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An easy to use XRD data analysis framework for users and scientists, online and offline

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Motivation

- When doing Xray diffraction experiments it is often necessary to perform several steps of data reduction and analysis in order to evaluate a result.
- In some cases data might even be found to be completely useless upon inspection after the experiment has concluded.
- Online analysis at the beamline can be useful in these cases.

Motivation contd.

- Users are not necessarily specialists in xray diffraction or scientific computing
- It would be nice to be able to give external users not just their data, but also the tools to process them, wouldn't it?

Implementation

Started xraylib as intern three months last summer. Continued this year from march as part of master degree “technical physics“ at NTNU, Norway.

Python

- High level \Rightarrow Quick and easy to develop and prototype.
- Yet high performance when using compiled libraries
- Evergrowing library of tools for scientific computing.
- No license necessary (unlike matlab)

Dependencies

- No dependency on ESRF computing infrastructure
- Python libraries
 - pyFAI Fast azimuthal integration on GPU / CPU
 - scipy / numpy Almost all you need for arrays/images/matrices
 - scikits-image Branch of scipy. More filters, including tomographic reconstruction (FBP, SART)

Installation

- Scripts for setting up xraylib for use *and* development are provided.
- In theory this is all you should need if you have system-wide access

```
git clone https://github.com/amundhov/xraylib.git
cd xraylib
./install.sh or ./develop.shp
```
- Python library dependencies maintained in **requirements.txt** and can be parsed by standard python package tools such as **pip** and **distutils**.

Installation cntd.

- In practice it is best to have your system administrator install the required python libraries. On debian based systems these are all available through APT.
- For development or local installation make use of python's virtual environments:
 - `virtualenv --system-site-packages venv`
 - `source venv/bin/activate`
 - [perform steps from previous slide]
- Whenever `venv/bin/activate` is sourced `xraylib` will be available on your path along with the scripts in `scripts/`

What's in it (for me)?

Some examples

- Calculation of sample properties such as xray absorption at given energy.
- Simplified file access (EDF, multiframe EDF, hdf5, anything fabio supports)
- Utility functions and examples for making small scripts and workflows.

We'll have a look at applications shortly.

xraylib + DAWN

- Data exploration. Rich support for slicing and visualising data in HDF5 format.
- Peak fitting and export.
- Integration with python scripts possible in their workflow tool. Lots of functionality coming, but currently not used.

In summary: process data with xraylib, visualise with DAWN.

Structure

batch
processing

examples/
integrate.sh

workflows

scripts/
xraylib-calibrate
...

DAWN workflow(?)

xraylib

files tomo fit calibration sample utils
formfactor

Libraries

pyFAI fabio h5py scikit-image scipy



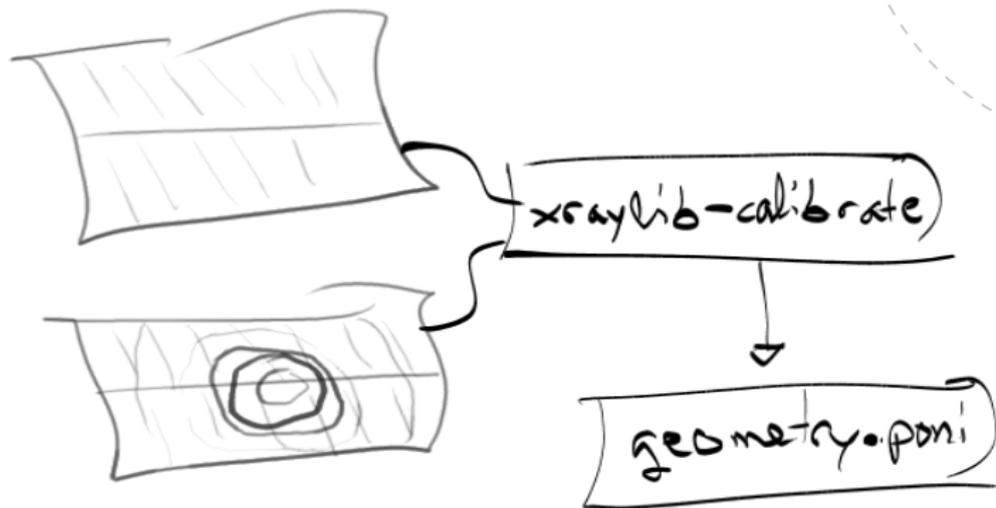
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Current applications of the framework

