### **NAME**

diff\_tomo - diff\_tomo

# **SYNOPSIS**

diff\_tomo [options] -p ponifile imagefiles\*

# **DESCRIPTION**

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.

## **OPTIONS**

### --version

show program's version number and exit

### -h, --help

show this help message and exit

### -o FILE, --output=FILE

HDF5 File where processed sinogram was saved

### -v, --verbose

switch to verbose/debug mode

### **-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

### -r NROT, --nRot=NROT

number of points in rotation

# **-c** NDIFF, **−−nDiff**=*NDIFF*

number of points in diffraction powder pattern

# -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

### -p FILE, --poni=FILE

file containing the diffraction parameter (poni-file)

# **-O** OFFSET, **−-offset**=*OFFSET*

do not process the first files

### -g, --gpu

process using OpenCL on GPU

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