

# *Principles of data processing with XDS*

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# Outline

- General information about *XDS*
- Usage, problems, diagnostics
- Demonstration of XDSgui: processing of students' data

throughout this talk: *program*, **file**

# The *XDS* program suite

Original author: Wolfgang Kabsch (Max-Planck-Institute Heidelberg);  
I joined in 2007

Distribution for Linux & Mac: new version every ca. 6 months (latest: Jan-2014; <http://xds.mpimf-heidelberg.mpg.de/>)

- *XDS*: the main program (indexing, integrating, scaling)
- *XSCALE*: scale several *XDS* intensity data sets together; zero-dose extrapolation; statistics
- *XDS CONV*: convert to other programs' formats

The following programs are independent of the *XDS* distribution:

- *XDS-Viewer* - inspect diagnostic images written by *XDS*, or (single) data frames (open source: [sourceforge.net](http://sourceforge.net)). Instead, *adxv* may be used
- *XDSSTAT* - additional statistics (not part of main distribution; download and use: see [XDSwiki](http://XDSwiki))
- *XDSGUI* – graphical user interface (open source: [sourceforge.net](http://sourceforge.net))

# interfaced to ...

- beamline software (generating **XDS.INP**)
- scripts: *xia2* (CCP4), *autoPROC* (Globalphasing), *xdsme* (Soleil), *autoxds* (SSRL), *autoprocess* (CMCF), ...  
*generate\_XDS.INP*
- CCP4: *pointless*, *xdsconv* (type CCP4, or CCP4\_I, or CCP4\_F)

# Sources of information

- XDS main website: <http://xds.mpimf-heidelberg.mpg.de> - complete, accurate, up-to-date documentation; download
- XDSwiki: [http://strucbio.biologie.uni-konstanz.de/xdswiki/index.php/Main\\_Page](http://strucbio.biologie.uni-konstanz.de/xdswiki/index.php/Main_Page)
- CCP4 bulletin board
- “XDS webinar” (<http://www.rigaku.com/downloads/webinars/kay-diederichs/>)
- “X-ray tutorial” (Faust *et al.* JAC 2008, 2010)
- Email to [kay.diederichs@uni-konstanz.de](mailto:kay.diederichs@uni-konstanz.de)

# XDSwiki

- started Feb 2008; ~ 60 pages at [http://strucbio.biologie.uni-konstanz.de/xdswiki/index.php/Main\\_Page](http://strucbio.biologie.uni-konstanz.de/xdswiki/index.php/Main_Page)
  - e.g. „Optimization“; explanations of task output
  - „Tips and Tricks“, „FAQ“
  - „Quality Control“ with datasets and results, and links to the projects of the ACA2011 and ACA2014 „data processing“ workshop
  - anybody can contribute!
- (same holds for CCP4wiki: ~ 90 pages at [http://strucbio.biologie.uni-konstanz.de/ccp4wiki/index.php/Main\\_Page](http://strucbio.biologie.uni-konstanz.de/ccp4wiki/index.php/Main_Page) )

# XDS features

(just a short selection)

- 3D - profiles of reflections are transformed into their own coordinate systems which makes them highly similar (Kabsch 1988 *J. Appl. Cryst.* **21**, 916-924.)
- Smooth scaling (*ibid.*)
- Zero-dose extrapolation (*XSCALE*) can help a lot in sub-structure determination (Diederichs *et al.* 2003, *Acta Cryst.* **D59**, 903-909.)
- Fast - two levels of parallelization

# How to use *XDS* ?

- XDS needs a single input file **XDS.INP** with parameters describing data reduction
- Keywords and their parameters have the form e.g. DETECTOR\_DISTANCE= 120.
- There are about 30 relevant keywords, but only about 15 are required (and may change between projects). All parameters have reasonable defaults where possible.
- shortcut: *generate\_XDS.INP* from XDSwiki
- Run *xds\_par* (on the commandline)



