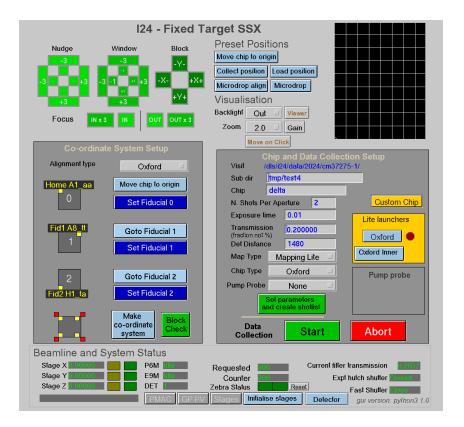
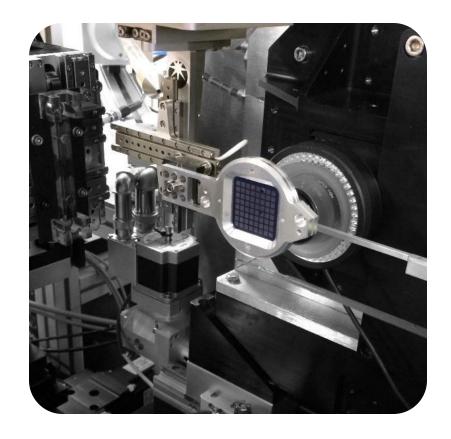
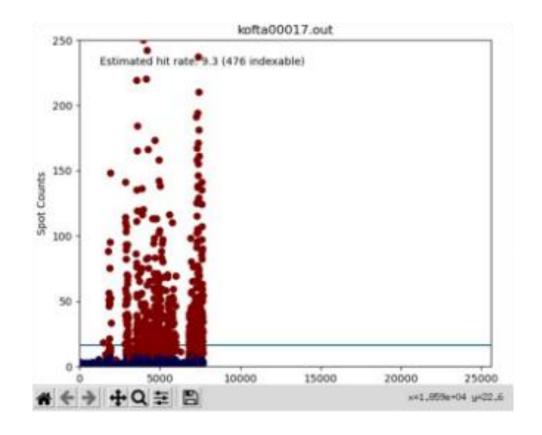
Automation for serial crystallography data collection and processing at Diamond Light Source





Dr James Beilsten-Edmands, 21/11/24



 Merging -7850 crystals in total scaled in space group P 43 21 2 Median cell: 79.226, 79.226, 38.161, 90.0, 90.0, 90.0 Merged mtz file: merged.mtz

Su	iggested Low High Overall
High resolution limit	1.60 4.34 1.60 1.32
Low resolution limit	56.02 56.06 1.63 56.02
Completeness	100.0 100.0 100.0 94.6
Multiplicity	94.1 169.9 39.1 61.5
I/sigma	20.9 69.7 1.4 12.6
Rmerge(I)	0.964 0.662 20.751 1.038
Rmerge(I+/-)	0.962 0.661 20.711 1.035
Rmeas(I)	0.968 0.664 21.022 1.045
Rmeas(I+/-)	0.971 0.665 21.231 1.048
Rpim(I)	0.094 0.052 3.333 0.112
Rpim(I+/-)	0.127 0.068 4.640 0.152
Rsplit(I)	0.077 0.046 1.253 0.195
CC half	0.996 0.995 0.316 0.959
Wilson B factor	9.883
Anomalous completeness	100.0 100.0 100.0 88.6
Anomalous multiplicity	50.9 103.2 20.6 33.8
Anomalous correlation	-0.017 -0.089 -0.031 -0.004
Anomalous slope	1.515
dF/F	0.090
dI/s(dI)	1.572
Total observations	1558766 158714 31224 1710375
Total unique	16566 934 799 27793

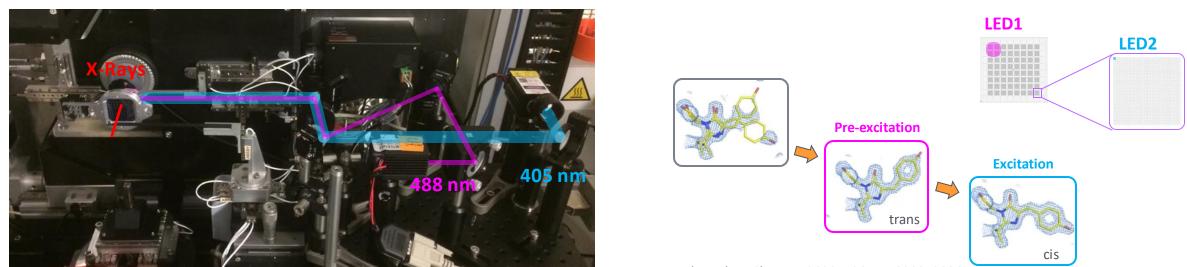


Serial crystallography

Serial still-shot crystallography is the measurement of 1 to N(<~10) diffraction patterns from given crystal, with no rotation. A complete, high-resolution dataset requires measurements of 1000s of crystals.

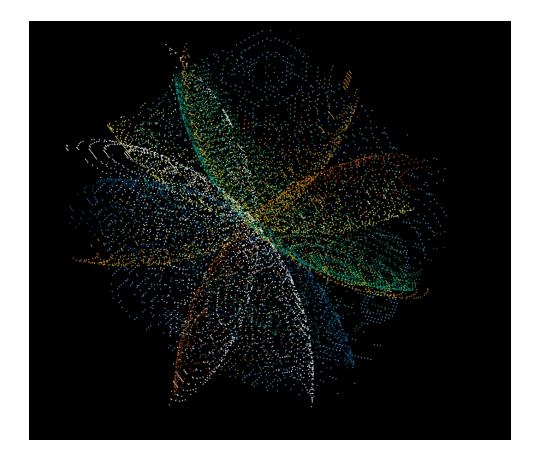
This technique is of particular importance for the study of dynamic biology at room temperature with minimal radiation damage, where processes on the timescale of sub-ms to seconds can be investigated at a synchrotron, or down to femtosecond timescales at an XFEL.

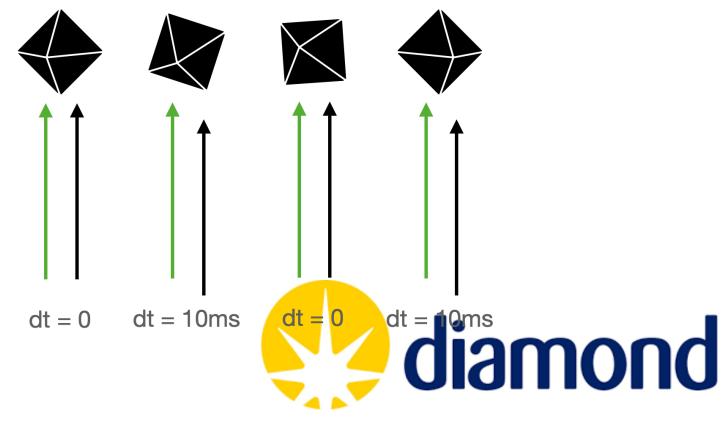
Typical experiments include the investigation of light-activated processes, chemical mixing/binding dynamics, studying of the effect of dose on metalloproteins.