1. Detector calibration. Detector tilt and beam origin.
2. Azimuthal integration.
3. Sinogram assembly of specific phases in diffraction tomography experiments [DSCT]
4. Sinogram correction and reconstruction

scripts/xraylib-calibrate



scripts/xraylib-calibrate

Usage: xraylib-calibrate <options> CALIBRATION_IMAGE [DARK_CURRENT1,DARK_CURRENT2,...]

XRD calibration routine based on ring shape.

Options:

-s, --silent supress output to terminal.
 -t, --timings Report execution times.
 --pixels Origin and calibration limits in pixels instead of mm.

File options:

--out=FILE Save calibration image after subtracting darkcurrent.
 --data-set=STRING Location to save data set.
 -p=FILE, --poni=FILE File to save detector geometry.

Detector options:

-D DETECTOR_NAME, --detector=DETECTOR_NAME
 Detector name
 --distance=distance [mm]
 Detector distance from sample
 --binning=x y Number of pixels that detector is set to group.
 --tilt=a b [degrees]
 --origin=x y [mm] Initial detector origin wrt beam

Calibration options:

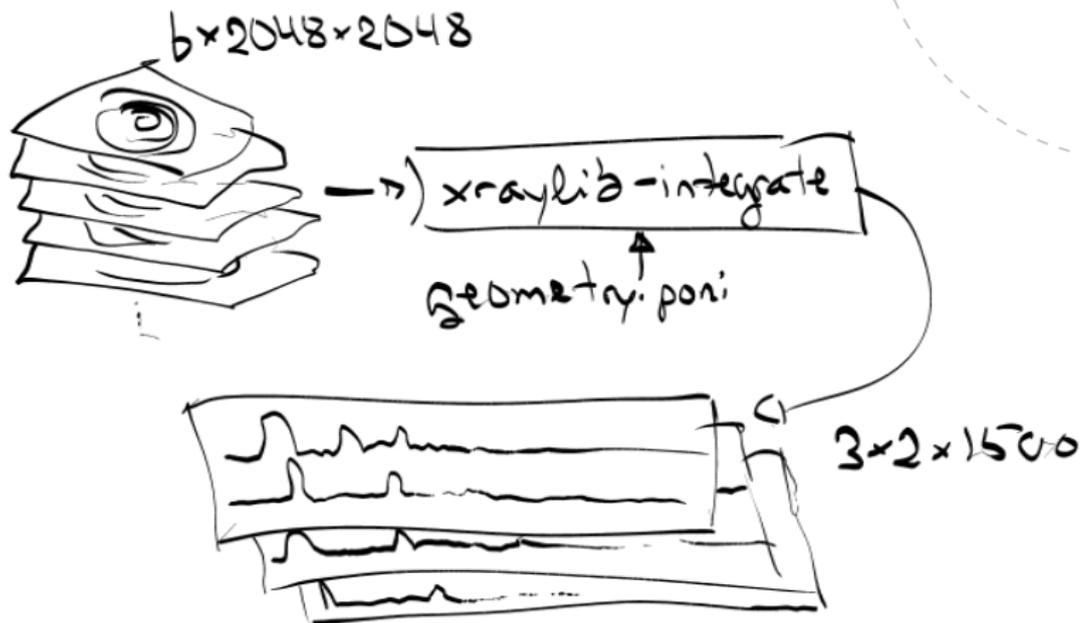
--limits=lower upper
 Radial distance [mm] to use for calibration.



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scripts/xraylib-integrate



scripts/xraylib-integrate

Usage: <options> --data-prefix=/mnt/data/./EXPERIMENT_...

