Oct. 21, 2025, SLAC National Accelerator Laboratory Productive, Performant Software for Large Scale Scientific Data Analysis

The Grand Bargain of Structural Biology at the kHz Frontier

Nicholas Sauter & David Mittan-Moreau

Lawrence Berkeley National Laboratory

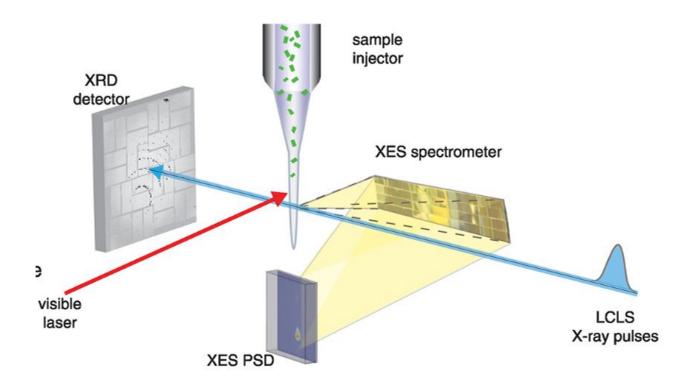


What is serial crystallography?

Serial crystallography

Serial vs. traditional crystallography

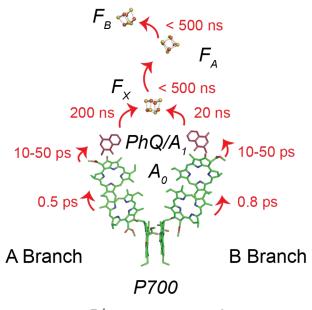
- Room temperature
- Free from radiation damage
- Pump probe



A 15-year track record of XFEL serial crystallography

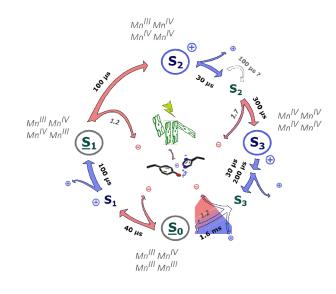
Light activation

Substrate mixing / gas activation



Photosystem I: Captures sunlight energy

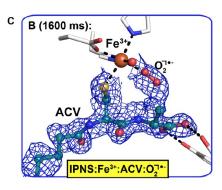
NADP + + 2e⁻ + H⁺ + 2
$$\gamma$$
 \rightarrow NADPH



Photosystem II: Generates atmospheric oxygen

$$2H_2O + 4\gamma \rightarrow O_2 + 4e^- +$$

4H+



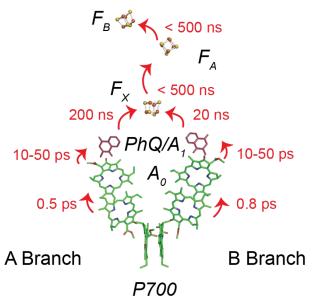
Isopenicillin N synthase: Production of $oldsymbol{eta}$ -lactam antibiotics

$$ACV + O_2 \rightarrow IPN + 2H_2O$$

A 15-year track record of XFEL serial crystallography

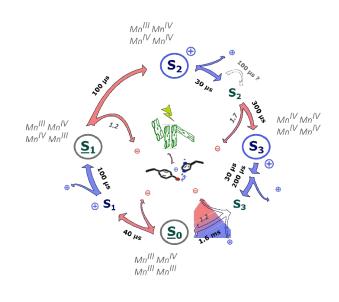
Light activation

Substrate mixing / gas activation



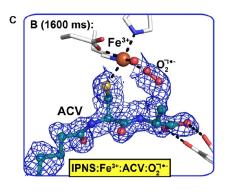
Photosystem I: Captures sunlight energy

NADP + + 2e⁻ + H⁺ + 2 $\gamma \rightarrow$ NADPH



Photosystem II: Generates atmospheric oxygen

 $2H_2O + 4\gamma \rightarrow O_2 + 4e^- + 4H^+$



Isopenicillin N synthase:

Production of β -lactam antibiotics

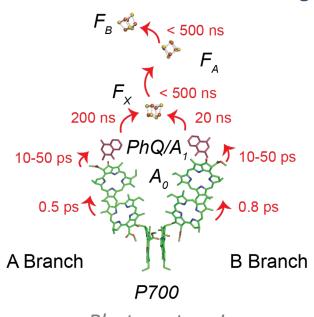
ACV + O₂ \rightarrow IPN + 2H₂O

S

A 15-year track record of XFEL serial crystallography

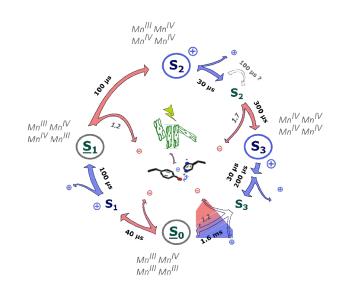
Light activation

Substrate mixing / gas activation



Photosystem I: Captures sunlight energy

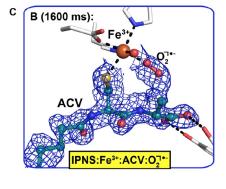
NADP + + 2e⁻ + H⁺ + $2\gamma \rightarrow$ NADPH



Photosystem II: Generates atmospheric oxygen

$$2H_2O + 4\gamma \rightarrow O_2 + 4e^- +$$

4H+



Isopenicillin N synthase: Production of $oldsymbol{eta}$ -lactam antibiotics

$$ACV + O_2 \rightarrow IPN + 2H_2O$$

fs / ps

ns

μs

ms

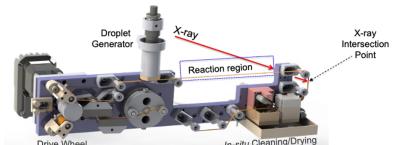
S

Drop-on-drop:

Protein crystals: 30 Hz, 160 µm drop, 2nL

Substrate: 1.6 kHz, 50µm drop, 60pL

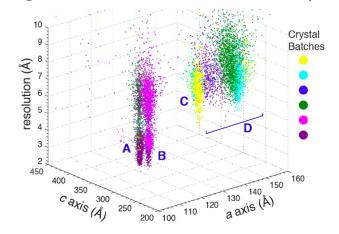
For $5\mu m$ crystals the diffusion time is ~5ms



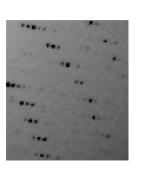
Sample delivery–conveyor belt

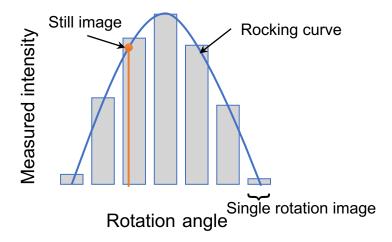
Why is speed a consideration for serial crystallography?

