

X-ray and electron detection - technology & how to get best data

***Andreas Förster, Application Scientist Crystallography
ReNaFoBis workshop, IGBMC, 2021-01-13***

Outline

- *Characteristics of X-ray and electron detectors*
- *Accurate data – best practice*
 - *Fine φ -slicing*
 - *Low intensity*
- *Think about your experiment*



X-ray detection

Mode of detection

- Direct detection
→ No intermediates*
- Indirect detection
→ Conversion into species
that can be detected*

More information

- Watch <https://www.youtube.com/watch?v=sxyjqGN8R18>
for a historic overview over X-ray detection.*
- Slides at <https://slideplayer.com/slide/12089838/>.*

Mode of quantification

- Counting
→ Each photon as it is
detected*
- Integration
→ Accumulation of signal
that is proportional to
number of photons*

Photographic film

Indirect detection

- *Blackening of silver halide*

Integrating

- *Estimation of spot intensity*
 - *Comparison by eye*
 - *Film scanners*

More information

- *Limited dynamic range, linearity, uniformity.*
- *Slow because of film development.*
- *Inaccurate when estimating intensities.*

Multiwire proportional counters

Direct detection

- Absorption of photons in gas (Xe) generates detectable electrons

Counting

- Charge pulses induced in wires at site of incidence.
- Delay lines make it possible to deduce wire/position from arrival time of pulse.

More information

- Developed in 1970s (ADSC, Xentronics).
- Low spatial resolution (1 x 2 mm pixels).
- Excellent temporal resolution (1 μ s).
- Up to 50 spots per image.

Image plates

Indirect detection

- Absorption of photons in storage phosphor ($\text{BaF}(\text{Br},\text{I}):\text{Eu}^{2+}$).

More information

- From early 1990s (marresearch, Rigaku).
- Large area, linear, simple.
- Large dynamic range.
- Slow, large point-spread function.

Integrating

- Excitation of visible light by laser scan.
- Emitted light proportional to absorbed X-ray intensity.

CCD detectors

Indirect detection

- *Absorption of photons in phosphor (Gd-based) generates visible light.*
- *Light usually travels down taper to small detector.*

Integrating

- *CCD collects light throughout exposure.*

More information

- *From the mid-1990s (ADSC, Rayonix, Rigaku).*
- *Small but can be tiled, fast.*
- *Small dynamic range, needs to be cooled.*
- *Large point-spread function, noisy.*

Pixel array detectors

Direct detection

- Absorption of photons in semiconductor (Si, CdTe) generates electron/hole pairs.
- Electric field drives electrons or holes into readout circuit.

More information

- From early 2000s (PSI, Medipix, DECTRIS).
- Small but can be assembled larger, with gaps.
- Extremely fast, simple.
- Single-pixel point-spread function, no background noise.
- Huge dynamic range.
- Large count-rate capacity.

Counting or integrating

- Depends on readout circuitry.

The optimal detector

Direct or indirect detection

- *Indirect detection always limited.*
- *Direct detection can achieve*
 - *Single-pixel point spread.*
 - *Near theoretical MTF.*
 - *Highest quantum efficiency.*

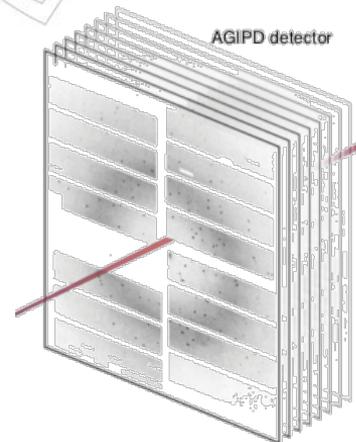
Counting or integrating

- *Depends on application.*
- *Counting: best when photons can be counted.*
- *Integration: best when photons arrive simultaneously.*

Integrating detectors

Direct detection – CS-PAD, JUNGFRAU, AGIPD, ePIX

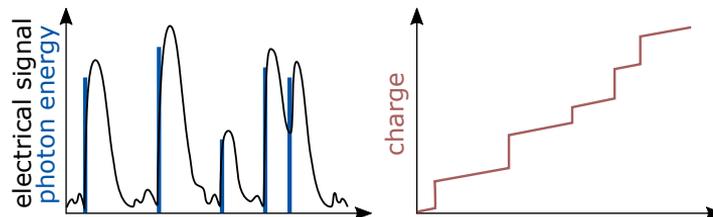
- Development projects.
- Noise suppression difficult (low operating temperature).
- Conversion from numbers on image to photons expensive.
- Extremely high uncompressed data rates.



2021 - JUNGFRAU 10M **2.2 kHz**

46 GB/s

@PSI

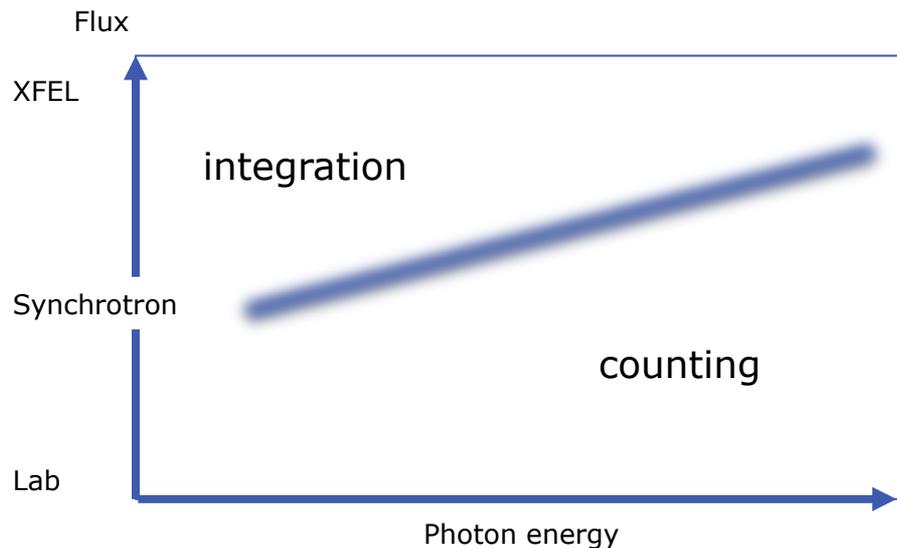


@EuXFEL

Counting vs. integration?

Detector depends on the source

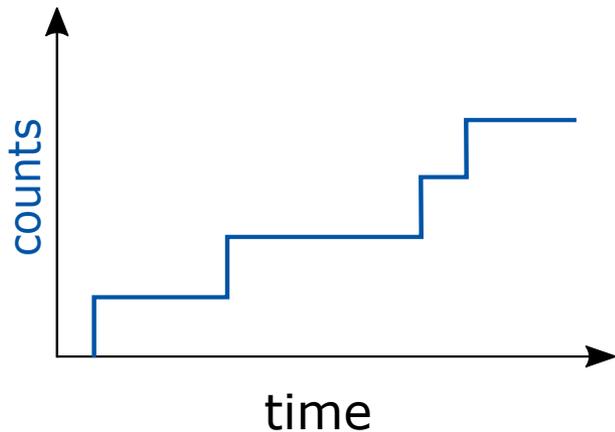
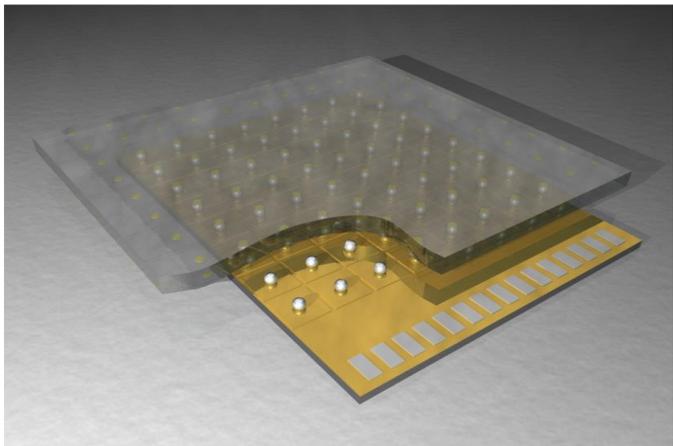
- Flux vs. energy
- Computational effort
- Pulses vs. continuous beam



