

XLI CT Workflow Cheat-sheet for Synchrotron Users

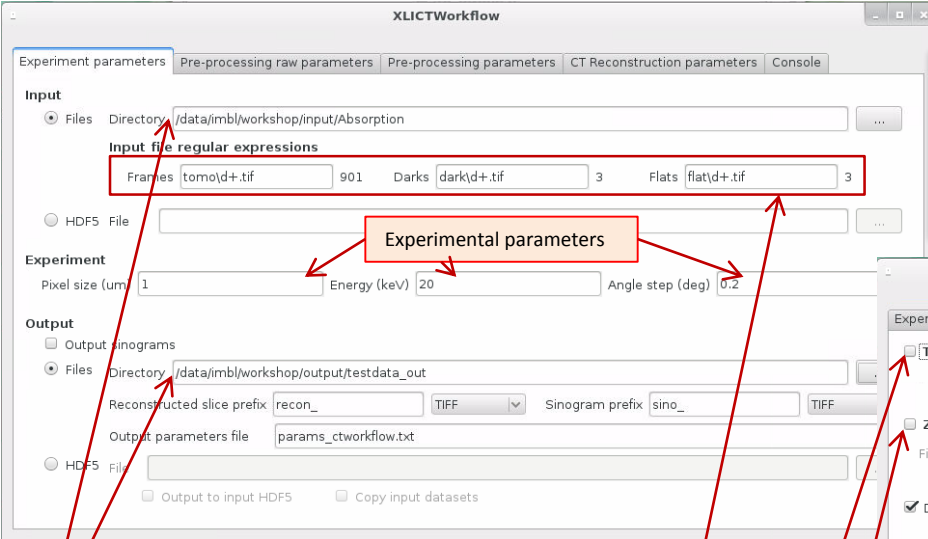
Getting started with XLI CT Workflow on ASCI

Login via asci.synchrotron.org.au using your synchrotron portal credentials and start an IMBL session by clicking the icon. The virtual desktop will then open from which applications like the XLI CT Workflow can be accessed. Once the ASCI desktop has started up you can access the XLI CT Workflow from: **Applications> ASCI> CSIRO XLI CT Workflow** (Applications menu is at the top left). Remote access via VPN will be made available shortly.



The Reconstruction Workflow Dialog

This provides a simplified interface suited to the reconstruction of synchrotron tomography data, and enables rapid reconstruction of datasets in one step. For similar datasets only the input and output directories need to be changed in the dialog to perform a new reconstruction. The filename patterns to search for in the chosen input directory are defined by regular expressions in the Experimental parameters tab of the workflow. Default output is floating point format, but the rescaling output option enables scaled output to integer format.



Input & output directories and output filenames (sinograms optional)

Filename regular expression definitions so the reconstruction wizard can identify frame, dark and flat files. These entries are typical for IMB data. "\d+" indicates a sequence of digits of any length and "\w+" a sequence of letters, so for instance the wizard will know to look for frame files starting with "SAMPLE_" followed by any number and ending with ".TIF". The numbers after the boxes display the number of corresponding files found

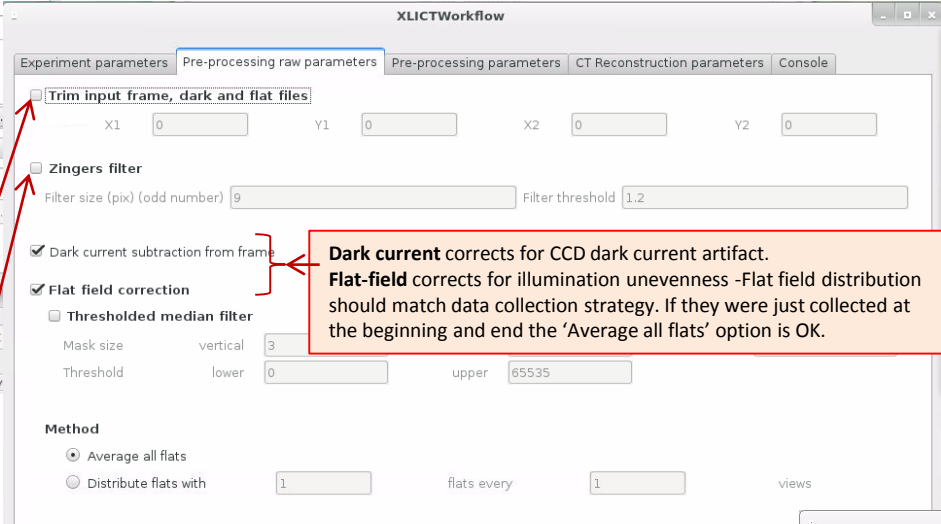
Trim files (option) specify top left & bottom right of trim area