Baxter et al., J. Phys. Chem. B, 2022, 126, 45, 9288-9296









Serial crystallography

Challenges from an automation perspective

Speed

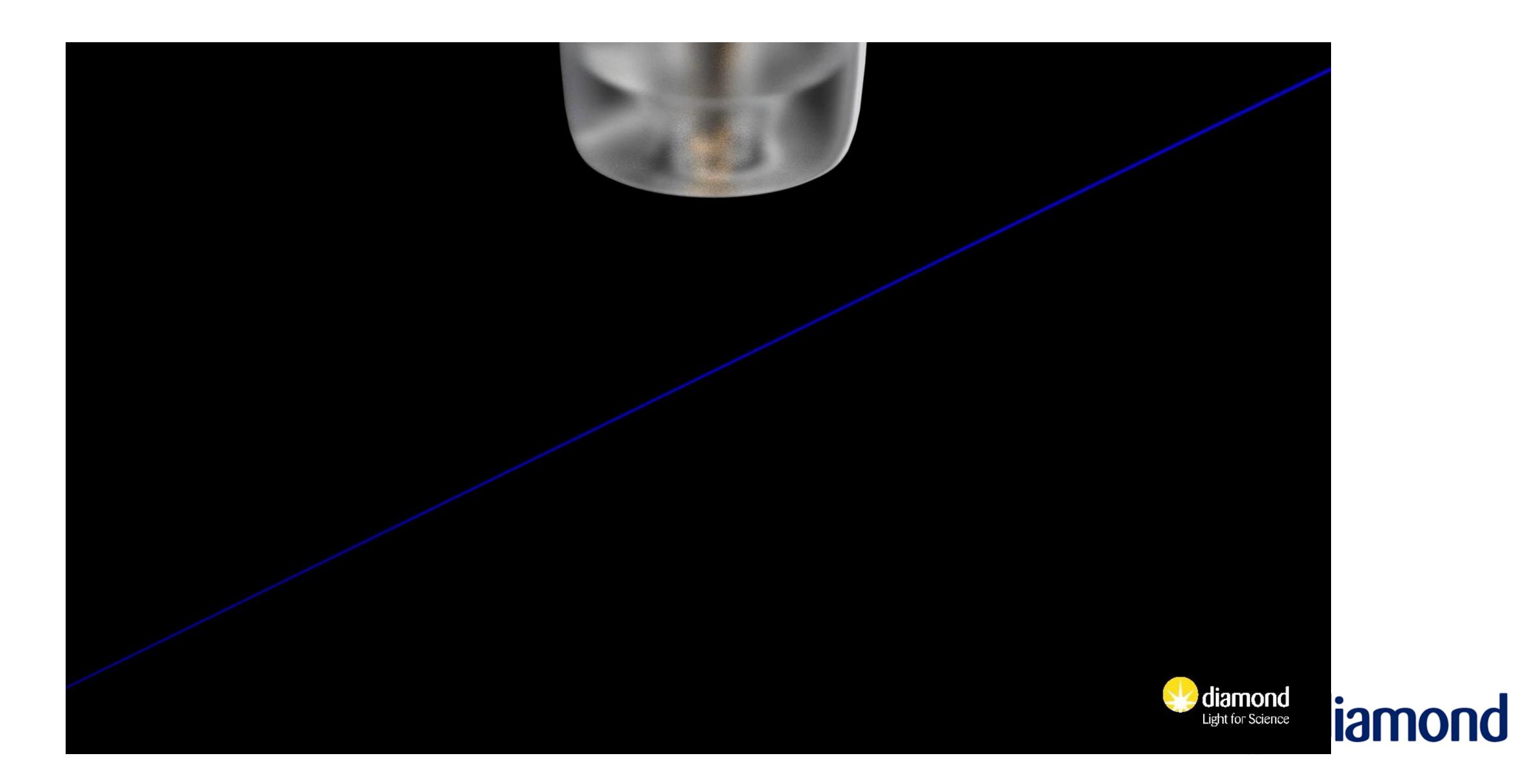
In theory you could collect new crystals at the detector collection frequency – 500Hz for Eiger, >kHz for newer detectors. Challenge is then the automation of the sample delivery process to achieve high crystal refresh rate. Following on from that, fast data processing and feedback are required to guide the experiment and make best use of available resources.

Complexity

Inherently more complex experiment type compared to rotation crystallography, different hardware options depending on biological question of interest, this extra metadata needs to be handled in processing and display of results.



Serial crystallography: extruder

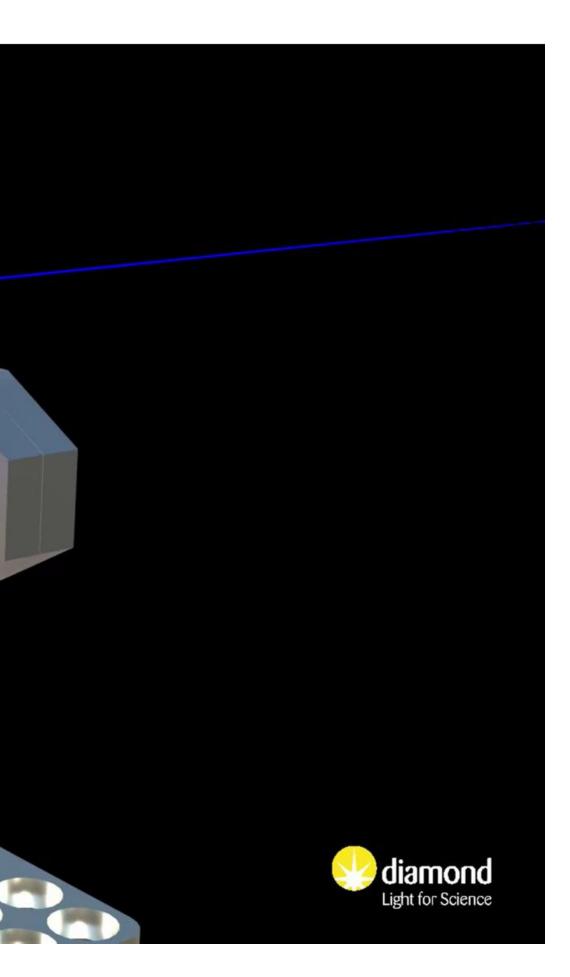




Serial crystallography: Fixed target

SSX: Fixed Target

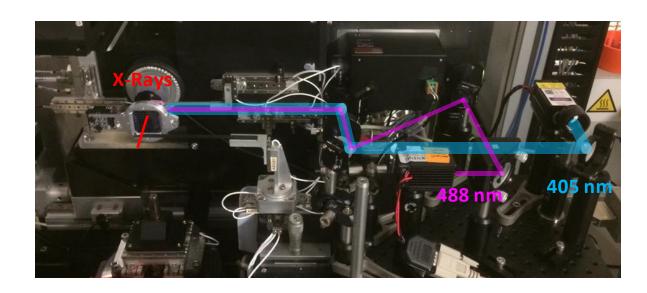
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1					100	Ne.	((0))		
a Charles	Contra Co	100	1000	icom)	(Q))	124	Sister in		