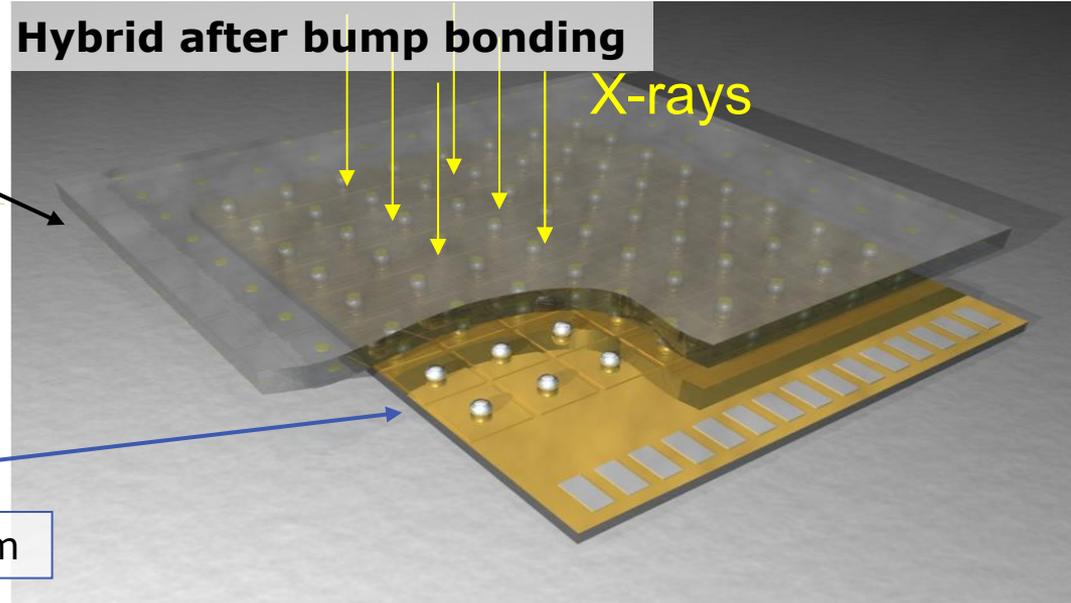
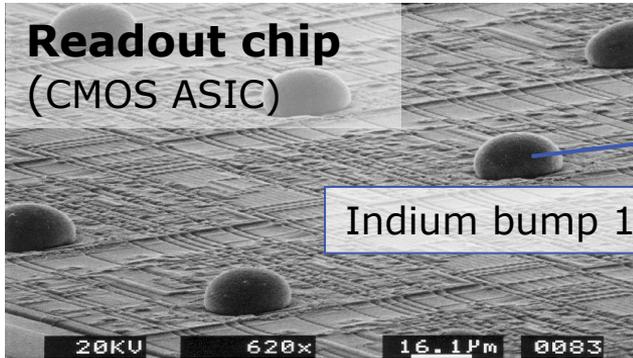
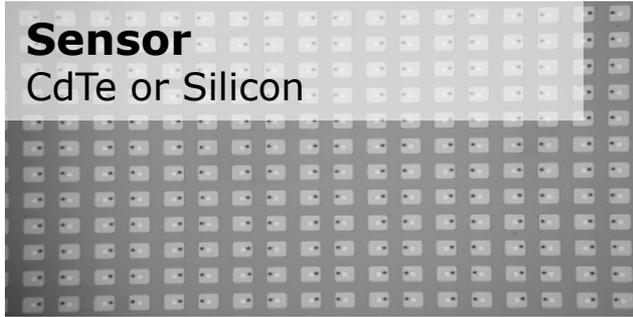
Philip Leonarski, PSI

The meaning of HPC

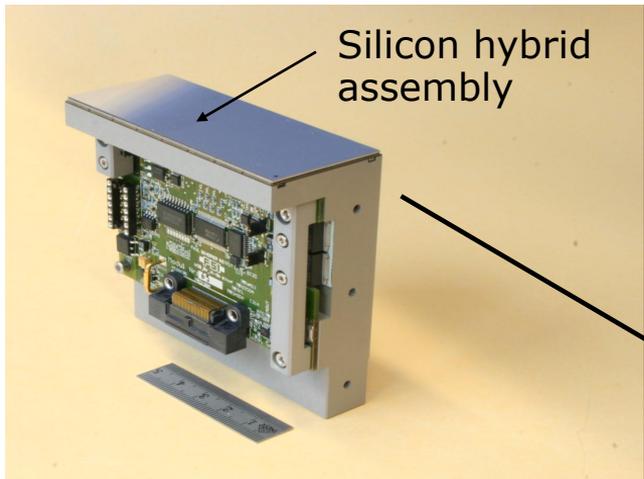
Hybrid Photon Counting = Hybrid pixels + photon counting



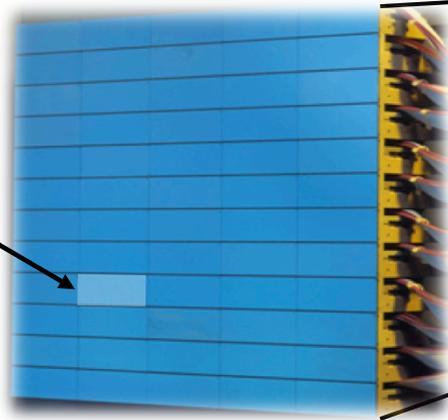
Hybrid pixel = sensor + readout



Modular HPC detectors



Silicon hybrid
assembly

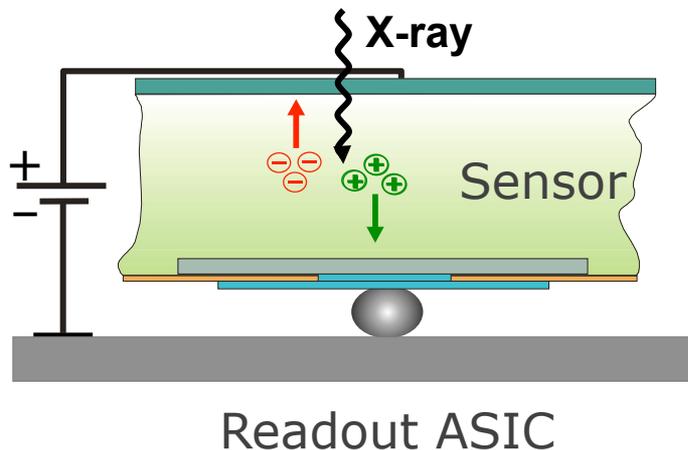


Module active area: $8 \times 4 \text{ cm}^2$

100k pixels on PILATUS ($172 \mu\text{m}$)

500k pixels on EIGER ($75 \mu\text{m}$)

Photon detection in hybrid pixels



Sensor pixel

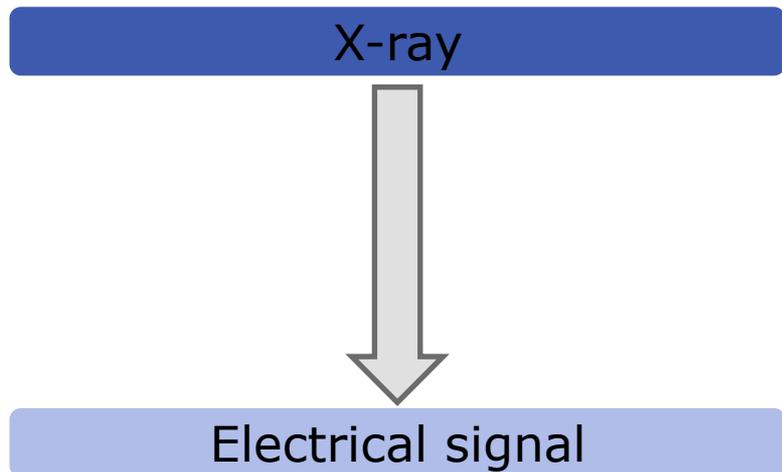
- Direct detection of X-ray photons
-> one $e^-/hole$ pair per 3.6 eV
- Charge is captured by electric field

