# Data processing and scaling with Mosflm and Aimless

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## Acknowledgements







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## Overview

- How to process and scale your data with Mosflm and Aimless
- Focus on interactive data processing in iMosflm
- Careful scaling using the CCP4i graphical interface

# What are we doing and why are we doing it?



Compute the intensity (and structure factor) of each bragg spot in a set of diffraction images

$$F_{hkl}| = \left(\frac{KI_{hkl}}{Lp}\right)^{\frac{1}{2}}$$

K = constant for given crystalL = Lorentz factorp = polarization factor

$$\rho(x, y, z) = \frac{1}{V} \sum_{h} \sum_{k} \sum_{l} F_{hkl} e^{-2\pi i (hx + ky + lz)}$$

Electron density at every point in the cell depends on the intensity of every reflection. We need to measure out intensities as well as possible!

### Warning: garbage in, garbage out



Data collection is the last experimental stage; if you collect bad data you are stuck with it! Data processing programs won't be able to rescue you!

## iMosflm

Data processing and scaling with Mosflm and Aimless

## Programs

Load images Find spots and index Refine cell parameters Integrate reflections

Check symmetry Scale and merge data Convert I to F Pointless

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Mosflm

- Aimless
  - Ctruncate



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#### The iMosflm GUI



#### **Action buttons:**

- 1. Create session
- 2. Open session
- 3. Save session
- 4. Add images

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Task palette: Only available tasks are live, *i.e.* when no images have been loaded, you can only load images (not index, refine, *etc.*)

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#### **Errors and Warnings:** Clicking will reveal popup with more information

#### **Click here to load images**

#### Adjust beam centre and detector distance manually



#### **Opens a window for you to inspect images**



Mask beam stop shadow Uses circle fitting to fit the beamstop shadow. This region of the detector will not be used during spot finding or integration.



#### Locate beam centre

Uses circle fitting to locate direct beam position. It is important to check since you can't always rely on the information in image headers to be correct!

# Indexing

Data processing and scaling with Mosflm and Aimless

## Purpose

#### Things we do know:

- detector position *etc*.
- where spots appear to be
- goniometer settings for each image

#### Things we don't know:

- unit cell
- miller index hkl
- sample orientation
- crystal lattice type



## Indexing in Mosflm

- 1. Find spots on the image
- 2. Convert 2D image co-ordinates to 3D scattering vectors
- 3. Index *via* Fast Fourier Transform
- 4. Reduce the cell
- 5. List 44 characteristic lattices for cell, with penalty value for each
- 6. Pick a likely solution
- 7. Estimate mosaic spread of the crystal



# Find spots on the diffraction images



Using the Ewald sphere construction, the observed spots  $(X_{d_i}, Y_d, \phi)$  can be mapped back into reciprocal space giving a set of scattering vectors **s**<sub>i</sub>



# This results in a set of points in reciprocal space

x a\*

Auto-indexing then attempts to use these points to find the cell and orientation of the crystal



#### **Indexing tab:**

iMosflm finds spots and automatically indexes when you click the indexing tab

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	⊞ 🖸 13 (reg)	mC	102	305.7	57.8	57.8	90.0	90.0	90.0	-	-	-		
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#### Solutions:

The 44 possible solutions are listed with penalty values
for each. The most likely solution is highlighted. Also gives the best guess for the lattice.

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		oC	1	81.7	81.7	150.1	90.0	90.0	90.0	0.14	0.06	0.36 ( 0.2)	1	
	⊞ <mark>11</mark> (req)	mC	102	305.7	57.8	57.8	90.0	90.0	90.0	-	-	-		
	⊞ 🖸 12 (reg)	oC	102	57.8	305.7	57.8	90.0	90.0	90.0	-	-	-		
	🗄 🚺 13 (reg)	mC	102	305.7	57.8	57.8	90.0	90.0	90.0	-	-	-		
	🗄 🔀 14 (reg)	mC	102	81.7	81.7	170.9	90.0	118.5	90.0	-	-	-		
	🗄 🔀 15 (reg)	mC	103	57.8	305.7	57.8	90.0	90.0	90.0	-	-	-		
	🗄 🚺 16 (reg)	mC	103	57.8	129.2	150.1	90.0	90.0	90.0	-	-	-		
	⊞ 17 (reg)	mC	103	57.8	305.7	57.8	90.0	90.0	90.0	-	-	-		
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#### **Reindexing:**

You can choose which images to use and reindex if necessary



#### **Mosaicity:**

During indexing, mosflm will also estimate the mosaicity





#### **Viewing predictions:**

The image viewer will be updated showing the predictions.