Integrate diffraction images and assemble into dataset.
Experiment parameters are assumed to be separated by underscore
NAME_xxx_yyy_zzz.edf will produce a data set with powder profiles in
dimensions x,y,z.

Options:

-s, --silent supress output to terminal.
-t, --timings Report execution times.
--nbuffer=NBUFFERS Number of files to buffer when loading files
--points=POINTS Number of points to keep radially.

Input options:

--data-path=/path/IMAGE_xyz_ Integrate files starting with this path.
--dark-path=/path/DARK_xyz_ Average darkcurrent files starting with this path.
--dark=DARK Use single darkcurrent image.
-p PONI_FILE, --ponit=PONI_FILE Name of poni file with detector geometry.

Output options:

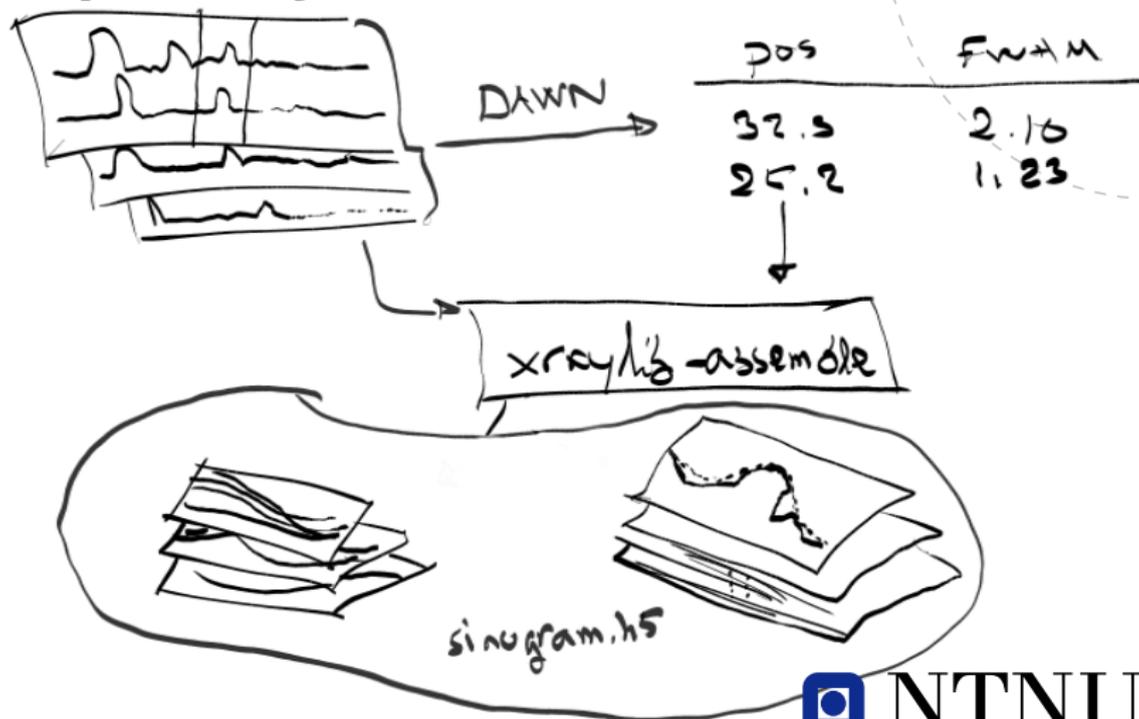
-o FILE, --out=FILE File to save integrated dataset.
--data-set=STRING Location to save data set.



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scripts/xraylib-assemble



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scripts/xraylib-assemble

Usage: xraylib-assemble <options> diffractogram.h5

Options:

-s, --silent supress output to terminal.
-t, --timings Report execution times.
--flip Flip every other scan line.