Readout electronics

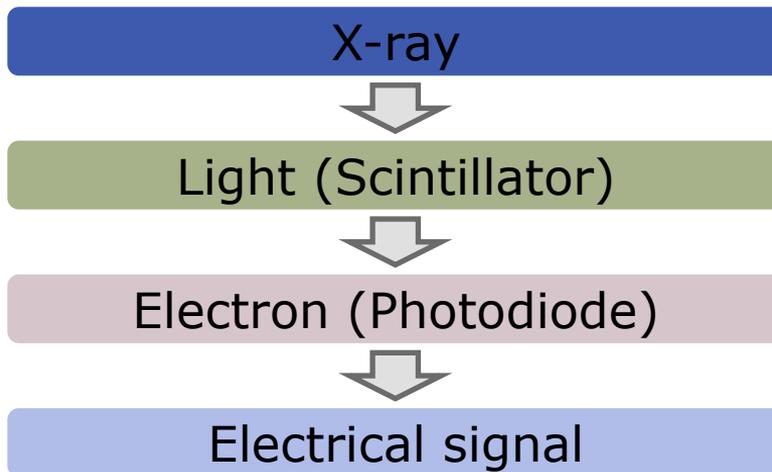
- Counting of charge pulses

Superiority of direct detection

Direct detection

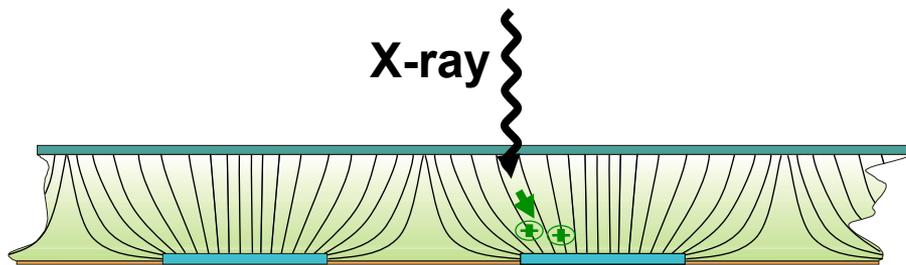


Indirect detection



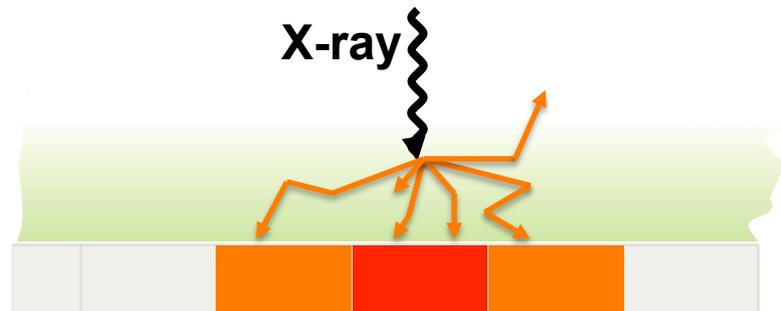
Superiority of direct detection

Direct detection



- Charge captured in electric field
- => **All photons captured**
- => **Signal remains in pixel**

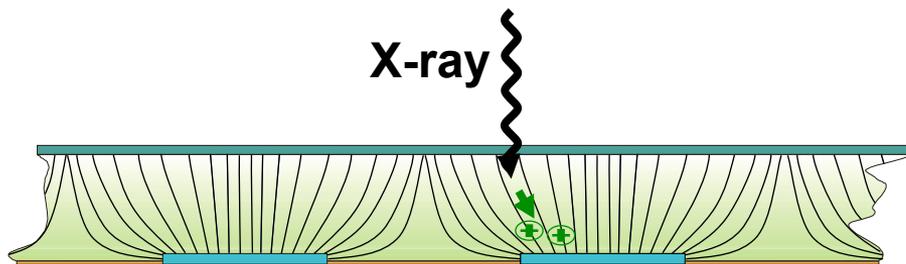
Indirect detection



- Radiation scattered in scintillator
- => **Signal spread across pixels**
- => **Light partially lost**

Superiority of direct detection

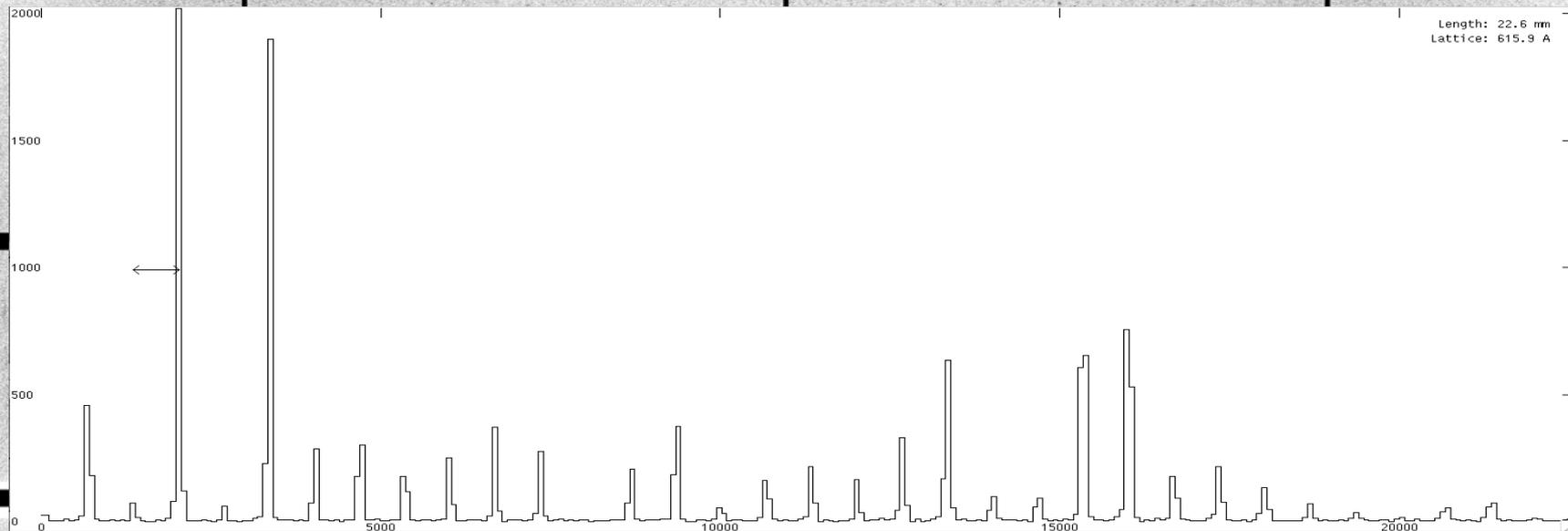
Charge captured in electric field



- *No photon loss*
- *Sharpest reflections*



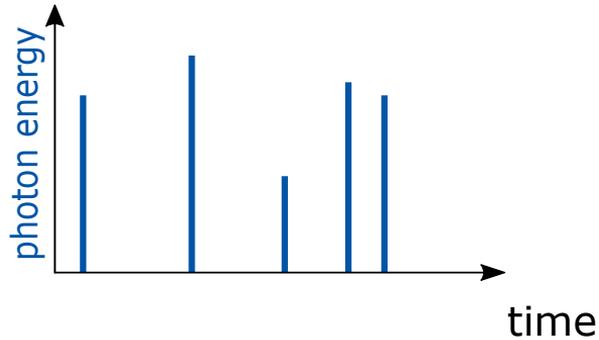
70S ribosome on EIGER X 16M



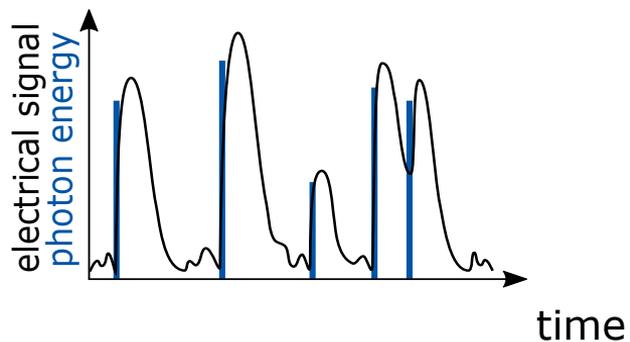
$a = 210 \text{ \AA}$, $b = 450 \text{ \AA}$, $c = 620 \text{ \AA}$
Diffraction to 2.3 \AA , Y. Polikanov, UIC