Make sure to inspect the images to see if predictions match observations!

Solutions:											
Solution	Lat.	Pen.	a	b	С	a	ß	τ	d (x,y)	$\sigma(\phi)$	<b>&amp;</b> beam
🕀 🎦 1 (ref)	aP	0	58.5	58.6	62.1	90.1	118.0	120.0	0.20	0.36	0.45 ( 0.1)
🖽 🎦 2 (ref)	аP	0	58.5	58.6	62.1	61.9	62.0	60.0	0.20	0.35	0.45 ( 0.1)
🕀 🎦 3 (ref) 🗌	mC	1	101.5	58.5	62.1	90.0	123.0	90.0	0.21	0.39	0.45 ( 0.2)
🗄 컱 4 (ref)	mC	2	101.5	58.5	62.1	90.0	123.0	90.0	0.21	0.39	0.45 ( 0.2)
🕀 🎦 5 (ref)	mC	2	101.4	58.6	62.2	90.0	123.0	90.0	0.19	0.42	0.44 ( 0.2)
🕀 🎦 6 (ref)	mC	2	101.5	58.5	62.1	90.0	122.9	90.0	0.20	0.36	0.46 ( 0.2)
🕀 🎦 7 (ref)	hR	4	58.6	58.6	156.4	90.0	90.0	120.0	0.21	0.36	0.46 (0.3)
🗄 🚺 8 (reg)	mC	59	85.3	85.5	58.5	90.0	133.2	90.0	-	-	-
🗄 🚺 9 (reg) 🗌	mC	59	103.5	62.1	58.5	90.0	124.3	90.0	-	-	-
🕀 🚺 10 (reg)	mC	60	101.5	58.5	62.1	90.0	123.0	90.0	-	-	-
🕀 🚺 11 (reg)	oI	60	58.5	62.1	85.5	90.0	90.0	90.0	-	-	-
🗄 🚺 12 (reg)	oI	60	58.6	62.2	85.3	90.0	90.0	90.0	-	-	-
🕀 🎦 13 (reg)	tI	61	60.4	60.4	85.3	90.0	90.0	90.0	-	-	-
🗄 🏹 14 (reg)	mC	61	101.5	58.5	62.1	90.0	123.0	90.0	-	-	-
🖽 📬 15 (rea)	hR	61	60.4	60.4	144.9	90.0	90.0	120.0	-	-	-
Spacegroup: h3	•										
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The solution with the highest symmetry from the group of solutions with low penalties (highlighted in blue) is usually chosen as the correct solution, but in cases of pseudosymmetry the rms error in spot positions ( $\sigma(x,y)$ ) is also important. Reasonable solutions in labelled in green.



# Check the predictions match the observations:

In this case the predictions are <u>not</u> nicely aligned with the spots



# Check the predictions match the observations:

In this case the predictions are better aligned with the spots

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	Show lattices summary [+] Spacegroup: h3		Search beam-cent	tre [-]							
	Mosaicity: 1.00 Estimate										
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After indexing you can refine the direct beam position to get better predictions

## Cell refinement

Data processing and scaling with Mosflm and Aimless



# To obtain a good estimate of cell parameters which can then be fixed during integration

Crystal	Detector	Beam
Cell dimensions	Position	Orientation
Orientation	Orientation	Divergence
Mosaic spread	Distortion	

**Refined parameters** 

## Cell refinement in Mosflm

- Uses the relative intensities of the parts of partial reflections that are spread across multiple images
- Minimises the differences between the observed and calculated spots on the Ewald sphere.
- Provides very accurate cell parameters
- Requires:
  - A reasonable knowledge of intensities: mosflm selects a few frames to be integrated
  - A model for how we expect the intensities of the parts to vary between images – the "rocking curve"
#### Fully and partially recorded reflections