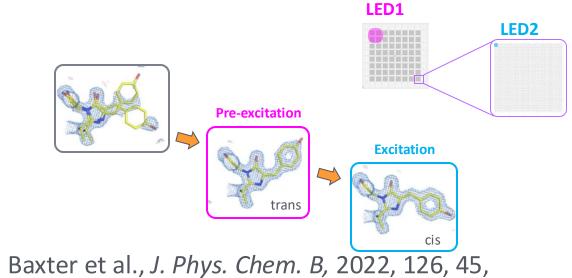
Horrell et al., *JoVE*, 2021, 168, e62200 Owen et al., *Acta Cryst.*, 2017, D73, 373- 378 Sherrell et al., *J. Synch. Rad.* 2015, 22, 1372-1378 

Chip 30 x 30 mm 8 x 8 city blocks 400 apertures on each city block Aperture size 7 – 20 µm 25600 positions ~ 8 min full data collection

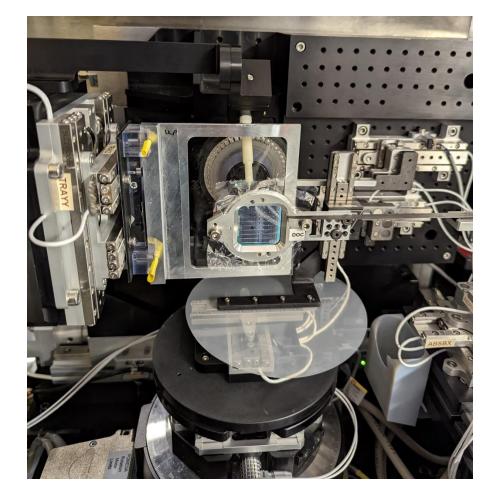


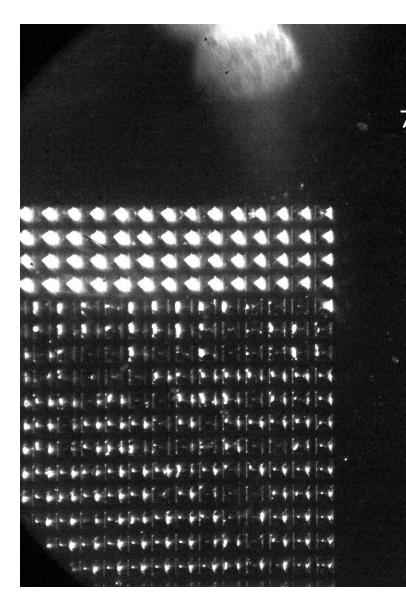
Serial crystallography: add-ons

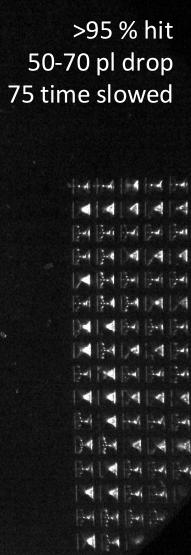










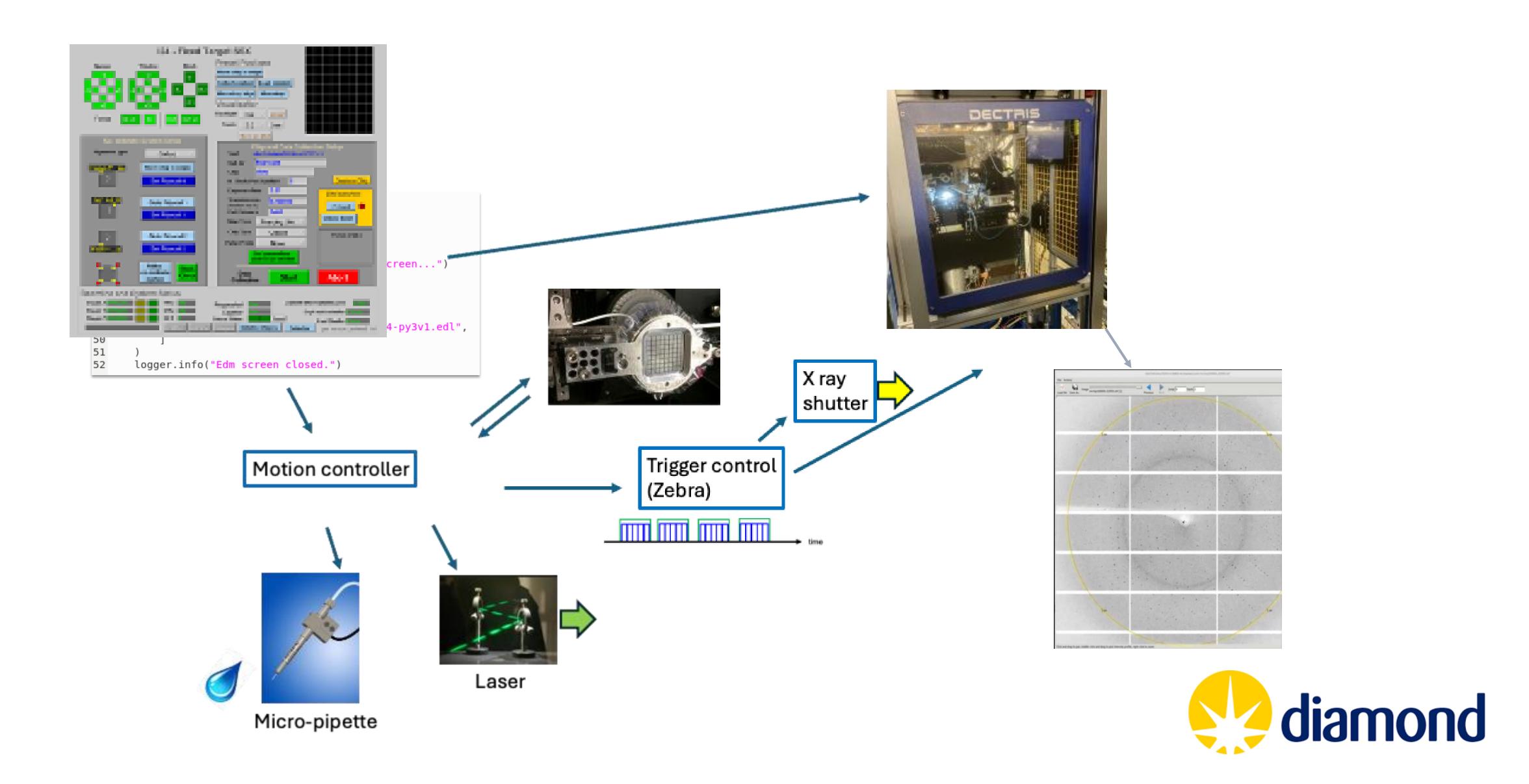


Laser excitation.