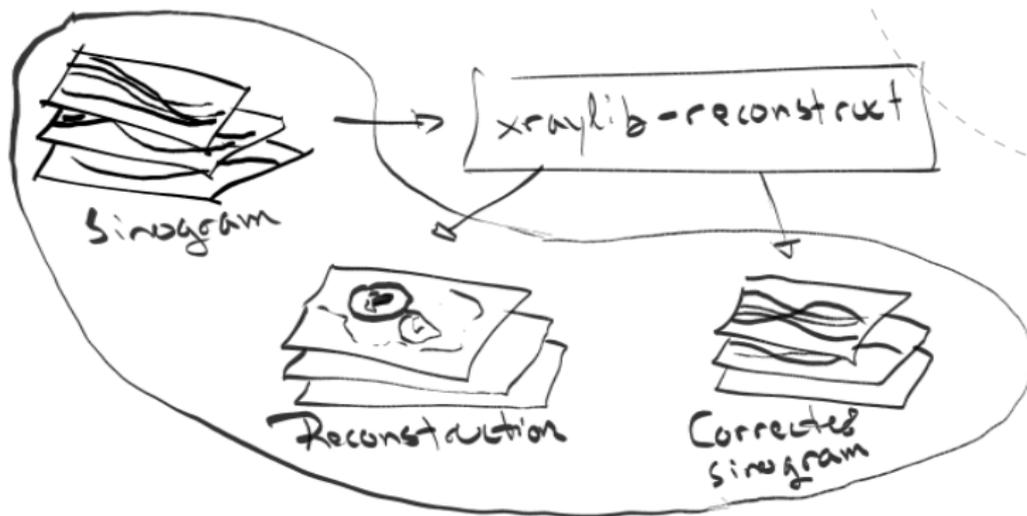
Input options:

--position=PEAK_POSITION Peak channel position
--fwhm=PEAK_FWHM Peak FWHM full width at half maximum
--shape=PEAK_SHAPE Peak shape. [gaussian|delta]
--peak-file=FILE Exported peaks from DAWN.
--input-set=STRING Override data set [default /xraylib/diffractogram].

Output options:

-o FILE, --out=FILE Output file.

scripts/xraylib-reconstruct



scripts/xraylib-reconstruct

Usage: xraylib-reconstruct <options>

Correct sinograms and perform reconstruction.
By default the sinogram is split into odd and even rows which are correlated to correct for offset in interleaved scans, followed by a search for the center of rotation.

Options:

-s, --silent supress output to terminal.
-t, --timings Report execution times.

Input options:

--sinogram-group=SINOGRAM_GROUP
--iterations=SART_ITERATIONS
 Number of iterations to perform SART reconstruction.
 [default=1]

Output options:

--output-sinogram
--output-reconstruction
-o FILE, --out=FILE
 Write reconstruction slices to file.



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Experimental application

Just two weeks ago diffraction tomography data was collected to test the diffraction tomography workflow.

Dummy sample consisting of small ($\approx 150\mu m$) glass spheres suspended from a needle using wax.

[unintentionally blank]

