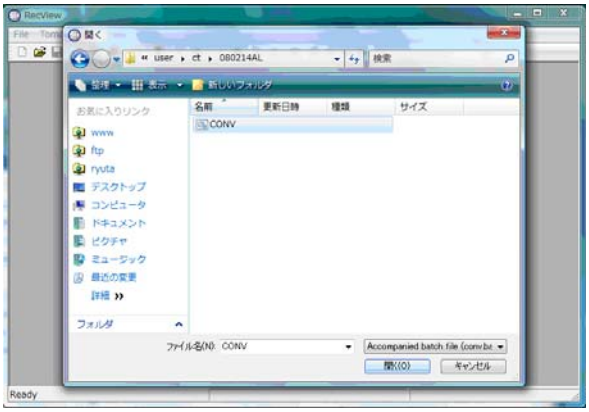
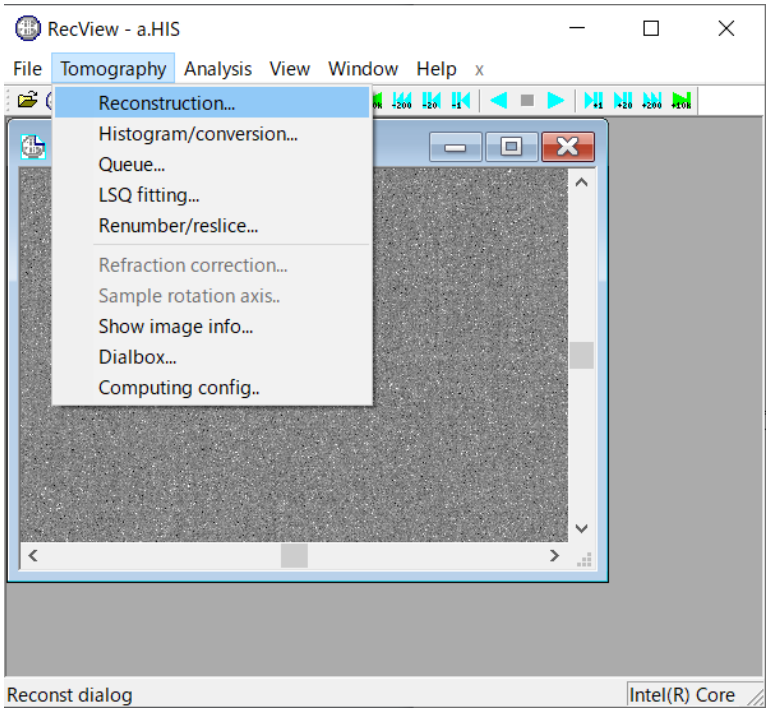
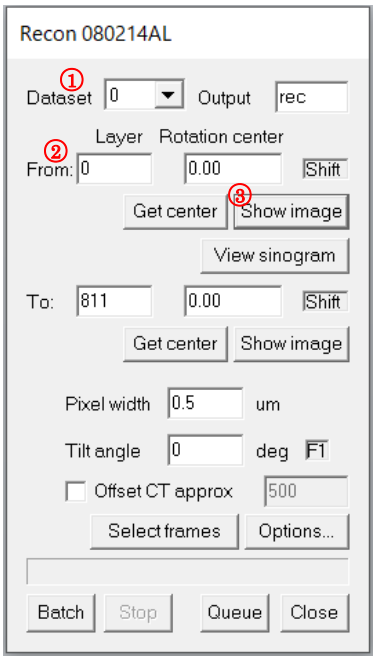
Reconstruction calculation using RecView

1. Open RecView (https://github.com/mizutanilab/RecView).
2. [img format only] Go to "File→Prepare files..." of the menu and open conv.bat in your data folder. This will average blank images and rewrite the file name.

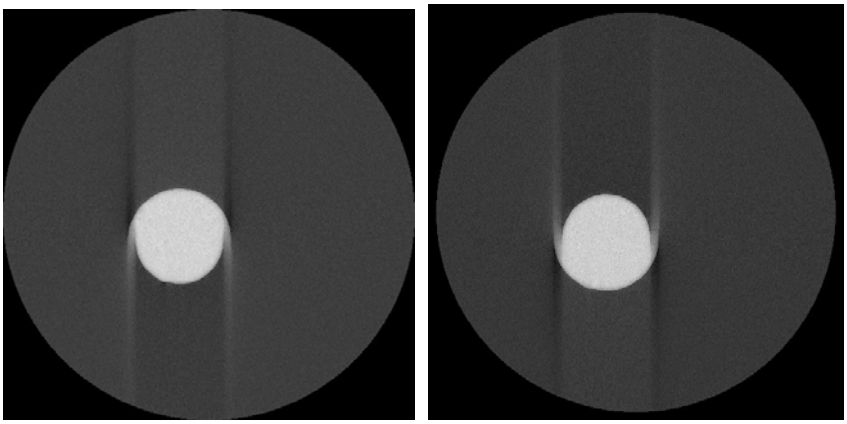


3. Go to "File→Open" of the menu and open a sample image in your data folder (a.his for his format, q0002.img for img format). Then open "Tomography → Reconstruction..." from the menu (see below).