Photon counting – one by one

– *Photons absorbed in sensor pixel*

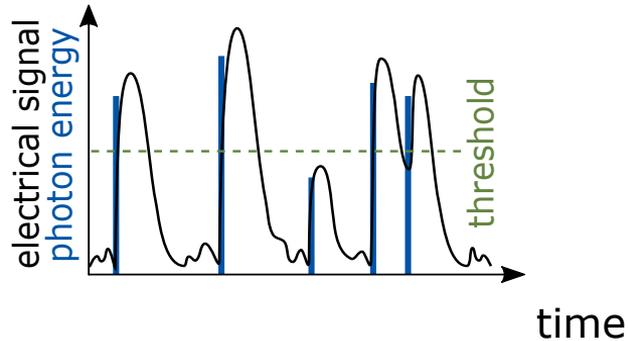


Photon counting – one by one



- *Photons absorbed in sensor pixel*
- *Charge pulse proportional to energy*

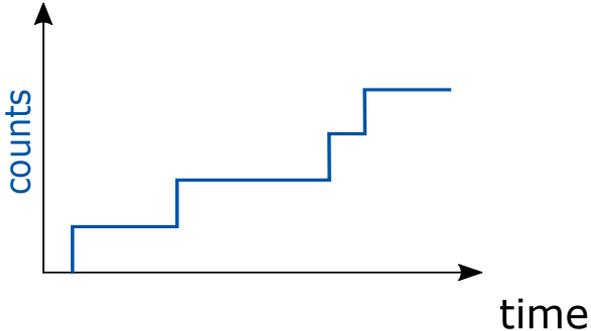
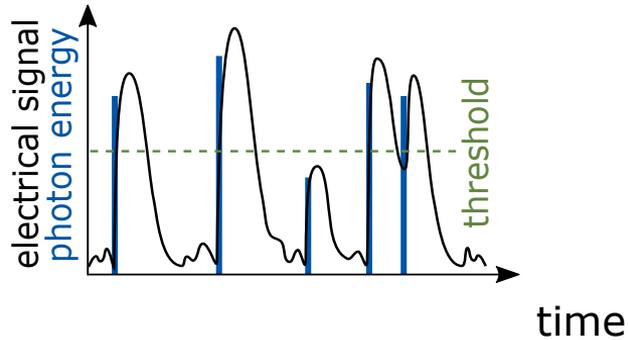
Photon counting – one by one



- Photons absorbed in sensor pixel
- Charge pulse proportional to energy
- Threshold to discard noise

- Signals above threshold are counted
- **Suppression of dark signal**
- **Suppression of electronic noise**

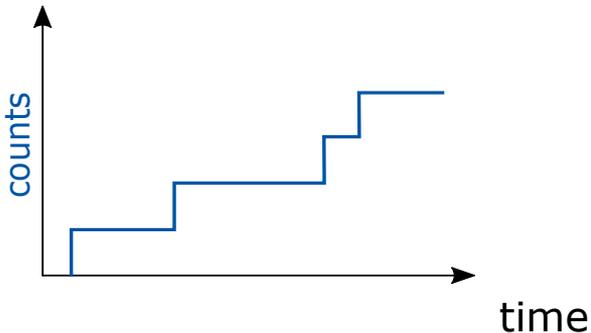
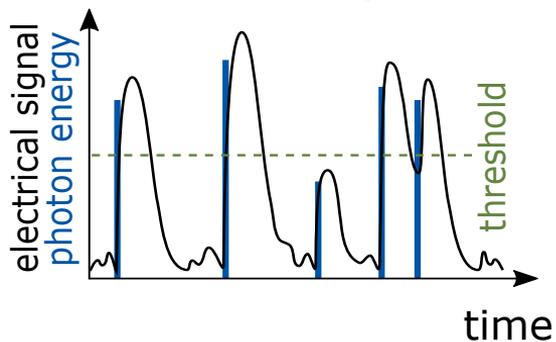
Photon counting – one by one



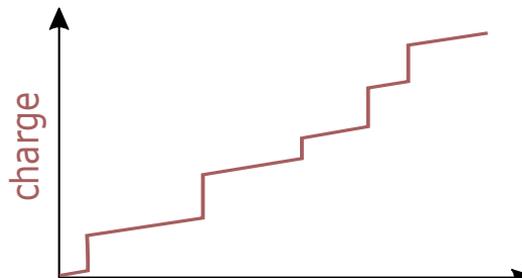
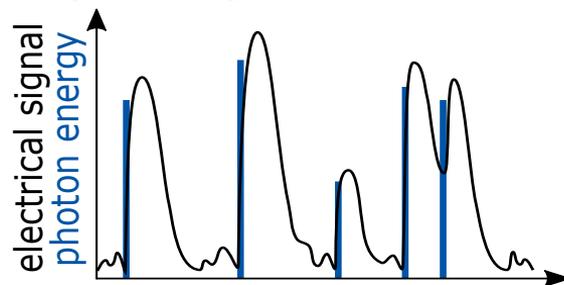
- Photons absorbed in sensor pixel
- Charge pulse proportional to energy
- Threshold to discard noise
- Signals above threshold are counted
 - **Suppression of dark signal**
 - **Suppression of electronic noise**
- On-the-fly digitization in digital counter
 - **No readout noise**
 - Fast readout
 - High dynamic range

