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### Outline

- › What is crystallographic data
- › Overview of data processing
- › Modeling the diffraction experiment
- › Data processing steps
- › Was processing successful?
- › Are the results good enough?
- › Data Processing Software:
  - › Mosflm, HKL2000, DIALS, XDS

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### What is crystallographic data?

The rotation method

- A set of successive images
- Collected while rotating crystal by small angle ( $\Delta\omega$ ) about fixed axis ( $\omega$ )
- Diffraction condition is satisfied when reciprocal lattice intersects the Ewald's sphere
- Diffraction pattern recorded on a detector (camera).

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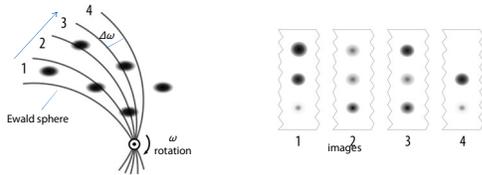
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## What is crystallographic data?



- Crystallographic data contains
  - information about the structure of the crystal in the cell dimensions and indices
  - Information about the contents of each unit cell (the protein/macromolecule) in the intensities.



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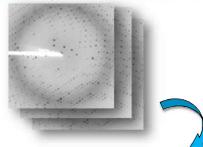
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## The Goal of Data Processing

- Extraction intensities and standard deviations of crystallographic reflections from diffraction images
- Steps
  - Model reflection positions
  - Integrate intensities
  - Correct, Scale and Refine Intensities
  - Assign Space-group
- All data reduction packages perform these steps
  - only differ in implementation



H	K	L	I	SIGMA(I)	XD	YD	ZD
0	0	-4	8.587E+07	1.819E+06	2183.2	2884.7	149.1
0	0	-6	7.899E+05	1.998E+04	2258.6	2101.2	144.4
0	0	-8	4.533E+05	1.627E+04	2334.3	2137.5	139.7
0	0	-10	4.341E+05	1.819E+04	2410.3	2133.4	135.0
0	0	-12	2.582E+05	2.051E+04	2486.6	2149.0	130.2
0	0	-14	2.036E+06	4.926E+04	1582.7	1938.0	191.3
0	0	-14	2.128E+06	5.324E+04	2583.5	2164.2	125.3
0	0	-16	1.309E+07	2.947E+05	1425.7	1923.2	106.2
0	0	-10	1.201E+07	2.889E+05	2640.9	2178.9	100.5
0	0	-18	6.215E+05	2.687E+04	1348.0	1909.1	201.2
0	0	-18	6.169E+05	3.147E+04	2718.8	2192.9	115.5
0	0	-20	2.451E+04	2.451E+04	1289.7	1895.6	206.2
n	n	n	0.871E+03	9.770E+04	9707.9	9706.1	110.6



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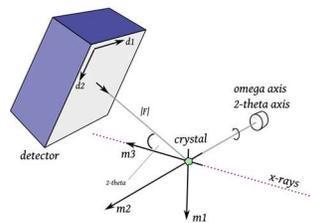
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## Modelling the diffraction experiment

- Coordinate systems
  - Detector coordinate system,
  - Goniostat coordinate system,
  - Crystal coordinate system
- Experimental Parameters:
  - Direction of incident beam,
  - detector origin, detector pixel size,
  - photon energy/wavelength,
  - starting  $\omega$  and  $\Delta\omega$  angle per oscillation, crystal to detector distance, beam divergence
- Note: different programs use different conventions



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## Modelling spot positions - XDS

- Detector coordinate system
  - Right-handed orthonormal  $\{d_1, d_2, d_3\}$
  - Origin closest point between detector and crystal  $(X_0, Y_0)$  found at distance  $|F|$  from crystal
  - Pixel  $(X, Y)$  on detector surface represented by vector

$$(X - X_0)d_1 + (Y - Y_0)d_2 + Fd_3$$

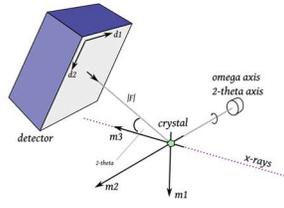
in lab coordinate system

- Goniostat coordinate system
  - Right-handed orthonormal  $\{m_1, m_2, m_3\}$
  - Origin at crystal
  - Determined from incident beam vector  $S_0$  and rotation axis  $m_2$  such that

$$m_1 = \frac{(m_2 \times S_0)}{|m_2 \times S_0|}$$

and

$$m_3 = m_1 \times m_2$$




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## XDS – Modelling spot positions and shape