# Example for MarCCD

```
JOB= XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT
ORGX=1546 ORGY=1552 !Detector origin (pixels); e.g. NX/2 NY/2
DETECTOR_DISTANCE=180 ! (mm)
OSCILLATION_RANGE=0.50 !degrees (>0)
X-RAY_WAVELENGTH=0.980243 !Angstroem
NAME_TEMPLATE_OF_DATA_FRAMES=frms/wga2-27_1_???.img
DATA_RANGE=1 360 !Numbers of first and last data image collected
BACKGROUND_RANGE=1 10 !Numbers of first and last data image for background
SPACE_GROUP_NUMBER= 19 !0 for unknown crystals; cell constants are ignored.
UNIT_CELL_CONSTANTS= 44.4 86.4 104.5 90 90 90
REFINE (IDXREF)=BEAM AXIS ORIENTATION CELL DISTANCE
REFINE (INTEGRATE)=DISTANCE BEAM ORIENTATION CELL ! AXIS
ROTATION_AXIS= 1.0 0.0 0.0
INCIDENT_BEAM_DIRECTION=0.0 0.0 1.0
FRACTION_OF_POLARIZATION=0.99 ! SLS X06SA
POLARIZATION_PLANE_NORMAL= 0.0 1.0 0.0
DETECTOR=CCDCHESS MINIMUM_VALID_PIXEL_VALUE=1 OVERLOAD=65000
DIRECTION_OF_DETECTOR_X-AXIS= 1.0 0.0 0.0
DIRECTION_OF_DETECTOR_Y-AXIS= 0.0 1.0 0.0
VALUE_RANGE_FOR_TRUSTED_DETECTOR_PIXELS= 7000 30000 !Used by DEFPIX
!for excluding shaded parts of the detector.
INCLUDE_RESOLUTION_RANGE=50.0 1.3 !Angstroem; used by DEFPIX,INTEGRATE,CORRECT
```

**Bold** keyword/parameter pairs are required. Complete documentation at

[http://xds.mpimf-heidelberg.mpg.de/html\\_doc/xds\\_parameters.html](http://xds.mpimf-heidelberg.mpg.de/html_doc/xds_parameters.html)

Templates for many detectors at

[http://xds.mpimf-heidelberg.mpg.de/html\\_doc/detectors.html](http://xds.mpimf-heidelberg.mpg.de/html_doc/detectors.html)

# Principle of *XDS* processing

- *The basic idea is simple*
- There is one JOB= line in **XDS.INP** which specifies a list of tasks/jobs:

```
JOB= XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT
```

