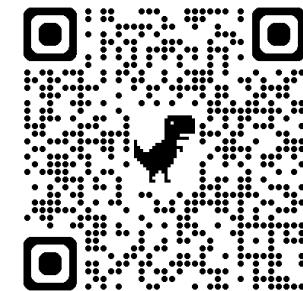


Acknowledgements

Robert Stroud James Fraser Nevan Krogan
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UCSF LBNL SLAC

ALS 8.3.1: TomAlberTron

NIH NIGMS R01 GM124149 (Holton)

NIH NIAID P50 AI150476 (Krogan)

NIH NIGMS P30 GM124169 (Adams)

DOE-BER IDAT (Hura)

NIH NIGMS P30 GM133894 (Hodgson)

Useful links

https://bl831.als.lbl.gov/~jamesh/powerpoint/?C=M;O=D

Index of /~jamesh/powerpoint

Name	Last modified	Size	Description
Parent Directory			
RapiData_XDTutorial_>	2024-04-30 09:21	1.6M	
RapiData_XDTutorial_>	2024-04-30 09:21	1.5M	
fear_no_Spacegroups.mp4	2024-03-13 13:47	326M	
fear_no_Spacegroups.pdf	2024-03-13 09:38	6.9M	
fear_no_Spacegroups...>	2024-03-12 20:27	106M	
Ringberg_tangle_2024...>	2024-02-15 05:54	7.0M	
SIBYLS_tangle_2024.pptx	2024-01-08 11:38	6.0M	
MX_at_ALS_JMH.pptx	2023-12-04 21:18	10M	

phasertng

ELVES

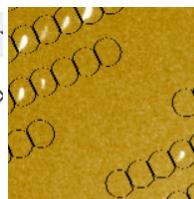
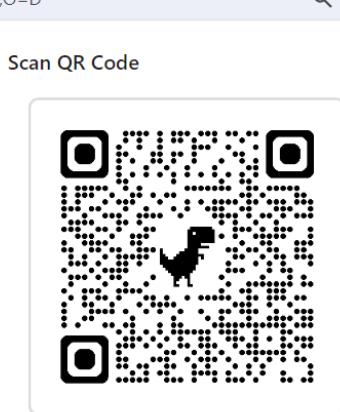
Chapter 7: Tips and Tricks

Neat-o unix commands

is the little sentence you type to run unix programs. The text that appears on each line to the left of the command prompt. This is a very old convention, but it is incredibly powerful. No graphical interface comes close to providing the detailed control that a command line gives you. The only problem with them almost always have obtuse syntax, and novice users have a really hard time figuring out what to do. I've created a quick guide for crystallographers who want to optimize their unix environment without reading all the unix manuals that I have. :)

The unix "shell"

Your "shell" program is probably tcsh (Turbo-C-shell). All a shell program does is accept your typed commands, find and run the unix program you have invoked, and then prompt you for another command. That's about it. However, the shell is



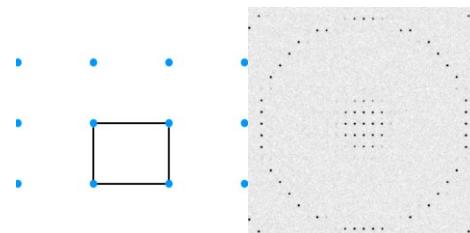
Page Discussion Read View

Difficult datasets

The following suggestions apply not only to or low-resolution, or otherwise difficult macromolecular datasets.

These datasets have few (or few strong, or few well-defined) reflections per frame. Therefore, the multitude of parameters describing the diffraction experiment needs to be reduced (in refinement one would say: to avoid overfitting). This means that some

Fear no Space Groups

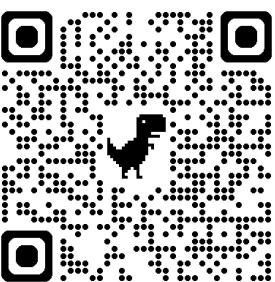
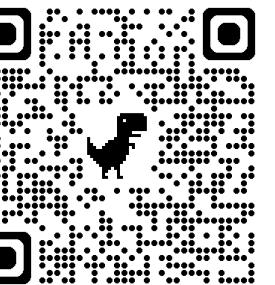


James Holton's Benchmarks...

Comparison of x-ray programs on different machines

The following tables are a comparison of standard x-ray data-processing, access to. The machine names have been omitted to protect the innocent. "major" process on the machine, and always from a local disk. The exact moved from machine to machine.

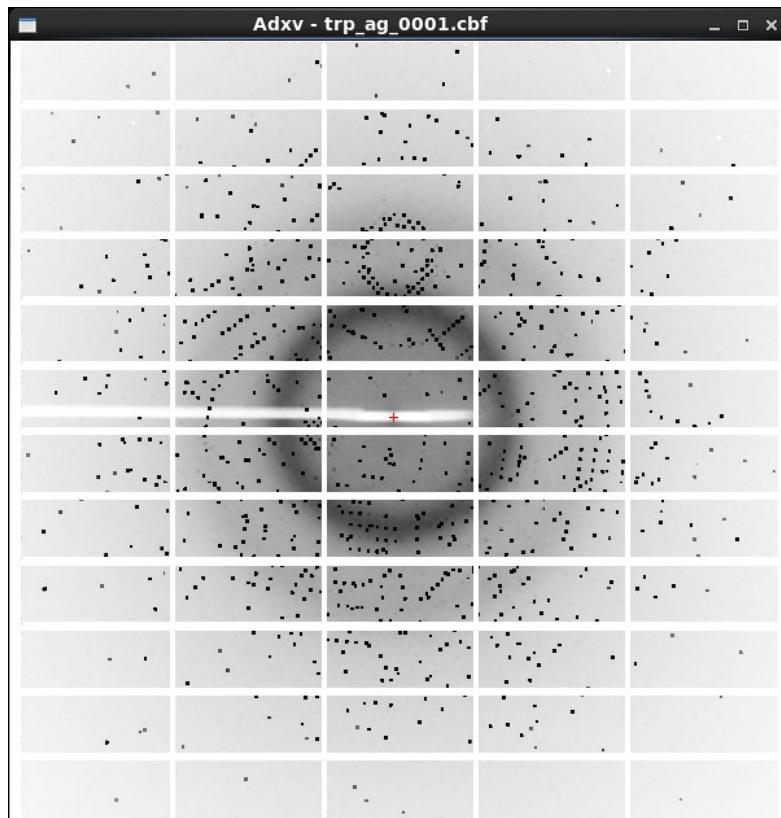
Speed of DIALS



XDS

X-ray diffraction data reduction engine

Diffraction image data



List of spot intensities (text)

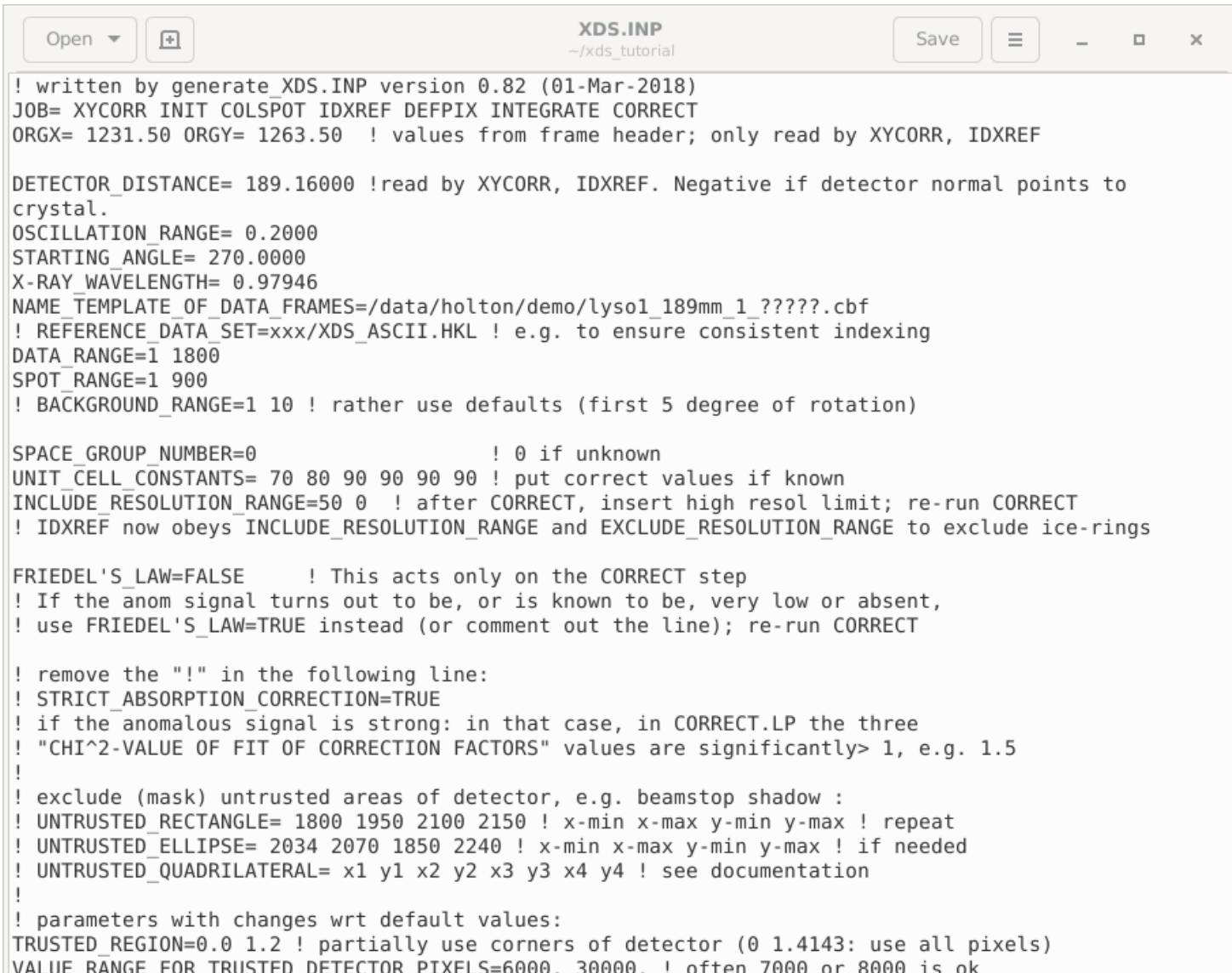
XDS_ASCII.HKL
/dev/shm/jamesh/bench

```
!DIRECTION_OF_DETECTOR_Y-AXIS= 0.00000 1.00000 0.00000
!VARIANCE_MODEL= 9.618E-01 2.594E-04
!NUMBER_OF_ITEMS_IN_EACH_DATA_RECORD=12
!ITEM_H=1
!ITEM_K=2
!ITEM_L=3
!ITEM_I0BS=4
!ITEM_SIGMA(I0BS)=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
 0   0      1 -4.155E-01  4.271E-01  1323.0  1256.5  24
 0   0      1 2.890E-01  4.948E-01  1323.0  1208.6  26
 0   0      1 2.898E-01  4.947E-01  1323.0  1208.6  22
 0   0      1 2.899E-01  4.941E-01  1323.0  1208.6  18
 0   0      1 -4.165E-01  4.266E-01  1323.0  1256.5  20
 0   0      1 2.897E-01  4.947E-01  1323.0  1208.6  33
 0   0      1 -4.155E-01  4.264E-01  1323.0  1256.5  35
 0   0      1 -4.162E-01  4.269E-01  1323.0  1256.5  31
 0   0      1 -4.157E-01  4.273E-01  1323.0  1256.5  27
 0   0      1 2.919E-01  4.946E-01  1323.0  1208.6  29
 0   0      1 -4.188E-01  4.267E-01  1323.0  1256.5  6
 0   0      1 2.896E-01  4.942E-01  1323.0  1208.6  8
 0   0      1 -2.905E-01  -4.040E-01  1323.0  1208.6  1
```

Plain Text ▾ Tab Width:

XDS

native user interface: a text file!



The screenshot shows a text editor window with the following details:

- File menu:** Open, Save, Minimize, Maximize, Close.
- Title bar:** XDS.INP, ~/xds_tutorial
- Content:** An XDS configuration file (XDS.INP) with the following text:

```
! written by generate_XDS.INP version 0.82 (01-Mar-2018)
JOB= XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT
ORGX= 1231.50 ORGY= 1263.50 ! values from frame header; only read by XYCORR, IDXREF

DETECTOR_DISTANCE= 189.16000 !read by XYCORR, IDXREF. Negative if detector normal points to
crystal.
OSCILLATION_RANGE= 0.2000
STARTING_ANGLE= 270.0000
X-RAY_WAVELENGTH= 0.97946
NAME_TEMPLATE_OF_DATA_FRAMES=/data/holton/demo/lysol_189mm_1_?????.cbf
! REFERENCE_DATA_SET=xxx/XDS_ASCII.HKL ! e.g. to ensure consistent indexing
DATA_RANGE=1 1800
SPOT_RANGE=1 900
! BACKGROUND_RANGE=1 10 ! rather use defaults (first 5 degree of rotation)

SPACE_GROUP_NUMBER=0 ! 0 if unknown
UNIT_CELL_CONSTANTS= 70 80 90 90 90 90 ! put correct values if known
INCLUDE_RESOLUTION_RANGE=50 0 ! after CORRECT, insert high resol limit; re-run CORRECT
! IDXREF now obeys INCLUDE_RESOLUTION_RANGE and EXCLUDE_RESOLUTION_RANGE to exclude ice-rings

FRIEDEL'S_LAW=FALSE ! This acts only on the CORRECT step
! If the anom signal turns out to be, or is known to be, very low or absent,
! use FRIEDEL'S_LAW=TRUE instead (or comment out the line); re-run CORRECT

! remove the "!" in the following line:
! STRICT_ABSORPTION_CORRECTION=TRUE
! if the anomalous signal is strong: in that case, in CORRECT.LP the three
! "CHI^2-VALUE OF FIT OF CORRECTION FACTORS" values are significantly> 1, e.g. 1.5
!
! exclude (mask) untrusted areas of detector, e.g. beamstop shadow :
! UNTRUSTED_RECTANGLE= 1800 1950 2100 2150 ! x-min x-max y-min y-max ! repeat
! UNTRUSTED_ELLIPSE= 2034 2070 1850 2240 ! x-min x-max y-min y-max ! if needed
! UNTRUSTED_QUADRILATERAL= x1 y1 x2 y2 x3 y3 x4 y4 ! see documentation
!
! parameters with changes wrt default values:
TRUSTED_REGION=0.0 1.2 ! partially use corners of detector (0 1.4143: use all pixels)
VALUFE RANGE FOR TRUSTED DETECTOR PTXELS=6000..30000. ! often 7000 or 8000 is ok
```

Generate XDS.INP

This script generates XDS.INP based on a list of frame names supplied on the commandline. It currently works for MarCCD, ADSC, Pilatus, Eiger, some Rigaku and one Bruker detector(s); since this is just a bash script, extension to other detectors should be very easy.

Contents [hide]

- [1 Usage](#)
- [2 The script](#)
- [3 System-wide or personal installation](#)
- [4 Copying generate_XDS.INP from XDSwiki webserver](#)
- [5 Obtaining generate_XDS.INP from this webpage](#)
- [6 Calling generate_XDS.INP from a Python script](#)
- [7 Dependencies](#)
- [8 Limitations](#)
- [9 See also](#)

Usage

Usage is just (don't forget the quotation marks!):

```
generate_XDS.INP "/home/myname/frms/mydata_1_???.img"
```

XDS supports bzip2-ed frames. Thus, when specifying the frame name parameter of the script, you should leave out any .bz2 extension.