200 μm

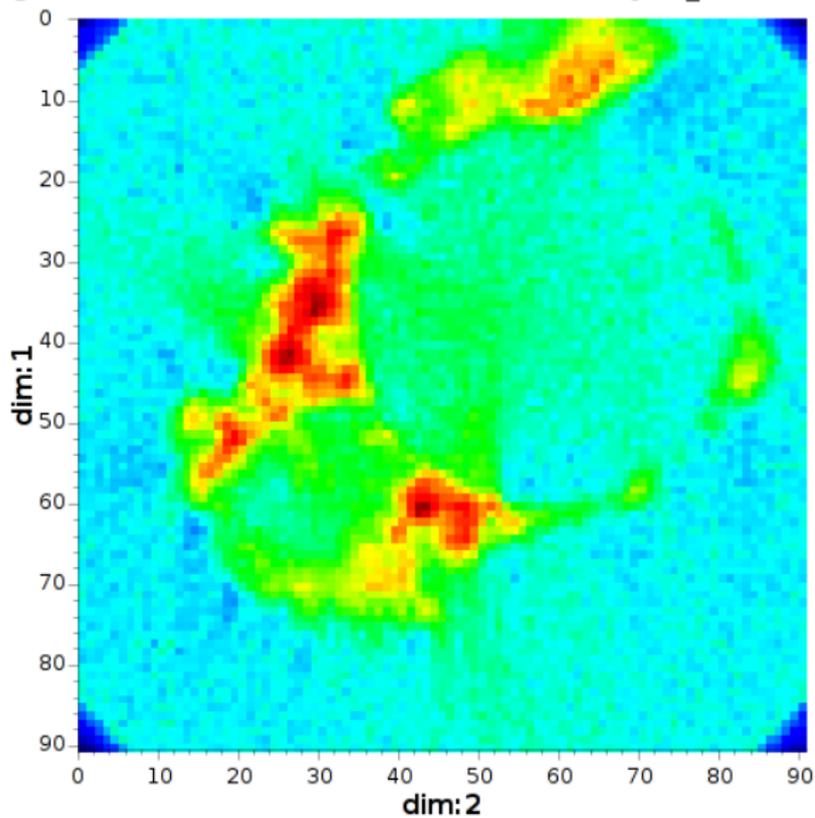
253.03 μm

154.89 μm

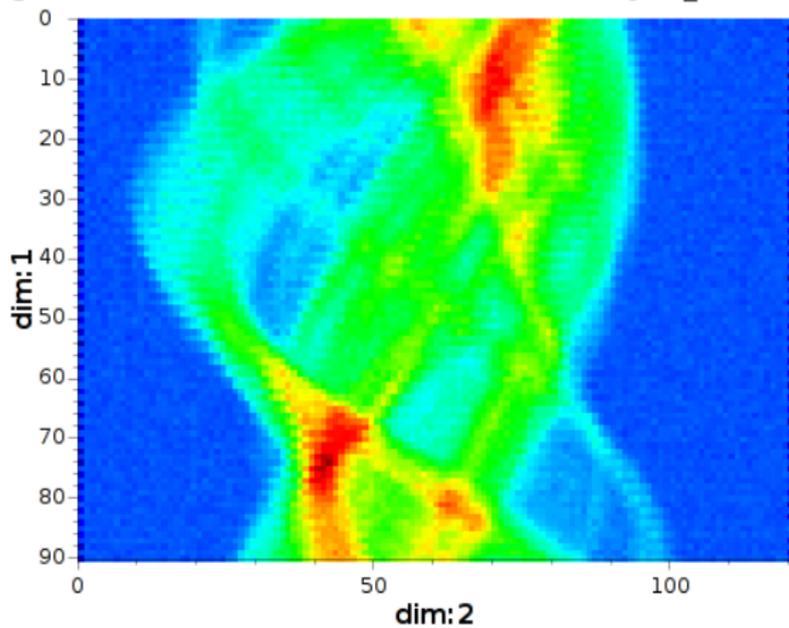
Results

We will see the sinograms, corrected sinograms and their respective reconstructions using filtered back projection.

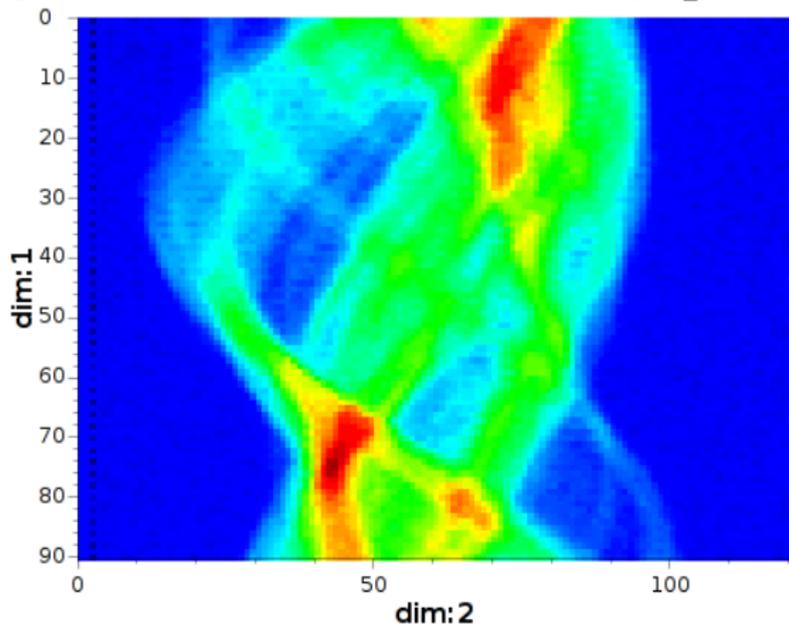
gaussian (83.96,4.82) (SINOGRAM-dummyA1_151.h5)