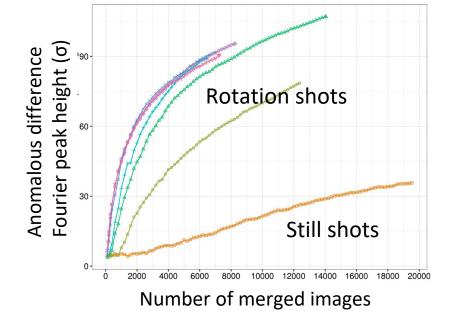
Partial diffraction patterns: merge data from thousands of crystals



Partial reflections & disperse beam: apply complex computational models to deduce structure factors







Continual assessment of whole data quality to decide stopping point, and compare alternate processing pipelines

Why is an MX XFEL Experiment so Stressful?

Jan Kern: "For a 5-shift Photosystem experiment (60 hrs @ 20 Hz) we brought 15 mL sample. Making 1 mL takes 1 week for 1.5 people, so 22 weeks FTE for 5 shifts."

Sample delivery:

- Is the beam hitting the sample?
- Can we further optimize our parameterization

Xray emission spectroscopy:

 Is our sample in the correct oxidation state?

Diffraction data processing:

- Diffraction to high resolution?
- Unit cells isomorphous?
- When can we stop collecting data?



Beamline operations:

Are there upstream issues?

PI Discussion:

• What sample or time point should we collect next?

Record high-level metadata in Google sheets

Structure solution:

 Do our results support our hypothesis?

Considering the enormous cost of the experiment in terms of sample and beamline operation, the most important mitigation we can offer is immediate data reduction with a 10-minute turnaround time, evaluating the final science metrics in order to know if the experiment is on track and when to move to the next sample.

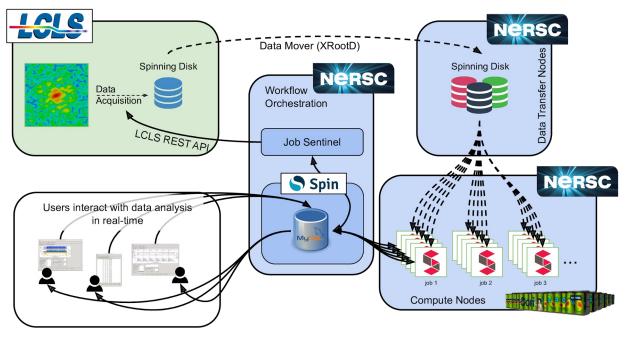
Collaboration with LCLS, ESNet & NERSC on the assessment pipeline

Long history

- 2014 Edison
- 2017 Cori
- 2021 Perlmutter
- 2027 Doudna

Continual evolution

- Beam
- Detector
- Compute cluster
- Algorithms



Current scale

- Jungfrau 16 Mpx x 2-byte depth
- Clocked at 120 Hz for 12 hrs
- 150 TB data

We have maintained our 10-minute turnaround for the past 8 years

What we have (and want to keep!):

- Dual implementation for FFB @ S3DF + complete workup at NERSC
- ESNet at 100 Gb/s
- Petabyte disk allocation
- 32 CPU nodes in the realtime queue on demand for 12 hours
- Immediate spinup of MySQL db

Things we would like, please

What we don't have now for serial crystallography at 2 kHz

- Clearer understanding of the goals, and which experiments benefit
- More accurate algorithms
- Much faster feedback to the experiment
- Failover to backup facility
- Data processing portability
- High level standardization
- More things automated

What could we accomplish at 2 kHz?

Current experience at 30 Hz

MFX-LU5017

- 48 hours
- 48% duty cycle
- 594,230 indexed images
- 54 data sets
- 1 mg of protein per data set
- 12 types of enzymes

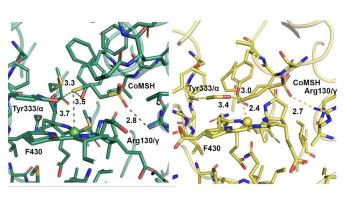
Chemical crystallography Mail-in pilot program

- 24 hours
- 44 samples screened
- 14 different user groups
- 11 structures solved

LCLS Mail-in small-molecule serial femtosecond crystallography

Submission Deadline:

1st February 2026

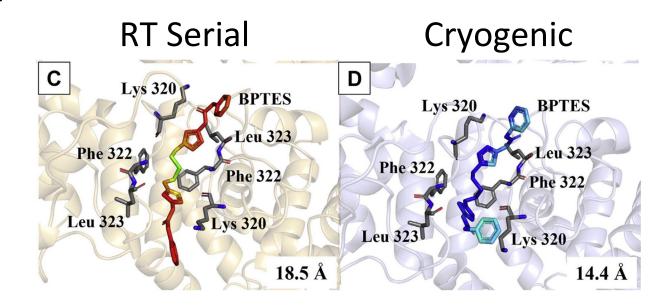


Now scale this to 2 kHz!

Structure Guided Drug Design

Serial crystallography is performed at room temperature without perturbation from cryoprotectants.

 Ligand binding pose is more physiologically relevant.