Rapid mixing with micro-drop ejector.

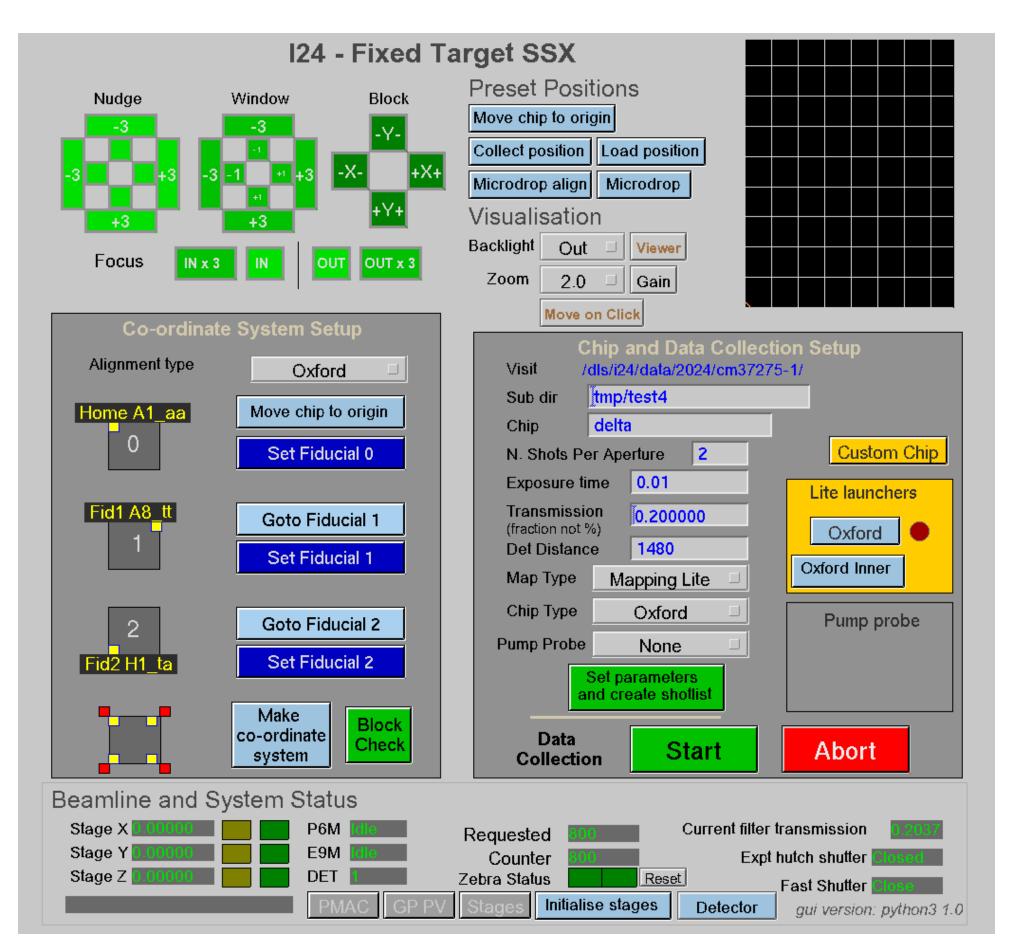


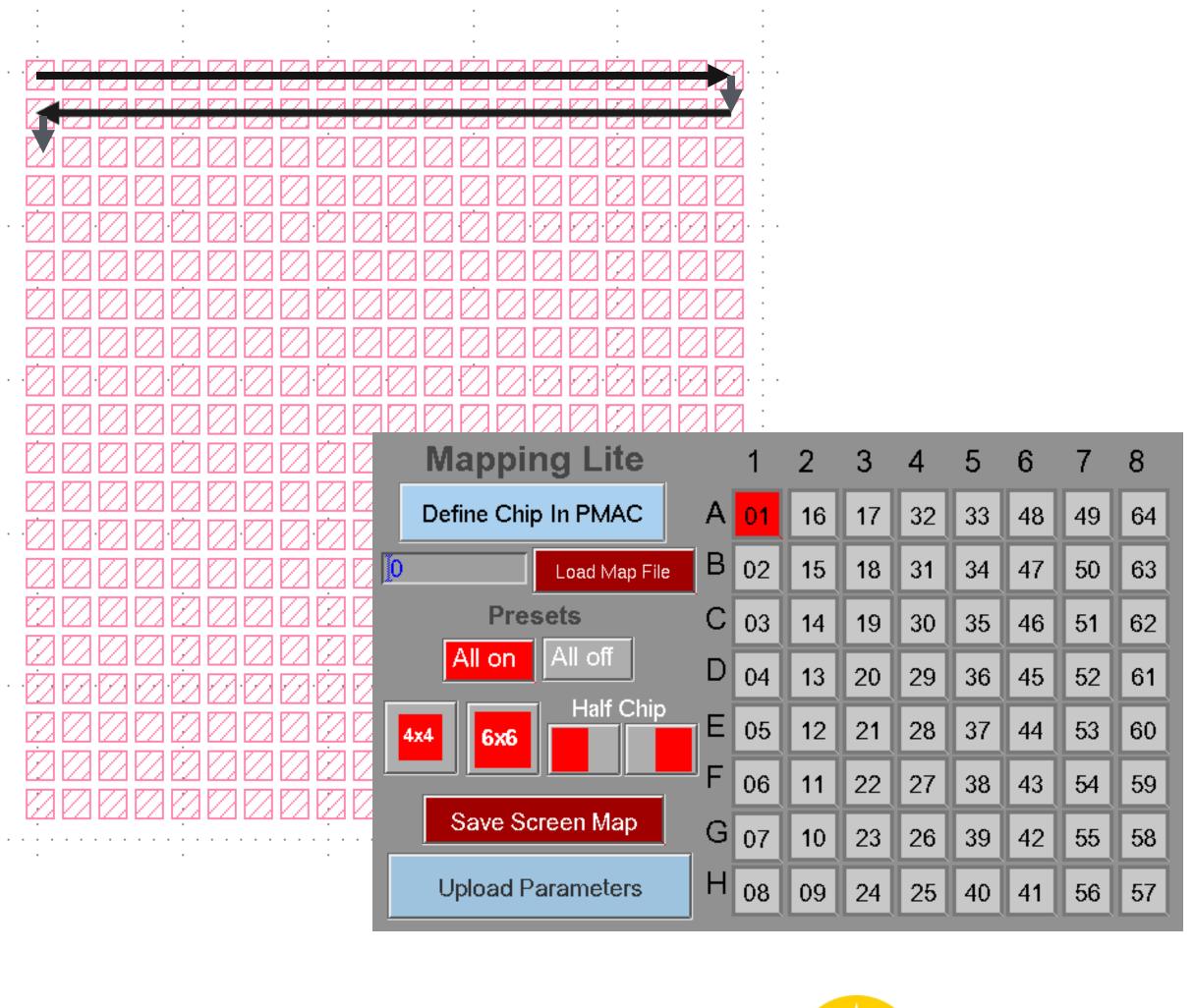
Automated data collection: I24 experiment control