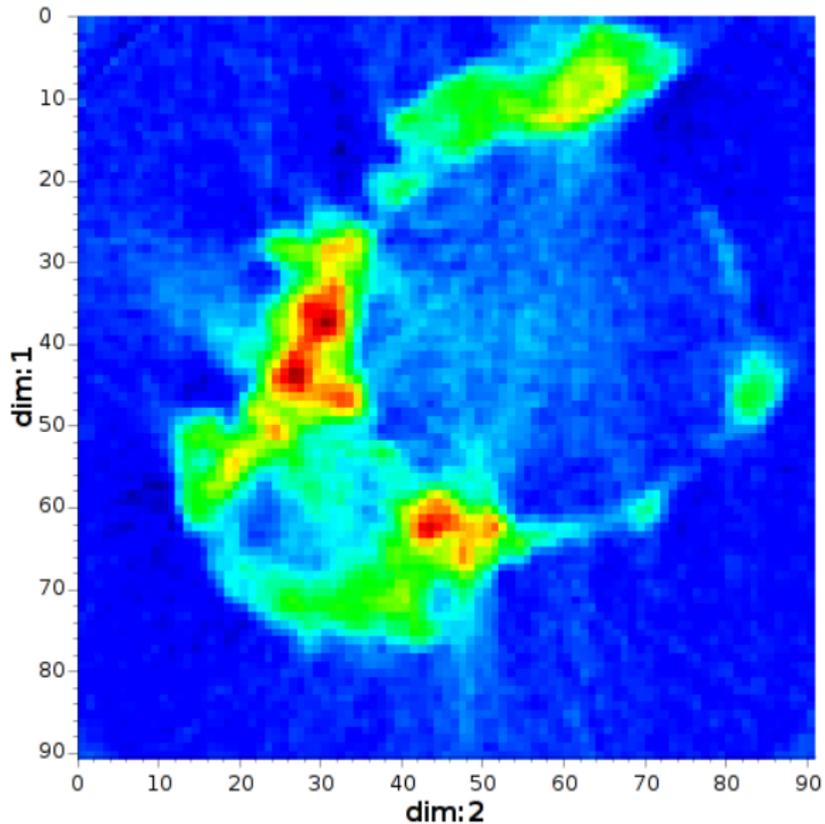
gaussian (83.96,4.82) (SINOGRAM-dummyA1_151.h5)