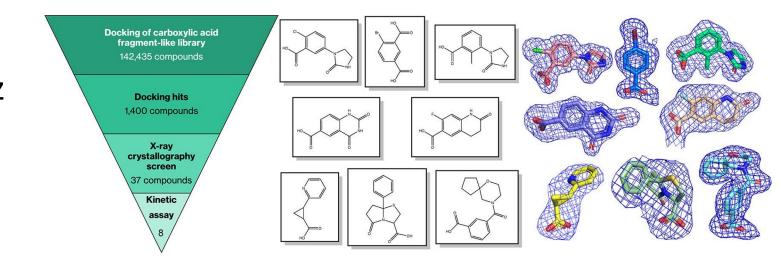


Milano, S, et al. (2022). New insights into the molecular mechanisms of glutaminase C inhibitors in cancer cells using serial room temperature crystallography. J. Biol. Chem. DOI: 10.1016/j.jbc.2021.101535

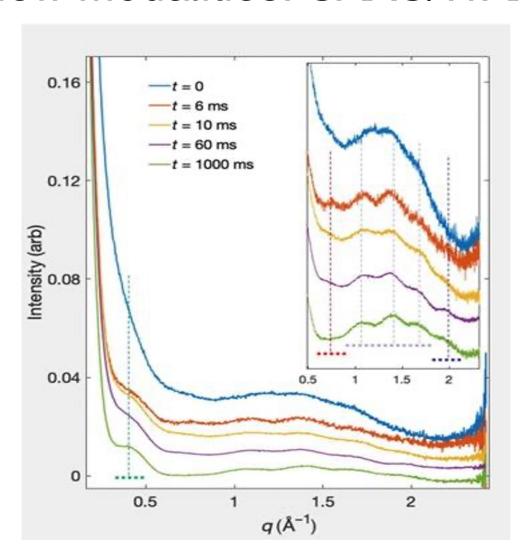
Structure Guided Drug Design

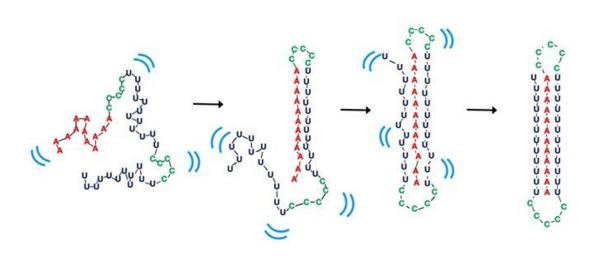
Fragment screening starts computationally, then high throughput binding assays.

Serial crystallography at 2 kHz would be a more informative high throughput assay.



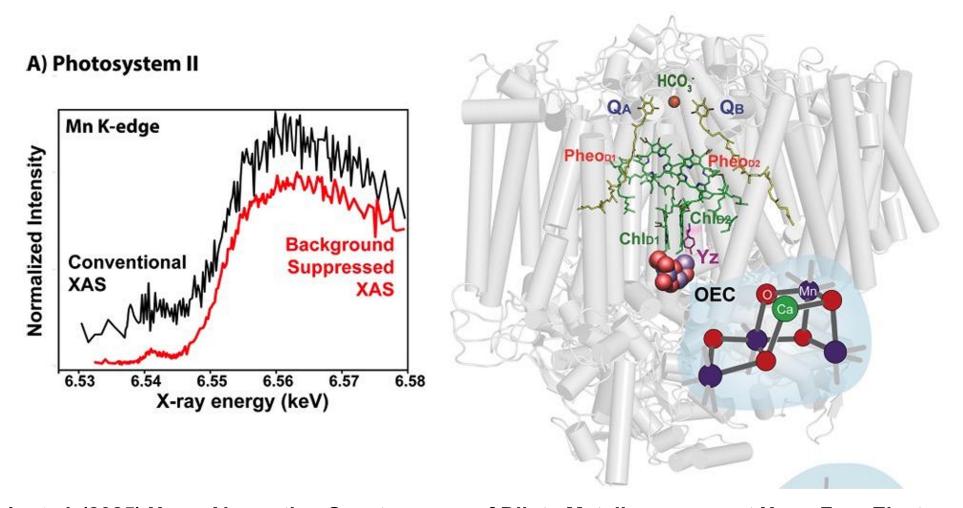
New Modalities: SAXS/WAXS





Zielinski, K. et al. (2023) RNA structures and dynamics with Å resolution revealed by x-ray free-electron lasers *Sci. Adv.* 9, DOI: 10.1126/sciadv.adj3509

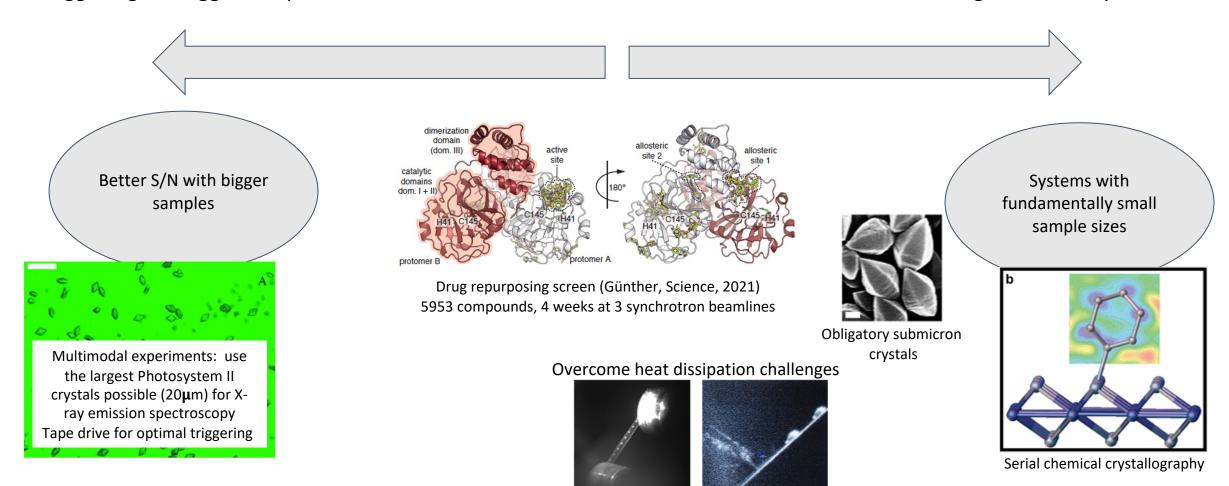
New Modalities: X-ray absorption spectroscopy



Bogacz, I. et al. (2025) X-ray Absorption Spectroscopy of Dilute Metalloenzymes at X-ray Free-Electron Lasers in a Shot-by-Shot Mode. J. Phys. Chem. Lett. DOI: 10.1021/acs.jpclett.5c00399

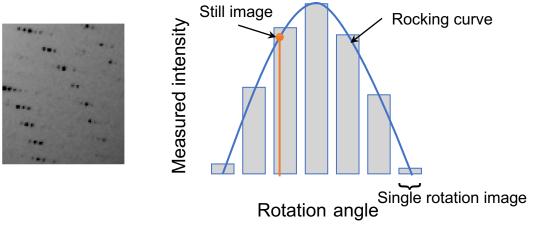
What experiments will benefit from kHz?

