NAME

diff_tomo - diff_tomo

DESCRIPTION

usage: diff_tomo [options] -**p** ponifile imagefiles* If the number of files is too large, use double quotes like "*.edf"

Azimuthal integration for diffraction tomography. Diffraction tomography is an experiment where 2D diffraction patterns are recorded while performing a 2D scan, one (the slowest) in rotation around the sample center and the other (the fastest) along a translation through the sample. Diff_tomo is a script (based on pyFAI and h5py) which allows the reduction of this 4D dataset into a 3D dataset containing the rotations angle (hundreds), the translation step (hundreds) and the many diffraction angles (thousands). The resulting dataset can be opened using PyMca roitool where the 1d dataset has to be selected as last dimension. This file is not (yet) NeXus compliant. This tool can be used for mapping experiments if one considers the slow scan direction as the rotation.

positional arguments:

FILE List of files to calibrate

optional arguments:

-h, --help

show this help message and exit

-V, --version

show program's version number and exit

-o FILE, --output FILE

HDF5 File where processed sinogram was saved, by default diff_tomo.h5

-v, --verbose

switch to verbose/debug mode, defaut: quiet

-P FILE, --prefix FILE

Prefix or common base for all files

-e EXTENSION, --extension EXTENSION

Process all files with this extension

-t NTRANS, --nTrans NTRANS

number of points in translation. Mandatory

-r NROT, --nRot NROT

number of points in rotation. Mandatory

-c NDIFF, --nDiff NDIFF

number of points in diffraction powder pattern, Mandatory

-d FILE, --dark FILE

list of dark images to average and subtract

-f FILE, ---flat FILE

list of flat images to average and divide

-m FILE, --mask FILE

file containing the mask, no mask by default

-р FILE, --рoni FILE

file containing the diffraction parameter (poni-file), Mandatory

-O OFFSET, --offset OFFSET

do not process the first files

-g, --gpu

process using OpenCL on GPU

-S, --stats

show statistics at the end

If the number of files is too large, use double quotes "*.edf"