4. Enter the pixel width in the "Pixel width" field. In the case of the his format containing multiple datasets, choose the "Dataset" (figure ①).
5. If necessary, make other settings such as offset CT.
6. Enter the y coordinate of the top edge of the sample in the "Layer" field of the "From" row (figure ②). Click the "Show image" button (figure ③).
7. After a few moments, a reconstructed image will be displayed. If the reconstructed image is an appropriate one, proceed to step 9. If the image is distorted as shown below, perform step 8.
8. [Optional] To adjust the rotation center, hold down the Shift key and rotate the mouse wheel. The slice image will be updated. Or you can enter the center value and press "Show image" to show another reconstructed image. If the resulting image is blurring downward (the left image below), increase the center value. If the image blurs upward (the right image below), decrease the center value. If you obtain a clear reconstructed image, your measurement was successful. If not, find the center value most appropriate.



[Offset CT] If the sample image is blurred like <·>, the center value should be adjusted to be smaller. If the image is blurred like >·<, the center value should be increased.

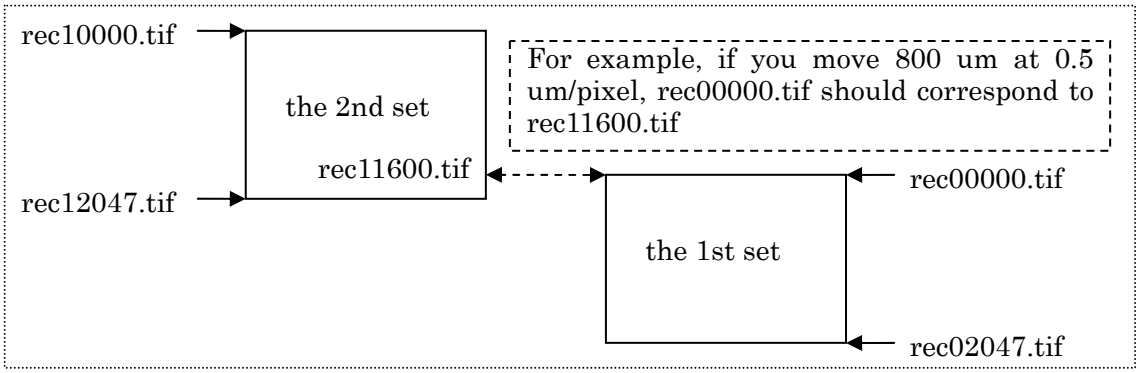
9. [Optional] You can adjust the image tilt by holding down the F1 key and rotating the mouse wheel. You can also enter the tilt value in the "Tilt angle" field and press the "Show image" button to show another reconstructed image.
10. Enter the y-coordinate of the bottom edge of the sample in the "Layer" field of the "To" row and press the "Show image" button. If the reconstructed image is distorted,

adjust it in the same way as above. If an appropriate image is obtained, proceed to the next step.

11. [When the sample is smaller than the entire field of view] To obtain slices of the sample with some vertical margins, set the y-coordinates in the "From" and the "To" rows to a position just above or below the upper or lower edge of the sample, respectively. If the center values differ greatly between the "From" and "To" fields, extrapolate them.
12. Press the "Queue" button to schedule the reconstruction calculation.
13. Go to "File→Close all" and click "OK". If you are asked whether you want to save the data or not, click "No". This will close all displayed images without storing them. If there are other datasets that need to be reconstructed, return to Step 2.
14. Open "Tomography→Queue..." from the menu and press "Start". Depending on the number of images and image pixels, it will take tens of minutes to several hours per dataset.

Stitching multiple vertical datasets

15. If multiple datasets are being measured from a single sample while shifting the sample position along the rotation axis, determine the superimposition point using the following procedure. Otherwise, proceed to "Data compression".
16. Open "Tomography→LSQ fitting".
17. If you do not know the approximate point of the superposition, first identify superposing frames between datasets roughly. If the sample is measured while being shifted up, the top of the first data set and the bottom of the second data set should be the same, Open the reconstructed image recXXXX.tif, and use the toolbar buttons  to move back and forth to determine the pair of images that are closest to each other (see the figure below).