120 Hz, 2 mJ X-ray pulse LCLS Copper LINAC Bigger signal, bigger sample 2 kHz, 0.2 mJ X-ray pulse LCLS-II-HE Small signal, more repetitions



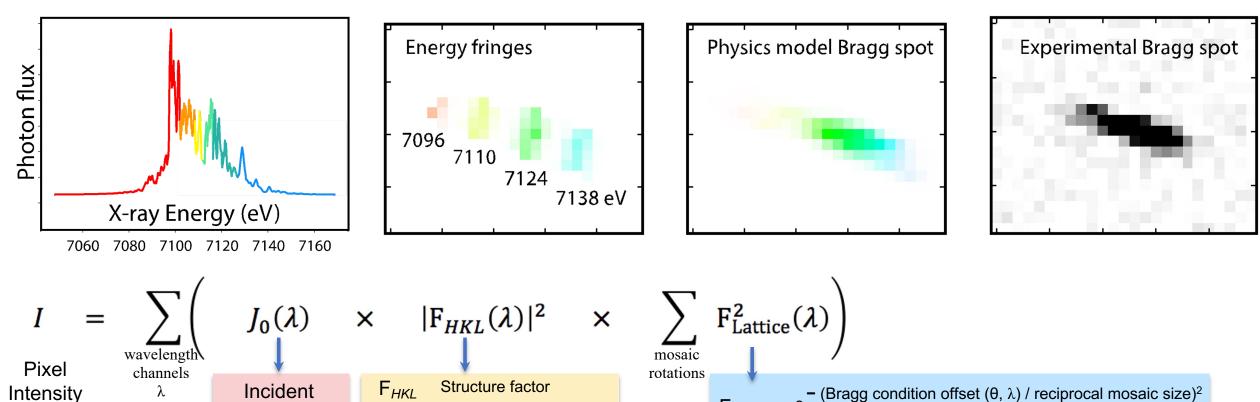
Improving accuracy

Partial reflections & disperse beam: apply complex computational models to deduce structure factors



nanoBragg / diffBragg

Use diffraction physics to model one pixel at a time, one photon at a time



Promises

More accurate results for tiny biological differences

Spectrum

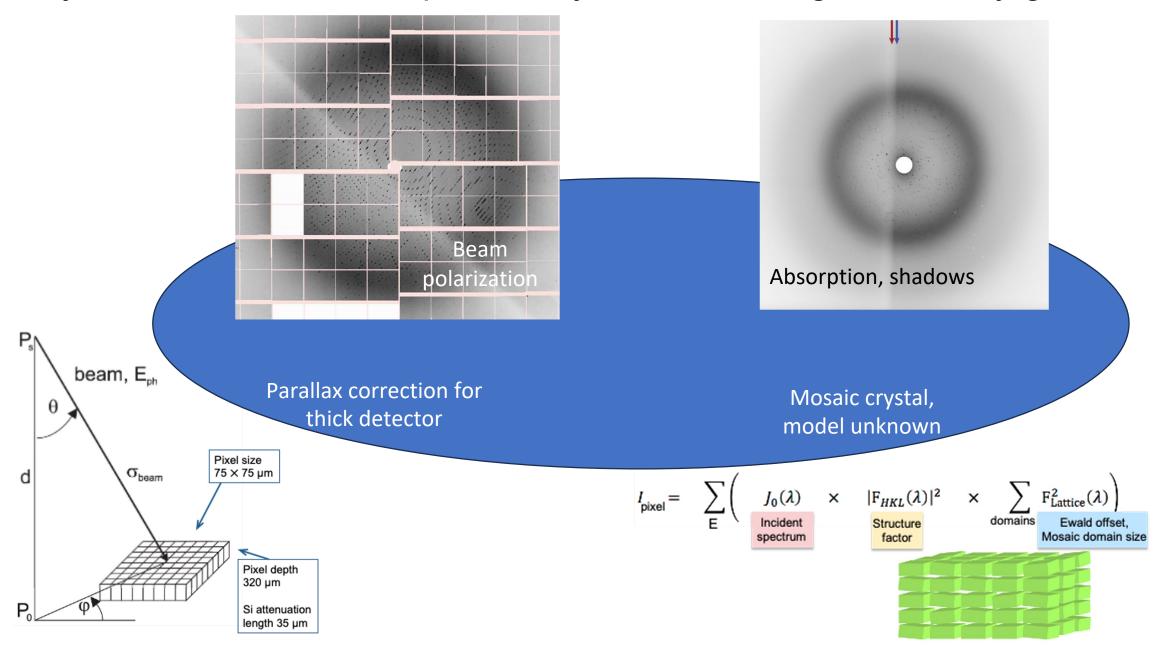
- Works great for simulated experiment
- Extends to new science, like metalloenzyme redox state

Challenges

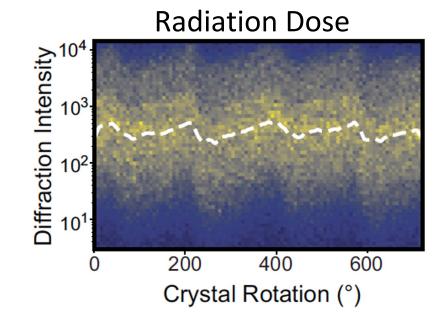
 $F_{Lattice}$

- Older code written in C++/CUDA
- Might require larger resources: 64 x GPU nodes
- Real experiments degraded by numerous systematic effects

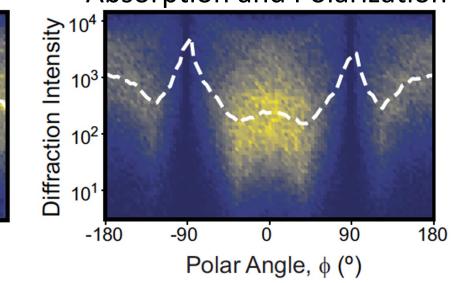
Systematic effects that potentially defeat our high-accuracy goals



Careless uses variational inference to scale Bragg spots







Promises

- NN learns how to scale data together
- Correctly model systematic effects with no physics

- Not scalable in memory, only uses one GPU node
- Relies on stochastic training to loop through >10⁴ images
- No integration trials especially at 2 kHz scale

Is the experimental feedback fast enough?

