



The European Synchrotron



- BioSAXS beamline
- FreeSAS software
- PyFAI software

Jérôme Kieffer
Algorithm & Data Analysis
Experiment Division

Beamline dedicated to macromolecular small angle scattering experiments

On behalf of the BM29 team:

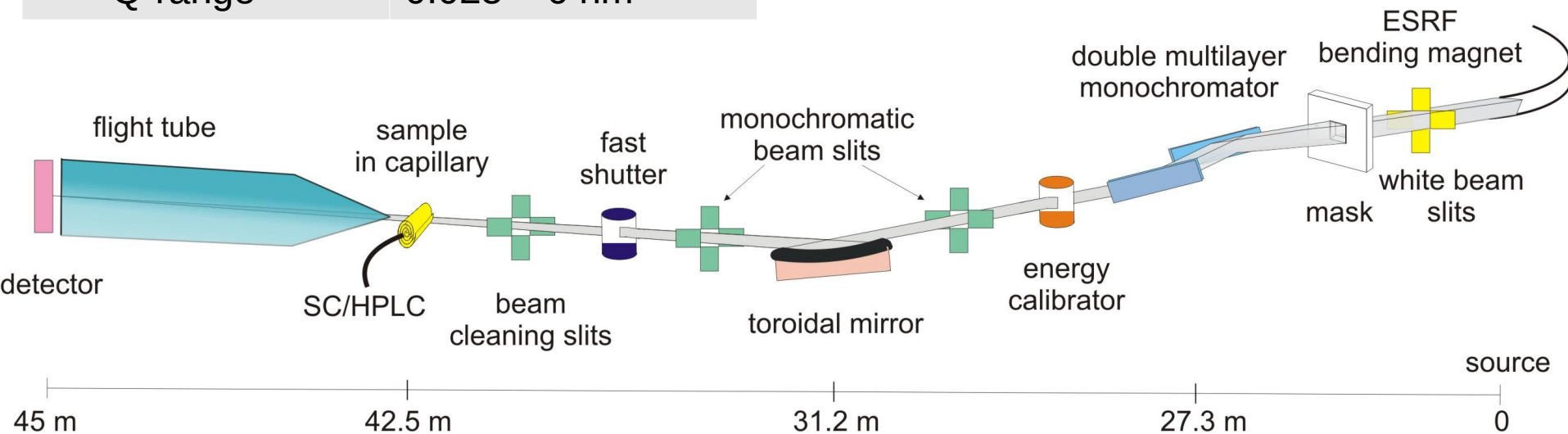
Mark Tully
Petra Pernot
Hayden Fisher

& Software support:

Antonia Beteva
Marcus Oscarsson
Jean-Baptiste Florial

Detector	Pilatus3 2M
• Pixel size	172 μm
• Distance	2.83 m
• Opening angle	$<4^\circ$
• Q-range	0.025 – 6 nm^{-1}

Source	2-pole wiggler
Energy	7-15 keV
Monochromator	Double multilayer
Bandwidth	1%
Beam size	200 μm x 100 μm
Flux	10^{13} ph/s

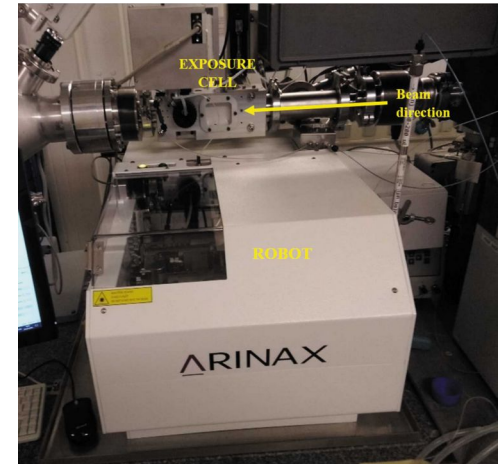


Tully & al (2023). BioSAXS @ ESRF-EBS
<https://doi.org/10.1107/S1600577522011286>

BM29: Experimental hutch



- **Robotic sample changer:**
 - Programmable Buffer-Sample-Buffer sequence
 - Based on 96-well plates with automatic pumping (5 μ L)
 - Flow-through the cell to limit radiation damage
 - Programmable temperature (5-60°C)
- **Size exclusion chromatography (HPLC)**
 - Separate the different oligomeric states of a macromolecule
 - Follow-up by UV spectrometry
- **Microfluidic setup**
 - Automatic dilution series programming
 - Lower the macromolecule consumption



Tully & al (2023). BioSAXS @ ESRF-EBS
<https://doi.org/10.1107/S1600577522011286>

Software stack at BM29: BSXCube v.3

BSXCuBE 3 Acquisition Acquisition result Beamline Setup System log Help User Logout

Safety shutter Fast shutter Beamstop Energy Transmission Ring Current
Data path: [./sample-name/protein-acronym/](#)

CLOSED CLOSED CLOSED 13.900 keV 2.42 % 0
Current collection
Sample name: - Run No.: - Frame No.: -
Attenuation: - % Exp. time: - s/frame

Sample Changer Load Parameters Save Sample Buffer

Sample : Buffer : Plate 1 : 96 Deep Well Plate

	1	2	3	4	5	6	7	8	9	10	11	12
A												
B												
C												
D												
E												
F												
G												
H												

Selected Well : 1:A:11

Sample Name : Buffer Name :

Concentration (mg/ml): SEU Temp. °C:

Volume µl : Storage Temp. °C:

Comment :

Add to Sample Table

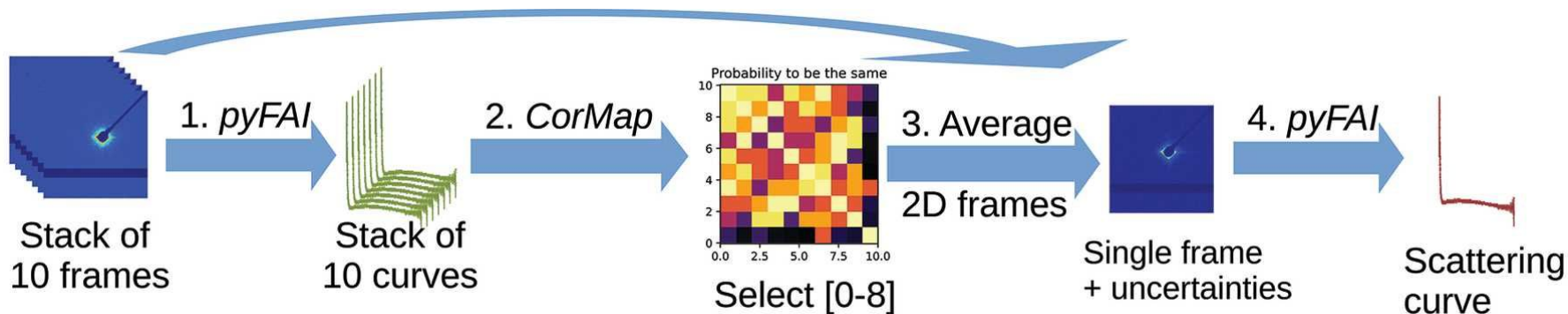
Clear Table Optimisation Expand Parameters: Parameters: Number of Sample's 3 (Selected 3)

	Name	Buffer	Plate	Row	Column	c (mg/mL)	Flow	Extra Flow t(s)	volume (µl)	SEU Temp. °C	Storage Temp. °C	Comment
<input checked="" type="checkbox"/>	sample	bn	1	A	11	1	<input checked="" type="checkbox"/>	5	50	4	4	
<input checked="" type="checkbox"/>	sample	bn	1	A	1	1	<input checked="" type="checkbox"/>	5	60	50	6	c
<input checked="" type="checkbox"/>	sample 1	bn1	2	B	2	0	<input checked="" type="checkbox"/>	5	67	58	66	c
<input checked="" type="checkbox"/>	sample 2	bn2	3	D	2	1	<input type="checkbox"/>	7	60	50	6	c