A better image viewer



The screenshot shows a web browser window with the title "Adxv". The address bar contains the URL <https://www.scripps.edu/tainer/arvai/adxv.html>. The main content area displays the heading "Adxv - A program to display X-Ray diffraction images" in bold black font. Below the heading is a paragraph of text describing the program's capabilities.

Adxv - A program to display X-Ray diffraction images

Adxv can be used to display and analyze 2-D area detector data. It is optimized to display X-Ray crystallography diffraction images. The data may be displayed as a 1-D cross section, 2-D image or 3-D surface. Sequential images may be displayed as an animation. The magnification, contrast and color mapping are adjustable. Displayed data may be saved in a variety of formats including ASCII, SMV/IMG, TIFF, JPEG and Postscript. Adxv will run on most versions of Linux and OSX. It is based on X11/Motif so an X-server is required. It will run on Windows if the Cygwin libraries and X-server have been installed.

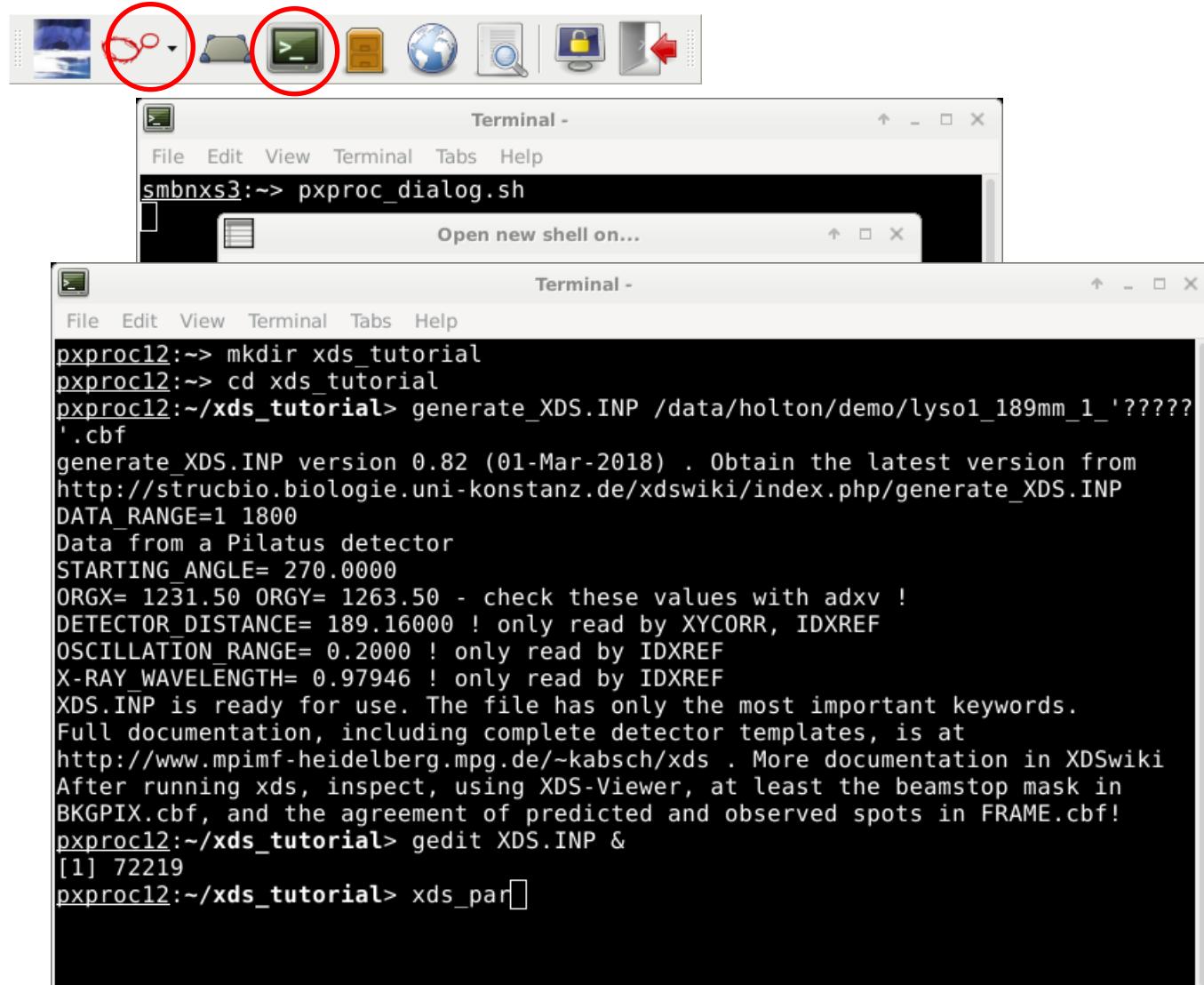
Many common detector and data formats are recognized, including:

- ADSC
- Mar ccd
- Mar image plate (old and new format)
- Raxis II & IV
- Crystallographic Binary Format (CBF)
- XDS .pck files
- European Data Format (EDF)
- Numerical Python (NUMPY)
- Hierarchical Data Format (HDF5)
- Tagged Image File Format (TIFF)
- Raw binary integer and floating point data



XDS

native user interface

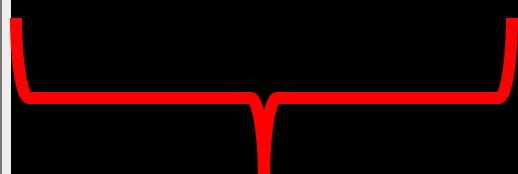




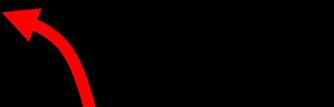
Terminal -

File Edit View Terminal Tabs Help

smbnxs3:~> □



The “prompt”



Cursor

does not move
with mouse

Mouse

can be used
To select and paste
But all pasted text
Goes to the cursor

too... much... typing!



- 1) Make sure X11 is running
- 2) Select some text with mouse
- 3) Move mouse over to your terminal
- 4) Hit middle mouse button
- 5) No keyboard required!

How to start XDS

prompt
Do not type!

```
proc:~> sss pxproc7  
proc:~> cd /data/$SER  
proc:~> mkdir xds_tutorial Enter  
proc:~> cd xds_tutorial  
proc:~> ln -sf /data/holton/demo .  
proc:~> xdsgui
```

Space!

underscore

Enter

Space!

period!

xdsgui – a graphical interface for XDS

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects Frame XDS.INP XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT tools statistics XDSCONV XSCALE

Folder with XDS configuration and output files

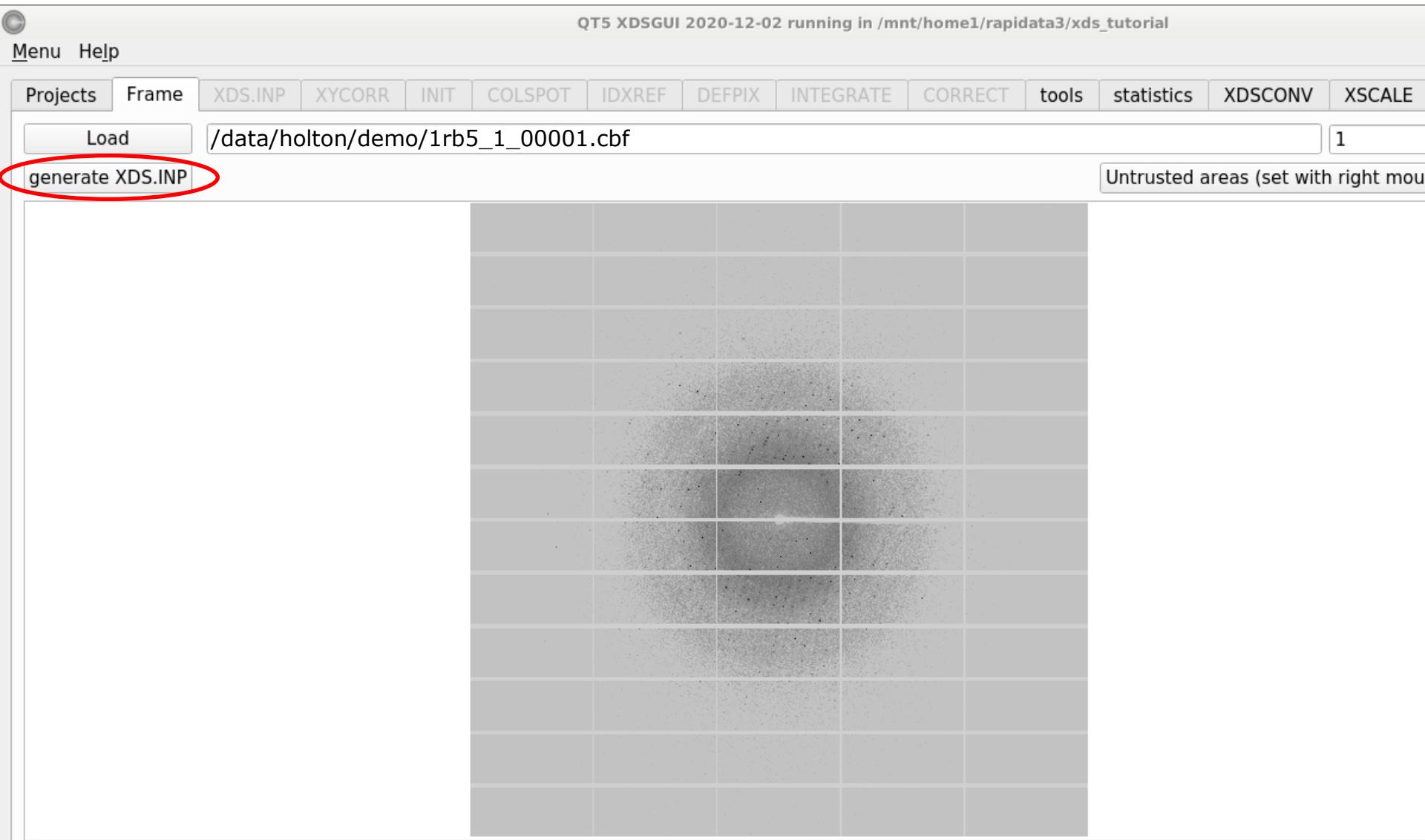
Default is the current directory. The title bar of the XDSGUI window shows the currently used folder.

Choose or create new folder

Load recent project

The screenshot shows a graphical user interface for the XDS GUI. At the top, there's a menu bar with 'Menu' and 'Help' options. Below it is a toolbar with various buttons: Projects, Frame, XDS.INP, XYCORR, INIT, COLSPOT, IDXREF, DEFPIX, INTEGRATE, CORRECT, tools, statistics, XDSCONV, and XSCALE. A status bar at the bottom displays the path '/mnt/home1/rapidata3/xds_tutorial'. The main area is a dialog box with two sections: 'Choose or create new folder' on the left and 'Load recent project' on the right. The 'Choose or create new folder' section contains a single button. The 'Load recent project' section is currently empty.

xdsgui – load an image



xdsgui – a GUI for text!

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects Frame XDS.INP XYCORR INIT COLSPOT IDXREF DEFFIX INTEGRATE CORRECT tools statistics XDSConv XSCALE

Save Run XDS

```
! written by generate_XDS.INP version 0.82 (01-Mar-2018)
JOB= XYCORR INIT COLSPOT IDXREF DEFFIX INTEGRATE CORRECT
ORGX= 1231.50 ORGY= 1263.50 ! values from frame header; only read by XYCORR, IDXREF

DETECTOR_DISTANCE= 189.16000 !read by XYCORR, IDXREF. Negative if detector normal points to crystal.
OSCILLATION_RANGE= 0.2000
STARTING_ANGLE= 270.0000
X-RAY_WAVELENGTH= 0.97946
NAME_TEMPLATE_OF_DATA_FRAMES=/data/holton/demo/1rb5_1_?????.cbf
! REFERENCE_DATA_SET=xxx/XDS_ASCII.HKL ! e.g. to ensure consistent indexing
DATA_RANGE=1 1800
SPOT_RANGE=1 900
! BACKGROUND_RANGE=1 10 ! rather use defaults (first 5 degree of rotation)

SPACE_GROUP_NUMBER=0 ! 0 if unknown
UNIT_CELL_CONSTANTS= 70 80 90 90 90 90 ! put correct values if known
INCLUDE_RESOLUTION_RANGE=50 0 ! after CORRECT, insert high resol limit; re-run CORRECT
! IDXREF now obeys INCLUDE_RESOLUTION_RANGE and EXCLUDE_RESOLUTION_RANGE to exclude ice-rings

FRIEDEL'S_LAW=FALSE ! This acts only on the CORRECT step
! If the anom signal turns out to be, or is known to be, very low or absent,
! use FRIEDEL'S_LAW=TRUE instead (or comment out the line); re-run CORRECT

! remove the "!" in the following line:
! STRICT_ABSORPTION_CORRECTION=TRUE
! if the anomalous signal is strong: in that case, in CORRECT.LP the three
! "CHI^2-VALUE OF FIT OF CORRECTION FACTORS" values are significantly> 1, e.g. 1.5
```

Xycorr – setting things up

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects Frame XDS.INP Xycorr INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT tools statistics XDSConv XSCALE

Save Run XDS

```
JOB= Xycorr
ORGX= 1231.50 ORGY= 1263.50 ! values from frame header; only read by Xycorr, IDXREF

DETECTOR_DISTANCE= 189.16000 !read by Xycorr, IDXREF. Negative if detector normal points to crystal.

DETECTOR= Pilatus MINIMUM_VALID_PIXEL_VALUE=0 OVERLOAD= 1179359 !PILATUS
SENSOR_THICKNESS= 0.32
X-RAY_WAVELENGTH= 0.97946
NX= 2463 NY= 2527 QX= 0.172 QY= 0.172 ! to make CORRECT happy if frames are unavailable

OSCILLATION_RANGE= 0.2000
!STARTING_ANGLE= 270.0000
DIRECTION_OF_DETECTOR_X-AXIS=1 0 0
DIRECTION_OF_DETECTOR_Y-AXIS=0 1 0
```

INIT – look at the background

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects Frame XDS.INP XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT tools statistics XDSConv XSCALE