Jan Kern:

For a 5-shift Photosystem experiment (60 hrs @ 20 Hz) we brought 15 mL sample. Making 1 mL takes 1 week for 1.5 people, so 22 weeks FTE for 5 shifts.

Aaron Brewster:

Oh, my word, that's 42 years of sample prep for 5 shifts at 2 kHz.

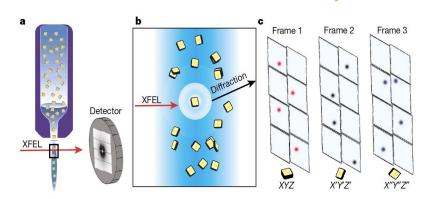
Nick Sauter:

A 10 minute data collection will burn through 40 days of sample prep. In the 2kHz regime we are justified in asking for feedback with 1 second turnaround.

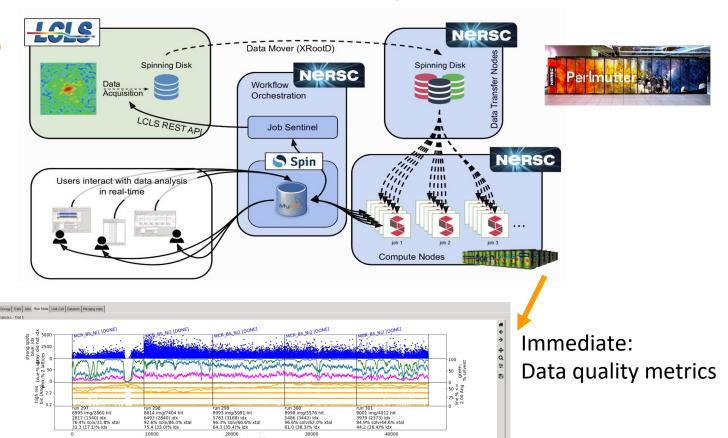
Experimental cycle



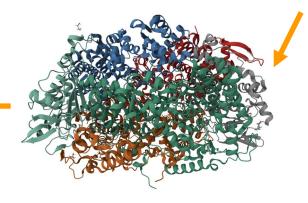
Data acquisition 5 minute run



Data transfer does not occur till the DAQ writes to hard disk



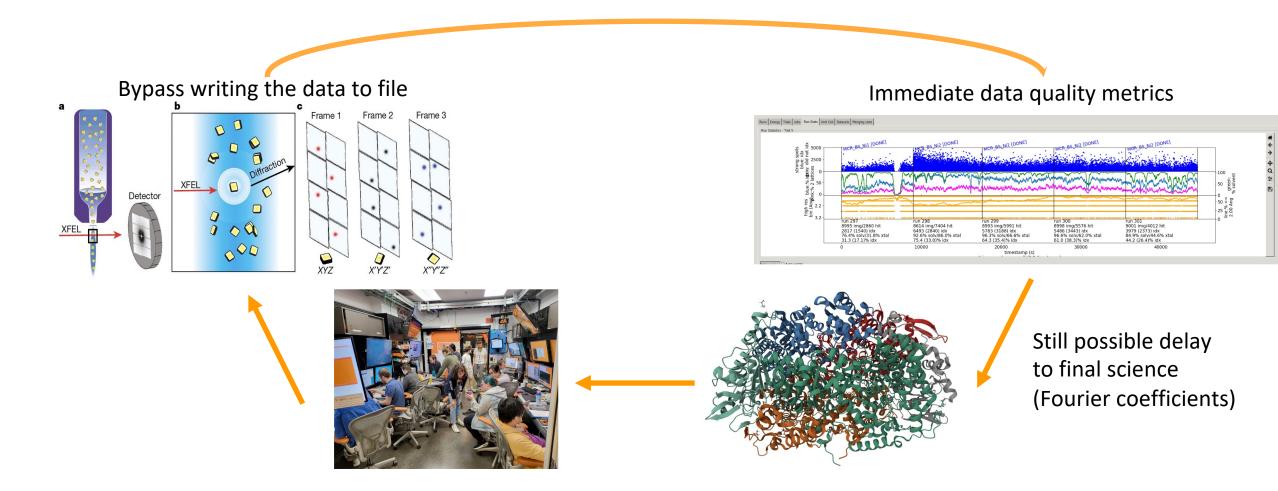




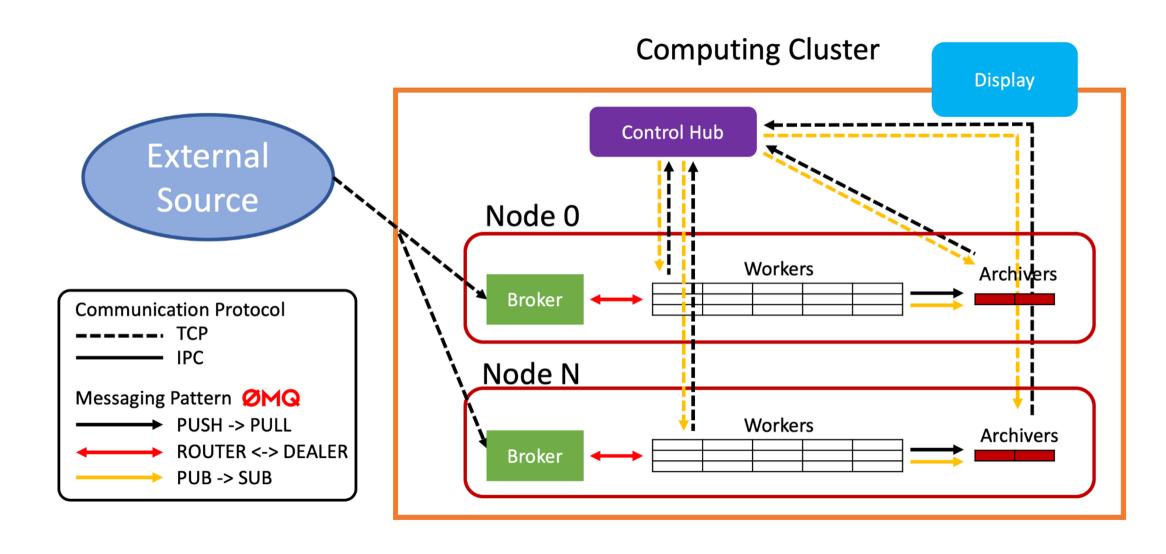
After 5 minutes: Final science (Fourier coefficients)

Experimental cycle

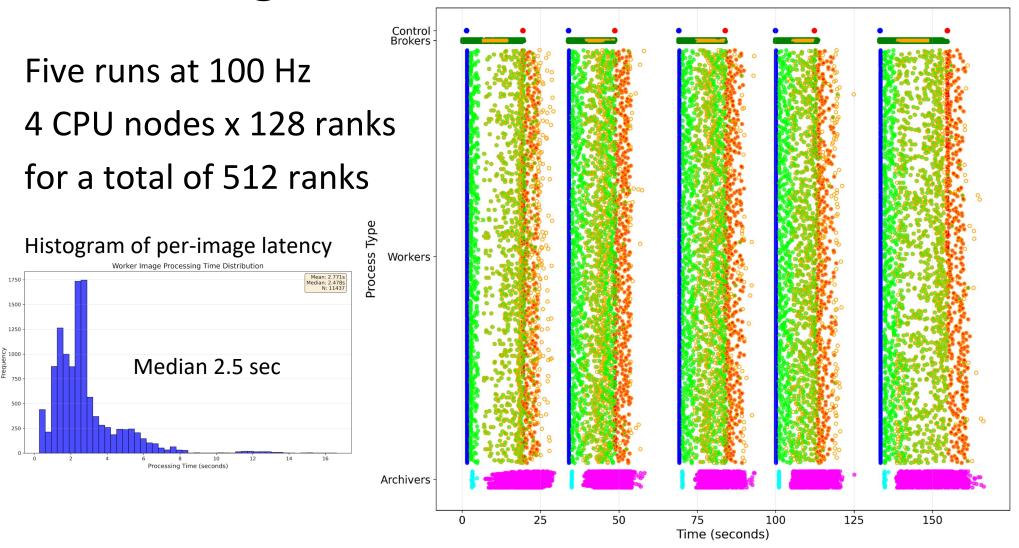