Add to Queue

Oskarsson et al. ICALEPCS2019
doi:10.18429/JACoW-ICALEPCS2019-WEPHA115

Data Analysis: Multi-frame integration

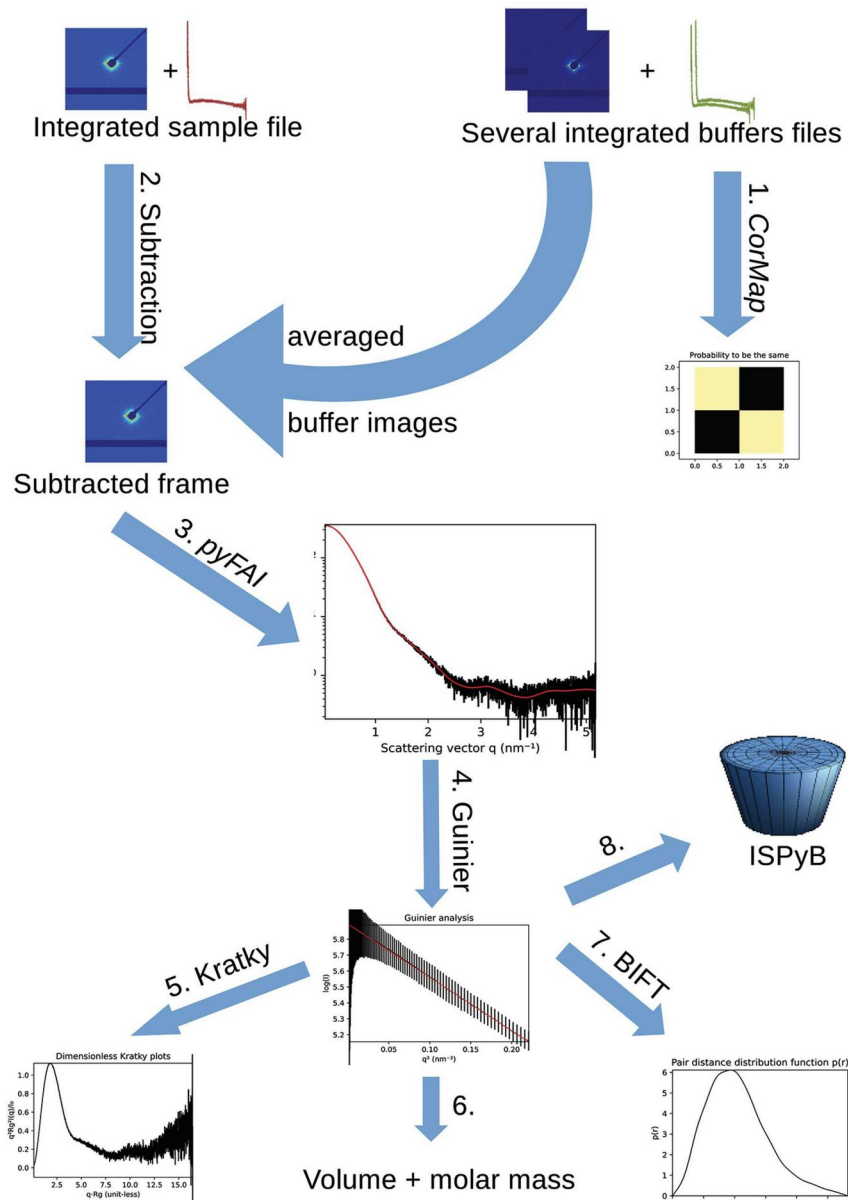


Data portal:
<https://data.esrf.fr>

The screenshot shows the data portal interface for the sample `test_bsa_20_10_5_sc`. The workflow includes steps for buffer and sample integration and subtraction. The metadata table below provides details for the dataset.

Name	Value	Units
SAXS_beam_center_x	564.7292386512835	NA
SAXS_beam_center_y	1127.4001384603537	NA
SAXS_code	T1	NA
SAXS_comments		NA
SAXS_concentration	20.0	mg/ml
SAXS_detector_distance	2.826838431400575	NA
SAXS_diode_currents	[0.00046159 0.00046383 0.00046334 0.00046435 0.00046416 0.00046382 0.00046296 0.00046471 0.00046462 0.00046444]	NA
SAXS_experiment_type	sample-changer	NA
SAXS_exposure_temperature	25.0	C
SAXS_frames_averaged	6-9	NA

Data Analysis: Buffer averaging and subtraction



Data portal:
<https://data.esrf.fr>

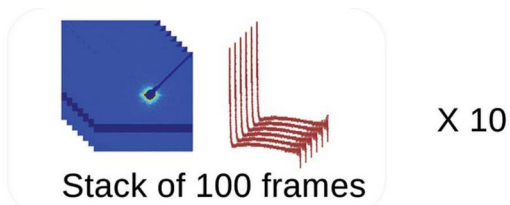
The screenshot shows a workflow diagram at the top with nodes for "buffer_after_T2", "sample_T2", "buffer_after_T1", "sample_T1", and "buffer_before_T1". Below the workflow, the "Name" is "subtract" and the "Sample" is "test_bsa_20_10_5_sc". The "Location" is "/test_bsa_20_10_5_sc_sample_T1/processed/subtract" and it was "Processed on 27/04/2024 09:55:43" with an "Elapsed time" of "00:00:00".

Four plots are displayed: "Scattering curve", "Dimensionless Kratky plot", "Dimensionless Kratky plot", and "Pair distance distribution function".

Below the plots, there are sections for "BIOSAXS", "Metadata list", and "Files 7".

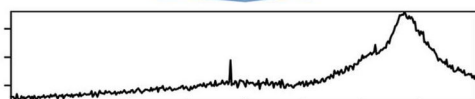
Name	Value	Units
SAXS_code	/entry_0000/T1	NA
SAXS_comments		NA
SAXS_concentration	20.0	mg/ml
SAXS_d_max	40.5±0.0	NA
SAXS_experiment_type	sampleChanger	NA
SAXS_exposure_temperature	25.0	C
SAXS_guinier_i0	0.8±0.0	NA
SAXS_guinier_points	52-83	
SAXS_guinier_rg	2.8±0.0	nm
SAXS_porod_volume	76.77868382189531	nm ³

Data Analysis: HPLC mode



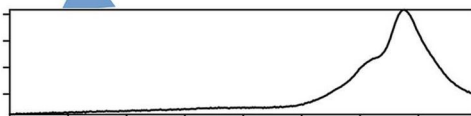
X 10

1. Concatenate curves



2. SVD

3. NMF

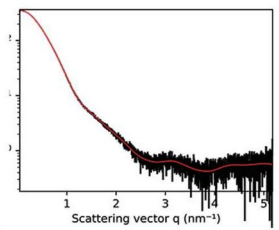


4. Bg



5. Sub.
+ peaks

6. SAS-analysis

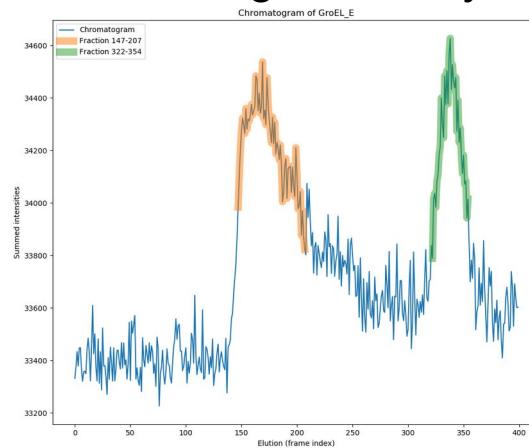


X Nb of fractions

7.

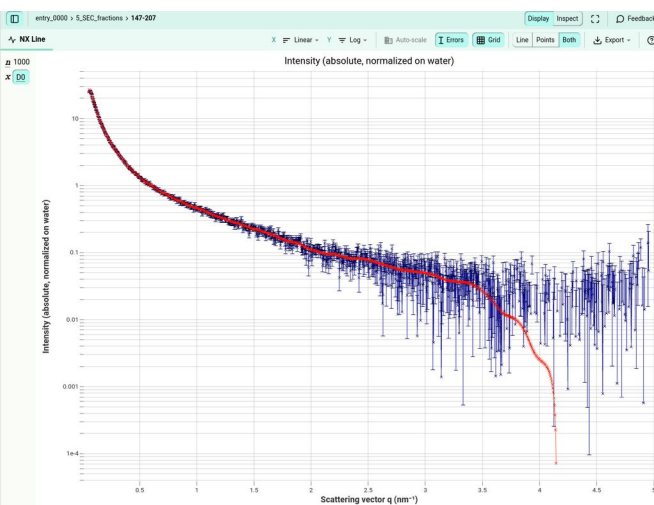


Chromatogram analysis



```

- entry_0000
  > 0_measurement
  > 1_chromatogram
  > 2_SVD
  > 3_NMF
  > 4_background
  > 5_SEC_fractions
    - 147-207
      > 1_average
      > 2_Guinier_analysis
      > 3_dimensionless_Kratky_plot
      > 4_invariants
      > 5_indirect_Fourier_transformation
      @ date
      @ first_frame
      @ last_frame
      @ sequence_index
    - 322-354
      > 1_average
      > 2_Guinier_analysis
      > 3_dimensionless_Kratky_plot
      > 4_invariants
      > 5_indirect_Fourier_transformation
      @ date
      @ first_frame
      @ last_frame
      @ sequence_index
    @ minimum_size
    @ sequence_index
  > 6_ISPyB
  > GroEL_E
  @ configuration
  @ end_time
  
```



Beamline independent SA(X)S software

Features:

- Guinier analysis
- Bayesian Inverse Fourier Transform
- Corelation Map

Credits:

- Martha Brennich
- Guillaume Bonami
- Jesse B. Hopkins
- Mayank Yadav

Kieffer et al., J. Synch Rad. (2022) doi:10.1107/S1600577522007238

How to determine THE best Guinier region ?