000		X iMosf	lm 1.0.7 – May 2012 (using M	osflm 7.0.9)			
Session Setting	IS						Help
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	💟 Final	57.78	57.78	150.03	90.00	90.00	
	Std dev	0.00	0.00	0.00	0.00	0.00	0.00
						No	) Warnings 🐼

#### **Cell refinement tab:**

Shows average profile

RMS residuals should be small

Shows initial and final unit cell parameters

# Integration/Refinement

Data processing and scaling with Mosflm and Aimless

### Purpose

#### What we know:

- Where the spots should be (i.e. orientation, cell, geometry)
- What Miller indices belong to the spots
- How many images the spots are on (mosaic spread)
  This is Integration

#### What we don't know:

• Spot intensities

168	192	188	179	175	162	185	192	198	179	161	172	176	172	180	156	155	146	149	153	157
150	174	169	184	186	186	186	182	172	160	151	185	163	189	169	171	143	143	152	156	162
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165	163	169	168	170	182	171	160	164	184	199	173	179	177	173	204	183	167	159	154	172
162	165	164	173	171	153	180	204	193	200	203	178	186	192	181	161	139	142	162	148	178
190	144	182	179	190	171	194	224	261	293	288	237	196	192	211	176	164	159	170	157	167
185	176	168	156	174	182	207	279	440	522	506	353	211	194	168	186	175	167	163	174	167
163	179	193	182	191	198	189	324	758	1119	1014	605	304	195	181	183	180	159	161	148	172
161	169	188	171	185	200	211	328	667	1082	1130	681	287	196	174	149	176	162	155	161	155
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141	143	153	172	166	198	187	197	192	239	242	210	177	164	170	140	139	161	191	169	144
165	159	161	156	162	173	183	169	163	184	192	178	157	178	169	151	165	175	167	174	160
160	163	158	170	174	164	144	141	144	174	145	178	169	162	179	165	162	169	157	159	159
148	171	167	191	179	160	169	167	175	164	165	165	173	158	157	170	179	161	153	182	159
168	161	168	182	173	184	168	159	175	168	169	168	164	154	145	155	171	146	174	182	162

This is a diffraction spot. All we want to do is measure the number of counts in the peak minus the background counts. Simple!

## Refinement and prediction

- Need to predict reflection positions accurately to avoid systematic errors in integration
- The detector parameters, crystal orientation and mosaic spread will be refined for every image during integration
- Cell parameters are kept fixed during integration
- Refined parameters such as the detector distance and YSCALE would not be expected to change during an experiment
- However, these parameters can compensate for errors in the cell parameters

### **Background subtraction**

- Create a peak/background mask by maximizing I/sigma
- Estimate background in peak region by fitting a plane to pixels in the background region and interpolating
- Errors in mask definition can give systematic errors in intensities



Parameters NRX, NRY, NC are optimised by maximising  $I/\sigma(I)$  (Lehmann & Larsen)



### Integration in Mosflm

Two methods:

- Summation integration: *signal = total counts background*
- Profile fitting: form standard profiles and fit to each reflection to estimate the intensity minimize  $\sum \omega_i (x_i Kp_i)^2$

## Profile fitting

Spots in the same region of the detector have similar profiles

Assume that the shape or profile of the spots is known. Then determine the scale factor which, when applied to the <u>known</u> spot profile, gives the best fit to be <u>observed</u> spot profile.

Profile fitting is more reliable for weak reflections than summation integration. Effectively "down-weight" peripheral peak pixels relative to the central pixels.

#### **Standard profiles:**

Determined empirically by computing the weighted mean of many spots.

The spot shape varies according to position on the detector.