Save Run XDS

JOB= INIT

```
!DETECTOR_DISTANCE= 189.16000 !read by XYCORR, IDXREF. Negative if detector normal points to crystal.
NAME_TEMPLATE_OF_DATA_FRAMES=/data/holton/demo/lyso1_189mm_1_?????.cbf
DATA_RANGE=1 1800
!SPOT_RANGE=1 900
BACKGROUND_RANGE=1 10 ! rather use defaults (first 5 degree of rotation)

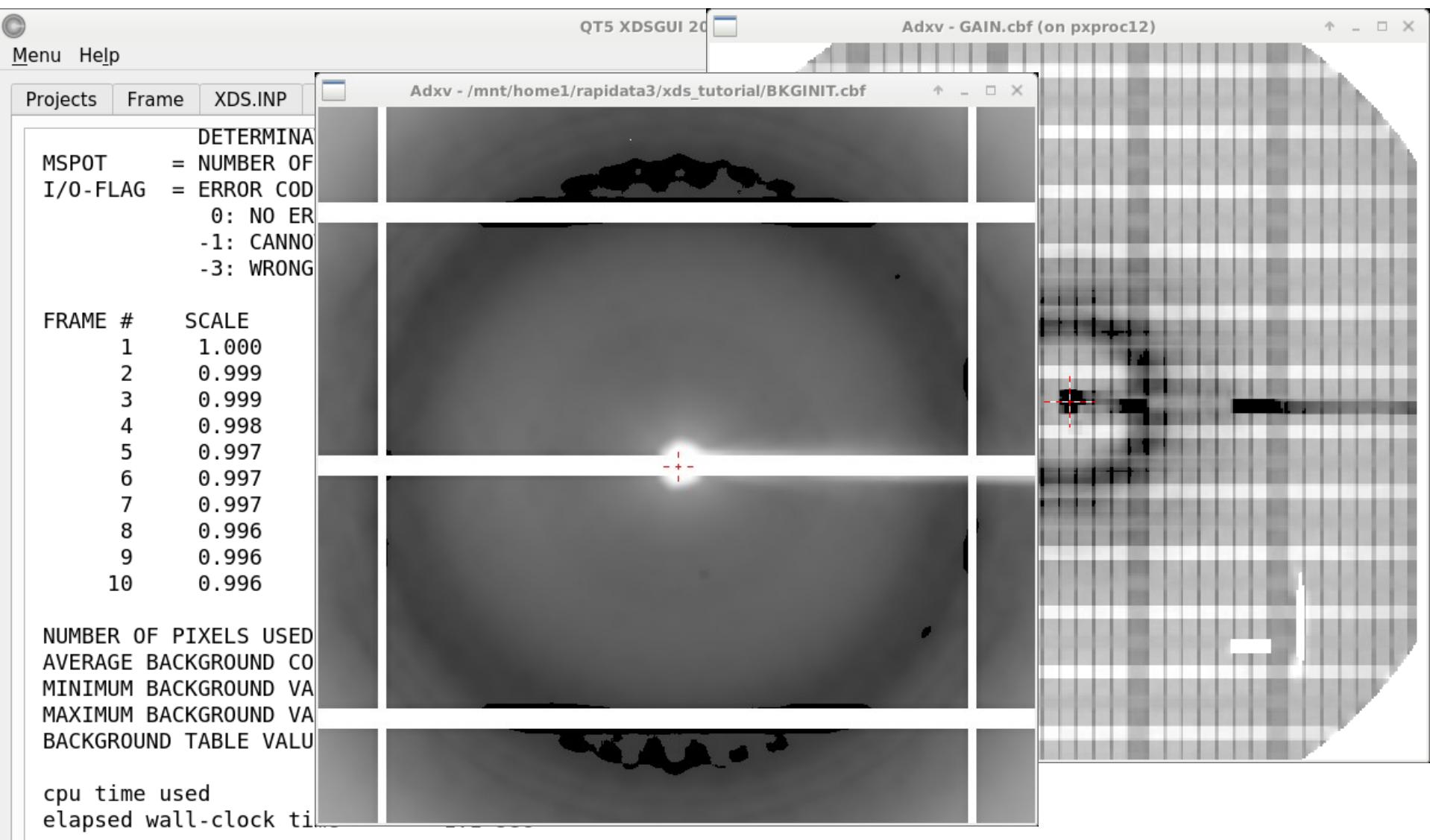
UNTRUSTED_RECTANGLE= 1800 1950 2100 2150 ! x-min x-max y-min y-max ! repeat
UNTRUSTED_ELLIPSE= 2034 2070 1850 2240 ! x-min x-max y-min y-max ! if needed
!UNTRUSTED_QUADRILATERAL= x1 y1 x2 y2 x3 y3 x4 y4 ! see documentation

TRUSTED_REGION=0.0 1.2 ! partially use corners of detector (0 1.4143: use all pixels)
```

DETECTOR= PILATUS MINIMUM_VALID_PIXEL_VALUE=0 OVERLOAD= 1179359 !PILATUS
!SENSOR_THICKNESS= 0.32
X-RAY_WAVELENGTH= 0.97946
NX= 2463 NY= 2527 QX= 0.172 QY= 0.172 ! to make CORRECT happy if frames are unavailable

OSCILLATION_RANGE= 0.2000
!STARTING_ANGLE= 270.0000
DIRECTION_OF_DETECTOR_X-AXIS=1 0 0
DIRECTION_OF_DETECTOR_Y-AXIS=0 1 0

INIT – look at the background



COLSPOT – the spot picker

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects Frame XDS.INP XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT tools statistics XDSConv XSCALE

Save Run XDS

JOB= COLSPOT

NAME_TEMPLATE_OF_DATA_FRAMES=/data/holton/demo/lyso1_189mm_1_?????.cbf

DATA_RANGE=1 1800

SPOT_RANGE=1 900

! BACKGROUND_RANGE=1 10 ! rather use defaults (first 5 degree of rotation)

STRONG_PIXEL=4 ! COLSPOT: only use strong reflections (default is 3)

MINIMUM_NUMBER_OF_PIXELS_IN_A_SPOT=3 ! default of 6 is sometimes too high

DETECTOR= PILATUS MINIMUM_VALID_PIXEL_VALUE=0 OVERLOAD= 1179359 !PILATUS

!SENSOR_THICKNESS= 0.32

X-RAY_WAVELENGTH= 0.97946

NX= 2463 NY= 2527 QX= 0.172 QY= 0.172 ! to make CORRECT happy if frames are unavailable

OSCILLATION_RANGE= 0.2000

!STARTING_ANGLE= 270.0000

DIRECTION_OF_DETECTOR_X-AXIS=1 0 0

DIRECTION_OF_DETECTOR_Y-AXIS=0 1 0

COLSPOT – the spot picker

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects	Frame	XDS.INP	XYCORR	INIT	COLSPOT
887	5364728	2689	0		
888	5364717	2700	0		
889	5364745	2672	0		
890	5364739	2678	0		
891	5364607	2810	0		
892	5364502	2915	0		
893	5364415	3002	0		
894	5364406	3011	0		
895	5364394	3023	0		
896	5364485	2932	0		
897	5364654	2763	0		
898	5364626	2791	0		
899	5364528	2889	0		
900	5364602	2815	0		

NUMBER OF STRONG PIXELS EXTRACTED FROM IMAGES

NUMBER OF DIFFRACTION SPOTS LOCATED
IGNORED BECAUSE OF SPOT CLOSE TO UNTRUSTED REGION
WEAK SPOTS OMITTED

NUMBER OF DIFFRACTION SPOTS ACCEPTED

total elapsed wall-clock time for COLSPOT

TASK	cpu time (sec)	elapsed wall-clock time (sec)
1	331.4	12.3

Coot 0.9.5 EL (ccp4)

File Edit Calculate Draw Measures Validate About Ligand

R/RC

Map

Display Manager

Successfully read coordinates file SPOT-notindexed.pdb. Molecule num...

CONV XSCALE

IDXREF – auto-indexing

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects Frame XDS.INP XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT tools statistics XDSConv XSCALE

Save

Run XDS

```
JOB= IDXREF
ORGX= 1231.50 ORGY= 1263.50 ! values from frame header; only read by XYCORR, IDXREF
DETECTOR_DISTANCE= 189.16000 !read by XYCORR, IDXREF. Negative if detector normal points to crystal.
OSCILLATION_RANGE= 0.2000
! STARTING_ANGLE= 270.0000
X-RAY_WAVELENGTH= 0.97946
! NAME_TEMPLATE_OF_DATA_FRAMES=/data/holton/demo/lyso1_189mm_1_?????.cbf
! REFERENCE_DATA_SET=xxx/XDS_ASCII.HKL ! e.g. to ensure consistent indexing
SPOT_RANGE=1 900

SPACE_GROUP_NUMBER= 96 ! 0 if unknown
UNIT_CELL_CONSTANTS= 78 78 37 90 90 90 ! put correct values if known
INCLUDE_RESOLUTION_RANGE=50 0 ! after CORRECT, insert high resol limit; re-run CORRECT
! EXCLUDE_RESOLUTION_RANGE= 3.93 3.87 !ice-ring at 3.897 Angstrom
TRUSTED_REGION=0.0 1.2 ! partially use corners of detector (0 1.4143: use all pixels)

REFINE(IDXREF)=CELL BEAM ORIENTATION AXIS ! refine POSITION only if known that header distance inaccurate
! MINIMUM_FRACTION_OF_INDEXED_SPOTS= 0.5

ROTATION_AXIS=1 0 0 ! Australian Synchrotron, SERCAT ID-22 (?), APS 19-ID (?), ESRF BM30A, Spring-8, SSRF BL
INCIDENT_BEAM_DIRECTION=0 0 1 ! only read by IDXREF

DETECTOR= PILATUS MINIMUM_VALID_PIXEL_VALUE=0 OVERLOAD= 1179359 !PILATUS
NX= 2463 NY= 2527 QX= 0.172 QY= 0.172 ! to make CORRECT happy if frames are unavailable
DIRECTION_OF_DETECTOR_X-AXIS=1 0 0
DIRECTION_OF_DETECTOR_Y-AXIS=0 1 0
```

First image number

XPARM.XDS

Starting phi

Delta-phi

XPARM.XDS

VERSION

Feb 5, 2021

BUILT=20210323

1

270.0000

0.2000

0.999971

0.007404

-0.001831

wavelen

0.979460

0.000711

0.000291

1.020970

spindle vector

space

78.8215

78.8215

37.1784

90.000

90.000

beam vector

group

96

36.338257

9.327419

-69.320709

number

26.357738

70.532730

23.307367

c cell vectors

30.559622

-16.002089

13.866352

b real space

det panels

1

2463

pixels

2527

0.172000

0.172000

pixel size

origin

1231.500000

1263.500000

189.160004

distance

1.000000

0.000000

0.000000

x Detector

0.000000

1.000000

0.000000

y fast/slow

0.000000

0.000000

1.000000

z

Panel #

1

1

2463

1

2527

0.00

0.00

0.00

1.000000

0.000000

0.000000

0.000000

1.000000

0.000000

IDXREF – auto-indexing

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects	Frame	XDS.INP	XYCORR	INI
LATTICE- CHARACTER	BRAVAIS- LATTICE	QUALITY OF FIT		
*	44	aP	0.0	
*	31	aP	0.2	
*	34	mP	1.5	
*	35	mP	1.8	
*	33	mP	2.9	
*	32	oP	3.1	
*	25	mC	4.5	
*	23	oC	4.9	
*	20	mC	5.1	
*	21	tP	6.2	
39	mC	248.6		
38	oC	249.9		
29	mC	250.0		
28	mC	250.9		
37	mC	251.4		
36	oC	252.7		
27	mC	498.8		
19	oI	501.9		
26	oF	622.5		
18	tI	625.6		
1	cF	999.0		
2	hR	999.0		
3	cP	999.0		
5	cI	999.0		

BRAVAIS- POSSIBLE SPACE-GROUPS FOR PROTEIN CRYSTALS [SPACE GROUP NUMBER, SYMBOL]

TYPE	
aP	[1, P1]
mP	[3, P2] [4, P2(1)]
mC, mI	[5, C2]
oP	[16, P222] [17, P222(1)] [18, P2(1)2(1)2] [19, P2(1)2(1)2(1)]
oC	[21, C222] [20, C222(1)]
oF	[22, F222]
oI	[23, I222] [24, I2(1)2(1)2(1)]
tP	[75, P4] [76, P4(1)] [77, P4(2)] [78, P4(3)] [89, P422] [91, P4(1)22] [92, P4(1)2(1)2] [93, P4(2)22] [94, P4(2)2(1)2]
	[95, P4(3)22] [96, P4(3)2(1)2]
tI	[79, I4] [80, I4(1)] [97, I422] [98, I4(1)22]
hP	[143, P3] [144, P3(1)] [145, P3(2)] [149, P312] [150, P3(1)21] [153, P3(2)12] [154, P3(2)21] [168, P3(2)2(1)2] [170, P6(5)] [171, P6(2)] [172, P6(4)] [173, P6(3)] [178, P6(1)22] [179, P6(5)22] [180, P6(2)22] [181, P6(2)2(1)2]
hR	[146, R3] [155, R32]
cP	[195, P23] [198, P2(1)3] [207, P432] [208, P4(2)32] [213, P4(1)32]
cF	[196, F23] [209, F432] [210, F4(1)32]
cI	[197, I23] [199, I2(1)3] [211, I432] [214, I4(1)32]

37.2 76.8 78.8 90.0 90.0 Range
87.2 87.1 111.4 50.3 50.3 Start

INTEGRATE – measure the spots!

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects Frame XDS.INP XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT tools statistics XDSConv XSCALE

```
JOB= INTEGRATE
NAME_TEMPLATE_OF_DATA_FRAMES=/data/holton/demo/lyso1_189mm_1_?????.cbf
DATA_RANGE=1 1800
! EXCLUDE_DATA_RANGE= 1000 1100
SPACE_GROUP_NUMBER=0 ! 0 if unknown
UNIT_CELL_CONSTANTS= 70 70 40 90 90 90 ! put correct values if known
INCLUDE_RESOLUTION_RANGE=50 0 ! after CORRECT, insert high resol limit; re-run CORRECT
!FRIEDEL'S_LAW=FALSE ! This acts only on the CORRECT step
REFINE(INTEGRATE)= POSITION BEAM ORIENTATION ! AXIS CELL
!NUMBER_OF_PROFILE_GRID_POINTS_ALONG_ALPHA/BETA=13 ! Default is 9 - Increasing may improve data
!NUMBER_OF_PROFILE_GRID_POINTS_ALONG_GAMMA=13 ! accuracy, particularly if finely-sliced on phi,
!BEAM_DIVERSION= 0.50204 BEAM_DIVERSION_E.S.D.= 0.05020
!REFLECTING_RANGE= 0.65025 REFLECTING_RANGE_E.S.D.= 0.09289

DETECTOR= PILATUS MINIMUM_VALID_PIXEL_VALUE=0 OVERLOAD= 1179359 !PILATUS
X-RAY_WAVELENGTH= 0.97946
NX= 2463 NY= 2527 QX= 0.172 QY= 0.172 ! to make CORRECT happy if frames are unavailable
OSCILLATION_RANGE= 0.2000
DIRECTION_OF_DETECTOR_X-AXIS=1 0 0
DIRECTION_OF_DETECTOR_Y-AXIS=0 1 0
```

CORRECT – scale all the “factors”

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects Frame XDS.INP XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT tools statistics XDSConv XSCALE