- **First order Taylor expansion at $q=0$:**

- Issue with aggregation !

$$I(q) = I_0 \exp\left(-\frac{R_g^2}{3} q^2\right)$$

- **Several implementation:**

- Like ATSAS:

- **Petoukhov et al, J. Appl. Cryst (2007)**
<https://doi.org/10.1107/S0021889807002853>

- Like BioXTAS-RAW

- **J. B. Hopkins, J. Appl. Cryst (2024)**
<https://doi.org/10.1107/S1600576723011019>

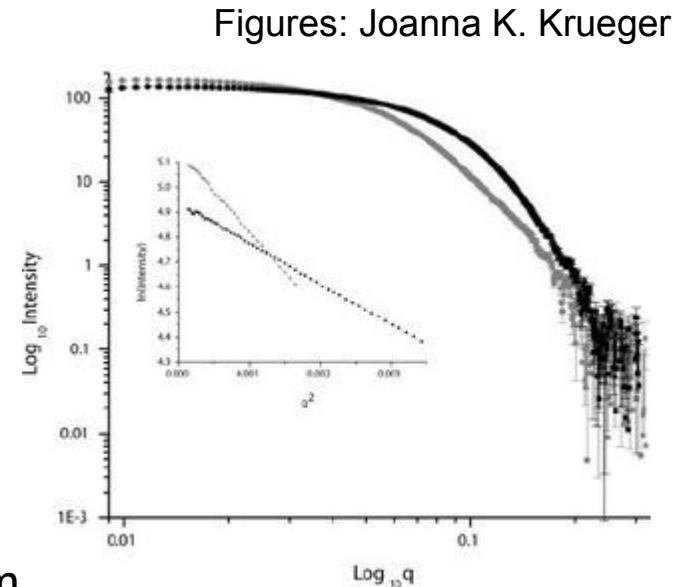
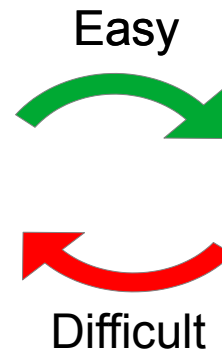
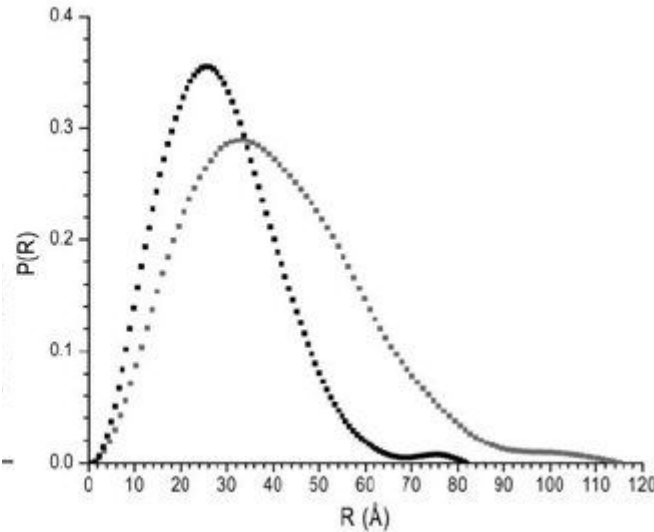
- Like GPA:

- **C. D. Putnam, J. Appl Cryst (2016)**
<https://doi.org/10.1107/S1600576716010906>

- DNN inspired from:

- **Molodenskiy et al. Structure (2022)**
<https://doi.org/10.1016/j.str.2022.03.011>

Bayesian Inverse Fourier Transform

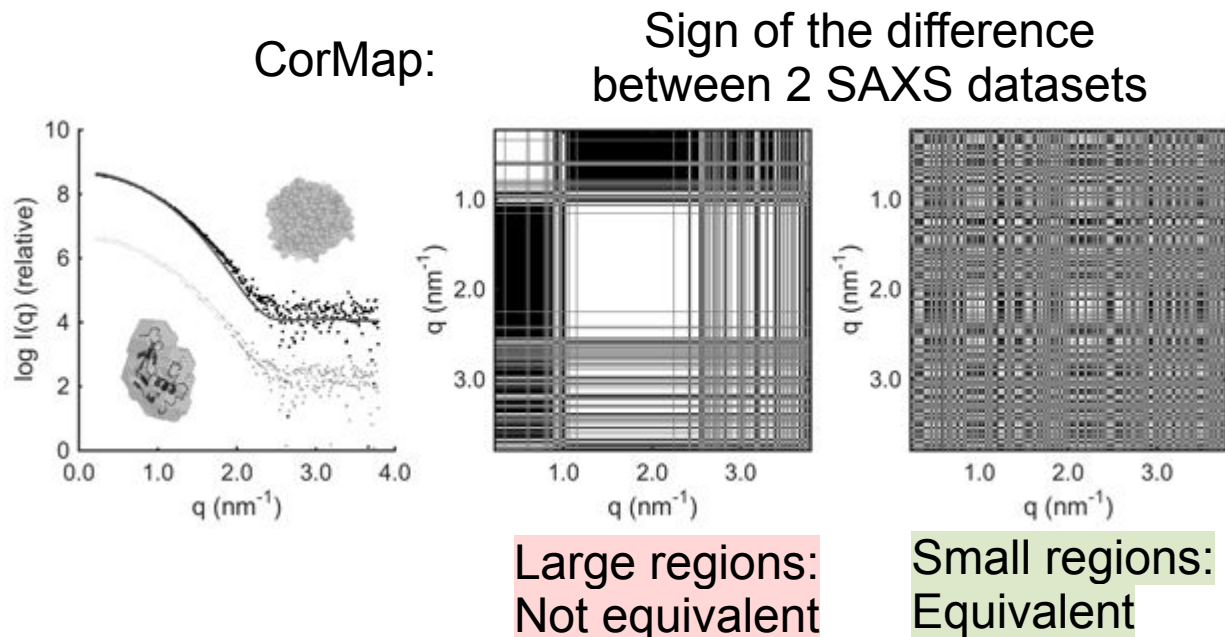


Ill-posed inverse problem

GNOM: Tikhonov regularization
BIFT: Bayesian regularization

- Implemented in Cython,
- Multi-threaded
- BLAS matrix multiplication
- Based on S. Hansen's paper
- J. Hopkins' code analysis (RAW)
→ Solution in ~ 1 second

Hansen, S. J Appl Cryst (2000) 33, 1415-1421.
DOI: [10.1107/S0021889800012930](https://doi.org/10.1107/S0021889800012930)



The largest region is compared with the total size of the pattern:
 The probability is the same a getting that many successive heads/tails when throwing a coins as many times as the pattern has points.

$$A_n(x) = \begin{cases} \sum_{j=0}^x A_{n-1-j}(x) & \text{for } n > x; \\ 2^n & \text{for } n \leq x. \end{cases}$$

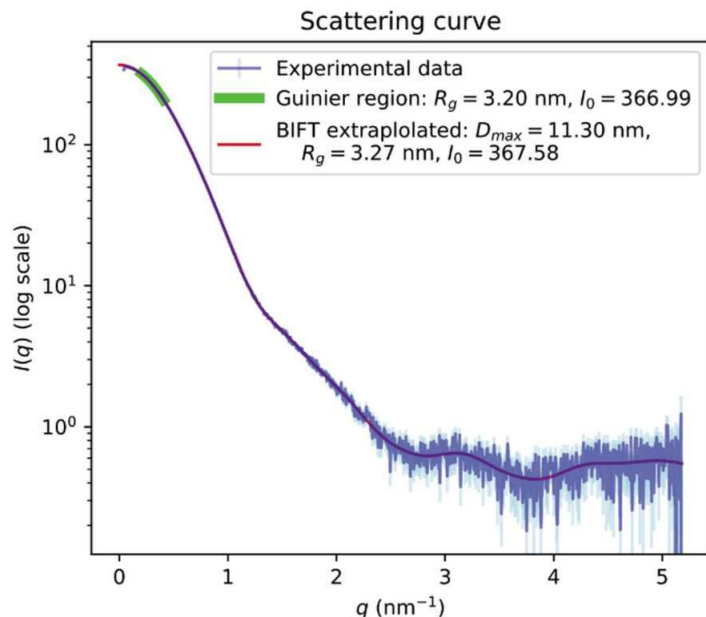
$$B_n(x) = 2A_{n-1}(x-1) \quad \text{for } x \geq 1.$$