This is done by forming a grid of standard profiles





Integration tab: To perform the integration, click on the integration tab and then click "Process"



# Refined detector parameters:

Check tilt and twist are stable; might need to fix. Yscale should also be ~1.0



#### Refined crystal parameters: Ensure that cell parameters are fixed





Details:	
The ratio of the observed variation in background pixels to that expected he BGRATIO) lies outside the range 0.9 to 1.1. Actual values: minimum: 1.1 The most likely explanation is that the GAIN of the detector is incorrect. N is 0.25 but the observed BGRATIO suggests it should be set to 0.34.NOTE fuse scatter can lead to an increased value of BGRATIO even when the gain e the gain for any detector should remain constant, it should be worked ou giving strong diffraction and clean spots (ie no disorder or diffuse scatt his value. Processing data with an incorrect gain will result in a systema of very weak reflections and incorrect standard deviations.	statistically (t 6 maximum: 1.16 The current GAI however that dif is correct. Sinc it for a crystal er)and kept at t tic overestimate
Hints:	[Interview ]
change GAIN to 0.34	Experiment Detector
Notes:	Refineable detector parameters
Sorry no further information	Offsets: radial: 0,000 tangen 0,000
	ccomega 0.00
	Detector tilt: 0.02 twist: 1.81
	Non-refineable detector parameters
	Detector: ADSC model: Q315
	Serial number: 921
	Gain. 0.23
	Pixel size: 0.10260
Sometimes the gain needs to be set manually	Default parameti Reset
	Close

# Quick scaling

Data processing and scaling with Mosflm and Aimless

### Purpose

Things we know:

- I, sig(I), corrected for geometric effects
- Lots of observations
- Symmetry

Things we don't know:

- |F|<sup>2</sup>
- Beam intensity
- Illuminated volume
- Absorption path through crystal
- Extent of sample decay

## Scaling

- Corrections for some of the things we don't know can be determined experimentally
- In most cases however empirical corrections are determined
- Have a model for: overall scale (beam intensity + illuminated volume) sample decay and absorption
- Refine model against data, to minimise differences between symmetry related intensities

## Scaling models

- Time or frame # dependent overall scale
- Time and resolution dependent decay
- Direction dependent absorption for example as spherical harmonics
- All depends on multiplicity



## **Objective of scaling**

- To model all of the unknown contributions to the measured intensity
- To recover I=k|F|<sup>2</sup> for each observation
- Achieved by minimizing the differences between observations internally consistent not necessarily correct!
- Final result of scaling is average  $||k||^2$  for each unique Miller index
- May want to keep I+ and I- separate

### Merging statistics

- Level of agreement between unmerged I is usually guide to data quality
- For strong measurements this is dominated by experimental effects e.g. radiation damage
- For weak reflections dominated by signal-to-noise
- Best merging statistics give a guide to how useful the averaged measurements are

## Programs

#### Pointless

- Determines likely point group
- Corrects space group *if* sufficient information
- Sorts reflections
- Detects screw axes & glide planes
- Re-indexes multiple datasets to a common setting

#### Aimless

- Merges partial reflections together
- Puts data onto a common scale
- Merges each set of symmetry equivalent reflections into a single observation

#### CTruncate

- Analyses scaled data according to an expected physical model
- Gives statistics on intensity distribution *e.g.* 
  - Wilson statistics
  - twinning analysis
- Outputs |F| values



Run Pointless, Aimless and cTruncate to scale the data

Run Pointless to check pointgroup

#### Quick Symmetry

#### Run of POINTLESS on 12/ 8/2013 at 12:52:29



Best Solution: space group P 41 21 2 Reindex operator: [h,k,1] Laue group probability: .000 Systematic absence probability: 973 Total probability: 0.9.3 Space group confidence: 0.962 Laue group confidence 1.000 Unit cell: 57.78 57.78 150 90 90 90 - Resolution range used for Laue group search 50.01 to 1.89 50.01 to 1.42 - Resolution range in file, used for systematic absence check Number of batches in file: 540 The data do not appear to be twinned, from the L-test

Check pointgroup is consistent with lattice used for integration



#### Quick Scale

Minimum and maximum SD correction factors: Fulls 0.90 1.86 Partials 0.69 9.08 Anomalous flag switched ON in input but the anomalous signal is weak



## Judging data quality

- Are there bad batches?
- Was the radiation damage such that you should exclude the later parts?
- What is the real resolution? Should you cut the high-resolution data?
- Is there any apparent anomalous signal?
- Is the outlier detection working well?
- Are the data twinned?
- What is the overall quality of the dataset?