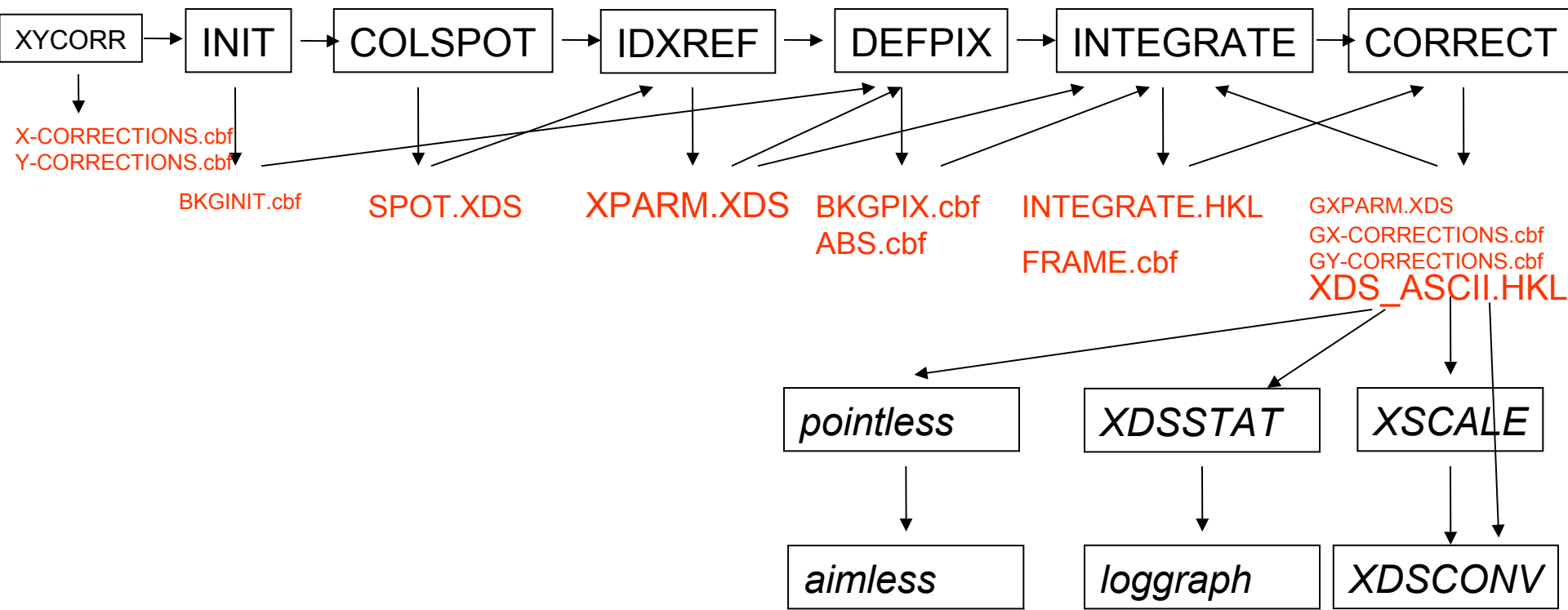
- data reduction is divided into tasks/jobs in **modular** way
- information storage/exchange/flow between tasks by data files which may be inspected/analyzed
- each task needs the result from the previous tasks
- fine-tuning of a task does *not* require previous tasks to be repeated
- each task writes its output file **<TASK>.LP**

# Using *XDS* – steps („JOBS“)

- XYCORR : write positional correction files  
( *X-CORRECTIONS.cbf*, *Y-CORRECTIONS.cbf* )
- INIT : find background pixels (defaults usually OK)
- COLSPOT: find reflection positions
- IDXREF : "index" reflections; user may supply/choose spacegroup
- XPLAN [not required] : strategy for data collection
- DEFPIX : find beamstop shadow (defaults mostly OK)
- INTEGRATE : evaluates intensities on all frames, writes *INTEGRATE.HKL* and *FRAME.cbf*
- CORRECT : scales, rejects outliers, statistics, writes *XDS\_ASCII.HKL* (and other files)

# Information flow

NAME_TEMPL	OSCILLATION	ORGX	DATA_RANGE
ATE_OF_DAT	_RANGE	ORGY	
A_FRAMES	SEPMIN	DETECTOR_DISTANCE	
DETECTOR	STRONG_PIX	X_RAY_WAVELENGTH	
	EL	SPACE_GROUP_NUMBER	



```

!FORMAT=XDS_ASCII    MERGE=FALSE    FRIEDEL'S_LAW=TRUE
!OUTPUT_FILE=XDS_ASCII.HKL          DATE= 3-Oct-2006
!Generated by CORRECT    (XDS VERSION August 18, 2006)
!PROFILE_FITTING= TRUE
!SPACE_GROUP_NUMBER= 92
!UNIT_CELL_CONSTANTS= 57.71    57.71    150.08    90.000    90.000    90.000
!NAME_TEMPLATE_OF_DATA_FRAMES= ../series_2_????.img
!DATA_RANGE= 1    399
!X-RAY_WAVELENGTH= 0.939010
!INCIDENT_BEAM_DIRECTION= 0.001872 -0.002230 1.064947
!FRACTION_OF_POLARIZATION= 0.980
!POLARIZATION_PLANE_NORMAL= 0.000000 1.000000 0.000000
!ROTATION_AXIS= 0.999995 0.002477 -0.001917
!OSCILLATION_RANGE= 0.500000
!STARTING_ANGLE= 30.000
!STARTING_FRAME= 1
!DETECTOR=ADSC
!DIRECTION_OF_DETECTOR_X-AXIS= 1.00000 0.00000 0.00000
!DIRECTION_OF_DETECTOR_Y-AXIS= 0.00000 1.00000 0.00000
!DETECTOR_DISTANCE= 189.286
!ORGX= 1541.25 ORGY= 1535.30
!NX= 3072 NY= 3072 QX= 0.102600 QY= 0.102600
!NUMBER_OF_ITEMS_IN_EACH_DATA_RECORD=12
!ITEM_H=1
!ITEM_K=2
!ITEM_L=3
!ITEM_IOBS=4
!ITEM_SIGMA(IOBS)=5
!ITEM_XD=6
!ITEM_YD=7
!ITEM_ZD=8
!ITEM_RLP=9
!ITEM_PEAK=10
!ITEM_CORR=11
!ITEM_PSI=12
!END_OF_HEADER