- Crystal coordinate system
  - Right-handed  $\{b_1, b_2, b_3\}$
  - Reciprocal basis  $\{b^1, b^2, b^3\}$
  - Represents un-rotated crystal (ie  $\omega = 0^\circ$ )
  - Any reciprocal-lattice vector can be expressed as

$$p_0 = hb_1^1 + kb_2^2 + lb_3^3$$

where  $h, k, l$  are integers  
 Location of all diffraction peaks can be calculated from the parameters  $S_0, m_2, b_1, b_2, b_3, X_0, Y_0, F, d_1, d_2, d_3, \omega_0$  and  $\Delta\omega$ .

- Only remaining parameters are spot shape and extent
- Spot shape and extent parameters
  - Gaussian model
  - $\sigma_1$ : Standard deviation of reflecting range (Mosaicity)
  - $\sigma_2$ : Standard deviation of beam divergence
  - Spot coordinate system  $\{e_1, e_2, e_3\}$  which transforms all spots to the same shape.

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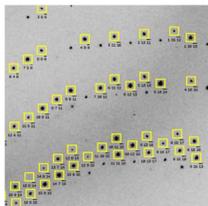
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## Auto-Indexing



H	K	L	I	SIGMA (I)
0	0	-4	8.587E+07	1.819E+06
0	0	-6	7.899E+05	1.998E+04
0	0	-8	4.535E+05	1.627E+04
0	0	-10	4.341E+05	1.819E+04
0	0	-12	3.582E+05	2.051E+04
0	0	14	2.036E+06	4.926E+04
0	0	-14	2.126E+06	5.314E+04
0	0	16	1.369E+07	2.947E+05
0	0	-16	1.301E+07	2.805E+05
0	0	18	6.215E+05	2.687E+04

Determines the

- Crystal orientation
- Approximate cell dimensions
- Possible crystal symmetry

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## Auto-Indexing

- ▶ A list of strong spots occurring in images is found
- ▶ A strong spot is one which exceeds the mean by a given number in units of  $\sigma$ , typically 3-5 $\sigma$ .
- ▶ Reciprocal basis vectors are found from the spots using various methods:
  - ▶ Mosflm, 1-D FFT
  - ▶ HKL2000, 3-D FFT
  - ▶ XDS, 3D difference vector cluster analysis
- ▶ A quality score is calculated
- ▶ Parameters are refined using more reflections.



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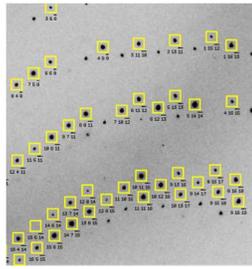
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## Auto-Indexing - XDS

- ▶ The process during which XDS determines the parameters
  - ▶ A list of strong spots occurring in images is found
  - ▶ A strong spot is one which exceeds the mean by  $>3-5\sigma$
  - ▶ Reciprocal basis vectors ( $\mathbf{b}_1^*$ ,  $\mathbf{b}_2^*$ ,  $\mathbf{b}_3^*$ ) are found from the spots using local indexing
    - ▶ Three independent vectors  $\mathbf{b}_1^*$ ,  $\mathbf{b}_2^*$ ,  $\mathbf{b}_3^*$  are selected which maximize a quality function
  - ▶ Ideally each spot corresponds to a reciprocal-lattice vector
    - ▶  $\mathbf{p}_0^* = h\mathbf{b}_1^* + k\mathbf{b}_2^* + l\mathbf{b}_3^*$
    - ▶ Unfortunately "alien" spots are often present



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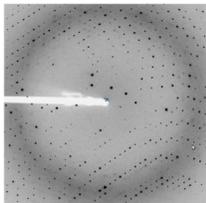
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## Integration



H	K	L	I	SIGMA (I)
0	0	-4	8.587E+07	1.819E+06
0	0	-6	7.899E+05	1.998E+04
0	0	-8	4.535E+05	1.627E+04
0	0	-10	4.341E+05	1.835E+04
0	0	-12	3.582E+05	2.051E+04
0	0	14	2.036E+06	4.926E+04
0	0	-14	2.126E+06	5.234E+04
0	0	16	1.369E+07	2.947E+05
0	0	-16	1.301E+07	2.805E+05
0	0	18	6.215E+05	2.687E+04