$$P_n(x) = 2^{\log_2(2^n - B_n(x)) - n}$$

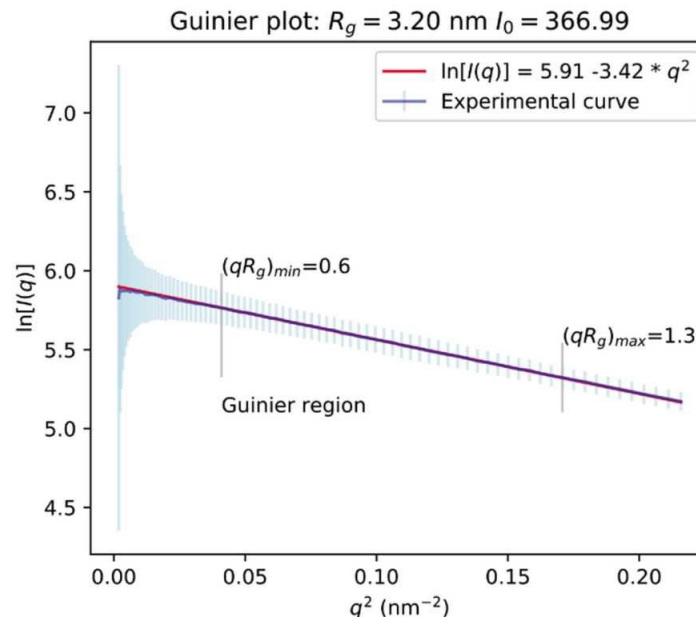
SAS analysis → all-in-one tool

sample_BSA_5mg-integrate-sub.dat

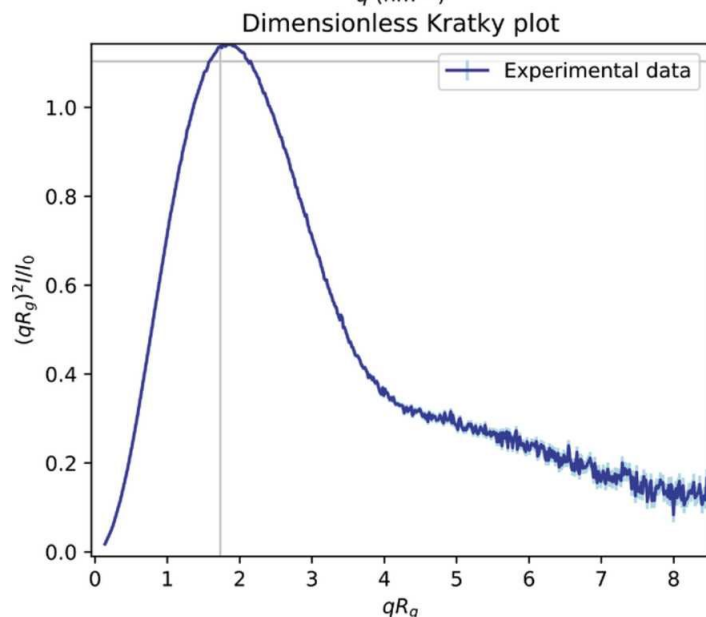
SAS
plot



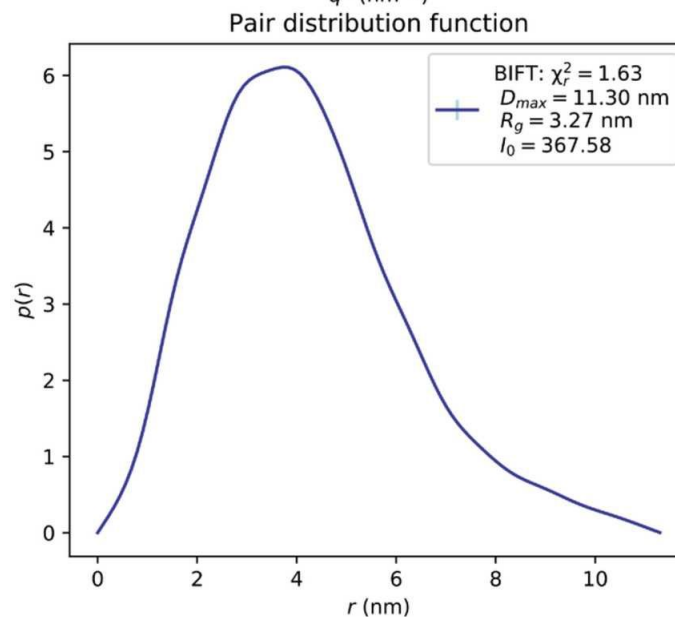
Guinier
plot



Kratky
plot

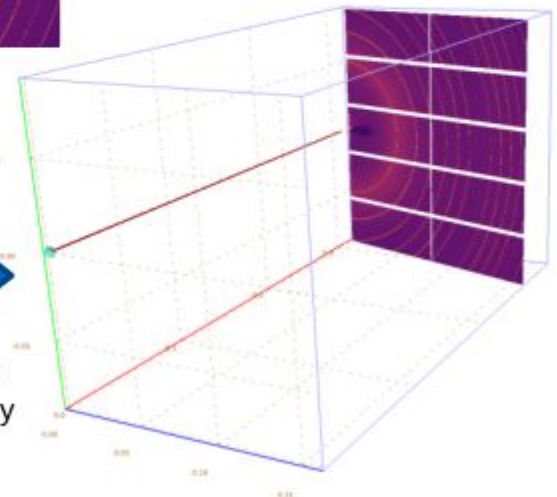
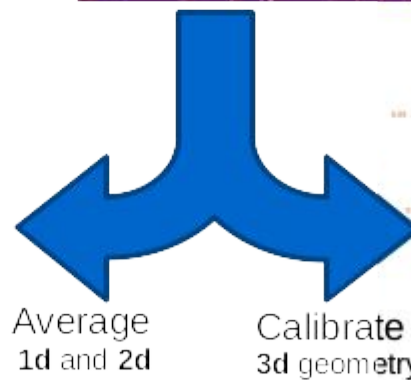
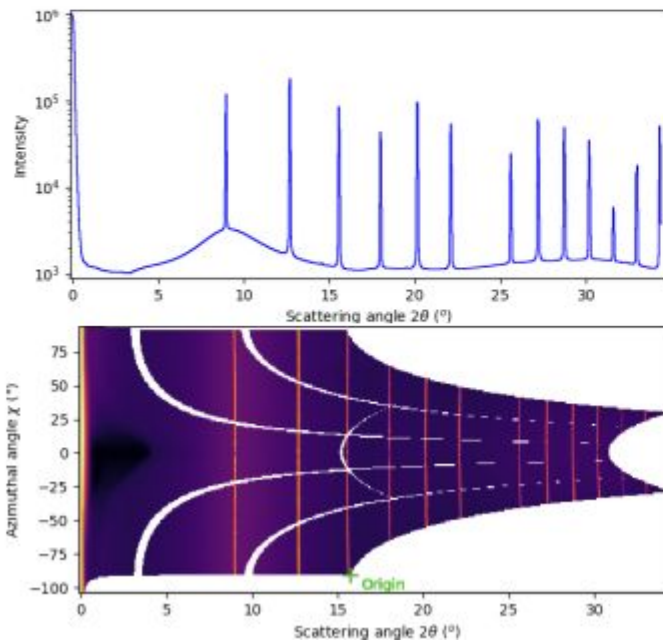
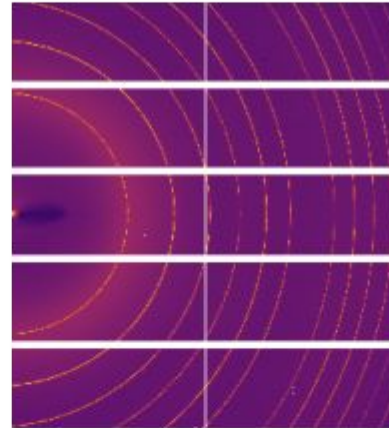


BIFT



Fast Azimuthal Integration library using Python

PyFAI
Fast Azimuthal Integration



Kieffer, J., Valls, V., Gutierrez-Fernandez, E., Ashiotis, G., Karkoulis, D., Nawaz, Z., Deschildre, A., Vincent, T., Picca, F. E., Massahud, E., Payno, H., Huder, L., Wright, J. P., Pandolfi, R., Jankowski, M., Paleo, P., Faure, B., Storm, M., De Nolf, W., Wright, C. J., Hopkins, J. B., Pascal, E., Weninger, C., Detlefs, C., Plaswig, F., Lavanchy, A., gbenecke, zxs-un, iltommi, & dodogerstlin
<https://doi.org/10.5281/zenodo.13756914>

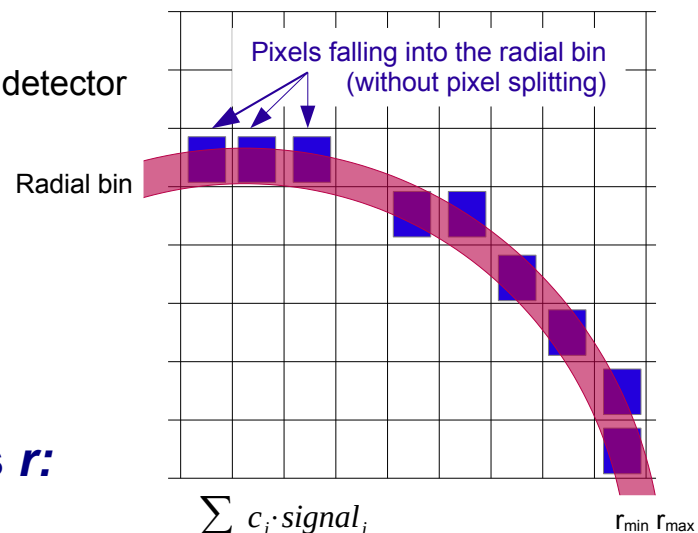
How azimuthal integration works

- Pixel-wise corrections:**

$$I_{cor} = \frac{I_{raw} - I_{dark}}{F \cdot \Omega \cdot P \cdot A \cdot I_0} = \frac{\text{signal}}{\text{normalization}}$$

Where: I_0 is the incoming flux (pixel independent)

- I_{raw} and I_{dark} are the signal measured from the detector
- F is the flat-field correction
- Ω is the solid angle for this pixel
- P is the polarization factor
- A is the parallax correction factor



- Averaging over a bin defined by the radius r :**

- Need for pixel splitting?
- c_i being the fraction of the pixel i contributing to bin $_r$

$$\langle I \rangle_r = \frac{\sum_{i \in \text{bin}_r} c_i \cdot \text{signal}_i}{\sum_{i \in \text{bin}_r} c_i \cdot \text{normalization}_i}$$

- Associated uncertainty propagation:**

- Assuming there is no correlation between pixels
- Pixel splitting can create correlation between bins...

$$\sigma(I_r) = \sqrt{\frac{\sum_{i \in \text{bin}_r} c_i^2 \cdot \text{variance}_i}{\sum_{i \in \text{bin}_r} c_i^2 \cdot \text{normalization}_i^2}}$$

$$\sigma(\langle I \rangle_r) = \sigma(I_r) \frac{\sqrt{\sum_{i \in \text{bin}_r} c_i^2 \cdot \text{normalization}_i^2}}{\sum_{i \in \text{bin}_r} c_i \cdot \text{normalization}_i}$$

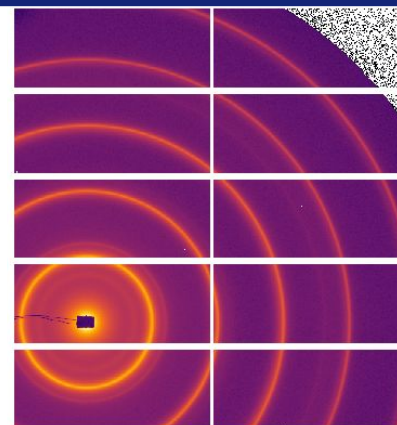


- **Image**

2D array of pixels as *numpy* array
read using *silx*, *fabio*, *h5py*, ...