```

XDS output file:  
**XDS\_ASCII.HKL**

```

0 0 4 4.287E-01 2.814E-01 1501.6 1514.4 99.4 0.00920 100 27 75.39
0 0 -4 2.243E-01 2.386E-01 1587.4 1548.6 91.6 0.00920 100 30 -79.02
0 0 5 5.976E-03 3.443E-01 1490.9 1510.2 100.4 0.01150 100 22 74.94

```

# What can go wrong?

Beamline: beam center wrong (90%) or unusual convention, rotation backwards; shutter jitter, beam flicker, vibrations ...

Detector: hot or cold pixels; distortions

Experiment: crystal with split reflections; ice rings; radiation damage

Interpretation of data: twinning overlooked, or wrong spacegroup

Phasing and refinement: anomalous signal too weak; low resolution; disorder; anisotropy

# The “error model”

Random error:  $\sigma_r(I) \approx \sqrt{I}$

this is what INTEGRATE calculates

Systematic errors:  $\sigma_s(I) \approx b * I$

this leads to deviations  $> \sigma_r(I)$  between sym-related reflections

New  $\sigma(I)$  estimate:  $\sigma(I) = \sqrt{a * (\sigma_r(I) + b * I^2)}$

with constants a,b fitted by CORRECT for the dataset

When random error vanishes (“asymptotically”),  
this results in  $I/\sigma(I) = 1/\sqrt{a*b}$

# A *proxy* for good data

$(I/\sigma)_{\text{asymptotic}} = ISa$  (reported in **CORRECT.LP**) is a measure of systematic error arising from beamline, crystal, and data processing

For a given data set,  $ISa$  increases: if the geometric parameterization is improved; if the correct choice of “FRIEDEL'S\_LAW=TRUE” or “FALSE” is made; if BEAM\_DIVERGENCE and REFLECTING\_RANGE are correct. In short: when the experimental data are well processed

*Maximizing  $ISa$  (good values are 30 and higher) means minimizing systematic errors;*

*This usually also optimizes  $CC_{1/2}$  at high resolution*



# *XDSgui*

- Simple GUI using Qt
- Adapted to the XDS philosophy
- User – extensible / modifiable commands
- Plots synchronously with processing
- Documentation and availability: XDSwiki

# References

- Kabsch, W. (1988) Evaluation of single-crystal X-ray diffraction data from a position-sensitive detector. *J. Appl. Cryst.* **21**, 916-924
- Kabsch, W. (2010) *XDS*. *Acta Cryst.* **D66**, 125-132 (open access)
- Kabsch, W. (2010) Integration, scaling, space-group assignment and post-refinement. *Acta Cryst.* **D66**, 133-144 (open access)
- Diederichs, K., McSweeney, S., Ravelli, R. (2003) Zero-dose extrapolation as part of macromolecular synchrotron data reduction. *Acta Cryst* **D59**, 903-909
- Diederichs, K., Junk, M. (2009) Post-processing intensity measurements at favourable dose values. *J. Appl. Cryst.* **42**, 48-57
- Diederichs K. (2009) Simulation of X-ray frames from macromolecular crystals using a ray-tracing approach. *Acta Cryst.* **D65**, 535-42
- Diederichs K. (2010) Quantifying instrument errors in macromolecular X-ray datasets. *Acta Cryst.* **D66**, 733-740

# Thank you!

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