Goal: 1 second



Streaming with dials.stills_process

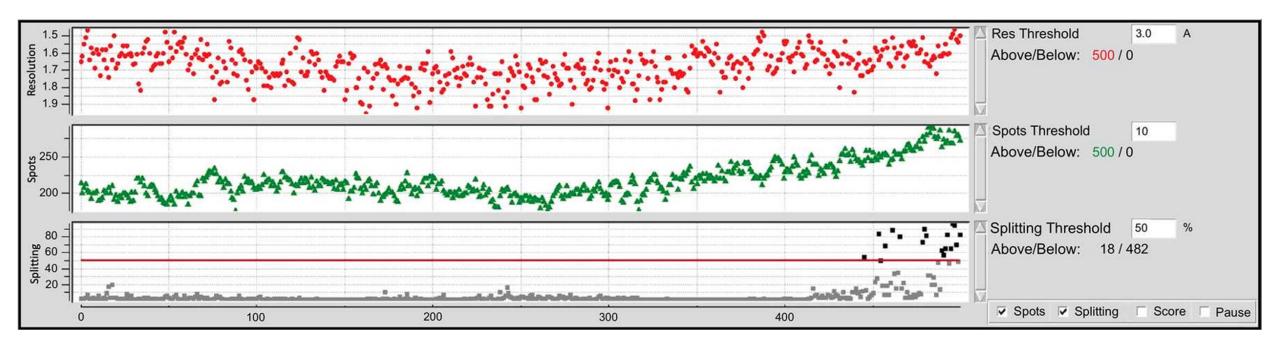


Processing at Scale



- Archiver: Start
- Archiver: Archived Image
- Worker: Start
 Worker: End
- Worker: Received Image
- Worker: Processed Image
- Broker: Sent
- Broker: Queued
- Control: Start
- Control: End

Resonet GPU spot analysis

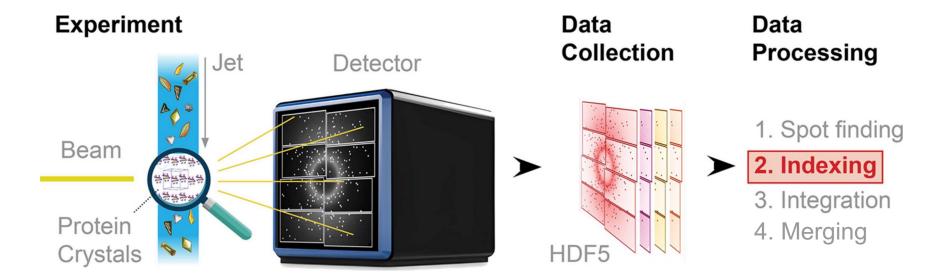


Promises

- GPU image quality metrics with NN
- Determine crystal resolution per pattern
- Identify overlapping lattices
- Suitable for 1-second decision making
- For rotation: helps check rad damage, crystal miscentering; asymmetric diffraction
- Network training is easy with simulated data

- No integration trials especially at kHz scale
- Can we convince user it is sufficient for event rejection?
- Might have to retrain network for specific beamlines