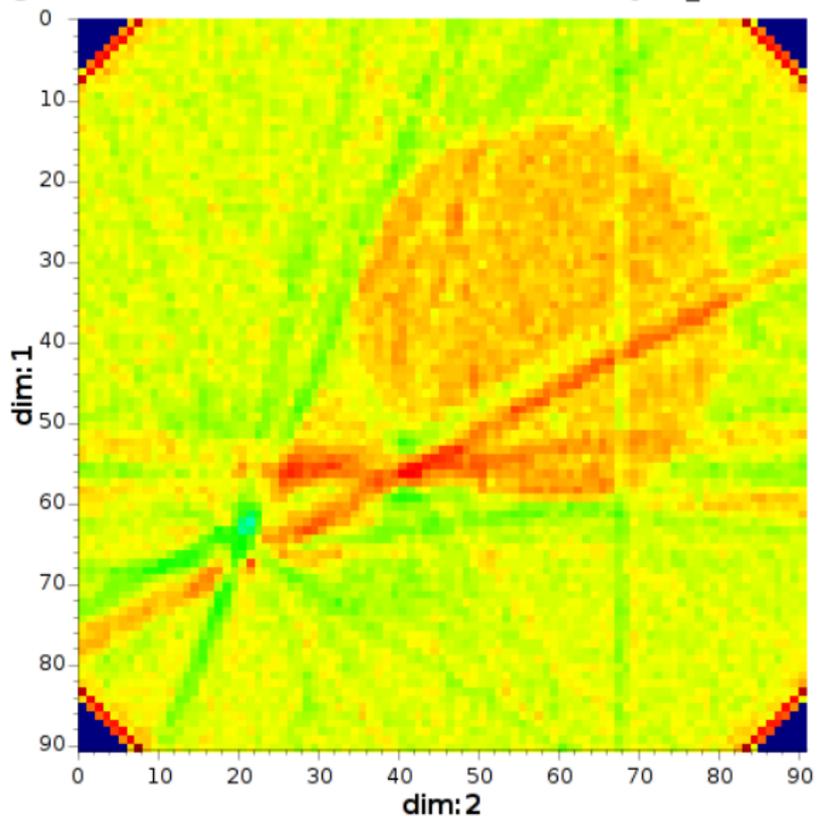
gaussian (83.96,4.82) (SINOGRAM-dummyA1_151.h5)



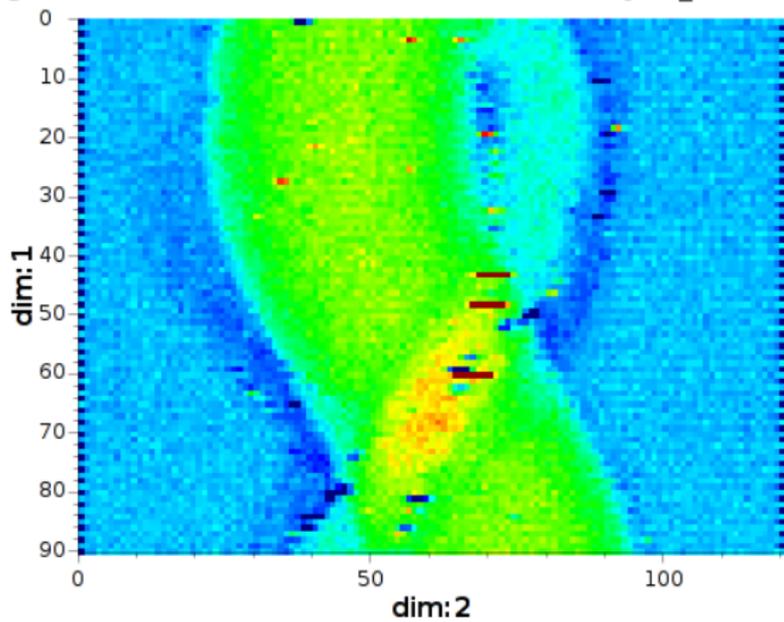
gaussian (83.96,4.82) (SINOGRAM-dummyA1_151.h5)