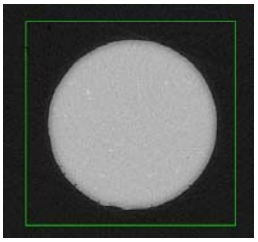
18. In the "Reference image" field, select the top 20 images of the first dataset from the

"Select" button (rec00000-00019 in the example above). Similarly, in the "Query image" field, select the bottom 20 images from the second dataset (rec11600 to 11619 in the example above). Because the image ends are usually noisy, you can superpose datasets in the rather middle.

19. Press "Start" to seek the point of superimposition. If you want to do the calculation later, you can set it as "Queue".
20. After the calculation finished, the obtained shift coordinate (x, y, z) of the superposition is displayed on the first line of the output field. If you execute it from the queue, it is represented as (x y z) at the beginning of each line. The values are also recorded in the log file named _recviewlog.txt in the dataset folder. If the shift coordinate is at the edge of the image, for example (-3 5 20), the calculation may be incorrect and should be examined manually. The obtained values will be used to specify the trimming box in the following data compression steps. For example, if you place the trimming box at the center coordinates (x0, y0) in the first dataset, the horizontal position of the second dataset can be corrected by adding the x and y values of the superposition to (x0, y0) to make (x0+x, y0+y).

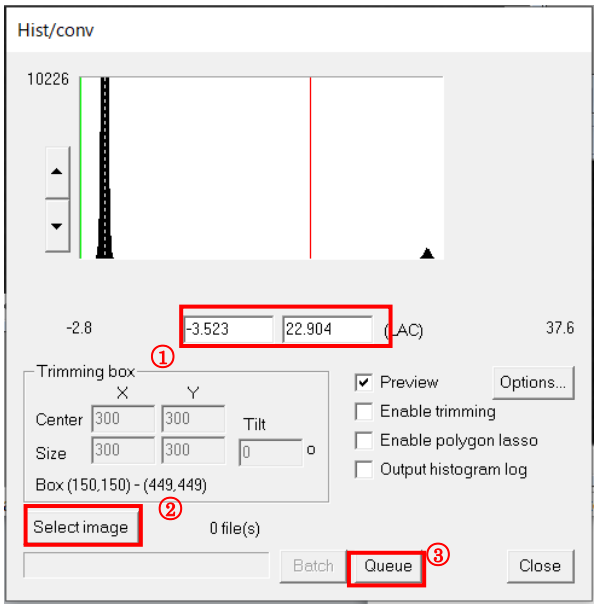
Data compression

21. Next, perform 8-bit conversion of the reconstructed images. From the menu, go to "File→Open" and open the first image of the reconstructed images recXXXXX.tif.
22. Hold down the left mouse button and move it so that the green box appears. Move the mouse to specify the region of interest (see below).



23. Use toolbar buttons  to view other images. Adjust the box for all slices so that the sample fits in the green box. Use the "10k" arrow to move between datasets. Finally, display a slice with good contrast for the next step.

24. Open the menu "Tomography → Histogram/conversion...". Enter a value in the LAC field (figure ①) and view the image. The green and red lines in the graph will be displayed to show the threshold. Enter the LAC range to output.
25. [Optional] When removing capillary pixels from the image, determine the thickness and the voxel value of the capillary, Open "Options" and set the thickness in the "Depth" and the voxel value in the "LAC threshold" field, respectively.



26. [Optional] When superimposing multiple datasets, correct the Center (x y) values with the results obtained in the steps 15-20 above. The shift along the z-direction is corrected by the file selection in the next step.
27. Select the file to be converted from the "Select image" button (figure ②).
28. "Queue" (figure ③) to schedule the execution.
29. Go to "File→Close all" and click "OK". If you are asked whether you want to save the data or not, press "No". If there are other datasets that should be processed, go to step 21.
30. Open "Tomography→Queue..." from the menu and press "Start". It takes several minutes to several tens of minutes depending on the number of images and the image size. If you are removing capillary voxels and if the removing did not work appropriately, you will see **Truncated** in the output field of the "Queue" window.
31. Close files with "File→Close all".
32. [Optional] If you have multiple datasets to be stitched, Open "Tomography→ Renumber/reslice files" and click "Add" to choose files to be renumbered. In the case of datasets taken by shifting the sample upward, choose datasets in the order of the last measurement to the first one. In the above example, first open files of rec10000 to 11599, then rec00000 to rec02047, and so on. The output path is set automatically, but can be changed if necessary. After choosing all of the images, click "Start" and wait until converted.
33. "File→Exit" to finish.