Photon counting vs. integration

Photon counting



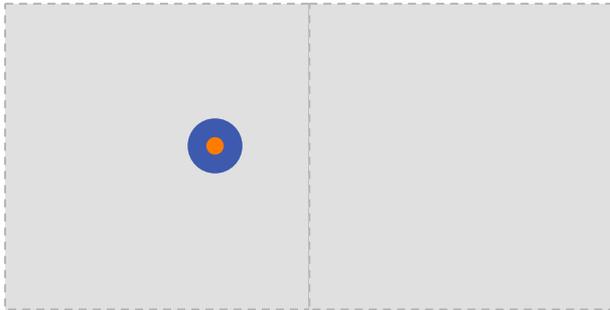
Charge integration



Counting with 50% threshold

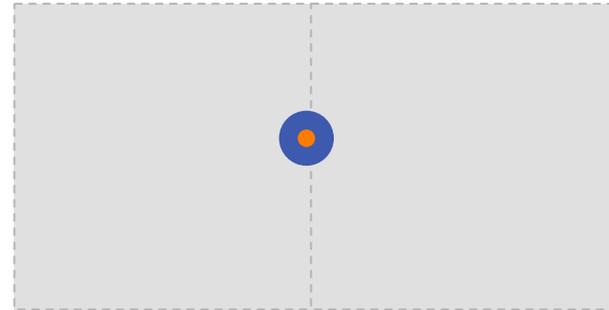
All signal counted within one pixel

1 photon



100% charge
1 count

1 photon

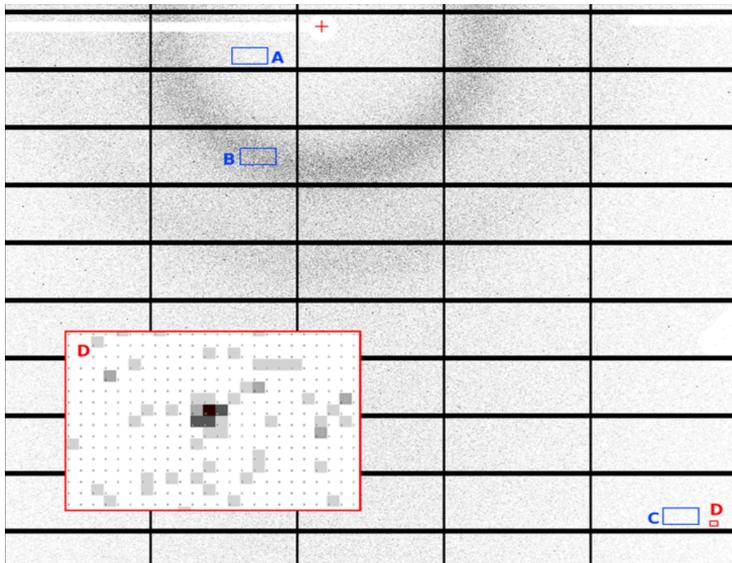


60% charge 40% charge
1 count -

Negligible background

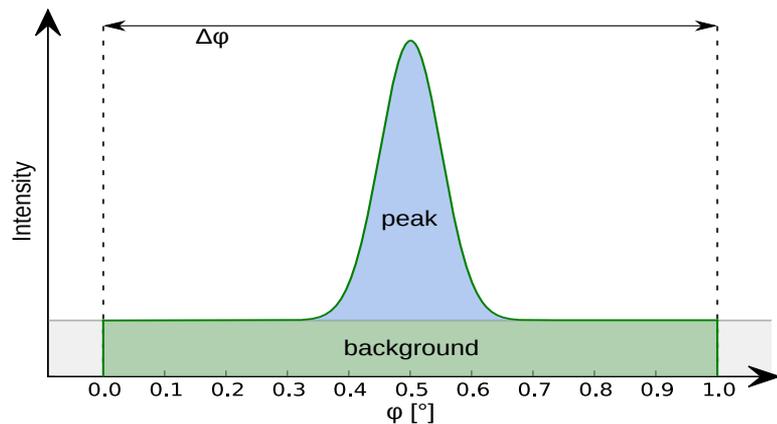
Protein crystallography in vacuum

PETase @ I23.



[Austin \(2018\) PNAS](#)

Accuracy of intensity estimates



Less background

=> Better data

$$\begin{aligned}
 Q &: \text{Quantity of photons} \\
 \text{var}(Q) &= Q \\
 \sigma(Q) &= [\text{var}(Q)]^{1/2} = Q^{1/2}
 \end{aligned}$$

$$\begin{aligned}
 I &: \text{Observed intensity} \\
 I &= \sum(\text{Peak}_i - \text{Bkg}_i) \\
 \text{var}(I) &= \sum[\text{var}(\text{Peak}_i) + \text{var}(\text{Bkg}_i)] \\
 R_{\text{err}} &= \sigma(I)/I
 \end{aligned}$$

Relative error [%]	Background [photons]		
Integrated intensity [photons]	0	500	1000
100	10.0	33.2	45.8
500	4.5	7.7	10.0
1000	3.2	4.5	5.5
10000	1.0	1.0	1.1

Pros and cons of fine φ -slicing

research papers

Acta Crystallographica Section D
**Biological
Crystallography**
ISSN 0907-4449

J. W. Pflugrath

Molecular Structure Corporation, 9009 New
Trails Drive, The Woodlands, TX 77381, USA

Correspondence e-mail: jwp@msc.com

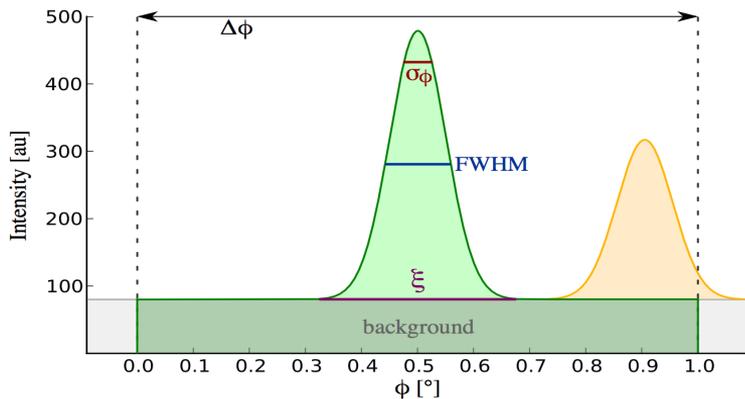
The finer things in X-ray diffraction data collection

X-ray diffraction images from two-dimensional position-sensitive detectors can be characterized as thick or thin, depending on whether the rotation-angle increment per image is greater than or less than the crystal mosaicity, respectively. The expectations and consequences of the processing of thick and thin images in terms of spatial overlap, saturated pixels, X-ray background and $I/\sigma(I)$ are discussed. The *d*TREK* software suite for processing diffraction images is briefly introduced, and results from *d*TREK* are compared with those from another popular package.

Received 6 May 1999
Accepted 5 July 1999

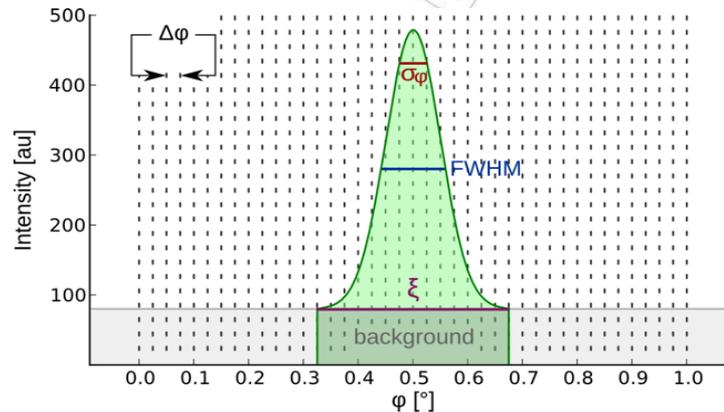
[Pflugrath \(1999\) Acta D](#)

Fine φ -slicing minimizes background



Wide φ -slicing

- $\Delta\varphi > \xi$
- Lots of background
- Few images



Fine φ -slicing

- $\Delta\varphi \ll \xi$
- Minimal background
- Many images

Advantages of fine φ -slicing

research papers 

Acta Crystallographica Section D
**Biological
Crystallography**
ISSN 0907-4449

**Marcus Mueller,*‡ Meitian
Wang and Clemens Schulze-
Briese‡**

Swiss Light Source at Paul Scherrer Institut,
CH-5232 Villigen, Switzerland

‡ Present address: DECTRIS Ltd,
Neuenhoferstrasse 107, CH-5400 Baden,
Switzerland.

**Optimal fine φ -slicing for single-photon-counting
pixel detectors**

The data-collection parameters used in a macromolecular diffraction experiment have a strong impact on data quality. A careful choice of parameters leads to better data and can make the difference between success and failure in phasing attempts, and will also result in a more accurate atomic model. The selection of parameters has to account for the application of the data in various phasing methods or high-resolution refinement. Furthermore, experimental factors such as crystal characteristics, available experiment time and the properties of the X-ray source and detector have to be considered. For many years CCD detectors have been the prevalent type of

Received 17 June 2011
Accepted 21 November 2011

Müller (2011) Acta D

Fine ϕ -slicing improves data quality

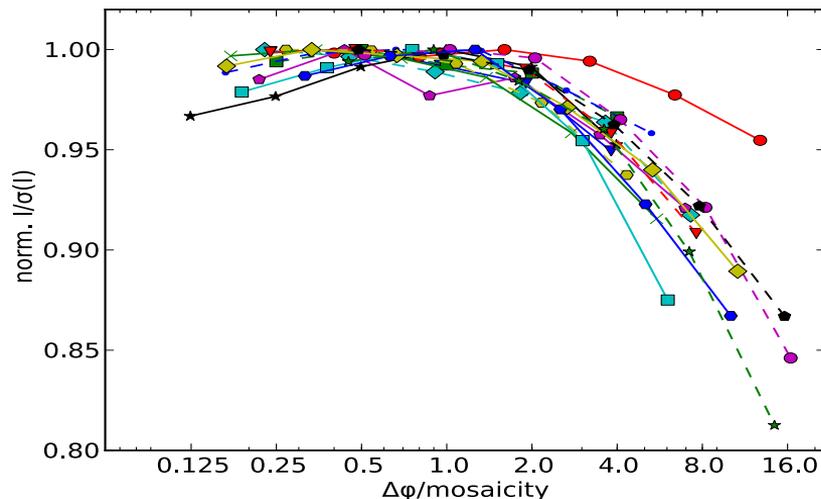
$\Delta\phi < \text{mosaicity}$ improves:

- overall statistics
- anomalous signal
- highest-shell statistics
- number of overlaps

on PILATUS.