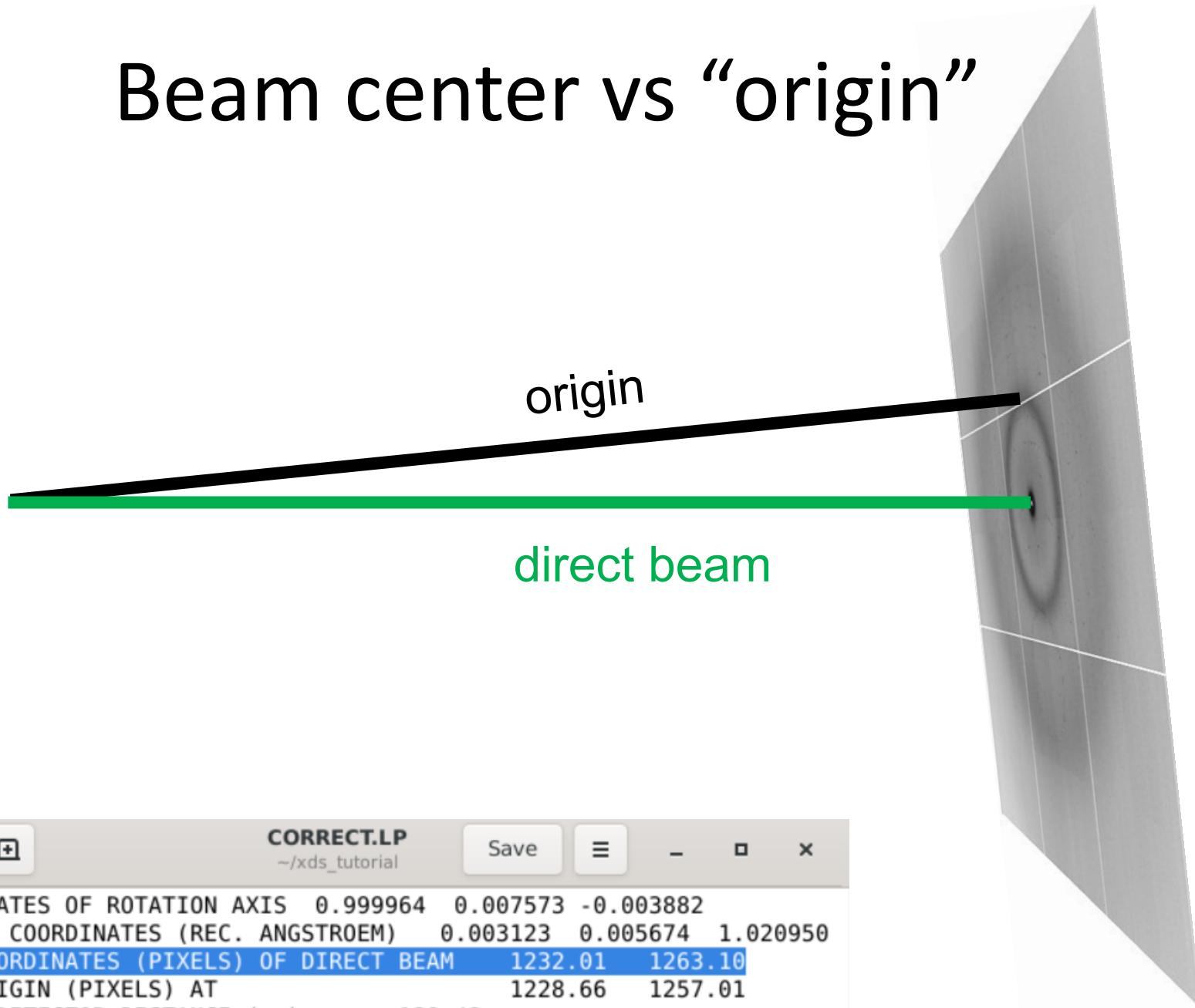
Save Run XDS

```
JOB= CORRECT
!NAME_TEMPLATE_OF_DATA_FRAMES=/data/holton/demo/lyso1_189mm_1_?????.cbf
! REFERENCE_DATA_SET=xxx/XDS_ASCII.HKL ! e.g. to ensure consistent indexing
DATA_RANGE=1 1800
! EXCLUDE_DATA_RANGE=1000 1100
SPACE_GROUP_NUMBER=0 ! 0 if unknown
UNIT_CELL_CONSTANTS= 70 70 40 90 90 90 ! put correct values if known
INCLUDE_RESOLUTION_RANGE=50 0 ! after CORRECT, insert high resol limit; re-run CORRECT
!EXCLUDE_RESOLUTION_RANGE= 3.93 3.87 !ice-ring at 3.897 Angstrom
FRIEDEL'S_LAW=FALSE ! This acts only on the CORRECT step
! STRICT_ABSORPTION_CORRECTION=TRUE
! REFINE(CORRECT)=CELL BEAM ORIENTATION AXIS POSITION ! Default is: refine everything
FRACTION_OF_POLARIZATION=0.98 ! better value is provided by beamline staff!
POLARIZATION_PLANE_NORMAL=0 1 0 ! only used by CORRECT

DETECTOR= PILATUS MINIMUM_VALID_PIXEL_VALUE=0 OVERLOAD= 1179359 !PILATUS
SENSOR_THICKNESS= 0.32
X-RAY_WAVELENGTH= 0.97946
NX= 2463 NY= 2527 QX= 0.172 QY= 0.172 ! to make CORRECT happy if frames are unavailable

OSCILLATION_RANGE= 0.2000
!STARTING_ANGLE= 270.0000
DIRECTION_OF_DETECTOR_X-AXIS=1 0 0
DIRECTION_OF_DETECTOR_Y-AXIS=0 1 0
```

Beam center vs “origin”



xdsconv – make an “mtz” file

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Menu Help

Projects Frame XDS.INP XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT tools statistics XDSConv XSCALE

save run XDSConv

```
! UNIT_CELL_CONSTANTS= 10 20 30 90 90 90
! SPACE_GROUP_NUMBER= 96
! GENERATE_FRACTION_OF_TEST_REFLECTIONS=0.05

INPUT_FILE=XDS_ASCII.HKL
OUTPUT_FILE=temp.hkl CCP4_I+F ! or CCP4_I or CCP4_F or SHELX or CNS
FRIEDEL'S_LAW=FALSE ! store anomalous signal in output file even if weak

! further options see http://xds.mpimf-heidelberg.mpg.de/~kabsch/xds/html\_doc/xdsconv\_parameters.html
```

output_file_name.mtz

Adding noise

$$1 + 1 = 1.4$$

$$\sigma_{\text{total}}^2 = \sigma_1^2 + \sigma_2^2$$

Adding noise

$$1^2 + 1^2 = 1.4^2$$

$$3^2 + 1^2 = 3.2^2$$

$$\sigma_{\text{total}}^2 = \sigma_1^2 + \sigma_2^2$$

Adding noise

$$1^2 + 1^2 = 1.4^2$$

$$3^2 + 1^2 = 3.2^2$$

$$10^2 + 1^2 = 10.05^2$$



signal vs noise

“If you don’t have
good data,
then you must
learn statistics.”

-James Holton

Sources of error for anomalous differences

- Shutter jitter (rms 0.5 ms)
- Beam flicker (0.15%/sqrt(Hz))
- Attenuation correction (< 2%)
- Radiation damage (1%/MGy)
- Detector calibration (3%)

anomalous signal

$$\frac{\Delta F}{F} \approx 1.2 f'' \sqrt{\frac{\# \text{ sites}}{\text{MW (Da)}}}$$

Crick, F. H. C. & Magdoff, B. S. (1956) *Acta Crystallogr.* **9**, 901-908.
Hendrickson, W. A. & Teeter, M. M. (1981) *Nature* **290**, 107-113.



Required crystal number or size calculator

$$n_{\text{xtals}} = \langle I_{\text{DL}} \rangle / 20 * f_{\text{NH}} * \text{MW} * V_M^2 / \exp(-0.5 * B/\text{reso}^2) / \text{xtalsize}^3 / (\text{reso}^3 - 1.53)$$

Enter values:

experiment goal =	subtle differences (MAD/SAD)		
number of sites =	<input type="text" value="1"/>	in asymmetric unit	
fpp =	<input type="text" value="4"/>	electrons	Bijvoet ratio = <input type="text" value="1.75"/> %
molecular weight =	<input type="text" value="30"/>	kDa in asymmetric unit	
resolution =	<input type="text" value="3.4"/>	Ang	signal to noise = <input type="text" value="81"/> at this resolution
reso on snapshot =	<input type="text" value="2.4"/>	Ang	→ Wilson B = <input type="text" value="35"/> Ang ²
background level =	<input type="text" value="100"/>	ADU/pixel	multiplicity = <input type="text" value="7.3"/>
spot size =	<input type="text" value="5"/>	pixels	
detector type =	ADSC Q210/315r (hwbin)		
solvent content =	<input type="text" value="50"/>	%	
xtal size _{beam} =	<input type="text" value="20"/>	microns	
xtal size _{vert} =	<input type="text" value="20"/>	microns	beam size _{vert} = <input type="text" value="100"/> microns
xtal size _{spindle} =	<input type="text" value="20"/>	microns	beam size _{spindle} = <input type="text" value="100"/> microns
<input type="button" value="Calculate n_xtals"/> ↓	<input type="button" value="Calculate size"/> ↑		
n _{xtals} =	<input type="text" value="1.4"/>	xtals you will need to merge	← <I _{DL} > <input type="text" value="11000"/> photons/hkl

Done



Re-indexing cheat sheet

Space group	Re-indexing
$P4$, ($P4_1$, $P4_3$), $P4_2$, $I4$, $I4_1$	$hkl \rightarrow kh\bar{l}$
$P3$, ($P3_1$, $P3_2$)	$hkl \rightarrow \overline{hkl}$ or $hkl \rightarrow kh\bar{l}$ or $hkl \rightarrow \overline{khl}$
$R3$	$hkl \rightarrow kh\bar{l}$
$P321$, ($P3_121$, $P3_221$)	$hkl \rightarrow \overline{hkl}$
$P312$, ($P3_112$, $P3_212$)	$hkl \rightarrow \overline{hkl}$
$P6$, ($P6_1$, $P6_5$), ($P6_2$, $P6_4$), $P6_3$	$hkl \rightarrow kh\bar{l}$
$P23$, $P2_13$, ($I23$, $I2_13$), $F23$	$hkl \rightarrow k\bar{h}l$

Zero-dose extrapolation (ZDE)

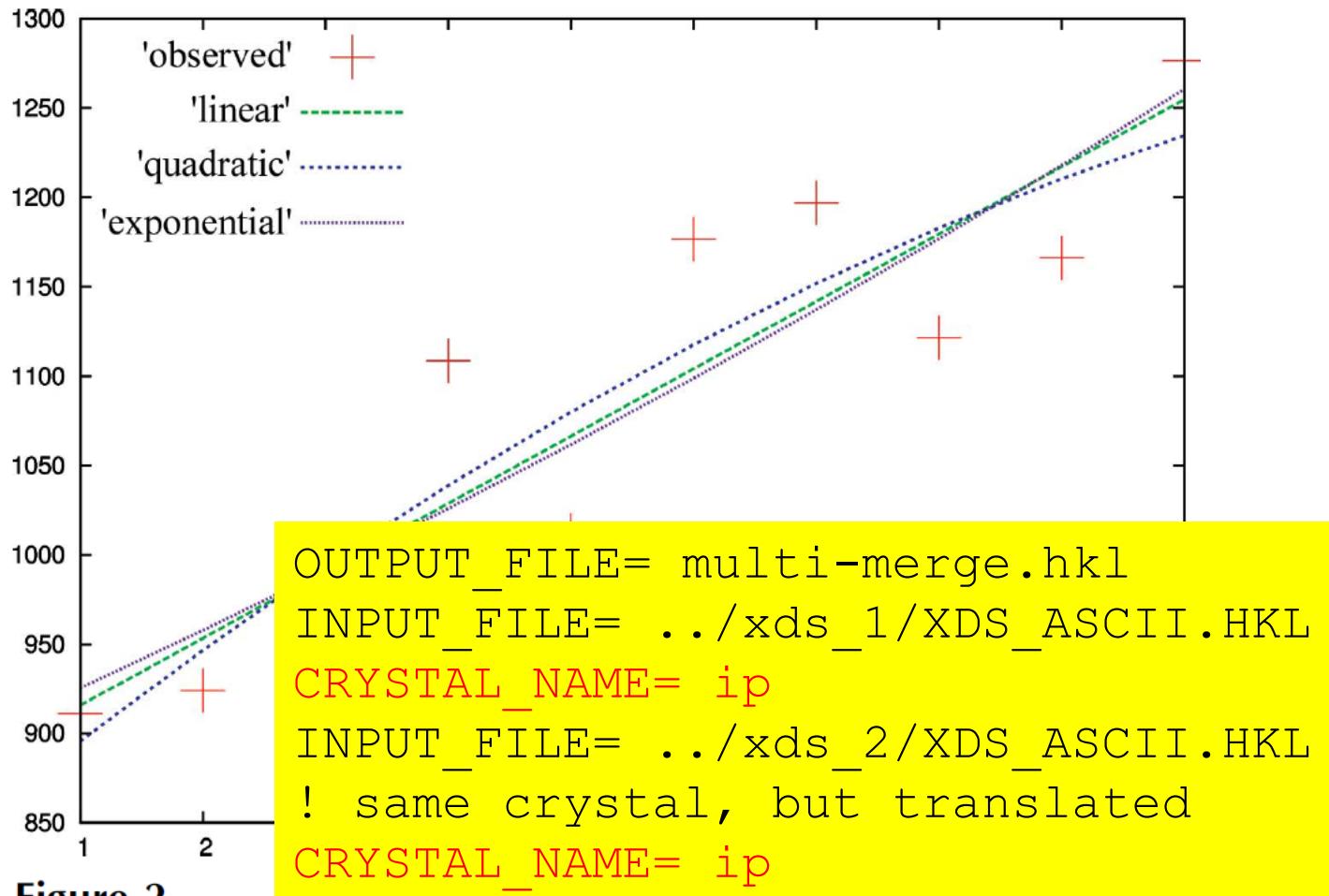


Figure 2

Example of noisy data points (marked by '+') fitted by a linear (green), a quadratic (blue) and an exponential function (purple). Near 1/4 and near 3/4 of the range, the values of the functions used for fitting coincide.