Determines

- ▶ The intensities of each reflection, i.e. the total number of photons scattered by the family of planes represented by each index.
- ▶ And their standard deviations



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## Integration

- ▶ **Successful integration is only possible if the model of the experiment is accurate**
  - ▶ Requires accurate experimental parameters
  - ▶ Requires successful auto-indexing



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## Integration

- ▶ In each region where a reflection is expected, pixels which belong to a reflection and those which belong to the background are identified
- ▶ The intensities of the non-background pixels are added up
  - ▶ Not possible if any pixels are overloaded.
- ▶ The total intensity of the background pixels is then subtracted
- ▶ Using counting statistics, an estimate of the error in the intensity ( $\sigma$ ) is calculated.



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## Integration

- ▶ Two types of integration algorithms:
  - ▶ 2D integration: Mosflm, HKL2000
    - ▶ Reflections are integrated using a 2D profile for each image
    - ▶ Partial reflections are only added together during scaling
    - ▶ Work better for images collected with "thick" slicing.
  - ▶ 3D integration: XDS, d\*Trek, DIALS
    - ▶ Reflection are integrated using a 3D profile which includes multiple adjacent images.
    - ▶ Produce better modelling of spot shape and more accurate spot centroids.
    - ▶ Works well with "thin"-sliced data which generally produce more accurate reflections.



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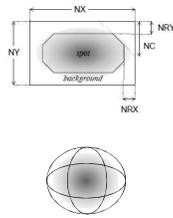
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## Integration

- ▶ Background determination differences
  - ▶ Mosflm/HKL2000
  - ▶ XDS/DIALS
    - ▶ Strong pixels are removed until remaining pixels represent samples from a random distribution
    - ▶ Background is the mean intensity of remaining pixels




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## Integration - XDS

- ▶ For each frame
  - ▶ Identify strong pixels in the image
  - ▶ Label each pixel with the indices of nearest reflection
  - ▶ 3D profile is determined for all pixels labelled with the same index
  - ▶ A reflection is rejected if its centroid deviates too much from expected position
  - ▶ Mosaicity ( $\sigma_p$ ) and Beam divergence ( $\sigma_b$ ) are estimated
    - ▶ 3D Gaussian fitting
  - ▶ Background is determined
    - ▶ Strong pixels are removed until remaining pixels represent samples from a random distribution
    - ▶ Background is the mean intensity of remaining pixels
  - ▶ Integrated intensity is estimated by profile fitting

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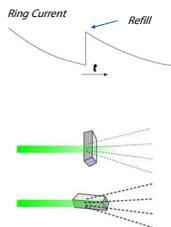
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## Correction & Scaling

- ▶ Integrated intensities need to be corrected for
  - ▶ Changes in beam intensity and variations of illuminated crystal volume
  - ▶ Absorption of incident and diffraction beams
  - ▶ Radiation damage
  - ▶ Variations in detector sensitivity on its surface
  - ▶ If multiple crystals were used
    - ▶ Differences in crystal sizes
    - ▶ Differences in crystalline order
  - ▶ Combined effect:
    - ▶ Correlations between reflection and frame number/angle
    - ▶ Correlations between reflection and spatial location on detector surface




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## Scaling

- Assumptions:
  - Statistically independent observations of intensities of symmetry related reflections recorded at different angles, frame numbers (time), spatial location on the detector surface, or different crystals, must be equal
  - If more than one crystal was used, intensities of equivalent reflections from different crystals must be equal.
- Scaling involves adjusting the integrated intensities to satisfy as many of those assumptions as reasonably possible.
- For MAD/MIR experiments relative intensity differences are more important than absolute intensities
  - multiple datasets should be scaled relative to each other.

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## Space-group assignment

- Identification of the correct space-group should be postponed for as long as possible until all intensities have been integrated.
- The correct space-group can be determined manually by examining systematic absences and unit cell parameters.
- Software can automate the process, e.g. POINTLESS, XDS, DIALS
- Re-integrating the data after space-group assignment may improve the data quality.

