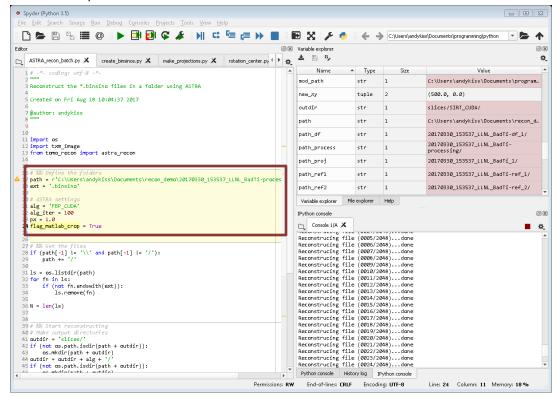
CREATE SINOGRAMS

- In Spyder, open create_binsinos.py
- Find the Settings cell and change the path variable, *root*, to the folder with the reference corrected projections
- Set the rotation axis, rot_axis, to the rotation axis value found in the previous step
- Ring artifacts in the reconstruction can be removed by using a filter. Set the ring removal filter flag, flag ring removal, to True to remove these.
- Run the script and wait for the sinograms to be output to the sinos folder



SINOGRAM RECONSTRUCTION

- In Spyder, open ASTRA_recon_batch.py
- Set the path to the sinograms, path
- Define your reconstruction settings
 - If possible, use a CUDA enabled algorithm as the GPU is much faster than the CPU
- Run the script

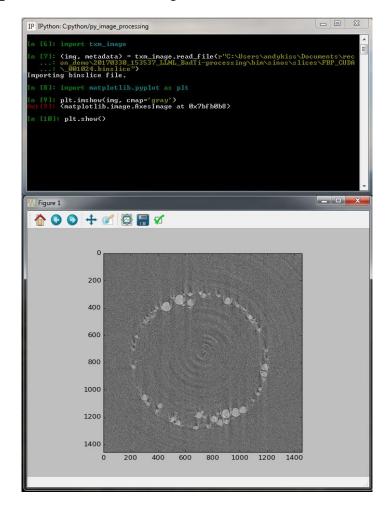


OPENING THE RECONSTRUCTED SLICES

• The reconstructed slices can be opened using Python, Fiji, or TXM Wizard

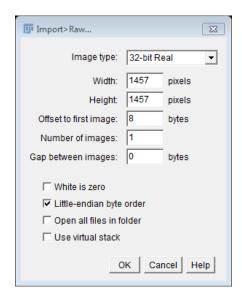
Python

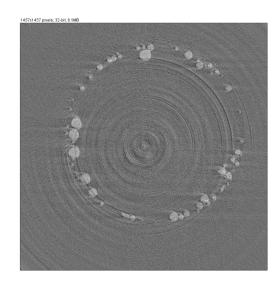
- Import the txm_image package
- Use the read_file function to load the image



Fiji

- File -> Import -> Raw...
- Choose the file you would like to open using the file dialog. If you want to open all the files in the folder, still only choose one.
- Use the settings listed below, 32-bit Real, 8-bit offset, Little-endian byte order to load the data
- Type in the width and height of the image
- If you want to open all the files in the folder, select that option





TXM Wizard

- Open TXM Wizard and go to Data Evaluation -> Image Handling
- Click Browse and select the files you would like to load from the file dialog. Make sure the file filter is set to *.binslice
- Click open and view