Automated data collection: I24 experiment control

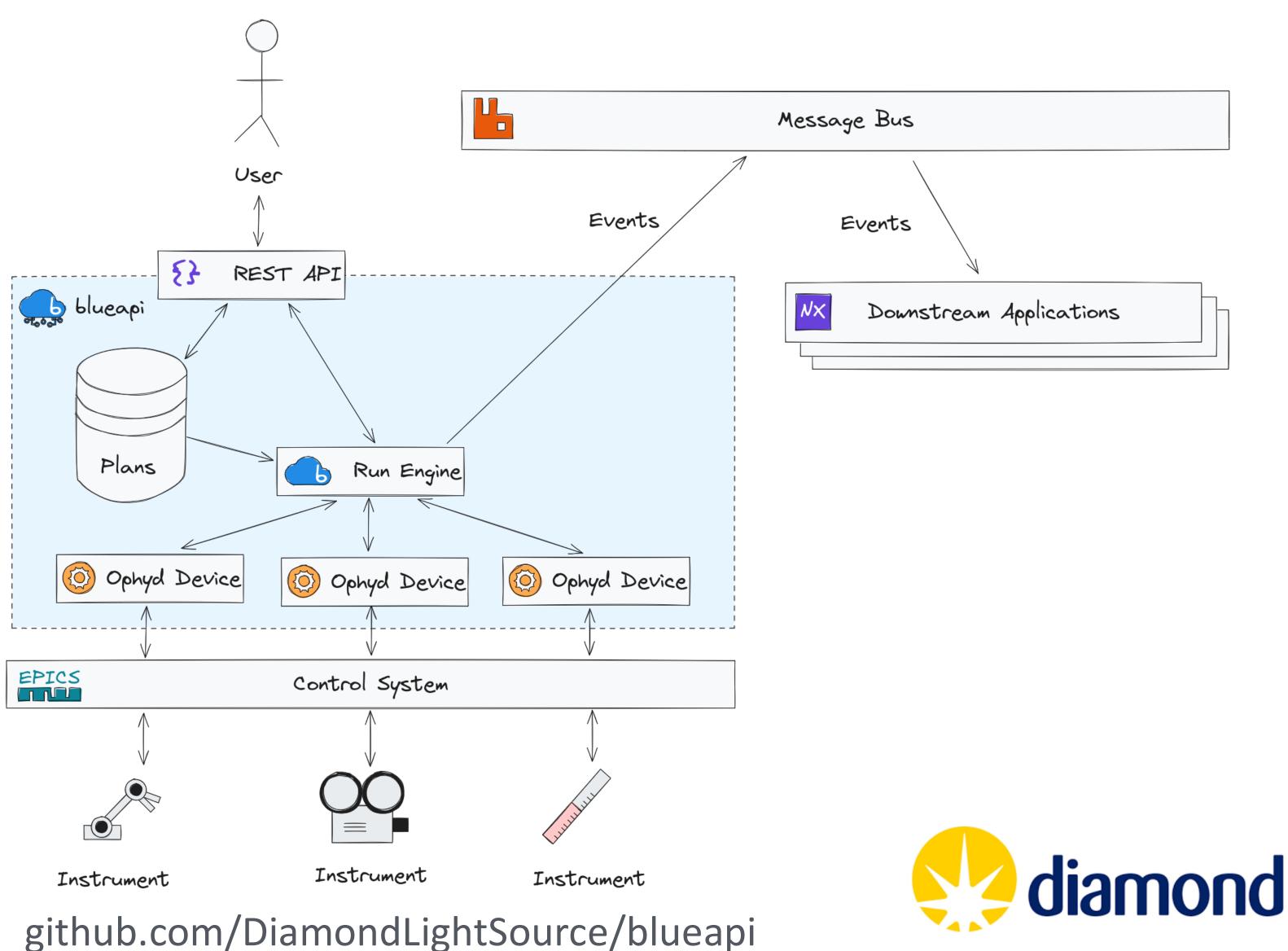
Fixed target GUI





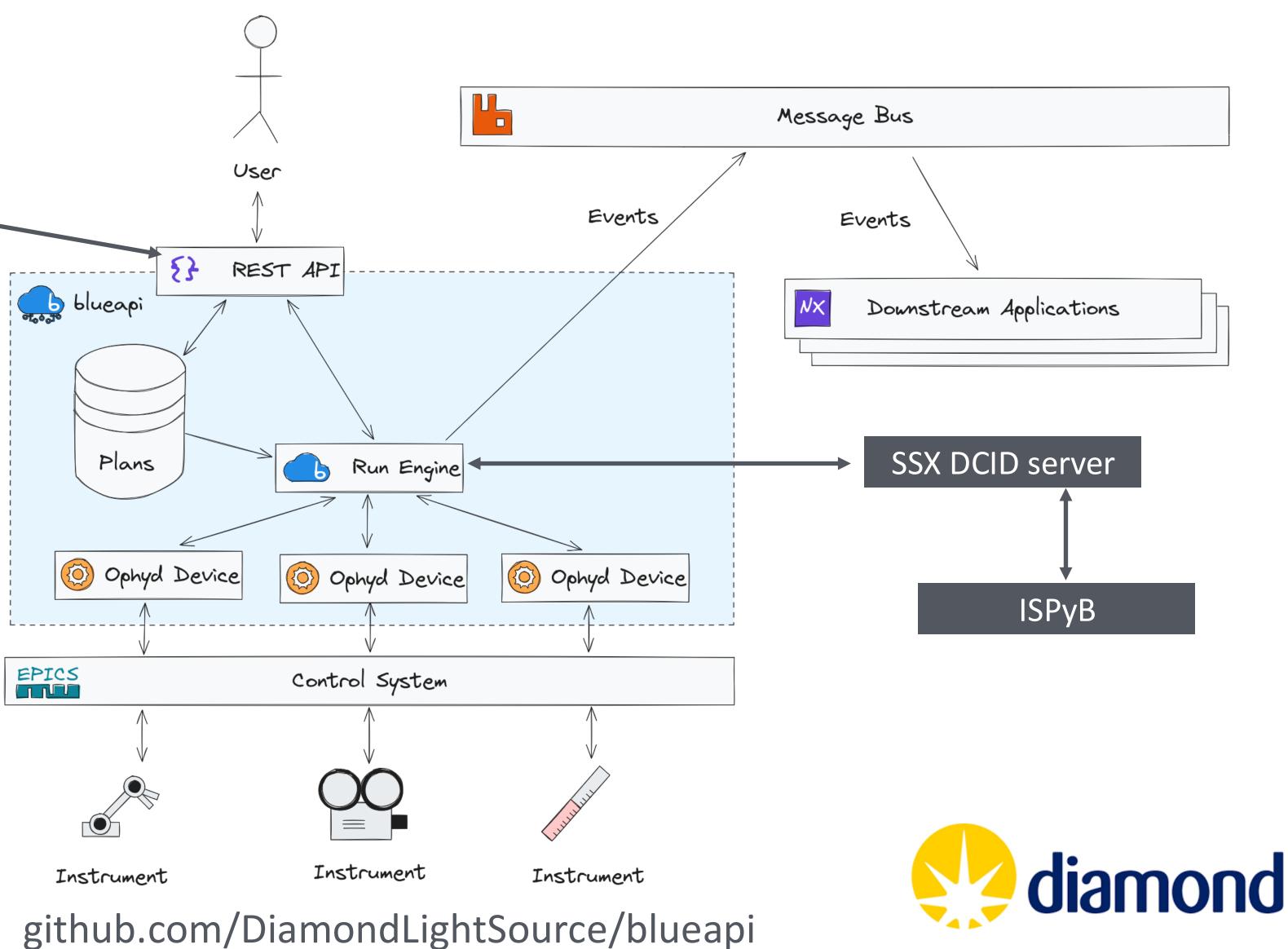


Automated data collection on I24: Bluesky



Automated data collection on I24: Bluesky

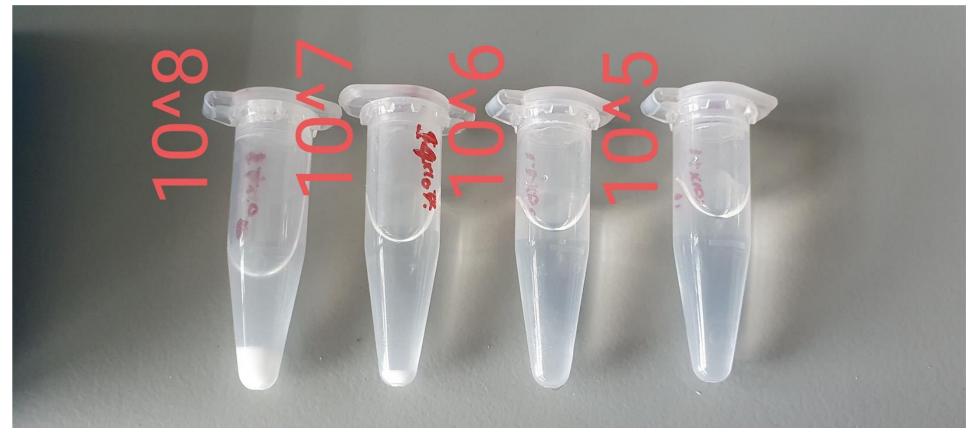
124 - 1	Extruder SSX		
Align Jet +Y x3 -X +X x3 -Y x5 IN OUT x5 Pump Probe Laser dwell 0 s Laser delay 0 s Laser delay 0 s Laser delay 0 s	Data Collection Setup Visit /dls/i24/data/2023/mx32727-11/ Sub-directory [a2a/syringe5/run5_10 Filename run5_10 Filename run5_10 Number of images 20000 Exposure time 0.01 Transmission (fraction not %) 0.200000 Det distance 320 Pump Probe False Start Abort Sample visualisation Viewer Gain Backlight OFF Zoom 2.0		Elucapi