- **Azimuthal integrator: core object**

- powder diagram using *integrate1d*
- “cake” image, azimuthally regrouped using *integrate2d*



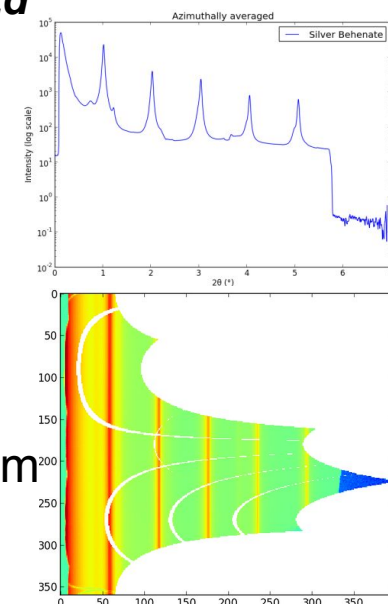
- **Detector object**

- Calculates the pixel position (distortions)
- Handles the mask for invalid pixels
→ saved as a HDF5 file

- **Geometry**

Position of the detector from the sample & incoming beam

→ saved as *PONI*-file

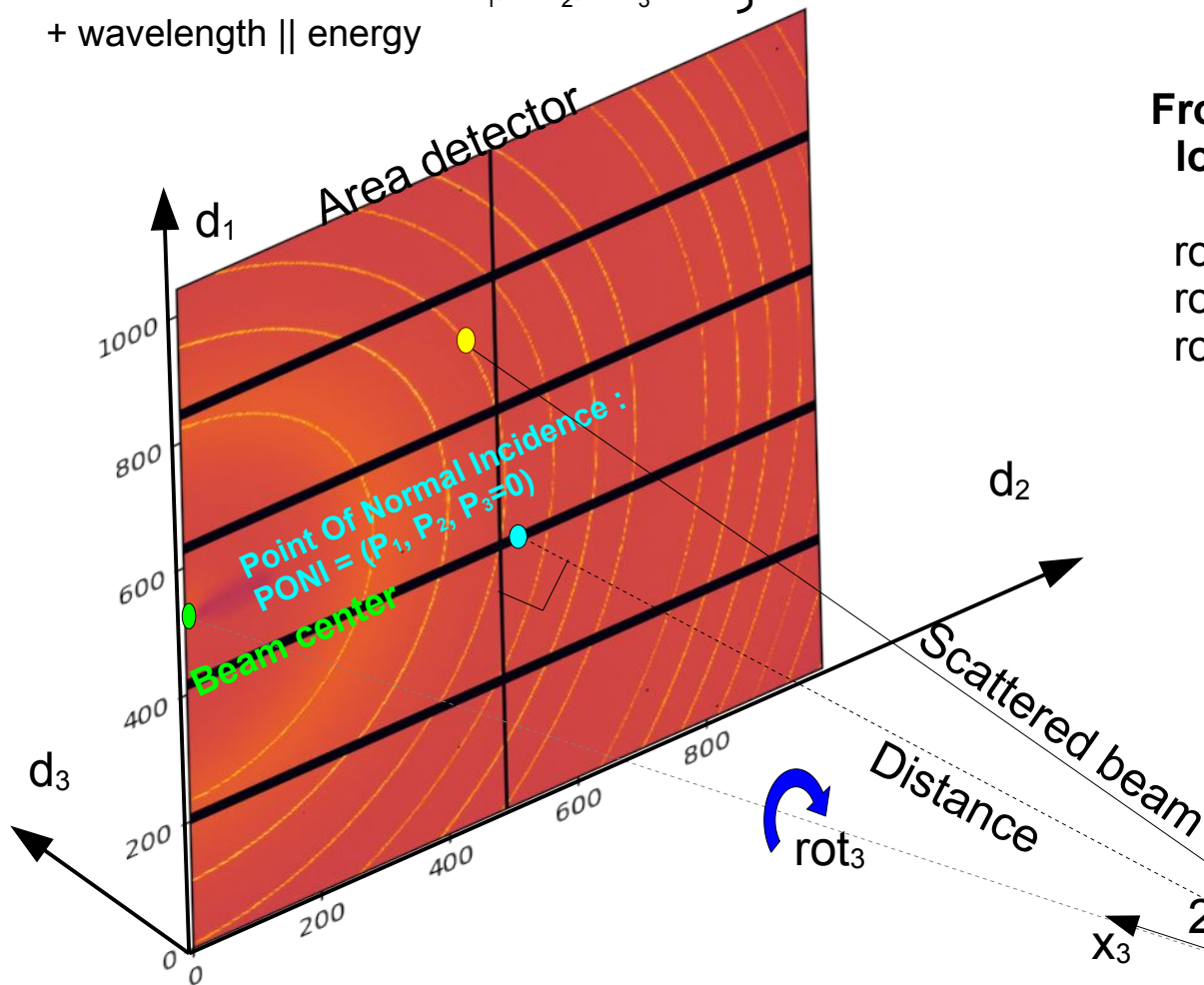


<http://www.silx.org/doc/pyFAI/dev/geometry.html#detector-position>

Geometry in pyFAI

Parameters:

- * 3 distances in meters: $dist$, $poni_1$, $poni_2$
 - * 3 rotations in radians: rot_1 , rot_2 , rot_3
 - + wavelength || energy
- } *PONI*-file



From the sample's point of view, looking towards the detector :

- rot_1 : moves detector → to the right
- rot_2 : moves detector ↓ downwards
- rot_3 : moves detector ↻ clockwise

Detector's origin:
lower left, looking from
the sample

Determine the position of
the detector vs sample

- **Geometry is best determined from the analysis of a known reference sample**
- **This calibration step is preferred to measuring distances and beam center position**
 - The prerequisite is:
 - **detector geometry and mask,**
 - **calibrant (LaB₆, CeO₂, AgBh, ...)**
 - **wavelength or energy used**
 - Only the position of the detector and the rotation needs to be refined:
 - **3 translations: dist, poni₁ and poni₂**
 - **32 rotations: rot₁, rot₂, rot₃**
- **It is divided into 4 major steps:**
 - 1) Extraction of groups of peaks
 - 2) Identification of peaks and groups of peaks belonging to same ring
 - 3) Least-squares refinement of the geometry parameters on peak position
 - 4) Validation by a human being of the geometry
- **PyFAI assumes this setup does not change during the experiment**
→ **Put the geometry in cache**

Calibration GUI in pyFAI

The screenshot displays the PyFAI Calibration GUI. The main window, titled "PyFAI Calibration", features a toolbar with icons for zooming, panning, and a "3D" button highlighted by a pink arrow. Below the toolbar is a "Display sample stage" window. This window contains a 3D plot of a sample stage, showing a blue cube with a red line representing the sample position and a blue line representing the detector position. The axes are labeled with values: 0.00, -0.05, 0.05, 0.10, and 0.15. To the right of the 3D plot is a "Object parameters" panel with a table of parameters.

Item	Value
Settings	
<input checked="" type="checkbox"/> Data	

At the bottom of the "Object parameters" panel, there are tabs for "Object parameters" and "Global parameters", and a "Close" button. The background of the main window shows a 2D plot of a detector with concentric circles and a red line representing the sample position. The status bar at the bottom of the main window displays: Pos: na Pixel: nan χ : nan 2θ : nan q: nan. The bottom left corner of the image shows "Online help..." and the bottom right corner shows "Next >".

A quest for speed:

- Histogram based algorithms
- Sparse matrix multiplication

What happens during an integration

1) Get the pixel coordinates from the detector, in meter.

There are 3 coordinates per pixel corner, and usually 4 corners per pixel.

1Mpix image → 48 Mbyte !

2) Offset the detector's origin to the PONI and rotate around the sample

3) Calculate the radial (2θ) and azimuthal (χ) positions of each corner

4) Assign each pixel to one or multiple bins.

If a look-up table is used, just store the fraction of the pixel.

Then for each bin sum the content of all contributing pixels.