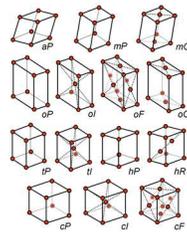


Image credits: © Bernhard Rupp

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## Was data processing successful?

- Always carefully inspect output files/reports to make sure each step was successful.
- Carefully inspect reflection profiles. Symptoms of problems include:
  - Off-centered profiles, Incorrectly predicted spots, (Mis-indexing, Crystal slippage, or change in incident beam direction)
  - Reflections extending to edge of profile
  - Many unintegrated reflections

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### Are the results good enough?

- ▶ Important indicators include,
  - ▶ completeness,
  - ▶ # of outliers, systematic absences if present,
  - ▶  $I/\sigma(I)$ , R-factors,  $CC_{1/2}$ , high resolution limit, anomalous signal, etc.
- ▶ R-merge is a poor guide to data quality
  - ▶ Does not take multiplicity into account
  - ▶ Not a good indicator of the high resolution limit
  - ▶ Variants such as R-meas and R-pim are only slightly better
- ▶ Better alternatives for checking internal consistency:
  - ▶  $I/\sigma(I) \geq 2.0$
  - ▶ Chi-squared  $\approx 1$
  - ▶ Rejecting data may improve the R-values but not the model. See *Acta Cryst. (2013) D69, 1215-1222*



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22

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### Are the results good enough?

- ▶ Pearson correlation coefficient (CC) is a better a better statistic.
- ▶  $CC \geq 0.3$  for anomalous signal is a good high resolution cut-off for phasing
- ▶  $CC_{1/2}$ , (related to CC) is a good statistic for assessing the information content in the reflections.
  - ▶ For  $CC_{1/2}$  around 0.2-0.4,  $I/\sigma(I)$  will be around 0.5-1.5 and there is little information left in the reflections.



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23

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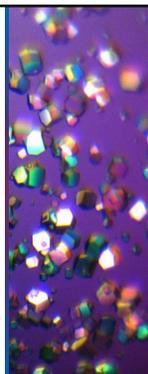
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### Data Processing Software



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## XDS – X-ray Data Streamer

- › Software for processing single-crystal monochromatic diffraction data recorded by the rotation method.
- › XDS can process small-molecule and macromolecular diffraction data from a wide variety of image formats
- › Developed by Wolfgang Kabsch at Max Planck Institute : <http://xds.mpimf-heidelberg.mpg.de/>
- › Free for academic and non-commercial use
- › Primarily command line
  - › Third Party GUI's available
- › References:
  - › *J. Appl. Cryst.* (1988). 21, 67-72.
  - › *J. Appl. Cryst.* (1988). 21, 916-924.
  - › *J. Appl. Cryst.* (1993). 26, 795-800.
  - › *Acta Cryst.* (2010). **D66**, 133-144.
  - › *Acta Cryst.* (2010). **D66**, 125-132.



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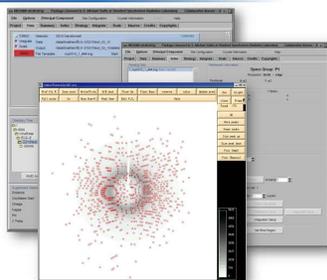
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## HKL2000

- › Software from HKL Research Inc
- › GUI
  - › Command line programs (denzo, scalepack)
- › License required to use
- › Not available at CMCF

<https://www.hkl-xray.com/hkl-2000>



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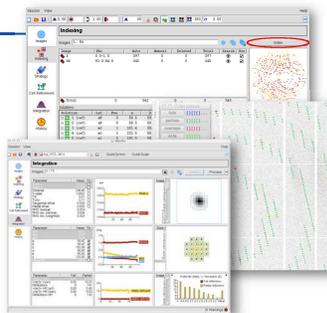
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## iMOSFLM

- › GUI for MOSFLM
- › Included with CCP4
  - › Can be installed separately
- › Available for Windows

<https://www.mrc-lmb.cam.ac.uk/harry/imosflm/>



13

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## DIALS - Diffraction Integration for Advanced Light Sources

- › Open Source Collaborative initiative
- › Newest Data Processing Package
  - › Uses knowledge acquired from history of crystallographic data processing
  - › Written in Python and C++
- › Command line interface
  - › GUI available in CCP4



<https://dials.github.io/>



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