Toro Indexer

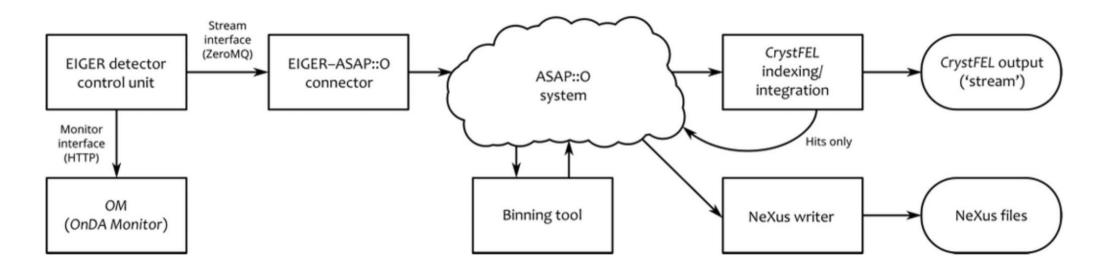


Promises

- Can index images at 1 kHz per A100-GPU node
- Result in fixed time, no sagas
- Suitable for 1-second decision making
- Sample-steering
- Feeds back a final-science metric, not just # spots
- Could be edge computing, could be streaming
- PyTorch so no direct involvement with C++/CUDA
- Robust methods instead of heuristic outlier rejection

- Only works if you have GPU spotfinder
- Works in parallel only if you pack 1,000 images
- No integration trials especially at kHz scale
- Can we convince user it is sufficient for event rejection?
- Tunable-might be slower for large unit cells
- Not a general indexer. Only works if you know the cell

ASAP::O & CrystFEL



Promises

- Entire CrystFEL pipeline optimized, not just one step
- Process 16 Mpx EIGER2 X at 133 Hz on one CPU node
- Latent time for one image is about 500 ms
- Elimination of the I/O bottleneck
- Dynamic scaling of computing resources.

- Sufficient computing resources must be available during experimentation. [Would require 15 CPU nodes at 2kHz]
- Need a robust data streaming platform (ASAP::O).
- Performant crystallographic software.
- Adequate and properly configured networking infrastructure.

Failover to backup facility

We want: 55MB compressed image $\times 2kHz = 820$ Gb/s $(66\mu s/evt)$ **NERSC -> NERSC** ESnet offers: 800 Gb/s (according to Google) 35 ms ALS **ALS -> NERSC ESnet NERSC** 75 ms S3DF -> NERSC 45 ms **LCLS** Points of Presence (POPs) S3DF -> OLCF SLAC S3DF SITES (Locations generalized for clarity) 1 s of ENERGY | Science

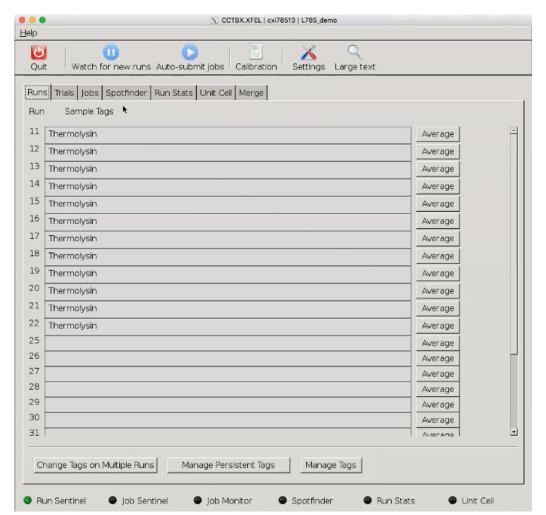
BERKELEY LAB

Is data processing portable?



Pros

Google sheet identifies all our runs: protein type, batch number, triggering conditions MySQL to organizes data reduction & science metrics; with auto-detection of new runs



Cons

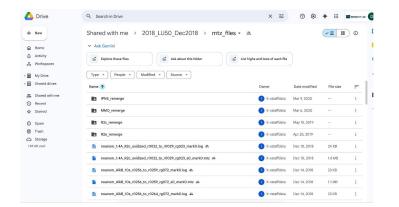
Information transferred to the GUI by hand!
Switching to NERSC required doing this all over again
Currently <1000 runs each beamtime. May not scale to 2kHz
High level metadata not portable, doesn't conform to any standard

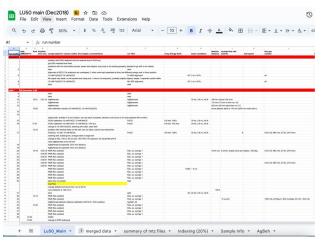
Resource pointers should be portable too!