Start with $0.1^\circ/\text{img}$

higher $I/\sigma(I)$



Fine φ -slicing with EIGER

research papers 

 STRUCTURAL BIOLOGY
ISSN 2059-7983

EIGER detector: application in macromolecular crystallography

Arnau Casanas,^a Rangana Warshamange,^a Aaron D. Finke,^a Ezequiel Panepucci,^a Vincent Olieric,^a Anne Nöll,^b Robert Tampé,^b Stefan Brandstetter,^c Andreas Förster,^c Marcus Mueller,^c Clemens Schulze-Briese,^c Oliver Bunk^a and Meitian Wang^{a*}

Received 9 June 2016
Accepted 29 July 2016

Edited by K. Diederichs, University of Konstanz, Germany

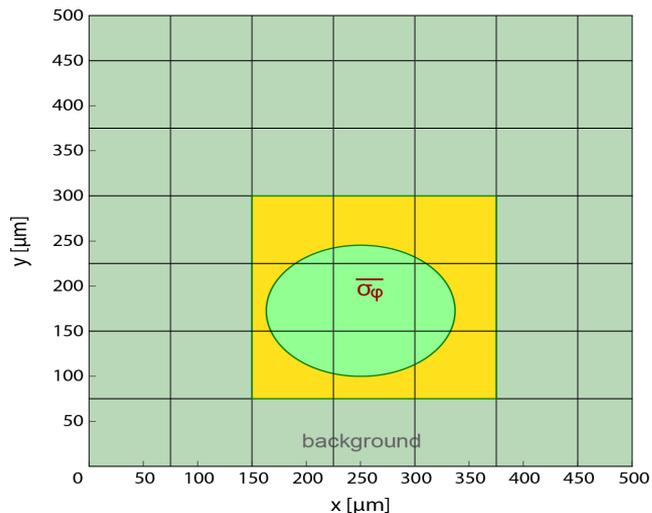
Keywords: X-ray detectors; EIGER detector; macromolecular crystallography; data-collection strategy.

^aSwiss Light Source, Paul Scherrer Institute, 5232 Villigen, Switzerland, ^bInstitute of Biochemistry, Biocenter, Goethe University Frankfurt, Max-von-Laue-Strasse 9, 60438 Frankfurt am Main, Germany, and ^cDECTRIS Ltd, Taeferweg 1, 5405 Baden-Dättwil, Switzerland. *Correspondence e-mail: meitian.wang@psi.ch

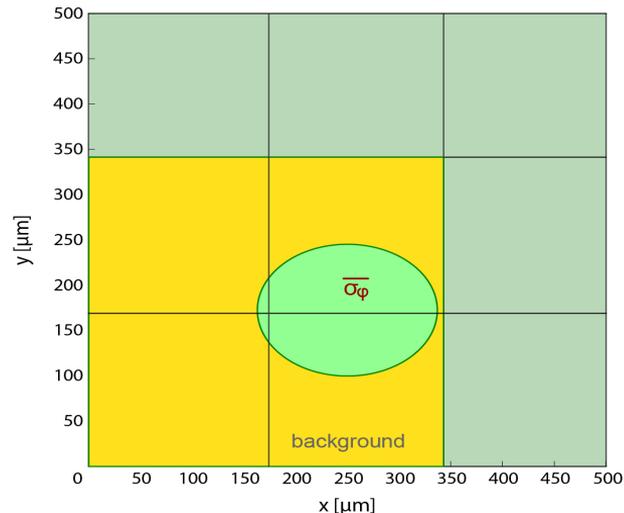
The development of single-photon-counting detectors, such as the PILATUS, has been a major recent breakthrough in macromolecular crystallography, enabling noise-free detection and novel data-acquisition modes. The new EIGER detector features a pixel size of $75 \times 75 \mu\text{m}$, frame rates of up to 3000 Hz and a dead time as low as $3.8 \mu\text{s}$. An EIGER 1M and EIGER 16M were

[Casanas \(2016\) Acta D](#)