Beamline and System S Current filter transmission Expt hutch shutter Fast Shutter Backlight Out Beamstop Data Collection Apertures	Detector in use P6M P6M E9M Observed Detector translation Demand 1480.0000 Nudge 25.0000 - + Detector gui version: python3 1.0		Plans
		i	



Automated data processing

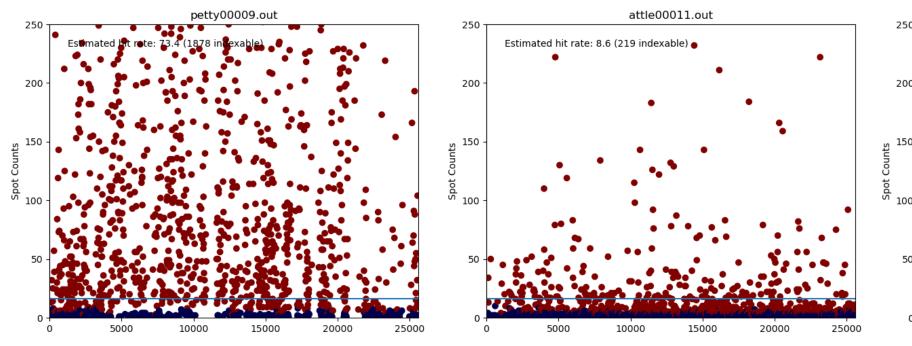
Fast feedback essential for understanding success of sample preparation and data quality.

Hit rate -> indexing success rate -> data quality statistics.



9%

Sam Horrell



75%



ewart00013.out Estimated hit rate: 1.3 (34 indexable

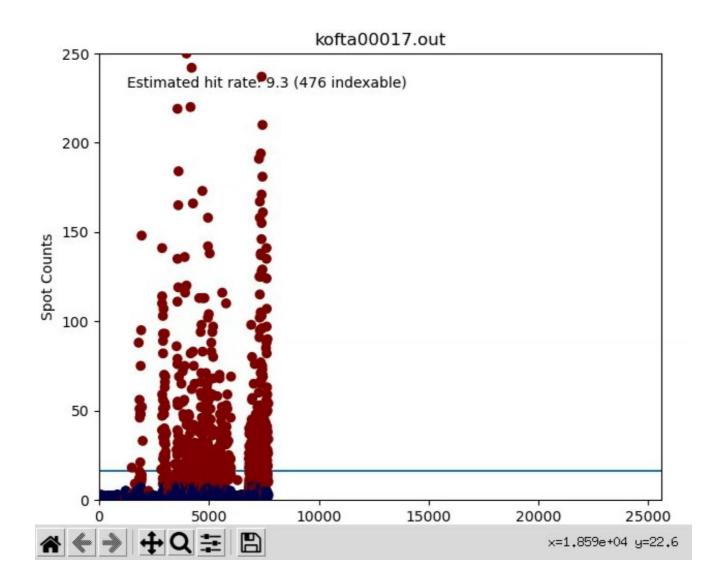






Automated data processing: fast feedback

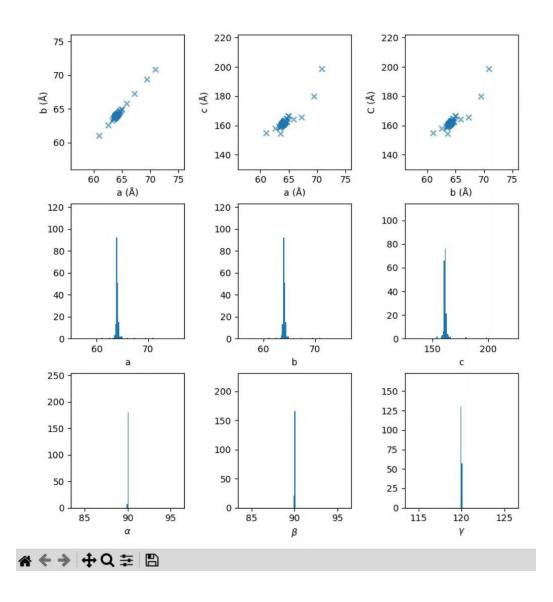
Live feedback from DIALS processing – dials.find_spots, dials.index