5) Histogram bin position with associated intensities

6) Histogram bin position with associated normalizations (i.e. solid angle)

7) Return bin position and the ratio of the two sums:



Can be performed with
sparse-matrix multiplications

$$\langle I \rangle_r = \frac{\sum_{i \in \text{bin}_r} c_i \cdot \text{signal}_i}{\sum_{i \in \text{bin}_r} c_i \cdot \text{normalization}_i}$$

Advantages of *histograms* vs matrix multiplication

Histograms

- Pro
- **Easier to understand**
 - **Low memory consumption**
 - **Fast initialization**

CSR matrix multiplication

- **Faster, even on a single core**
- **Many-core friendly**
 - OpenMP and OpenCL

- Con
- **Pretty slow**
 - **Hardly parallelizable**

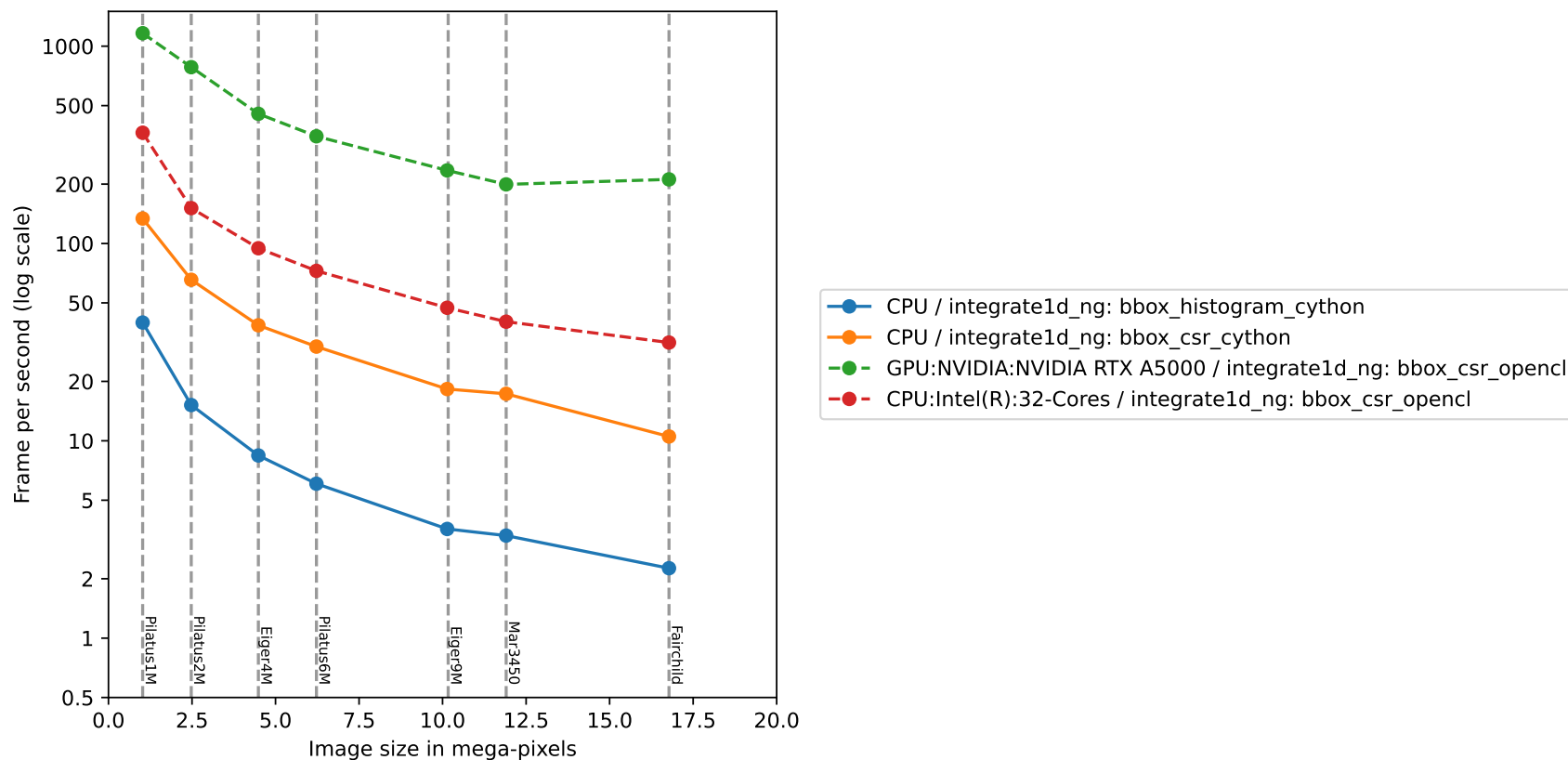
- **Slower initialization**
- **The sparse matrix can be large**

Rule of thumb: < 5 frames

≥ 5 frames

Benchmark: Let's speak about speed !

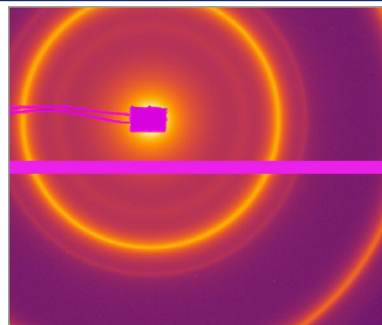
CPU: AMD Ryzen Threadripper PRO 3975WX 32-Cores
GPU: NVIDIA RTX A5000



High frequency noise issue

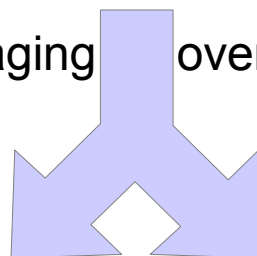
Where pixel splitting comes-in

Example with SAXS data integrated in 2D



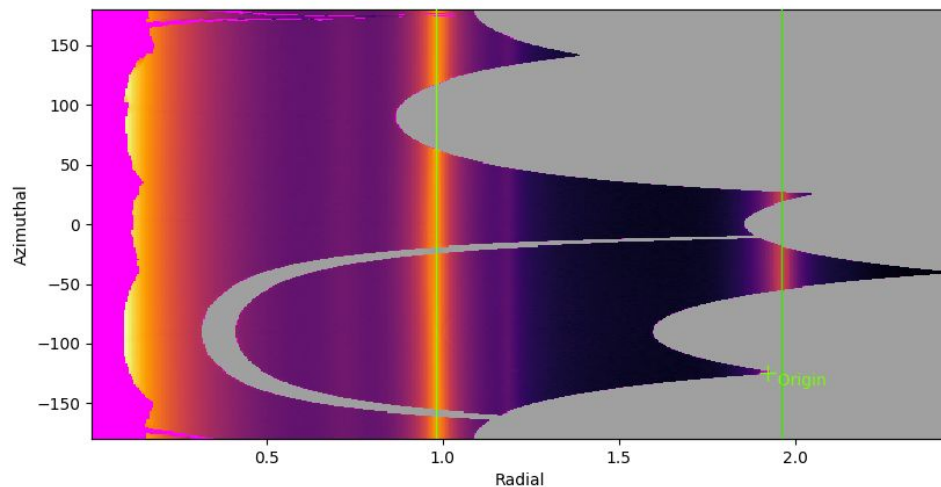
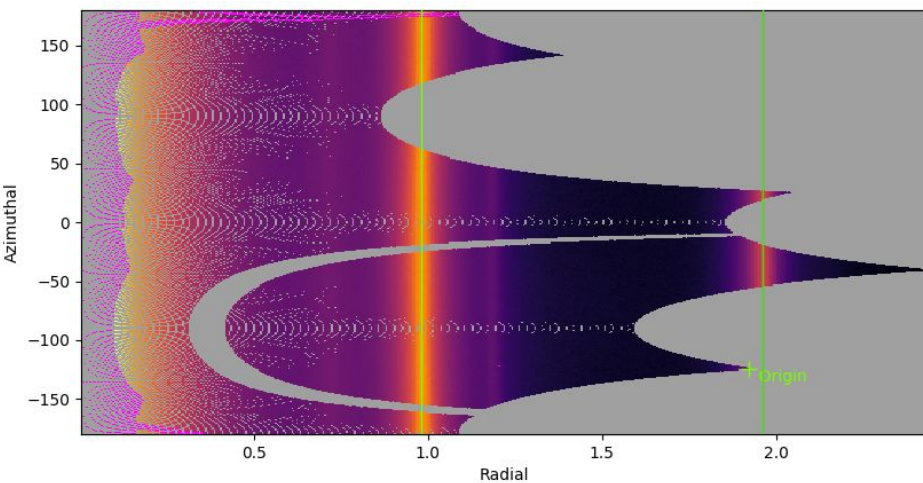
Pilatus 200k:
~500 x 400 pixels

2D averaging over 512x360 bins



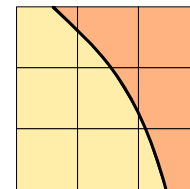
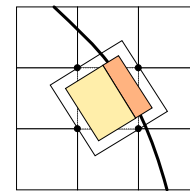
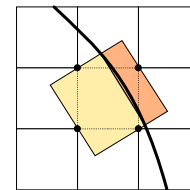
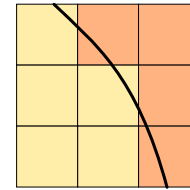
Without pixel splitting