Smaller pixels improve data quality

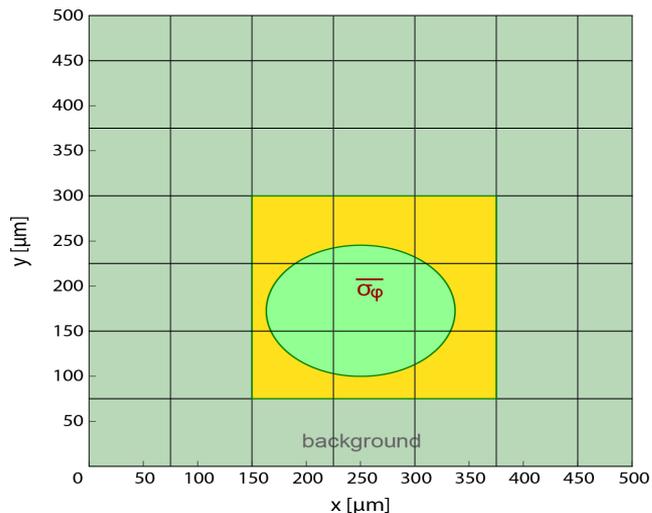


Reflection on EIGER

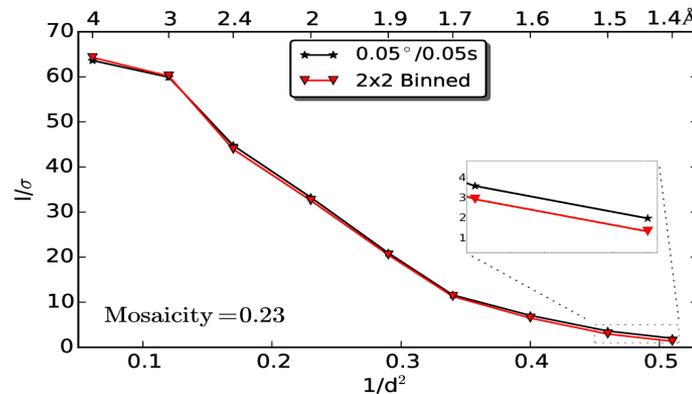


Reflection on PILATUS

Smaller pixels improve data quality



Reflection on EIGER

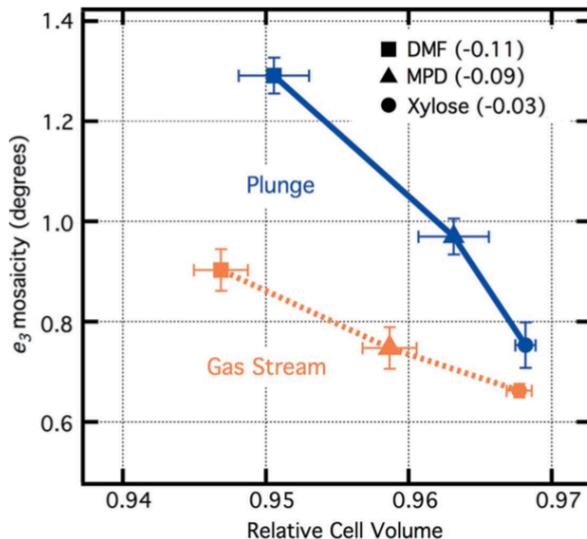
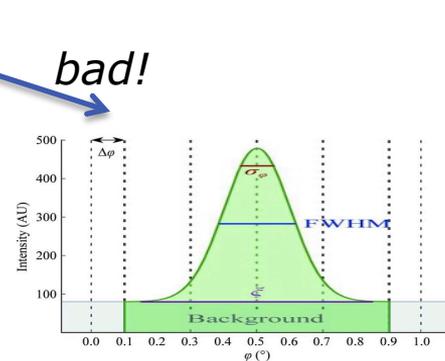
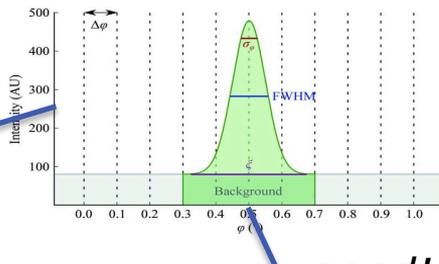
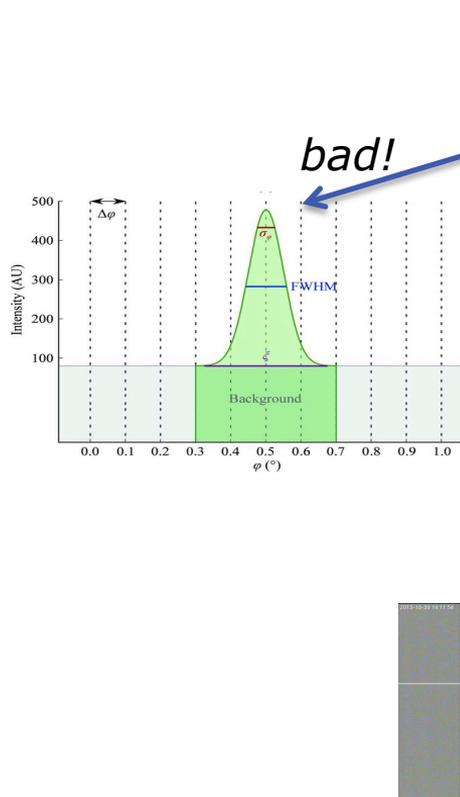


Better high-resolution data

Get best data by

- Using EIGER and PILATUS detectors*
- Using fine φ -slicing ($0.1^\circ/\text{img}$)*
- Minimizing other sources of error*

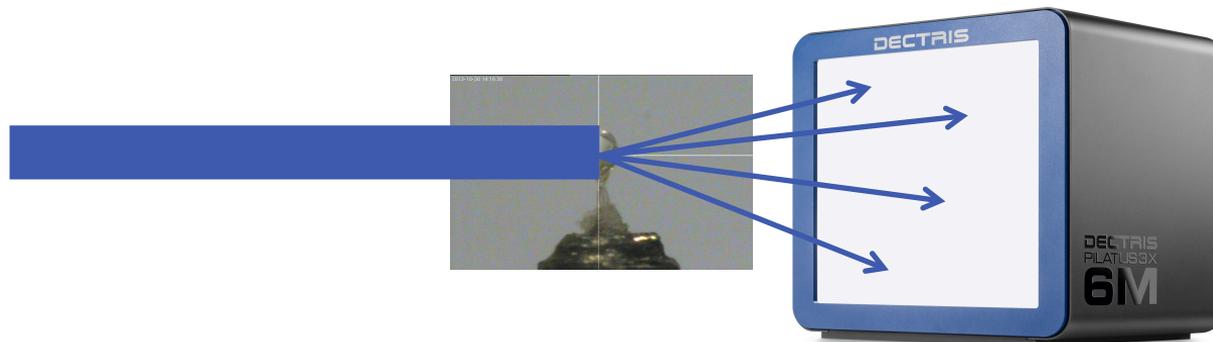
Decrease absolute background



Reduce mosaicity!!

Harrison (2019) J Appl Cryst

Decrease absolute background



Get best data by

- Using EIGER and PILATUS detectors*
- Using fine φ -slicing ($0.1^\circ/\text{img}$)*
- Minimizing absolute background*
- Collecting 360° of data*

Low-intensity data collection

research papers 

 STRUCTURAL BIOLOGY
ISSN 2059-7983

How best to use photons

Graeme Winter,* Richard J. Gildea, Neil G. Paterson, John Beale, Markus Gerstel, Danny Axford, Melanie Vollmar, Katherine E. McAuley, Robin L. Owen, Ralf Flaig, Alun W. Ashton and David R. Hall

Diamond Light Source, Harwell Science and Innovation Campus, Didcot, Oxfordshire OX11 0DE, UK. *Correspondence e-mail: graeme.winter@diamond.ac.uk

Received 12 October 2018
Accepted 13 March 2019

Keywords: radiation damage; data collection; data processing; data analysis.

Supporting information: this article has supporting information at journals.iucr.org/d

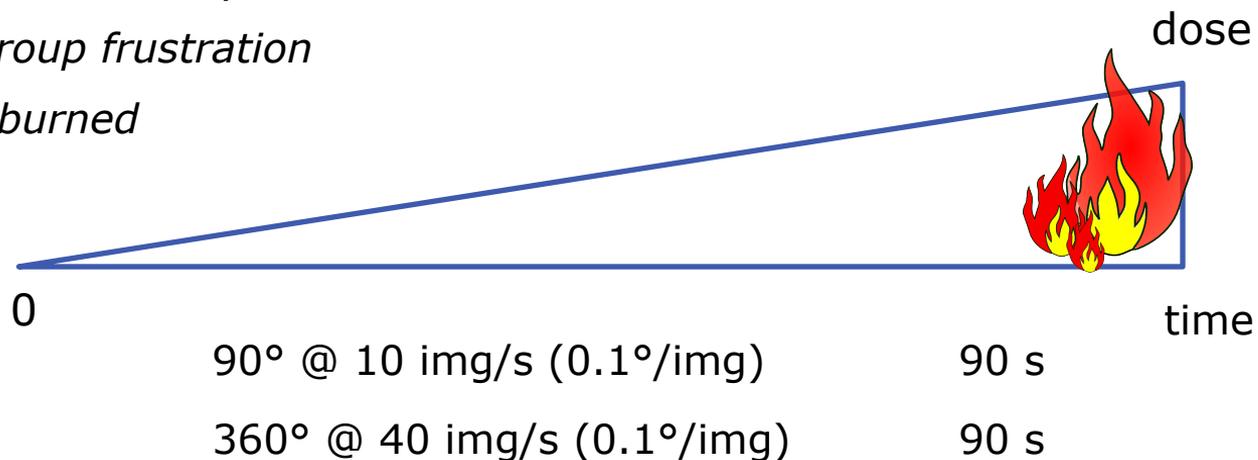
Strategies for collecting X-ray diffraction data have evolved alongside beamline hardware and detector developments. The traditional approaches for diffraction data collection have emphasised collecting data from noisy integrating detectors (*i.e.* film, image plates and CCD detectors). With fast pixel array detectors on stable beamlines, the limiting factor becomes the sample lifetime, and the question becomes one of how to expend the photons that your sample can diffract, *i.e.* as a smaller number of stronger measurements or a larger number of weaker data. This parameter space is explored *via* experiment and synthetic data treatment and advice is derived on how best to use the equipment on a modern beamline. Suggestions are also made on how to acquire data in a conservative manner if very little is known about the sample lifetime.

[Winter \(2019\) Acta D](#)

The American method

Collect 360° of data

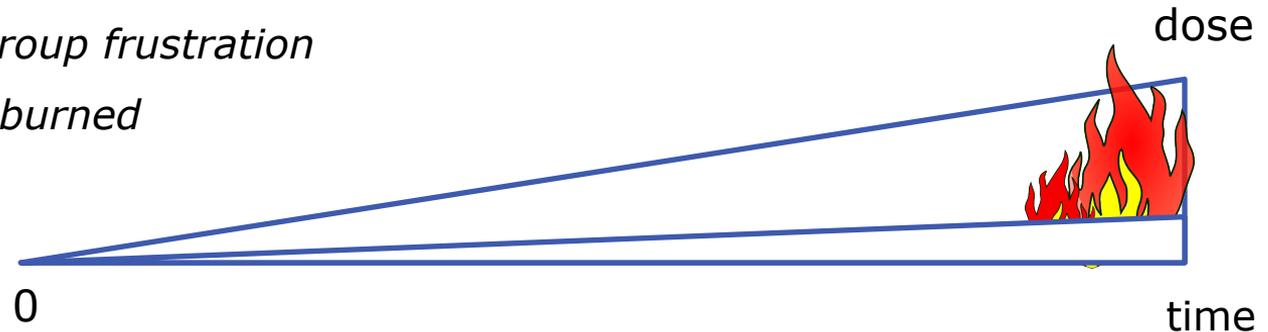
- To get more precise intensity estimates
- To avoid space group frustration
- To avoid getting burned