Zingers filter to remove bright 'speckle' artifacts from the images

Normalisation enables images to be normalised based on a selected region which is free of the sample in all images. The row-wise normalisation is useful if the illumination is moving up and down. An optional 3x3 pixel smoothing filter can also be applied to the data.

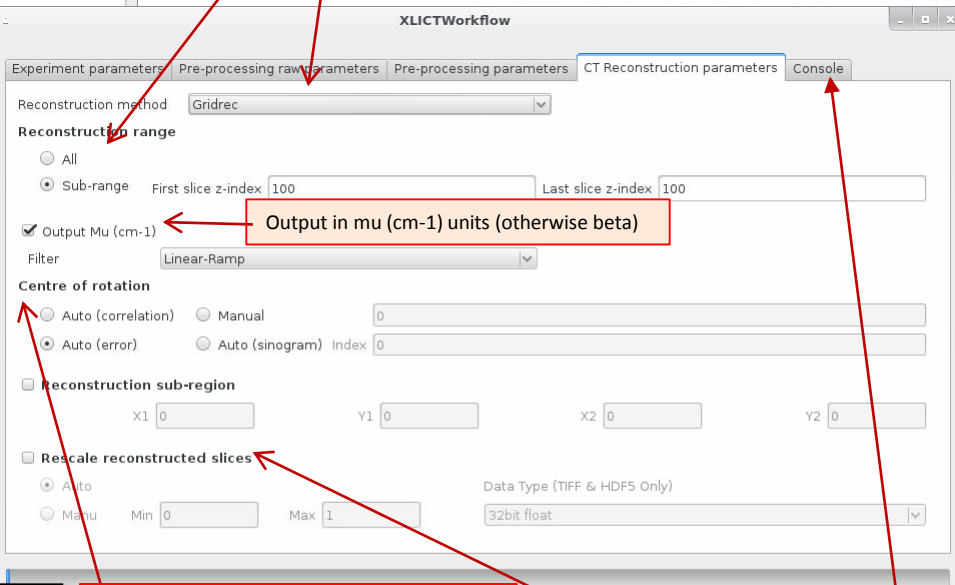
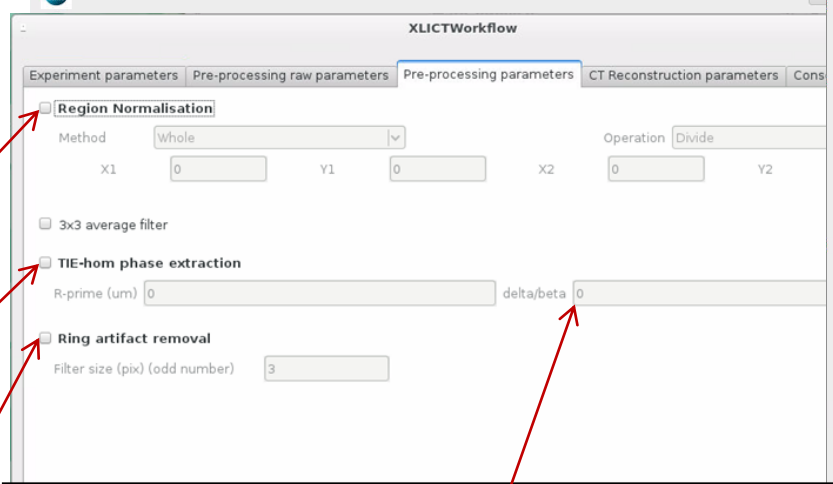
TIE-HOM phase-extraction. The R-prime is the sample to detector (scintillator) distance. The delta/beta ratio for the material is also required. You can guess this with the help of the chart below right. Simply choose a value for a material most like your sample.