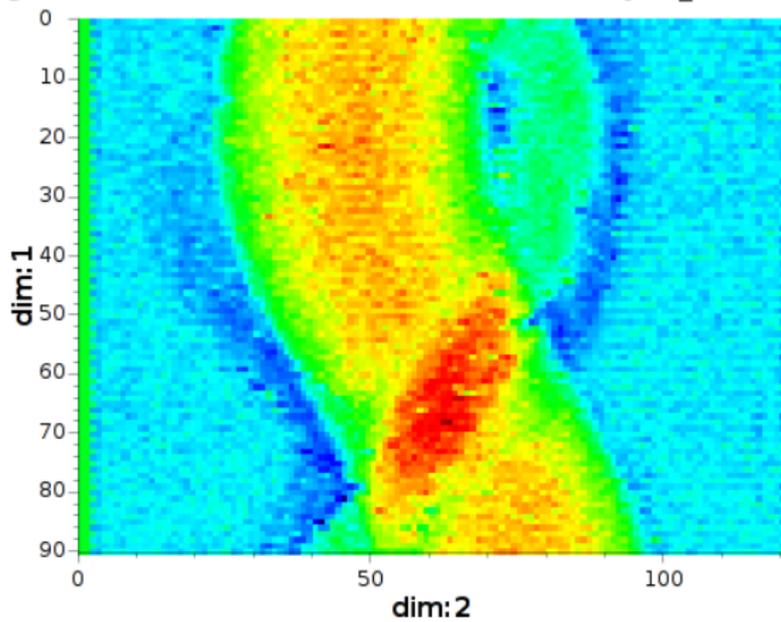
gaussian (230.0,30.0) (SINOGRAM-dummyA1_151.h5)



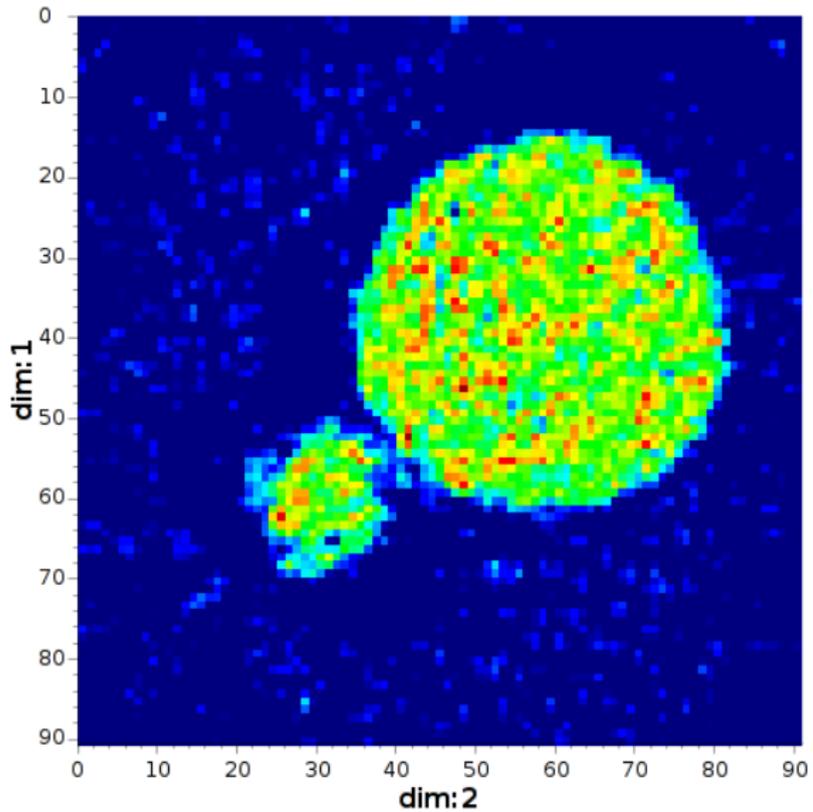
gaussian (230.0,30.0) (SINOGRAM-dummyA1_151.h5)



gaussian (230.0,30.0) (SINOGRAM-dummyA1_151.h5)



gaussian (230.0,30.0) (SINOGRAM-dummyA1_151.h5)



Issues / Further work

- Easy to use?
 - Not everyone comfortable working from the command line.
 - Keep the number of options down, or hidden for power-users
 - Investigate closer integration with DAWN.
 - Beamlines could provide presets for detector calibration and batch scripts.
- More applications. Use beyond basic data reduction and Diffraction Tomography.
- Extend test coverage beyond

The biggest problem of them all!

We need to call the module something.
Xraylib is already taken.

Suggestions are welcome. . .

Questions?

Live demonstration of results in DAWN.