With pixel splitting



creates bin cross-correlation

- **No pixel splitting: default histograms**
 - Each pixel contributes to a single bin of the result
 - No bin correlation but noisy
 - The pixel has no surface: sharpest peaks
- **Bounding-box pixel splitting**
 - The smoothest integrated curve
 - Blurs a bit the signal
- **Pseudo pixel splitting (deprecated)**
 - Scale down the bounding box to the pixel area, before splitting.
 - Good cost/precision compromise, similar to FIT2D
- **Full pixel splitting**
 - Split each pixel as a polygon on the output bins.
 - Costly high-precision choice



- **Histogram based algorithms:**
 - Each pixel is split over the bins it covers.
 - The corner coordinates have to be calculated (4x slower initialization)
 - The slow down is function of the oversampling factor, for every image
- **Sparse matrix multiplication based algorithms**
 - The sparse matrix contains already the pixel splitting scheme
 - Longer initialization time related to the oversampling factor
 - There are *NO* performance penalty on the integration itself

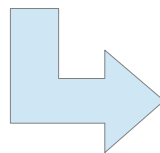
All those consideration are independent of the programming language

Nevertheless, Python which is interpreted is expected to be 1000x slower than:

- compiled code like C, C++, Fortran, ...
- JIT compiled code like Java, Julia or numba

Grazing incidence data visualization

Edgar Gutierrez-Fernandez
Thomas Dane



Poster

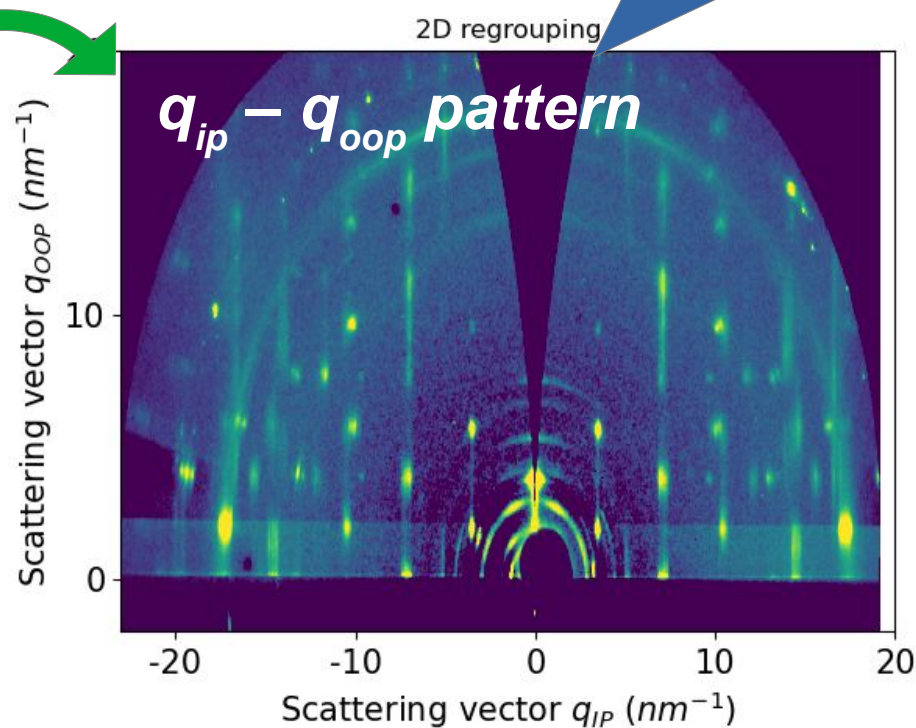
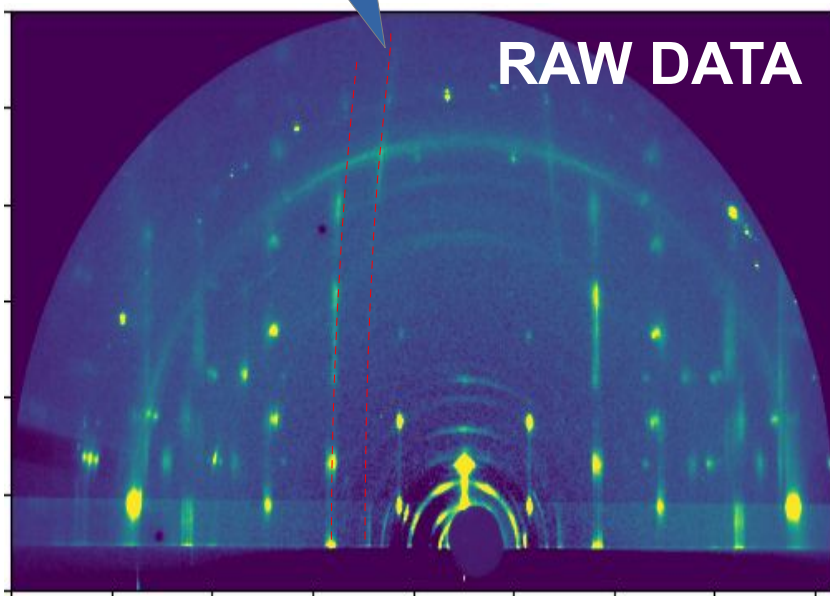
Reshaping into the components of \vec{q}

$$\vec{q} = \vec{q}_x(\text{beam}) + \vec{q}_y(\text{horz}) + \vec{q}_z(\text{vert})$$

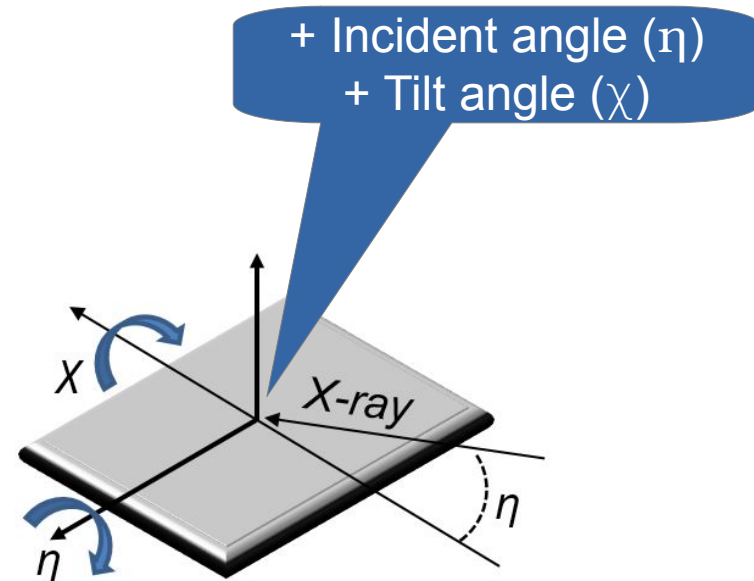
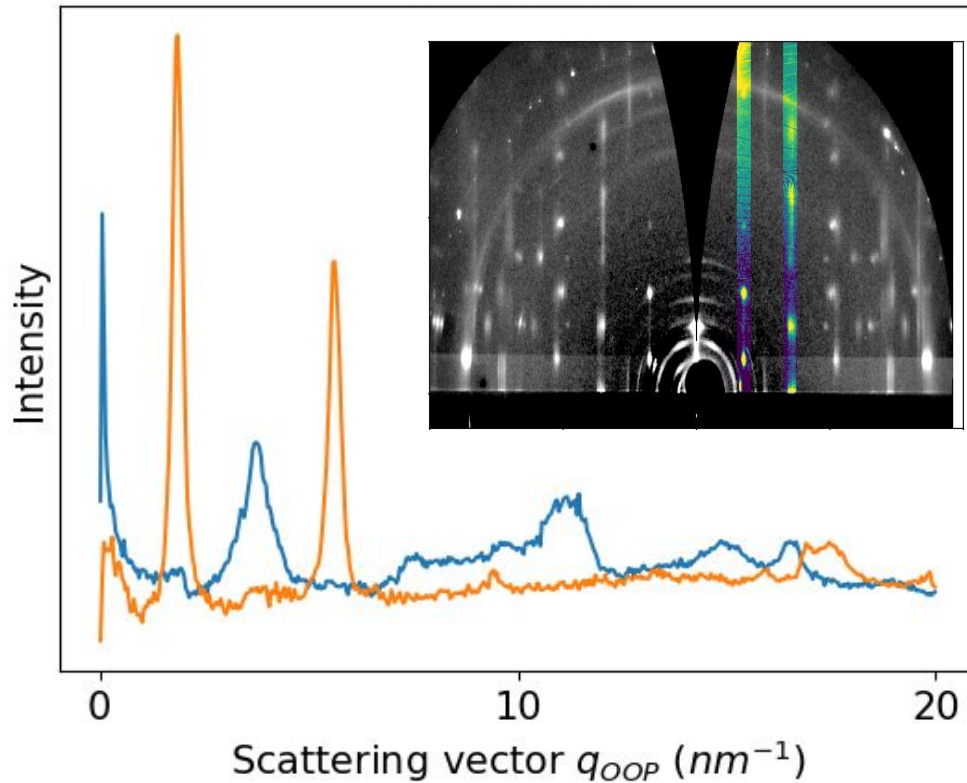
$$q_{IP} = \sqrt{q_x^2 + q_y^2} \quad q_{OOP} = q_z$$

In a flat detector, the diffraction rods are curved

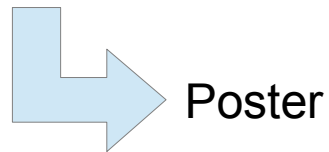
Missing wedge: the probed region of the reciprocal space is a sphere.