Diederichs, K. (2006). "Some aspects of quantitative analysis and correction of radiation damage." *Acta Cryst. D* **62**(1): 96-101.

xscale – final stats

QT5 XDSGUI 2020-12-02 running in /mnt/home1/rapidata3/xds_tutorial

Help

ects Frame XDS.INP XYCORR INIT COLSPOT IDXREF DEFPIX INTEGRATE CORRECT tools statistics XDSConv XSCALE SHELX

save

run xscale

show XSCA

SUBSET OF INTENSITY DATA WITH SIGNAL/NOISE >= -3.0 AS FUNCTION OF RESOLUTION											
RESOLUTION LIMIT	NUMBER OF REFLECTIONS OBSERVED	NUMBER OF UNIQUE REFLECTIONS	NUMBER OF POSSIBLE REFLECTIONS	COMPLETENESS OF DATA	R-FACTOR observed	R-FACTOR expected	R-FACTOR COMPARED I/SIGMA	R-meas	CC(1/2)	Anomalous Corr	
4.82	15416	1089	1091	99.8%	1.1%	1.8%	15416	145.67	1.2%	100.0*	89*
3.41	24671	1848	1955	94.5%	1.4%	1.9%	24666	140.26	1.5%	100.0*	69*
2.78	36341	2537	2537	100.0%	1.6%	1.9%	36341	132.84	1.7%	100.0*	46*
2.41	37752	3013	3014	100.0%	2.1%	2.1%	37752	106.63	2.2%	100.0*	41*
2.16	46702	3405	3405	100.0%	2.6%	2.4%	46702	96.90	2.7%	100.0*	36*
1.97	51923	3756	3756	100.0%	3.3%	2.9%	51923	78.79	3.4%	100.0*	19*
1.82	51323	4111	4111	100.0%	4.7%	4.0%	51323	54.26	4.9%	99.9*	14*
1.71	57891	4362	4362	100.0%	7.2%	6.3%	57891	38.45	7.5%	99.9*	9
1.61	64156	4680	4680	100.0%	9.8%	9.1%	64156	28.17	10.2%	99.8*	3
1.53	68501	4943	4943	100.0%	14.3%	14.1%	68501	19.31	14.9%	99.7*	3
1.45	64913	5219	5219	100.0%	20.3%	20.4%	64913	13.20	21.2%	99.3*	0
1.39	72865	5446	5447	100.0%	32.4%	33.9%	72865	8.63	33.7%	98.5*	-5
1.34	77152	5660	5660	100.0%	47.7%	50.5%	77152	5.99	49.6%	97.3*	-1
1.29	74358	5893	5893	100.0%	66.2%	70.6%	74358	4.13	69.0%	94.9*	-3
1.25	78139	6102	6103	100.0%	97.4%	105.1%	78139	2.82	101.4%	88.6*	-1
1.21	83395	6304	6304	100.0%	131.6%	143.4%	83395	2.07	136.8%	82.6*	-4
1.17	82112	6550	6551	100.0%	172.1%	189.4%	82112	1.45	179.4%	70.6*	-2
1.14	57381	6701	6701	100.0%	232.2%	256.3%	57381	0.80	247.1%	41.3*	-5
1.11	41788	6847	6918	99.0%	307.2%	341.0%	41689	0.46	335.7%	19.2*	1
1.08	26251	6266	7081	88.5%	456.8%	513.1%	25593	0.22	518.3%	7.1	0
total	1113030	94732	95731	99.0%	2.9%	3.2%	1112268	26.85	3.0%	100.0*	2

XDS: CORRECT.LP or XSCALE.LP

COMPARED	I/SIGMA	R-meas	CC (1/2)	Anomal	SigAno
Corr					
3018	33.77	2.3%	99.9*	21*	1.012
4585	22.56	3.6%	99.8*	9	0.914
5327	19.99	4.0%	99.7*	9	0.859
6094	12.27	6.8%	99.3*	-1	0.784
7068	6.01	14.2%	97.8*	-2	0.799
8185	3.10	29.4%	88.8*	-4	0.776
8981	1.90	48.8%	75.9*	2	0.765
5991	1.14	87.3%	53.5*	-2	0.722
2520	0.59	170.4%	21.9*	4	0.693
51769	8.97	9.5%	99.5*	2	0.804

XDS: CORRECT.LP or XSCALE.LP

CORRECTION PARAMETERS FOR THE STANDARD ERROR OF REFLECTION I

The variance $v_0(I)$ of the intensity I obtained from counting statistics is replaced by $v(I)=a*(v_0(I)+b*I^2)$. The model parameters a , b are chosen to minimize the discrepancies between $v(I)$ and the variance estimated from sample statistics of symmetry related reflections. This model is valid in an asymptotic limit $ISa=1/SQRT(a*b)$ for the highest $I/\Sigma(I)$. An experimental setup can produce (Diederichs (2010) Acta Cryst D66: 1020-1027)

a	b
3.806E+00	1.080E-04

ISa
49.32

CCP4: aimless log

\$TABLE: Analysis against resolution, XDSdataset:

\$GRAPHS:I/sigma, Mean Mn(I)/sd(Mn(I)):0|0.216023x0|137.14:2,13,14:

:Rmerge, Rfull, Rmeas, Rpim v Resolution:0|0.216023x0|1.70834:2,4,5,6,7:

:Average I, RMSdeviation and Sd:0|0.216023x0|1650.8:2,10,11,12:

:Fractional bias:0|0.216023x0|0:2,15:

\$\$

N	1/d^2	Dmid	Rmrg	Rfull	Rcum	Rmeas	Rpim	Nmeas	AvI	RMSdev	sd	I/RMS	Mn(I/sd)	Frc
1	0.0064	12.55	0.020	0.020	0.020	0.021	0.006	13115	1651	57	42	29.2	137.1	
2	0.0191	7.24	0.027	0.027	0.024	0.028	0.008	24753	1171	47	42	25.0	105.2	
3	0.0318	5.61	0.038	0.038	0.029	0.040	0.012	32197	857	46	43	18.4	79.6	
4	0.0445	4.74	0.034	0.034	0.031	0.035	0.010	37743	1212	57	53	21.4	91.2	
5	0.0572	4.18	0.036	0.036	0.032	0.038	0.011	42642	1181	59	57	19.9	83.8	
6	0.0699	3.78	0.049	0.049	0.036	0.052	0.015	47224	883	59	57	15.1	65.1	
7	0.0826	3.48	0.065	0.065	0.040	0.068	0.020	51052	685	59	58	11.7	50.9	
8	0.0953	3.24	0.096	0.096	0.045	0.100	0.029	54636	448	56	56	8.0	35.0	
9	0.1080	3.04	0.151	0.151	0.050	0.158	0.046	58072	268	53	53	5.1	22.7	
10	0.1207	2.88	0.229	0.229	0.056	0.240	0.070	60731	171	51	51	3.3	15.4	
11	0.1334	2.74	0.314	0.314	0.063	0.329	0.097	63807	125	51	51	2.4	11.3	
12	0.1461	2.62	0.406	0.406	0.070	0.425	0.125	66241	98	51	52	1.9	8.7	
13	0.1588	2.51	0.537	0.537	0.078	0.562	0.166	68272	76	53	53	1.4	6.5	
14	0.1715	2.41	0.627	0.627	0.081	0.707	0.207	71170	61	52	51	1.1	4.4	

CCP4: aimless log

\$TABLE: Correlations CC(1/2) within dataset, XDSdataset:

\$GRAPHS: Anom & Imean CCs v resolution:0|0.216023x0|1:2,4,7:

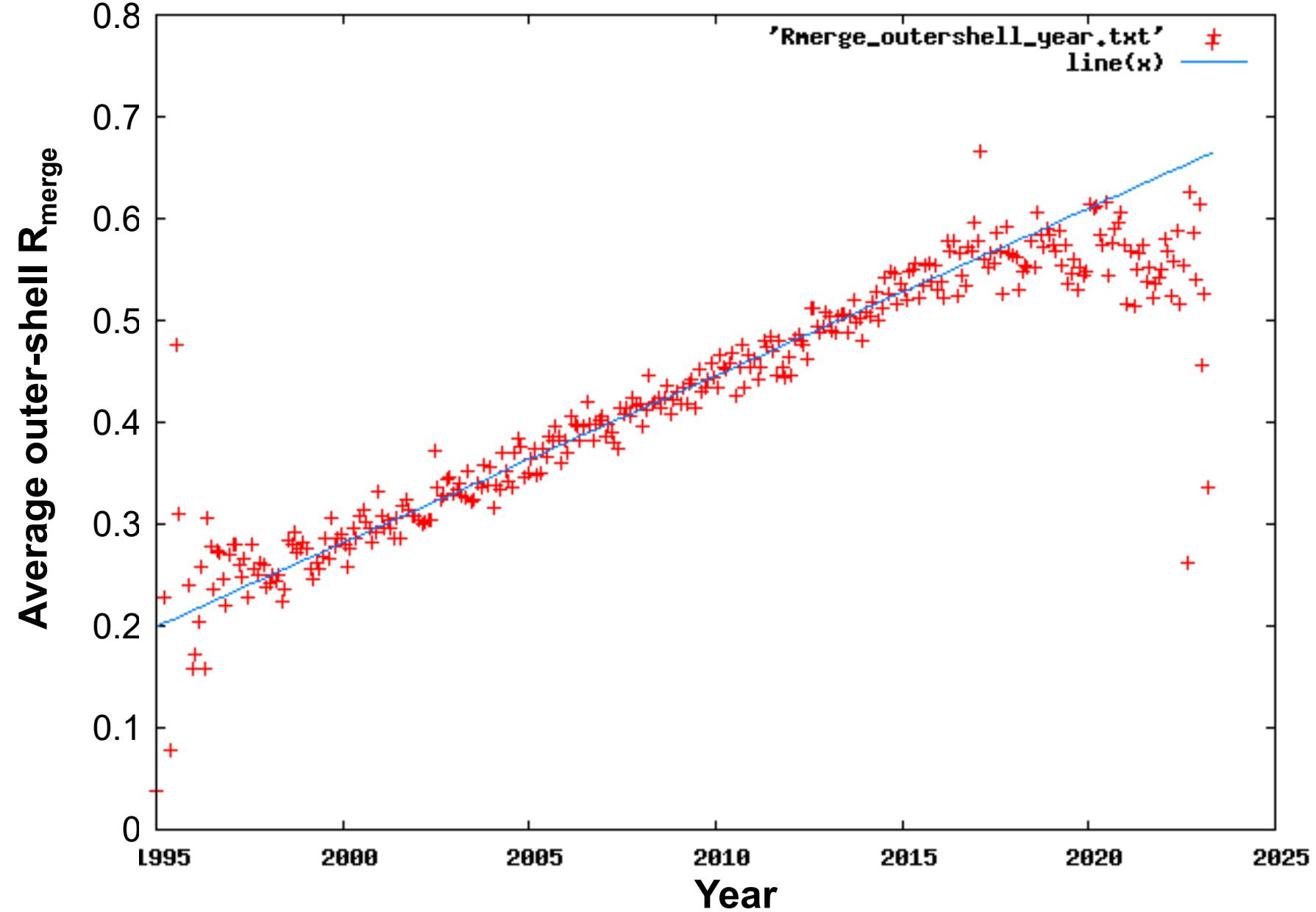
: RMS correlation ratio :0|0.216023x0|2.20344:2,6:

\$\$

N	1/d^2	Dmid	CCanom	Nanom	RCRanom	CC1/2	NImean	\$
1	0.0064	12.55	0.659	499	2.203	1.000	669	
2	0.0191	7.24	0.550	975	1.853	1.000	1155	
3	0.0318	5.61	0.527	1295	1.798	1.000	1479	
16	0.1970	2.25	0.037	2123	1.038	0.711	2275	
17	0.2097	2.18	0.043	1682	1.044	0.460	1877	

Resolution cutoff?

R_{merge} at the resolution limit in PDB



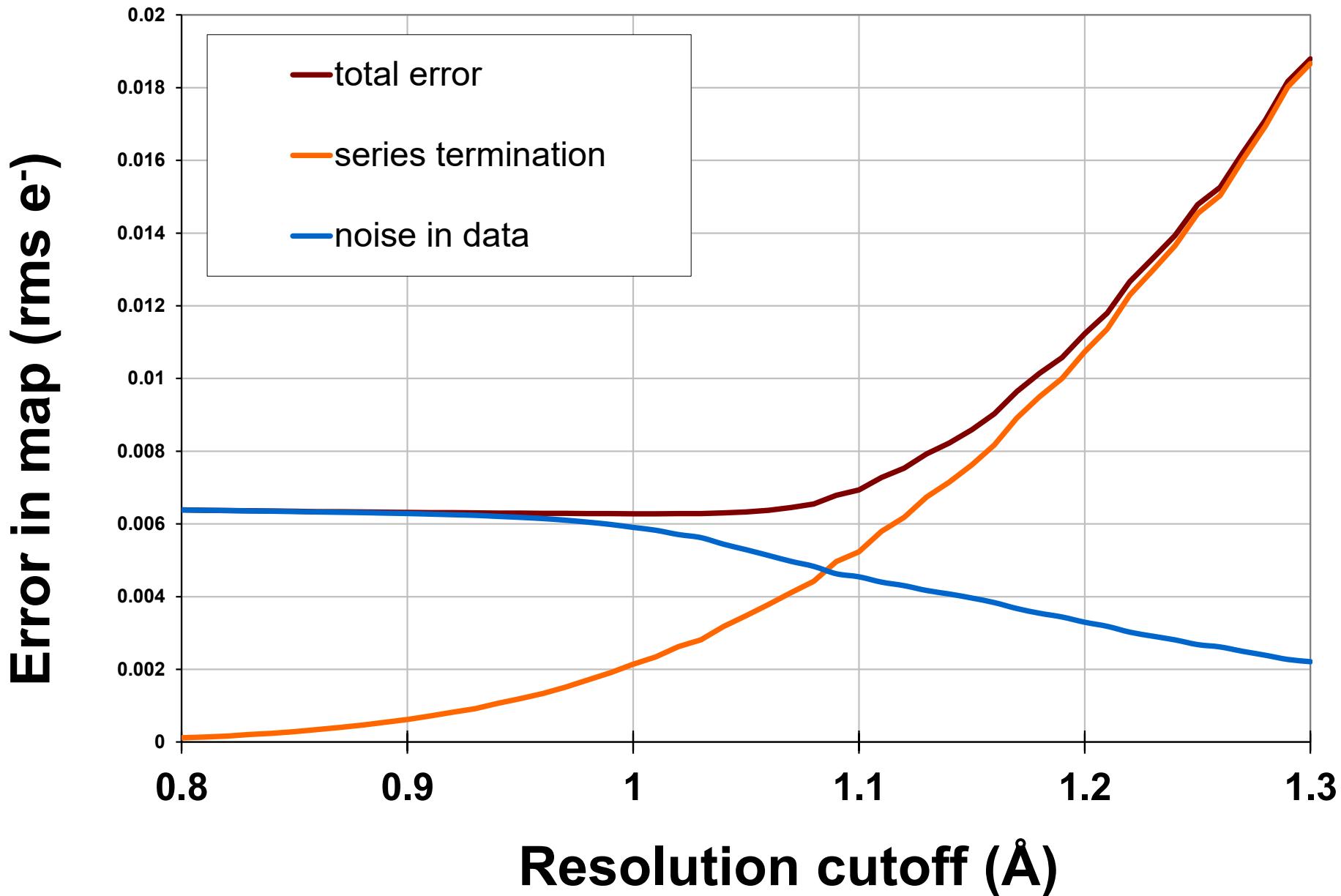
Expected R_{merge} as $I_{\text{obs}} \rightarrow 0$

$$R_{\text{merge}} = \frac{\sum |I_{\text{obs}} - \langle I \rangle|}{\sum I_{\text{obs}}}$$

Optimum resolution cutoff is:

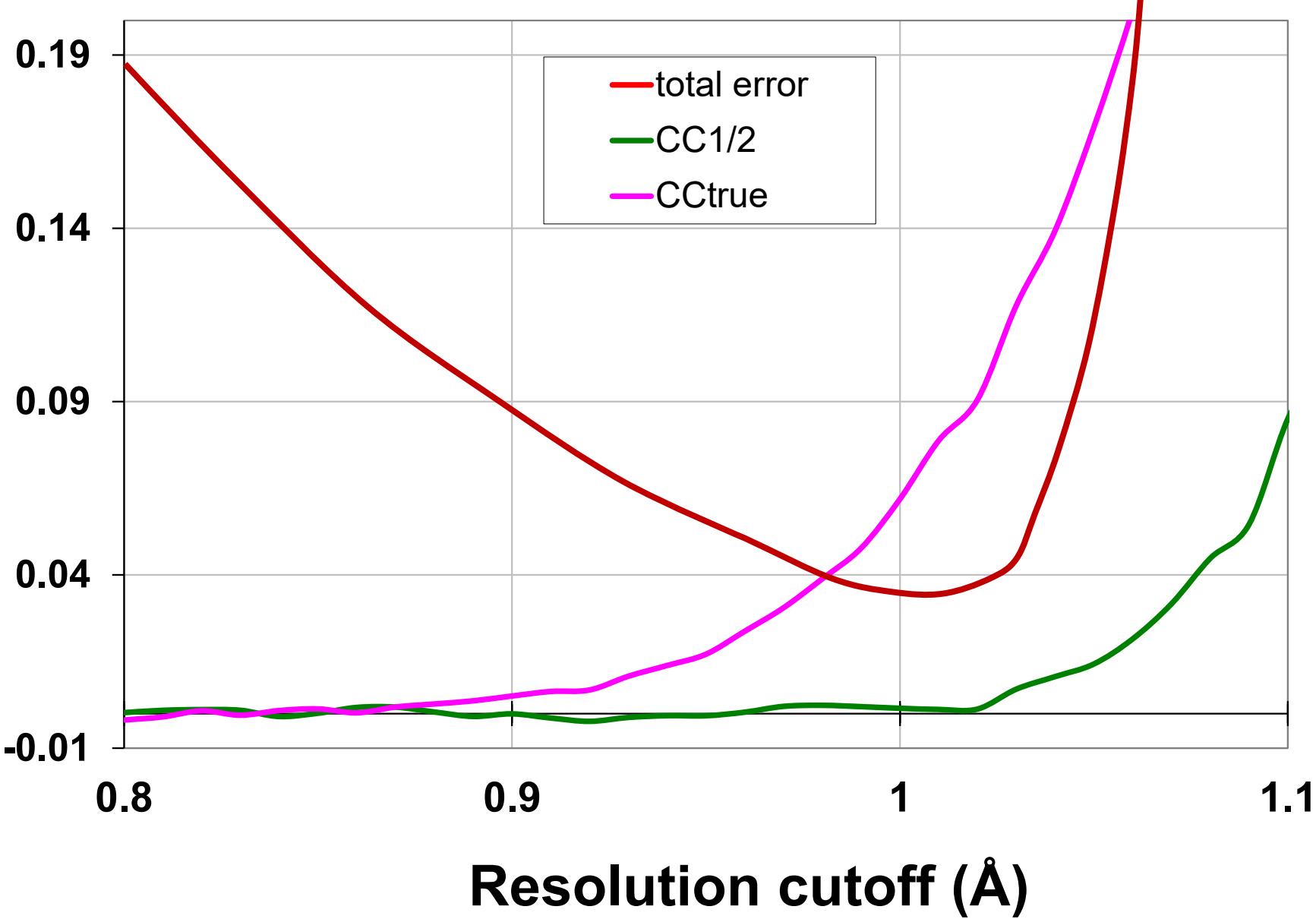
- Too optimistic: add nothing but noise
- Too pessimistic: series-termination error
- Happy medium?
- Simulate:
 - Random atoms, compute F^2
 - Add Gaussian noise, RMS = 1
 - Truncate
 - Subtract “right” map, RMS difference