Ring filter - for removing ring artefacts from the reconstructed slices. The filter size should be an odd number (17 is a good starting value).



Dark current corrects for CCD dark current artifact. Flat-field corrects for illumination unevenness - Flat field distribution should match data collection strategy. If they were just collected at the beginning and end the 'Average all flats' option is OK.

Select reconstruction method from the drop-down list (On ASCI Gridrec is most suitable), and enter the range of slices (in z) to be reconstructed.



Output in mu (cm-1) units (otherwise beta)

this enables selection from three possible methods of automatic centre-of-rotation detection, or else manual entry of the centre of rotation (given in pixels relative to the image centre). Auto (error) is the default and works most of the time. If automatic methods fail the manual method can be used to find the centre of rotation by trial and error.

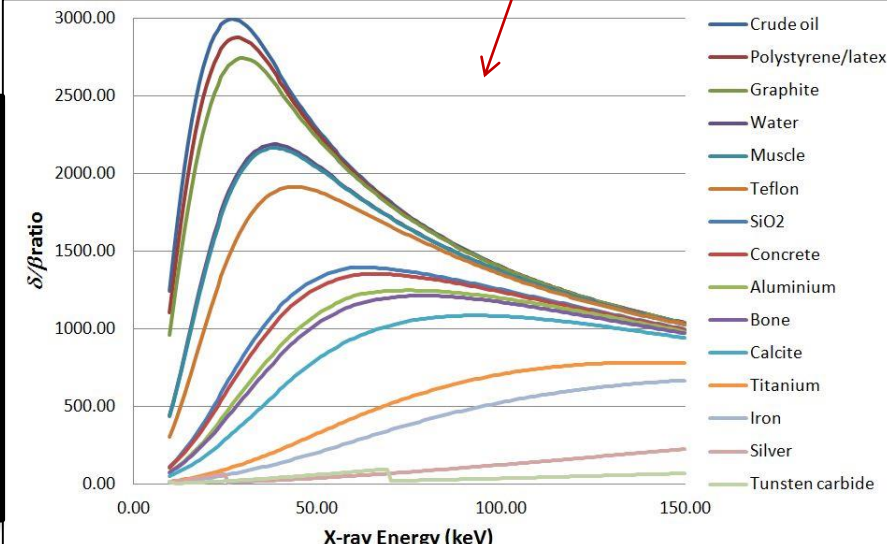
Option for output to be in rescaled integer format rather than default floating point. Automatic or user-specified scaling can be used.

Press 'Process' to start

Viewing, rendering, analysing and saving data on ASCI

From the SCI desktop you can open the Fiji application:
Applications>ASCI> Fiji
 Image files can be viewed individually by dragging and dropping to Fiji. Alternatively, a whole reconstructed stack can be read in using:
File> Import > Image Sequence...
 There is also a basic 3D viewer under the Plugins menu in Fiji which you can use once you have imported an image stack

The Avizo software is suited for or more advanced 3D image rendering/display and 3D image analysis. This is can be accessed on the MASSIVE cluster if required.



XLI CT Workflow on the command line

The XLI CT software can be run from the command line. A basic command line example is shown below. Look under the cosole tab of GUI to see the input parameters corresponding to your last reconstruction run.

```
Mylogin:> opt/x-tract/bin/XLICTWorkflowMPI --indir /data/imbl/workshop/input/Absorption --outdir /data/imbl/workshop/output/Mayo/Absorption --proj "tomo\d+.tif" --darks "dark\d+.tif" --flats "flat\d+.tif" --dark_correction 1 --flat_correction 1 --angle_step 0.2 --energy 10 --recon_method 1 --pixel_size 10 --recon_out_mu 1 --cor_method 2 --file_prefix_ctrecon "slice.tif"
```