#### Rmerge: finding bad batches



Would like to have relatively stable rmerge across all batches

#### Scales and B-factors: radiation damage



Ideally have constant scaling factor of 1; except if crystals have an irregular shape. Drop in B factor below -10 indicates radiation damage

#### Number of rejections per image

Ν	Run.Rot	MidPhi	Batch	Bfactor	Mn(k)	0k	Number	NumReject
1	1.1	-49.50	1	-0.694	1.0651	0.9940	1703	0
2	1.2	-48.50	2	-0.688	1.0622	0.9905	2193	0
3	1.3	-47.50	3	-0.677	1.0564	0.9851	2219	0
4	1.4	-46.50	4	-0.668	1.0453	0.9774	2202	0
5	1.5	-45.50	5	-0.656	1.0339	0.9671	2198	0
6	1.6	-44.50	6	-0.641	1.0180	0.9542	2217	1
7	1.7	-43.50	7	-0.629	1.0017	0.9395	2208	0
8	1.8	-42.50	8	-0.614	0.9811	0.9185	2217	0

Want low number of rejected reflections per image; a maximum of around 5





### Anomalous differences

Anomalous differences



A slope > 1 in the centre indicates that the measured anomalous differences are greater than would be expected from the standard deviations.

### Detecting twinning

- Depends on moments of intensity distributions
- Acentric E<sup>4</sup> is useful: if 2 probably not twinned, if 1.5 probably twinned
- Measures the spread of the merged intensity distribution
- Look at ctruncate output
- More twinning tests are performed, check ctruncate log


### Data Quality: Rmerge vs intensity

Rmerge v Intensity



Rmerge is always large for small intensities. For large intensities it should be in the range 0.01 to 0.04 for good data. Larger values suggest that there are systematic errors.

#### Data Quality: completeness



Completeness of data should be as close to 100% as possible. Watch out for data with < 95% completeness. Some loss of completeness can be tolerated in the outermost resolution bins. If you integrate to the corners of the detector, you may have low completeness at high resolution.

# More scaling

Data processing and scaling with Mosflm and Aimless

## After iMosflm

- Quick scaling useful to see if there is nothing pathological with your data set however...
- Move on to using CCP4i
- Probably easiest to create a new "project" and copy in the MTZ file from iMosflm
- N.B. take care with consistent indexing scaling multiple data sets



○ ○ ○ X Aimless - Pointless, Aimless, Ctruncate			
		Help	
Job title Scale data with Aimless			
Custom scaling options: default is to determine Laue group, refine & apply scales, and write merged	l data		
🔲 Customise symmetry determination 🔲 Option to skip scaling & just merge 🔲 Customise	e output options		
Separate anomalous pairs for outlier rejection & merging statistics			
Run Ctruncate to output Wilson plot and SFs after scaling and output a single MT	rz file		
Ensure unique data & add FreeR column for 0.05 fraction of data.			
Input reflection file type: MTZ file 🔤 🔄 treat filenames as Mosfim templates (ie t	o match multiple file	es)	
Project name: DEMO crystal name: THAUMATIN dataset name: NATIVE			
HKLIN #1 THAUMATIN - th_8_2_0001.mtz	Browse View	v	
	Add File	e	
UKLOUT THAUMATIN the 9-2-0001 cooled mtz	Drawna 1 Mar		
	Browse		Mostim MTZ file name
Resolution and batch exclusions			
Exclude data resolution less than 50.010 Angstrom or greater than 1.422 Angstrom			
_ Exclude selected baches		_	
	,		
Scale with automatic default settings			
Define Runs			
Accepted and Excluded Data			
Reject Outliers			
SD Correction Protocols			
Observations Used & Handling of Partials	I		
Scaling Details			1
Truncate: convert to structure amplitudes and final output			Z
Run - Save or Restore -	Close		

# Selecting scaling models

- If you have or expect an anomalous signal, tell the scaling program
- Try different scaling models if you don't need a correction, don't apply it
- If you have multiple data sets (MAD data set or multi-pass) scale them together now
- For multiple wavelengths assign different DATASET names

### MAD



## Multi-pass



# Radiation damage



# Thank you for listening!

http://www.ccp4.ac.uk