Per-image spot-finding, hit rate estimate



dials.github.io



Per-hit indexing – cell parameter distributions



Automated data processing: infrastructure

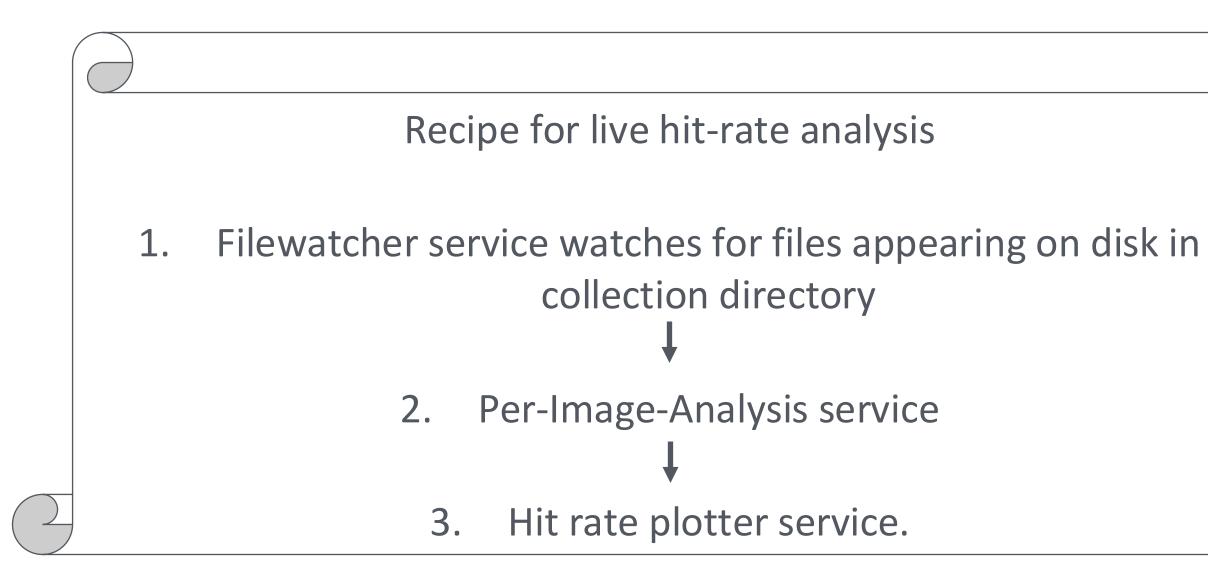
Analysis infrastructure at Diamond

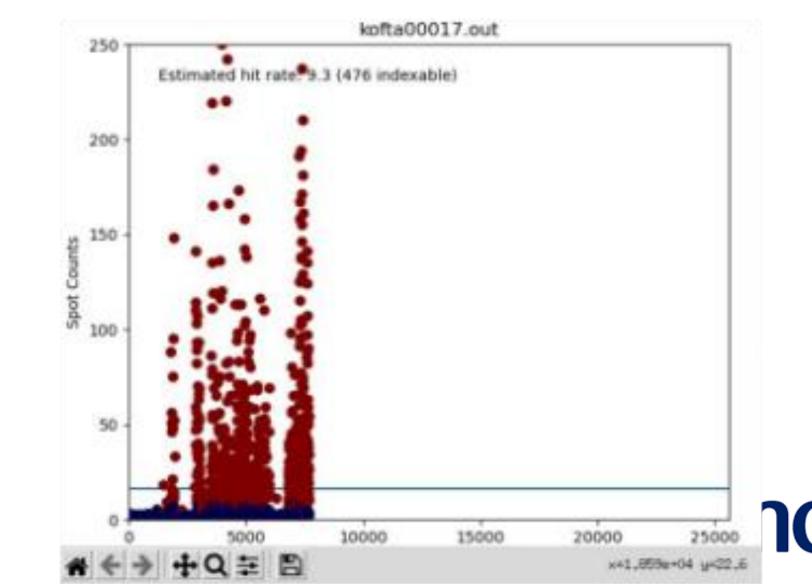
Data analysis managed by zocalo software. github.com/DiamondLightSource/python-zocalo

Zocalo defines a set of services (run on Kubernetes cluster at DLS) – these run continuously and wait for work – via messages managed by RabbitMQ server.

Zocalo also defines wrappers – run processing commands on demand (e.g. xia2 processing job).

Finally have a set of recipes which define workflows based on these services/wrappers as a flowchart/graph.











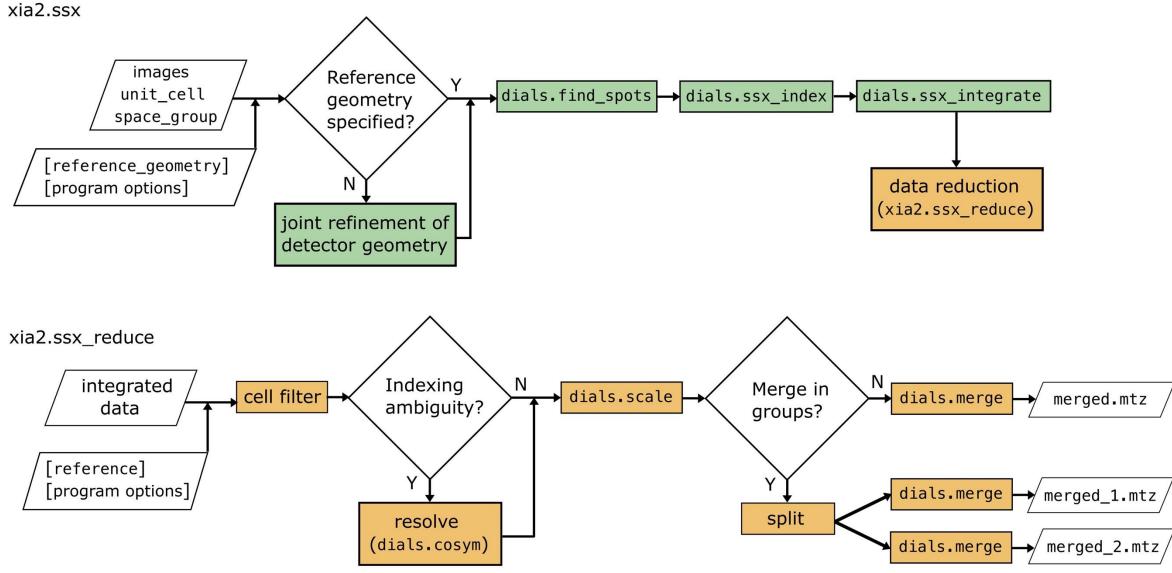
Automated data processing: full processing

Full post-processing with xia2.ssx triggered automatically after data collection.