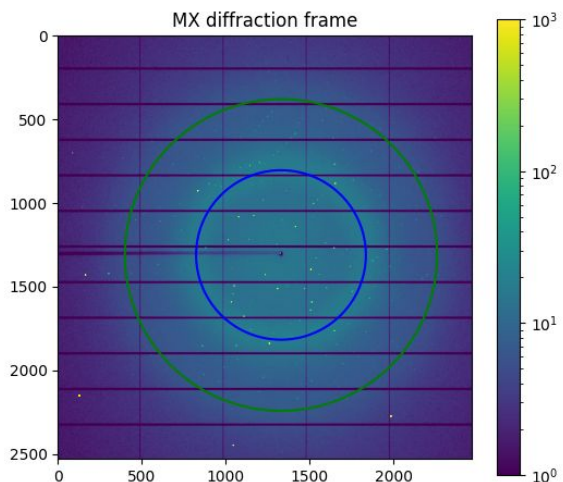
1D-Integration along \vec{q} components



Outlier rejection: Sigma-clipping Median filtering

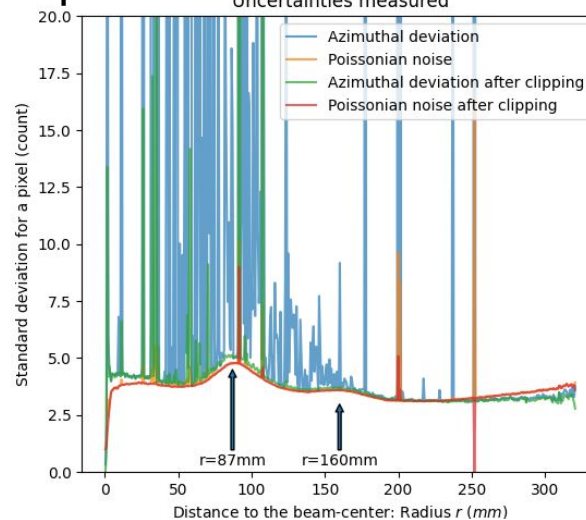
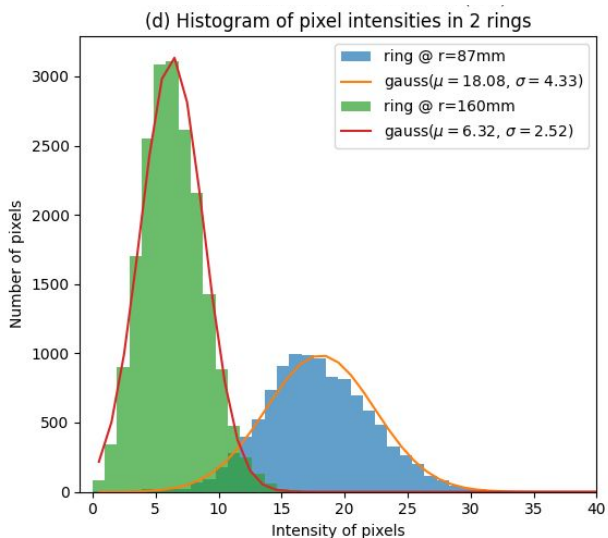
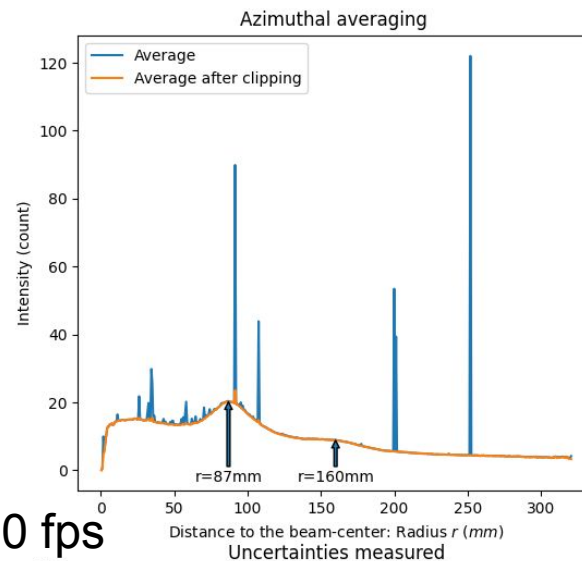


Sigma clipping



Implemented in:

- Python
- Cython
- OpenCL → 250 fps

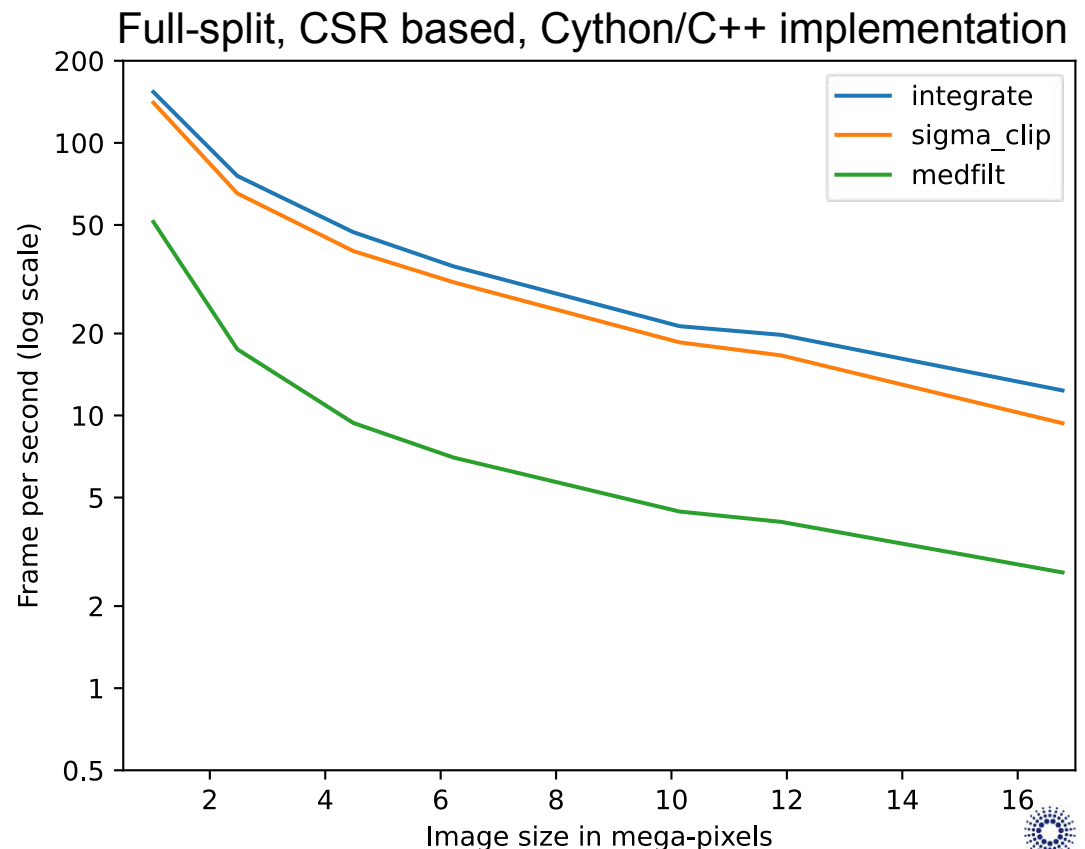


No pixel splitting

- **Outlier rejection based on extrema rejection**
 - Oversampling for Rietveld refinement with large pixel size
- **Requires one sort per azimuthal bin, thus expensive !**
 - Implementations:
 - **Python**
 - **Cython**
 - **OpenCL (*)**

* New parallel sort algorithm suitable for variable size ensembles.

Unpublished / experimental work



- Using pyFAI as a library
- Alternative software

Other applications relying on pyFAI: 40 on github!

- **NanoPeakCell: Serial crystallography pre-processing**
 - Nicolas Coquelle, IBS Grenoble
- **PySaxs: data analysis for SAXS experimental station**
 - Olivier Taché, CEA Saclay
- **Dpdak: online data analysis for Saxs data**
 - Gunthard Benecke, Petra III
- **Dioplas: offline data analysis for high pressure diffraction**
 - Clemens Percher, APS → EuXFEL
- **Bubble: online data analysis for Saxs/Waxs data**
 - Vadim Diadkin, Dubble & SNBL CRG beamlines
- **Project for materials and strain analysis**
 - Jozef Keckes, Loeben university, Austria
- **xPDFsuite**
 - Prof. Simon Billinge, U. of Columbia

<http://www.silx.org/doc/dev/pyFAI/ecosystem.html>

Many different tools exist ...

Name	License	Language	Owner	Details
PyFAI	MIT	Python/ C++	ESRF	GPU possible
FIT2D	MIT	Fortran	ESRF	Discontinued
XRDUA	GPL	IDL	U. Antwerp	diff-map
Dawn	EPL	Java	Diamond	
DataSqueeze	Shareware	Java	U. Pennsylvania	
Foxtrot	Academic	Java	Xenocs/Soleil	SAXS only
Maud	Freeware	Java	U.Trento	Focus on materials
GSAS-II	BSD	Python/ Fortran	APS / U.Chicago	
Scikit-Beam	BSD	Python	NSLS-II / BNL	
AzInt	MIT	Python/C++	Max-IV	FPGA possible
SAXSdog	-	Python	TU-Graz	

Questions ?