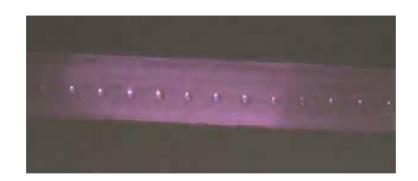
```
> more redoscamerge/42937958/PSII_SPREAD_1F_spread_000428.expt
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  "experiment": [
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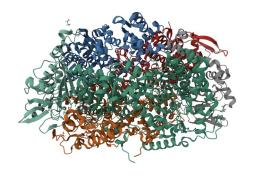
XFEL data are multimodal

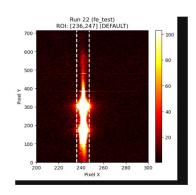
- Sample metadata
- Sample delivery videos
- FEE spectrometer
- Elastic spectrometer
- XES spectra
- Diffraction images
- Results & conclusions

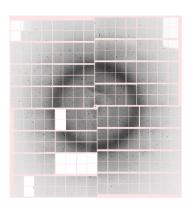


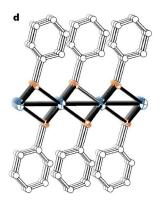






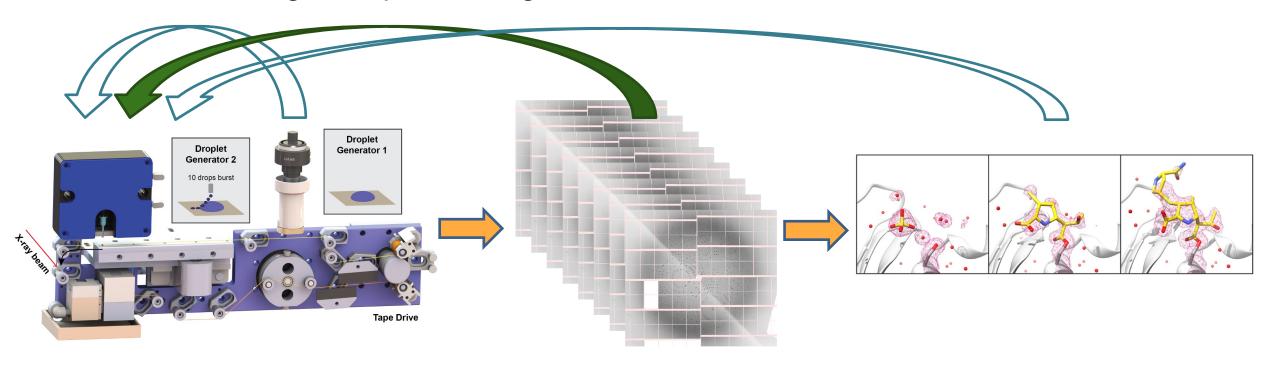




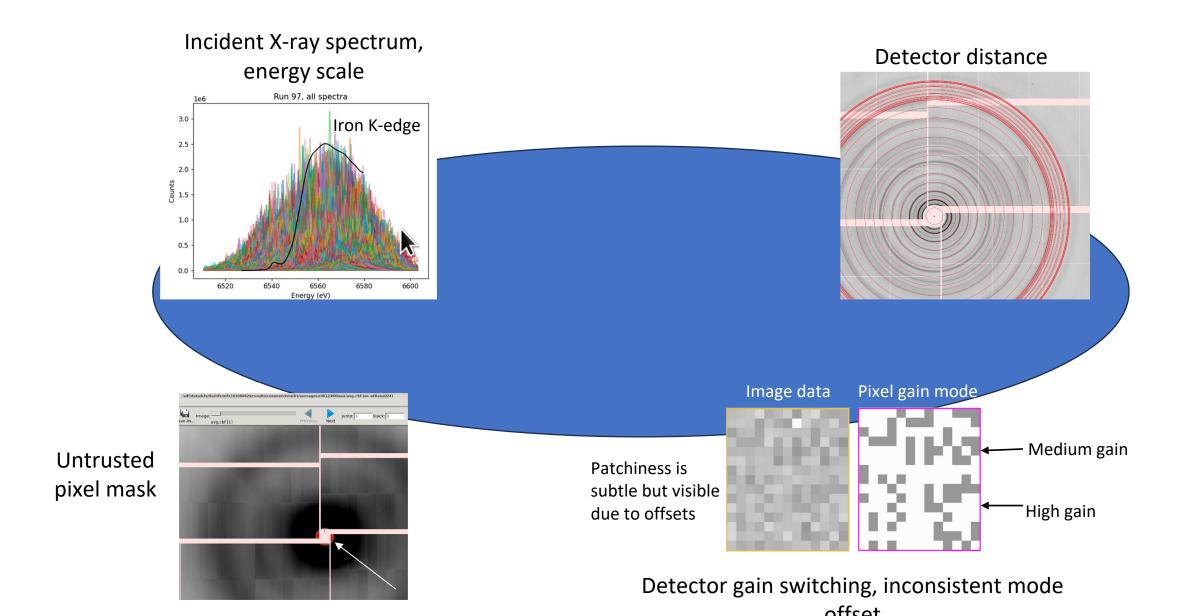


Autonomous experimentation

Streaming data processing



Many calibrations with various levels of reliability



Things we would like, please

What we don't have now for serial crystallography at 2 kHz

- Clearer understanding of the goals, and what experiments benefit
 - Discussion of sample prep and sample delivery
- Better algorithms for better accuracy
- Goal of 1 second feedback to the experiment
 - Data streaming
 - Reliance on GPU and/or ML
- Failover to backup facility
- Database portability, resource portability (like file pointers)
- Better standardization
 - Have a rich metadata layer describing the sample (run,time point, chemical species, conditions, trigger detail)
 - GUI doesn't scale to 2kHz
- Automate more steps

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- Automate more steps

Everything here would help us at 120 Hz too!

Acknowledgements



Berkeley Lab Biosciences

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Jana Thayer

Valerio Mariani

Fred Poitevin

Kevin Dalton

Doris Mai

Katalin Mecseki

NERSC

Johannes Blaschke



OLCF

David Rogers



ALS Gemini Beam Line

Daniil Prigozhin John Taylor



Current Funding

LBNL/LDRD Self Driving Serial Crystallography
NESAP for Doudna "CCTBX+LCLS+ALS"
NIGMS US DIALS National Resource
NIGMS R35 Serial Crystallography Computation

Discussion time-Nick Sauter, Structural Biology at 2kHz

- What have you **learned**? (Particularly in areas outside your core expertise)
 - O Great alignment of goals both within immediate collaboration with LCLS and within larger light source community as expressed by Hannah Parrage (single interface for cross facility awareness, use streaming in live experiment)
- What key challenges and opportunities must be addressed to achieve our goals?
 - O High-level metadata describing the experiment is recorded (duplicated) in three different places, and none is portable in case a different compute resource is needed.
 - The generalization to GPU and multimode should be easier. Mike Bauer (NVIDIA), "all parallelism should be implicit".
 Brad Chamberlain "with Arkouda you don't have to worry about nodes and ranks."
 - O Wah Chiu, "no funding body to help people process data...this is extremely lacking". This should include both the computing services and the expert advice.
 - O The small calibrations must also be done automatically or else they will consume a large percentage of the time if they must still be done by hand. "We can't have human beings touching things anymore".
- What time-dependent factors may influence decisions in the near term? (E.g., American Science Cloud)
 - O Both the ALS and LCLS will have down time in the next three years, interfering with the ability to test data processing and self-driving experiments on live data.
 - O We (David Mittan-Moreau) have one year of LDRD funding to work at the ALS / GEMINI beamline so it would be good to work on a well defined stepping stone, like "Process the data at 100 Hz data acquisition with a processing latency of 1 second, and use the results to automatically drive at least 1 motor control."