Relies on a small configuration (.yaml) file detailing expected unit cell and space group.

xia2.ssx – processes images to merged MTZ running DIALS programs.

xia2.ssx_reduce – reduces integrated together from multiple collections.



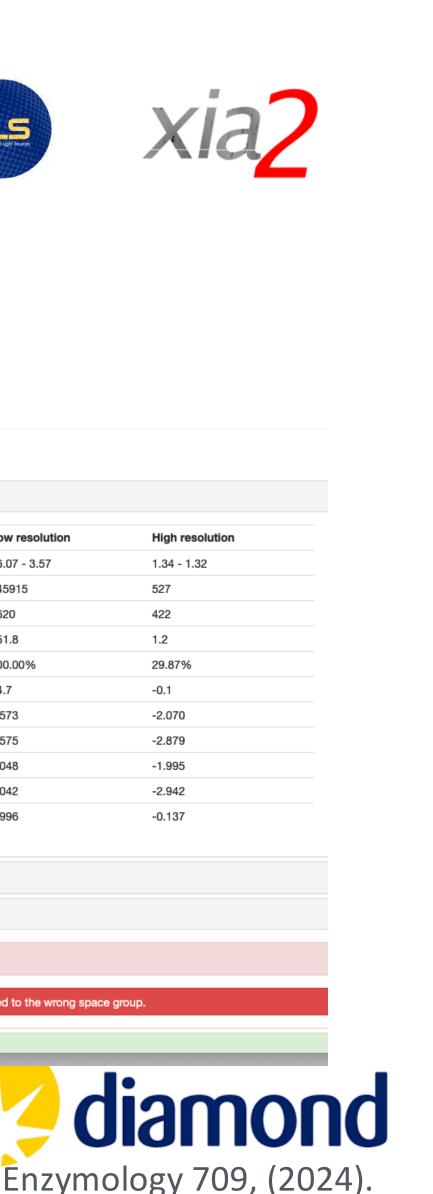


DIALS merge report

Merging statistics

Overall									
		Overall	Low resolution	High resolution					
	Resolution (Å)	56.02 - 1.32	56.07 - 3.57	1.34 - 1.32					
	Observations	1710375	245915	527					
	Unique reflections	27793	1620	422 1.2 29.87% -0.1 -2.070 -2.879 -1.995					
	Multiplicity	61.5	151.8						
	Completeness	94.62%	100.00%						
	Mean I/σ(I)	12.6	74.7						
	R _{merge}	1.038	0.573						
	R _{meas}	1.045	0.575						
	R _{pim}	0.112	0.048						
	R _{split}	0.195	0.042	-2.942					
	CC _½	0.959	0.996	-0.137					
	Resolution shells								
	Xtriage								
	× 1 serious warning								
	× The merging statistics indicate	igned to the wrong space group							
	& checks passed								
-									
			ih V	0000					

J. Beilsten-Edmands et al., Methods in Enzymology 709, (2024).

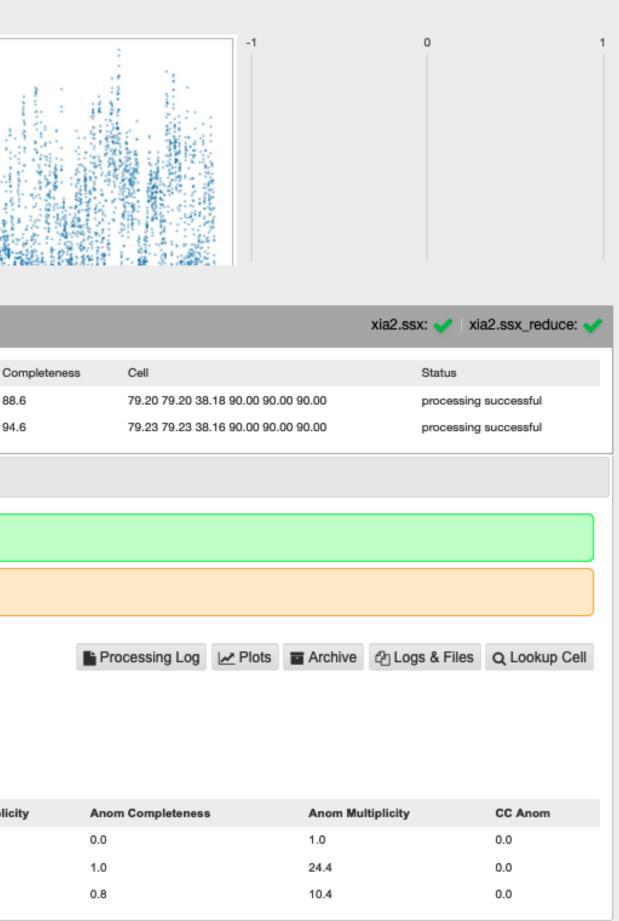


Automated data processing: full processing

Results displayed in SynchWeb on a per-chip basis. Multiple chips of the same condition merged together automatically. Access to log files, html report and merged MTZ file.

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outerShell	1	68			160		1.32 - 1.34	-1.065	-0.1	0.5		11.3			1.1
innerShell	6	6946			1619		3.57 - 56.06	0.566	46.1	1.0		100.0			41.4
overall	4	75439			25988		1.32 - 56.00	0.990	8.8	0.9		88.6			18.3

stream Processin



No processing re

Timescale ~15-30 mins





Automated serial data processing: future directions

- Acceleration of live processing through migration to GPU devices.
- Extension of live processing to cover the full processing, enabling complete metrics on fast timescale.
- Completion of metadata models to cover all serial experiment types (dose/time series).
- Web-based GUI for live display of results
- Migration from reliance on file systems to stream-based workflows.



Acknowledgements

Data acquisition team, in particular Noemi Frisina, David Perl, Dominic Oram

124 Beamline team – Robin Owen, Danny Axford, Sofia Jaho, Do-Heon Gu + many others over last 10+ years

Data Analysis/DIALS team, in particular Nick Devenish, James Parkhurst, Graeme Winter

github.com/DiamondLightSource/blueapi

nsls-ii.github.io/bluesky/

dials.github.io. xia2.github.io

github.com/DiamondLightSource/python-zocalo

Slide material: Danny Axford, Robin Owen, Sam Horrell

Grant funding from Wellcome trust, CCP4/UKRI, EU grant funding.