The American method

Collect 360° of data

- To get more precise intensity estimates
- To avoid space group frustration
- To avoid getting burned



90° @ 10 img/s (0.1°/img)

90 s

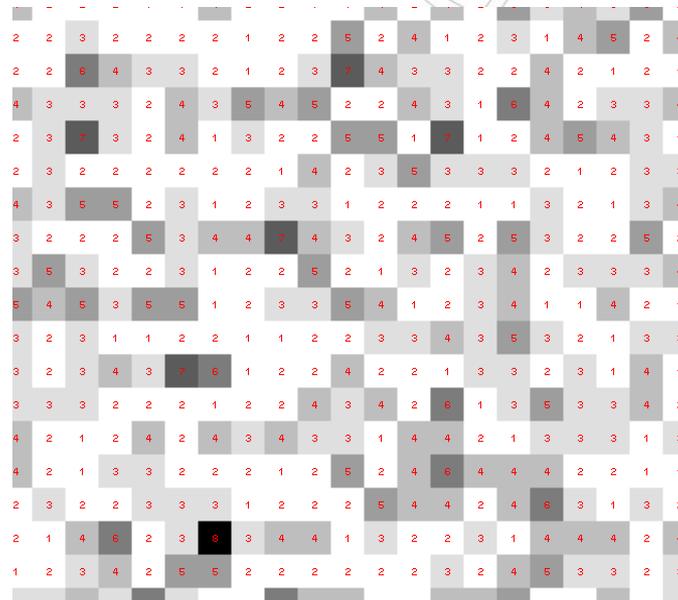
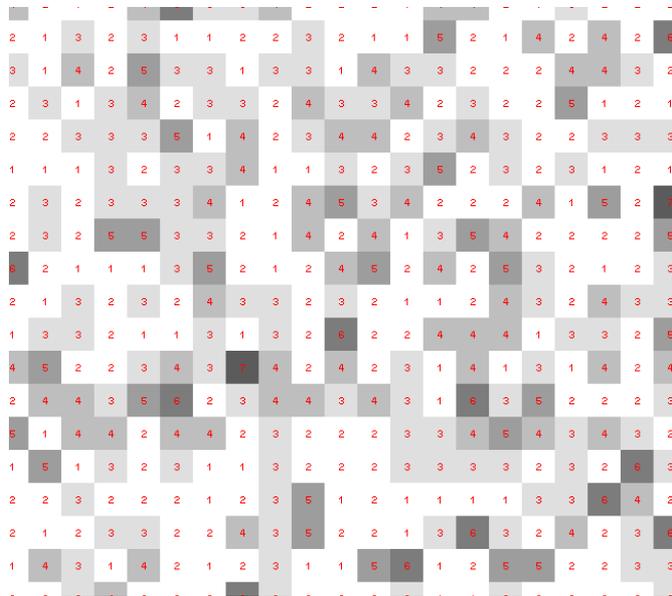
360° @ 40 img/s (0.1°/img)

90 s

Attenuate beam 4-fold + 360° @ 40 img/s (0.1°/img)

90s

Are these spots?



Fine ϕ -slicing + low-intensity data collection make for very weak spots

There is always anomalous signal

Current paradigm

- *Molecular replacement*
- *In case of failure*
 - *Se-Met substitution*
 - *Heavy atom soaking*

Always measure anomalous differences

- *Experimental phasing*
- *Improved MR phases*
- *Identify metal ions*
- *Without extra work*

Always measure 360° of data.



Get best data by

- Using PILATUS and EIGER detectors*
- Using fine φ -slicing ($0.1^\circ/\text{img}$)*
- Minimizing absolute background*
- Collecting 360° of low-intensity data*

Sophisticated strategies

Collect 360° of data

- From starting angle suggested by strategy software*
- With detector at correct distance*
- With optimized exposure time/attenuation*
- At non-standard energy*
- With inverse beam method*
- From aligned crystal*
- Multiple times (dose fractionation)*

Never measure less than 360° of data.

Simple native SAD strategy

research papers 

 STRUCTURAL BIOLOGY
ISSN 2059-7983

Making routine native SAD a reality: lessons from beamline X06DA at the Swiss Light Source

Shibom Basu,^a Aaron Finke,^b Laura Vera,^a Meitian Wang^a and Vincent Olieric^{a*}

^aSwiss Light Source, Paul Scherrer Institut, Villigen PSI, Switzerland, and ^bMacCHESS, Cornell University, Ithaca, New York, USA. *Correspondence e-mail: vincent.olieric@psi.ch

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Supporting information: this article has supporting information at journals.iucr.org/d

Native single-wavelength anomalous dispersion (SAD) is the most attractive *de novo* phasing method in macromolecular crystallography, as it directly utilizes intrinsic anomalous scattering from native crystals. However, the success of such an experiment depends on accurate measurements of the reflection intensities and therefore on careful data-collection protocols. Here, the low-dose, multiple-orientation data-collection protocol for native SAD phasing developed at beamline X06DA (PXIII) at the Swiss Light Source is reviewed, and its usage over the last four years on conventional crystals (>50 µm) is reported. Being experimentally very simple and fast, this method has gained popularity and has delivered 45 *de novo* structures to date (13 of which have been published). Native SAD is currently the primary choice for experimental phasing among

[Basu \(2019\) Acta D](#)

Maximize anomalous signal

- ***Multiplicity amplifies anomalous signal***
 - *Change crystal orientation for true multiplicity*
- ***Radiation damage must be avoided***
 - *Low-intensity data collection*
 - *Collect more images at lower dose*
- ***Combine data from multiple crystals***

Detector must be free of readout noise.

Get best data by

- Using PILATUS and EIGER detectors*
- Using fine φ -slicing ($0.1^\circ/\text{img}$)*
- Minimizing absolute background*
- Collecting at least 360° of low-intensity data*
- Thinking about your experiment*

Use beam time *effectively*

- *Mount crystal – 1 min*
 - *Center crystal – 1 min*
 - *Collect a dataset – 1 min*
 - *Eight-hour shift – 480 min*
- **Person A :**
 - *Collects 82 datasets*
 - **Takes 1 TB of data home**
 - **Person B :**
 - *Thinks about experiment*
 - *Talks to beamline scientist about hardware/best strategy*
 - *Has a tea to focus*
 - *Collects a dataset*
 - *Has a chat with her mate*
 - *Collects two more datasets*
 - **Solves structure**

Conclusions

- *Optimize your sample!*
- *With PILATUS, collect 360° of data with weak beam*
- *With PILATUS, $\Delta\phi \approx 1/2$ XDS mosaicity for best data*
- *There is no native data*
- *Ask your beamline scientist / think !*

An abstract graphic consisting of multiple thin, light blue lines that form a series of overlapping, wavy shapes across the top and middle of the page. The lines are more densely packed in some areas, creating a sense of depth and movement, resembling a stylized wave or a data visualization.

Ask if things are unclear

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Read more

- Förster et al. **Transforming X-ray detection with hybrid photon counting detectors.** [Philos Trans A. 2019;377:20180241.](#)
- Pflugrath. **The finer things in X-ray diffraction data collection.** [Acta D. 1999;55:1718.](#)
- Müller et al. **Optimal fine φ -slicing for single-photon-counting pixel detectors.** [Acta D. 2012;68:42.](#)
- Casanas et al. **EIGER detector: application in macromolecular crystallography.** [Acta D. 2016;72:1036.](#)
- Winter et al. **How best to use photons.** [Acta D. 2019;75:242.](#)
- Basu et al. **Making routine native SAD a reality: lessons from beamline X06DA at the Swiss Light Source.** [Acta D. 2019;75:262.](#)
- Förster and Schulze-Briese. **A shared vision for macromolecular crystallography over the next five years.** [Struct Dynam. 2019; 6:064302.](#)