Optimal resolution cutoff



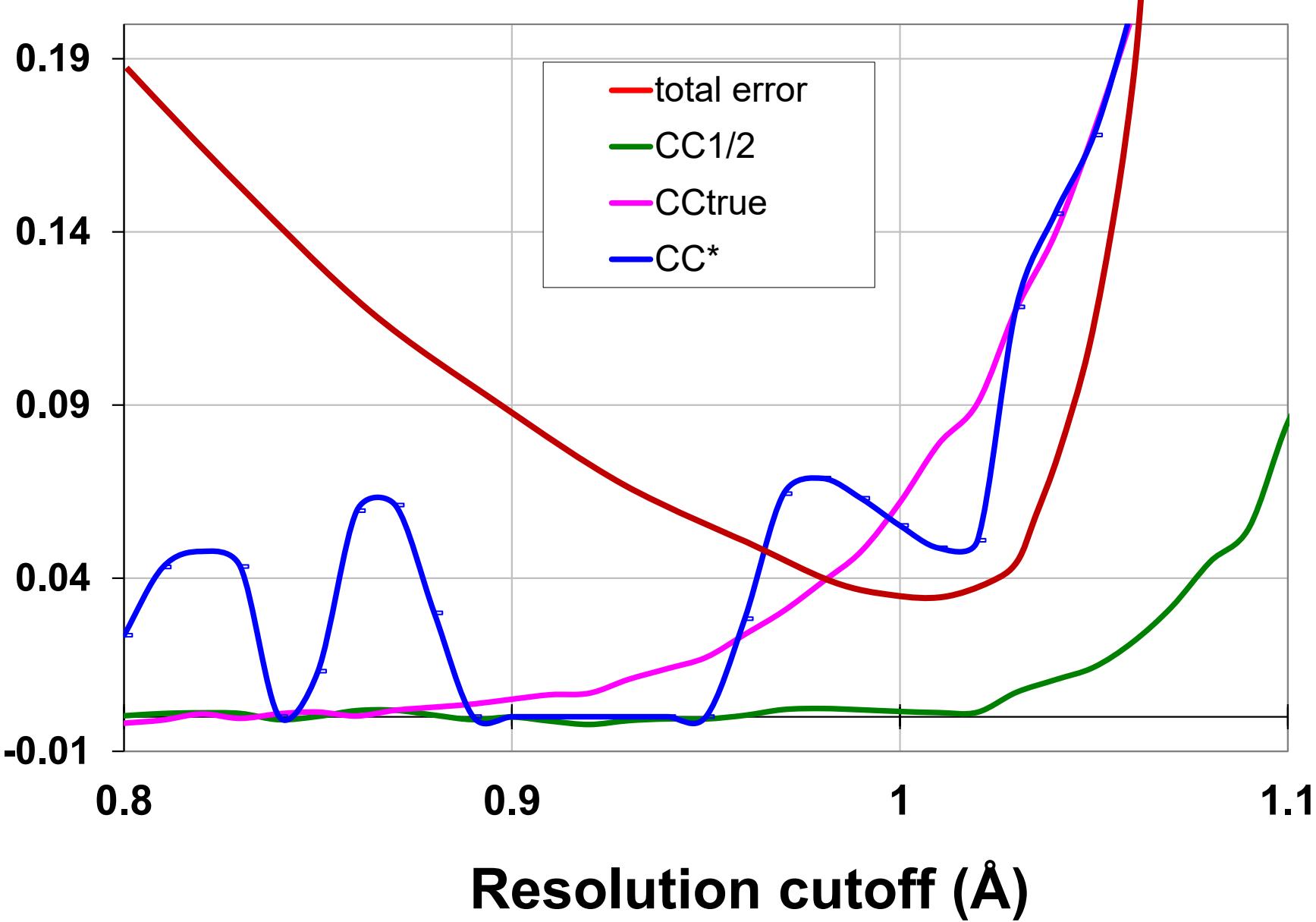
Optimal resolution cutoff

Correlation Coefficient

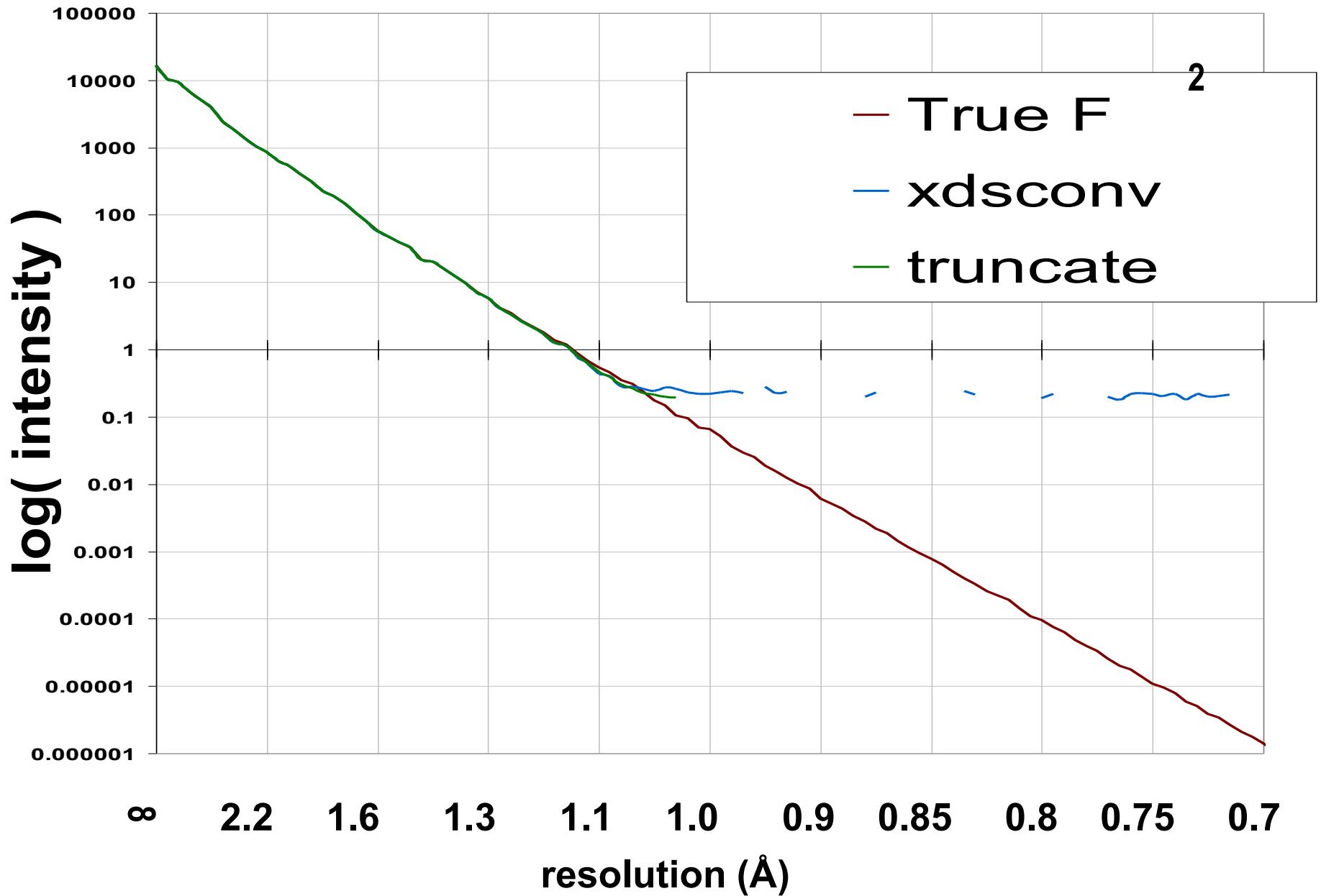


Optimal resolution cutoff

Correlation Coefficient



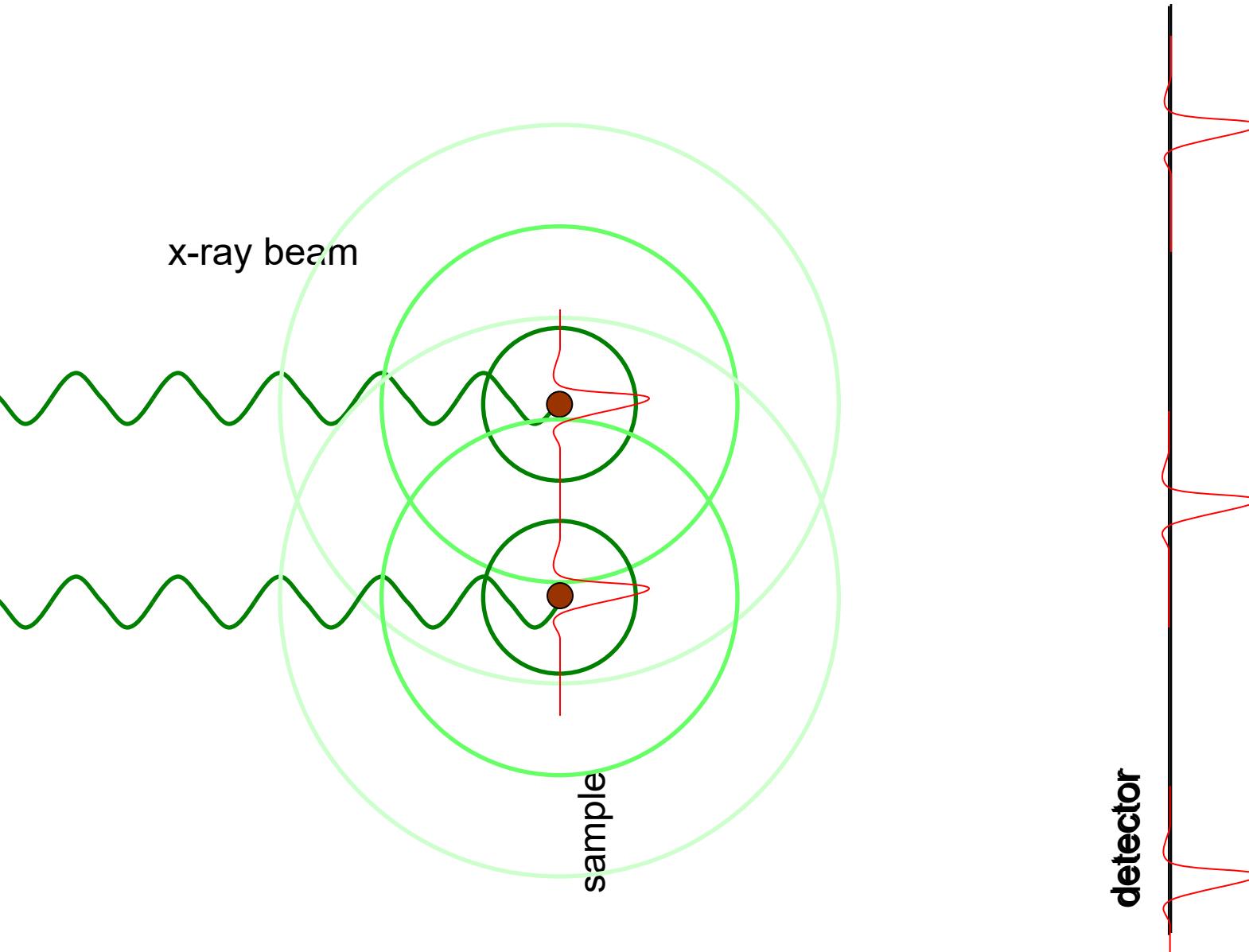
Wilson Plot

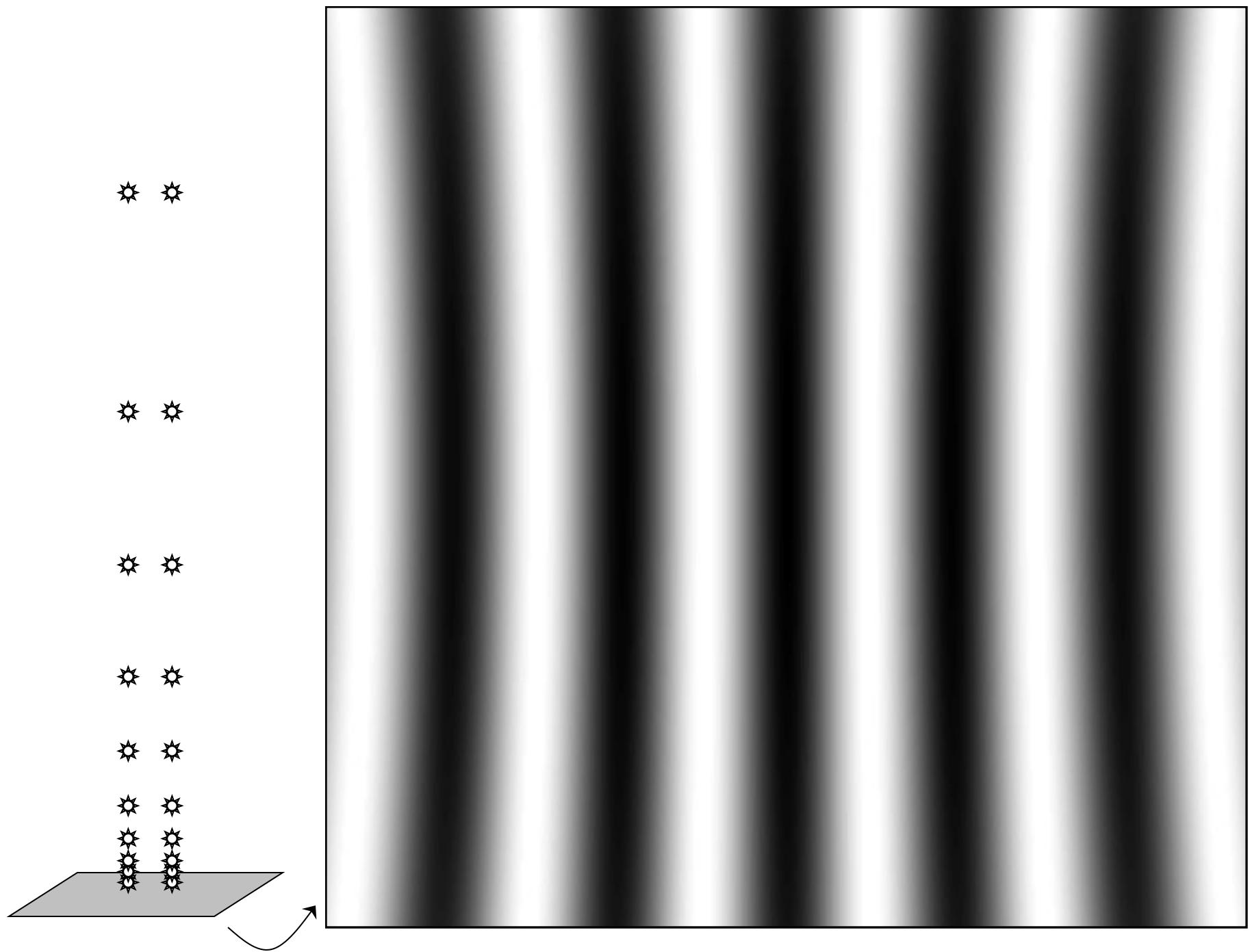


Optimum resolution cutoff is:

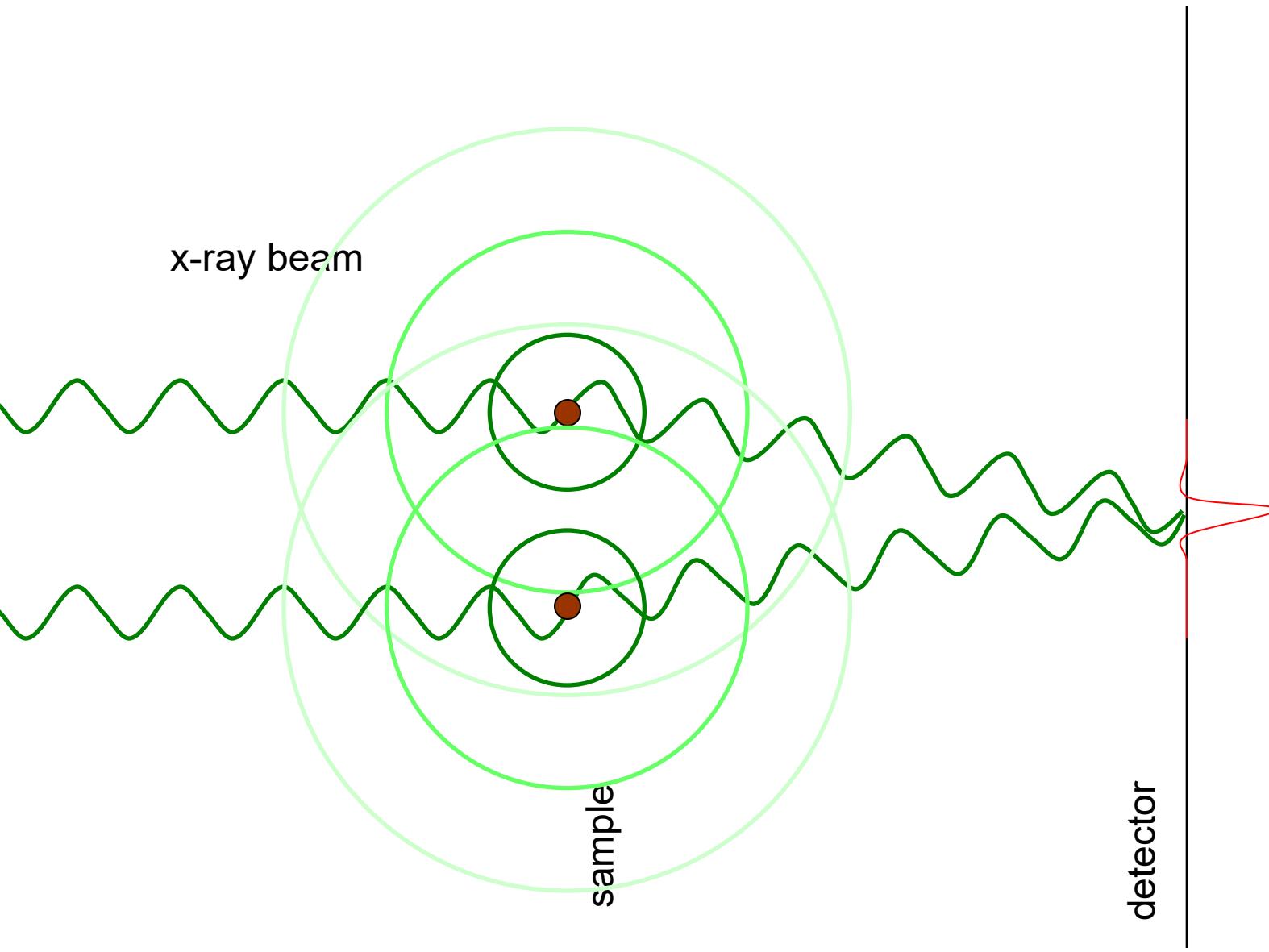
0.0 Å

scattering

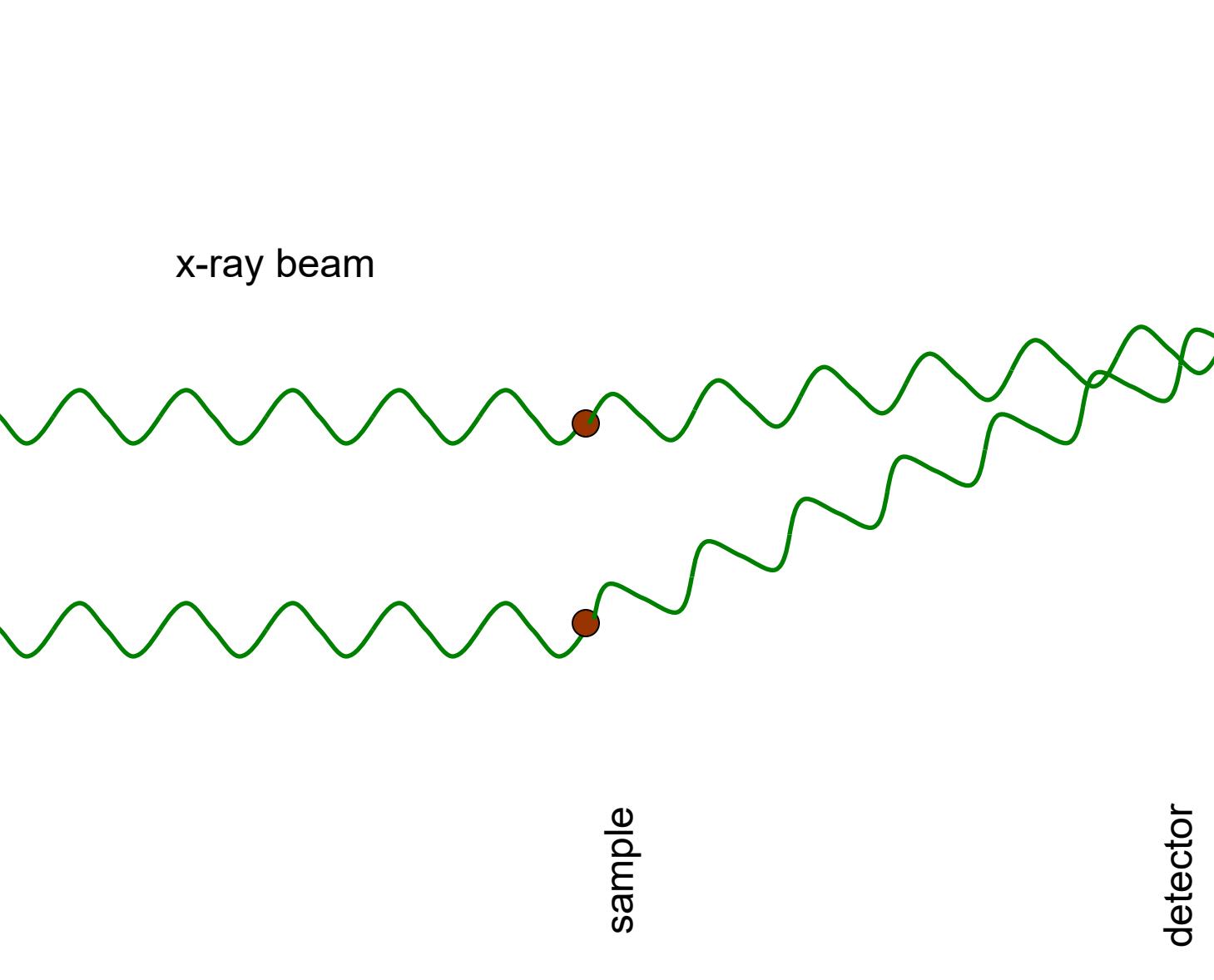




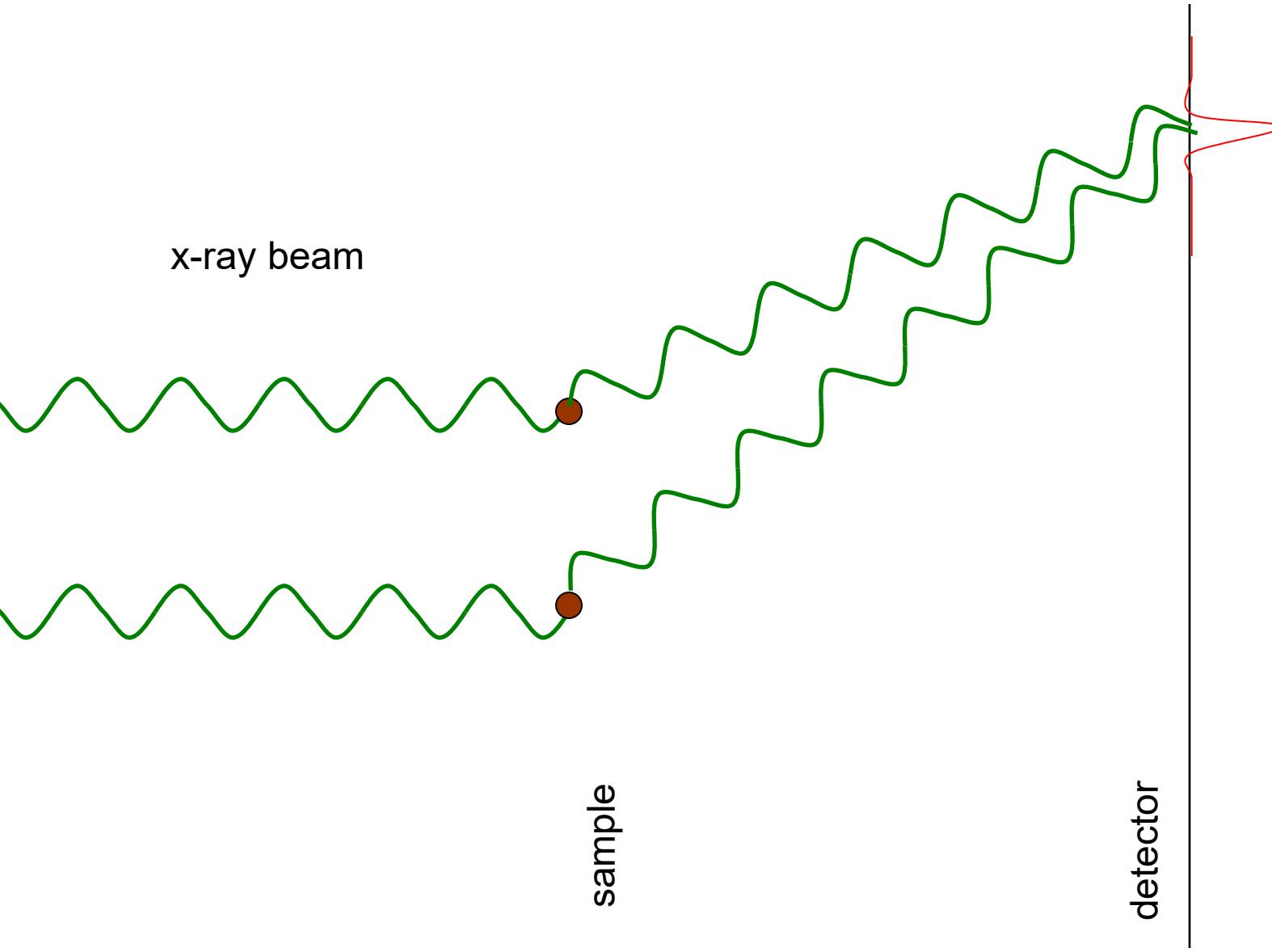
scattering



scattering

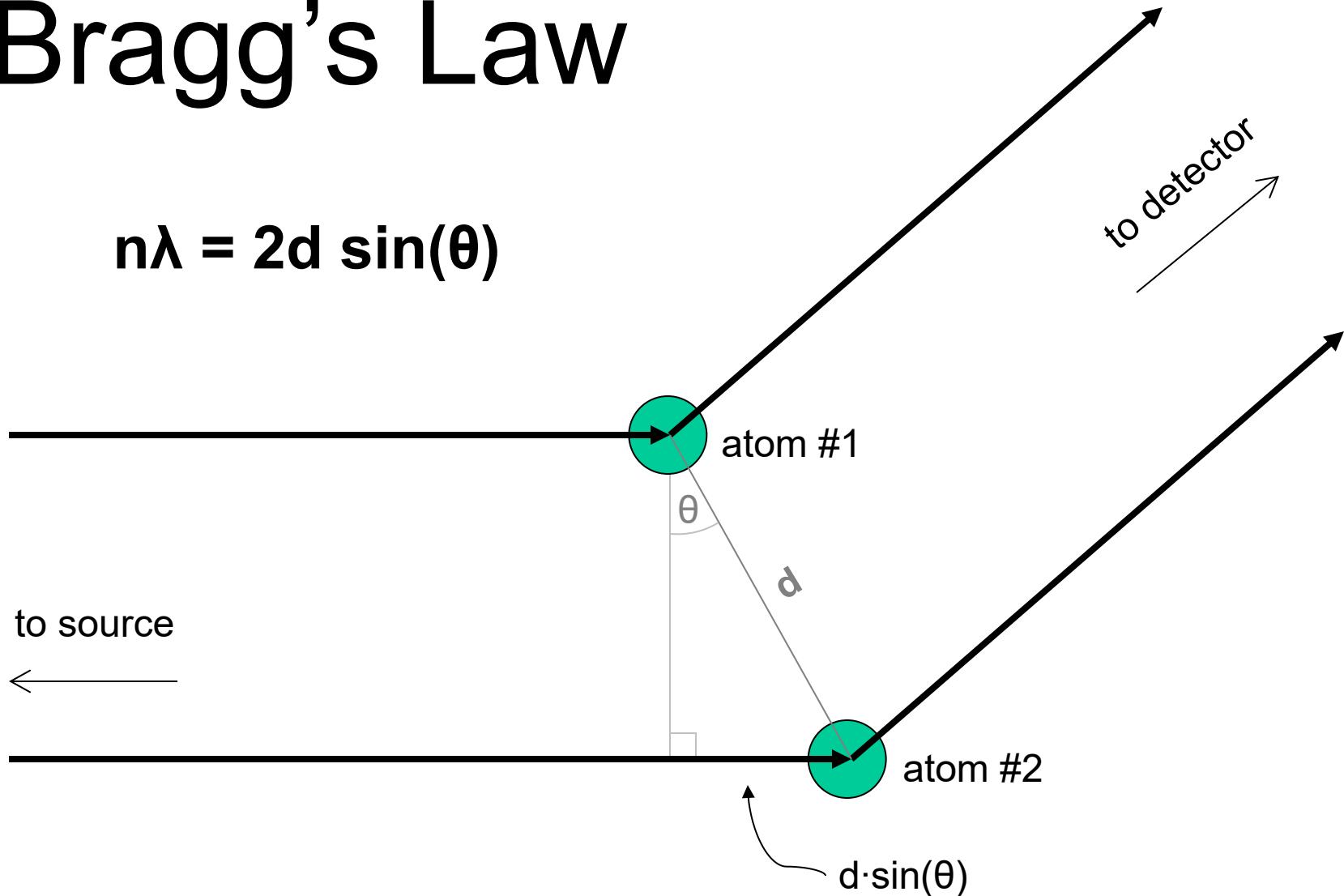


scattering



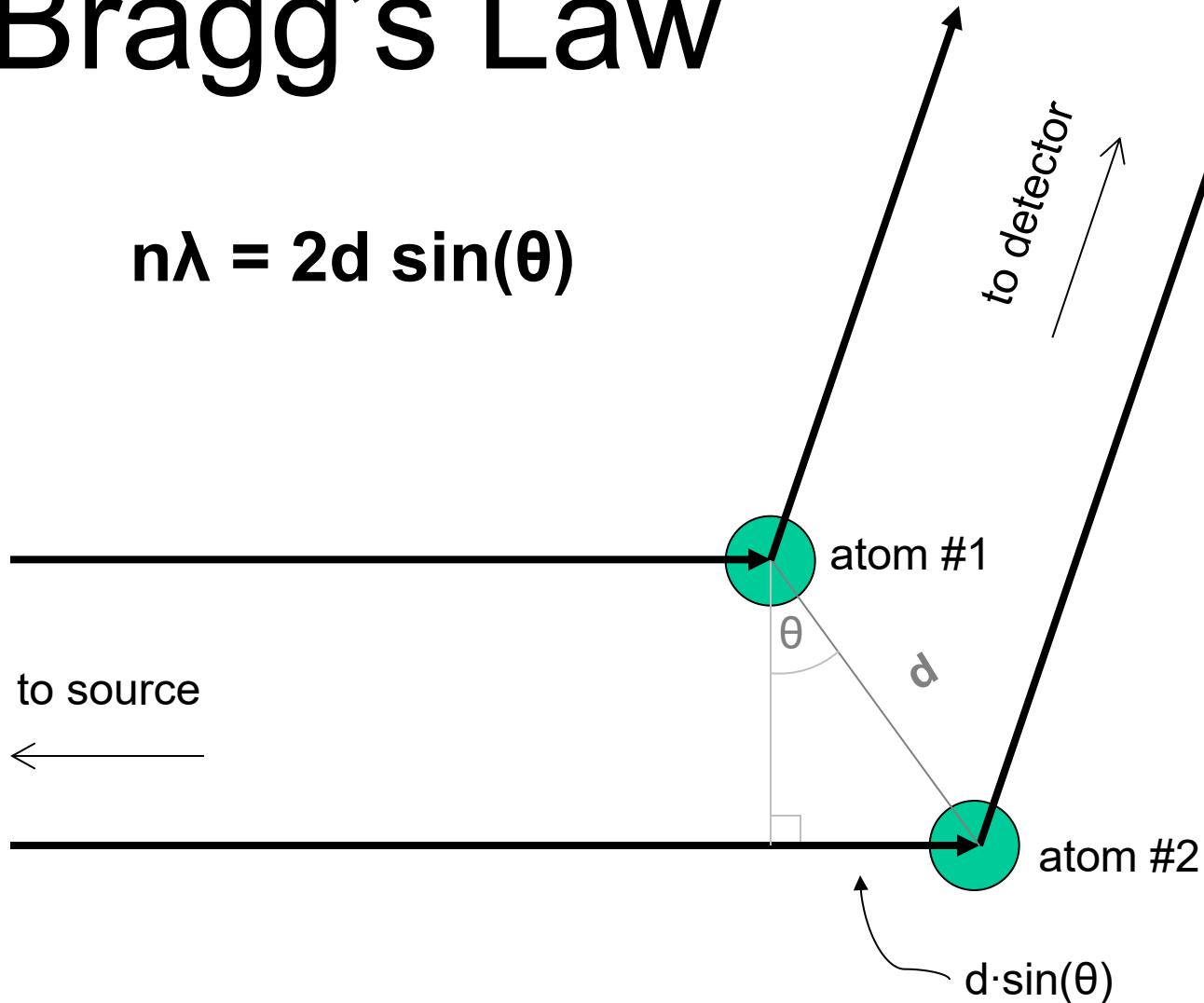
Bragg's Law

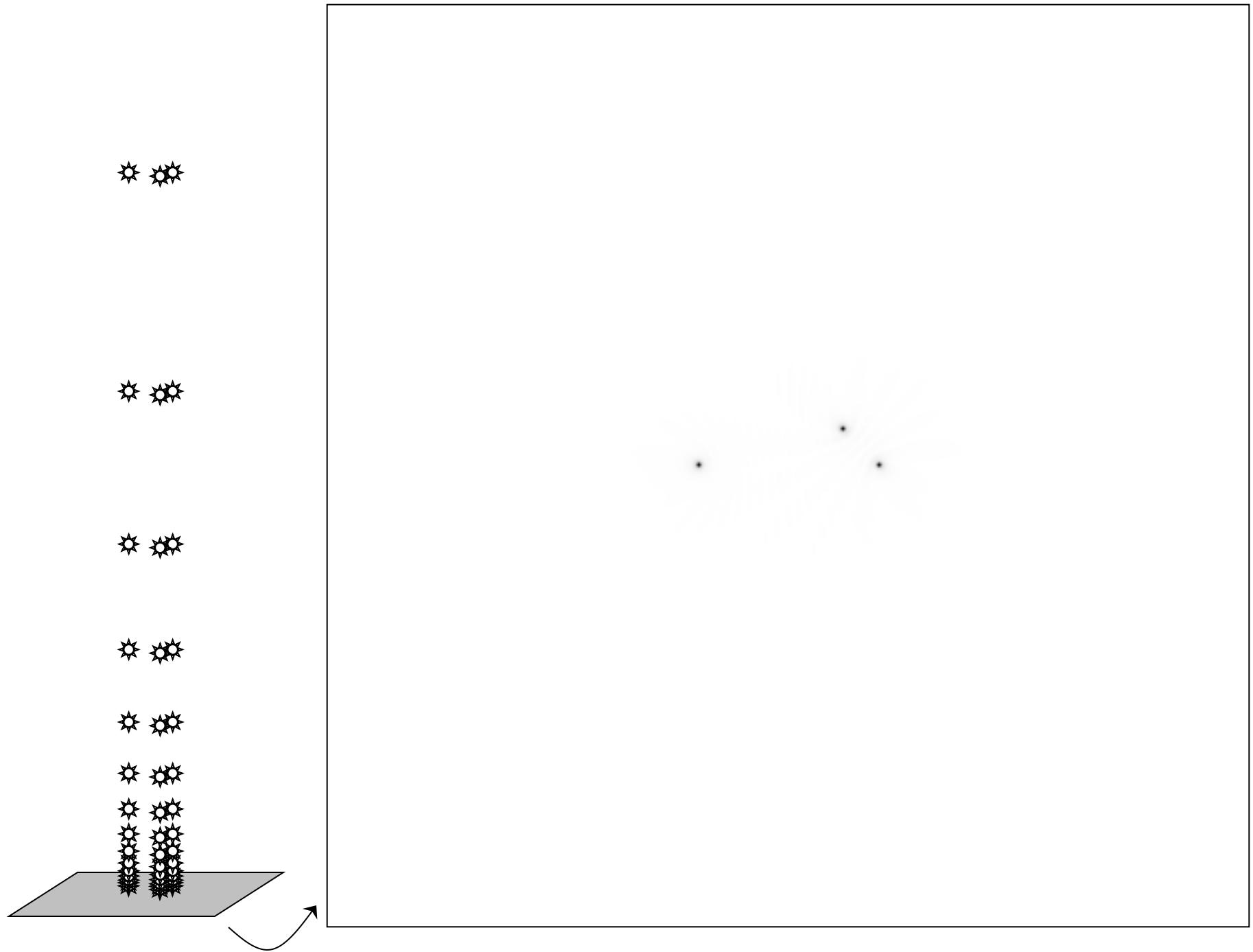
$$n\lambda = 2d \sin(\theta)$$



Bragg's Law

$$n\lambda = 2d \sin(\theta)$$

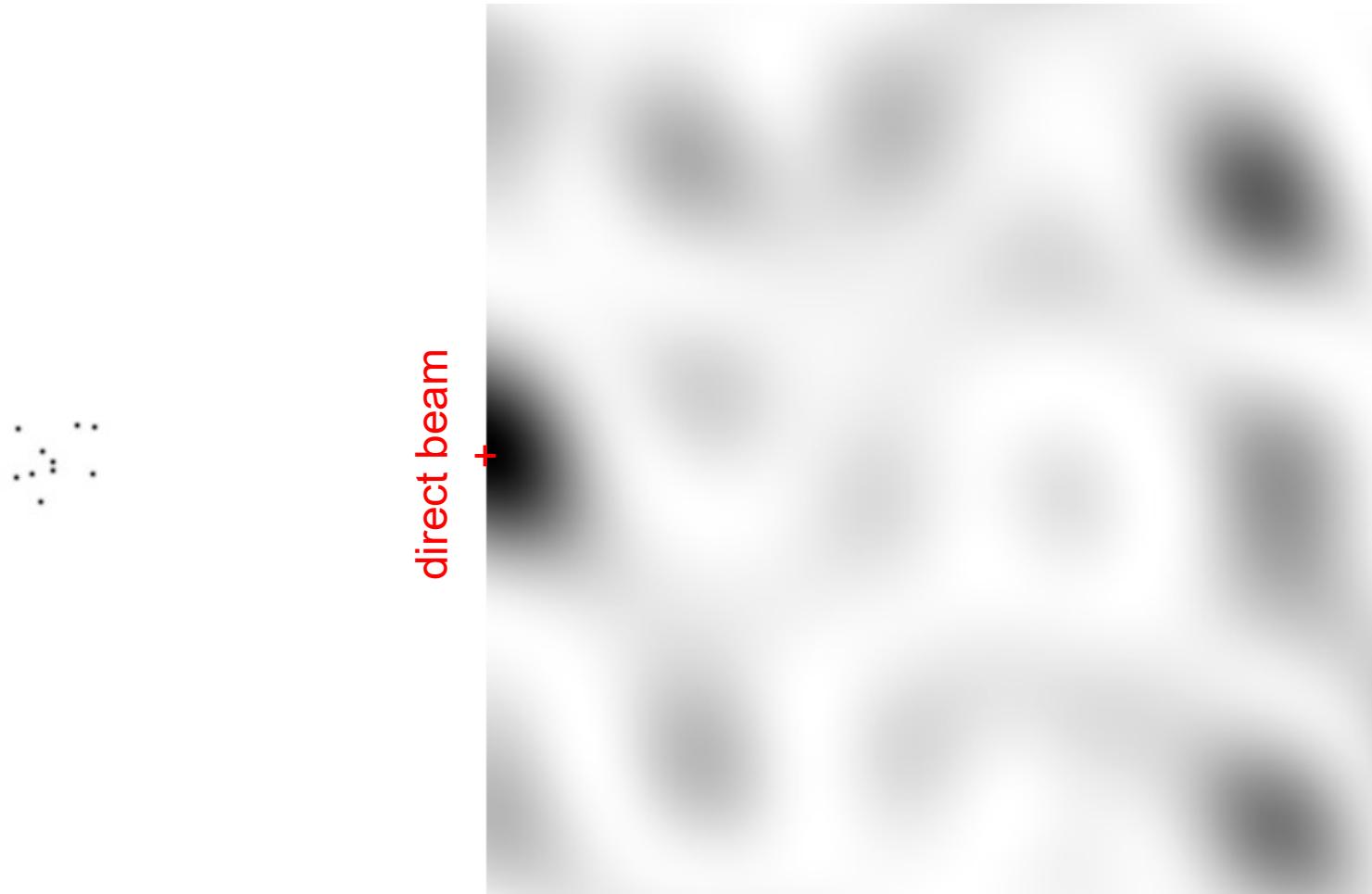




scattering from a structure

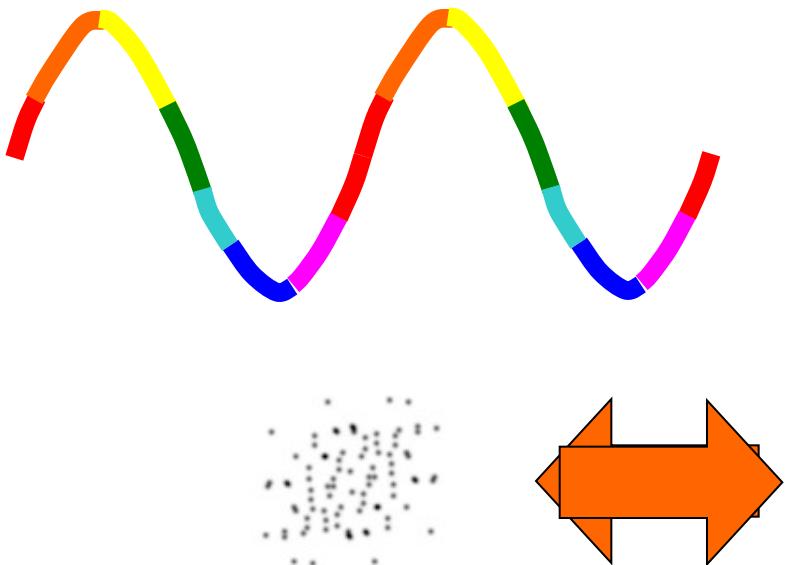
sample

detector



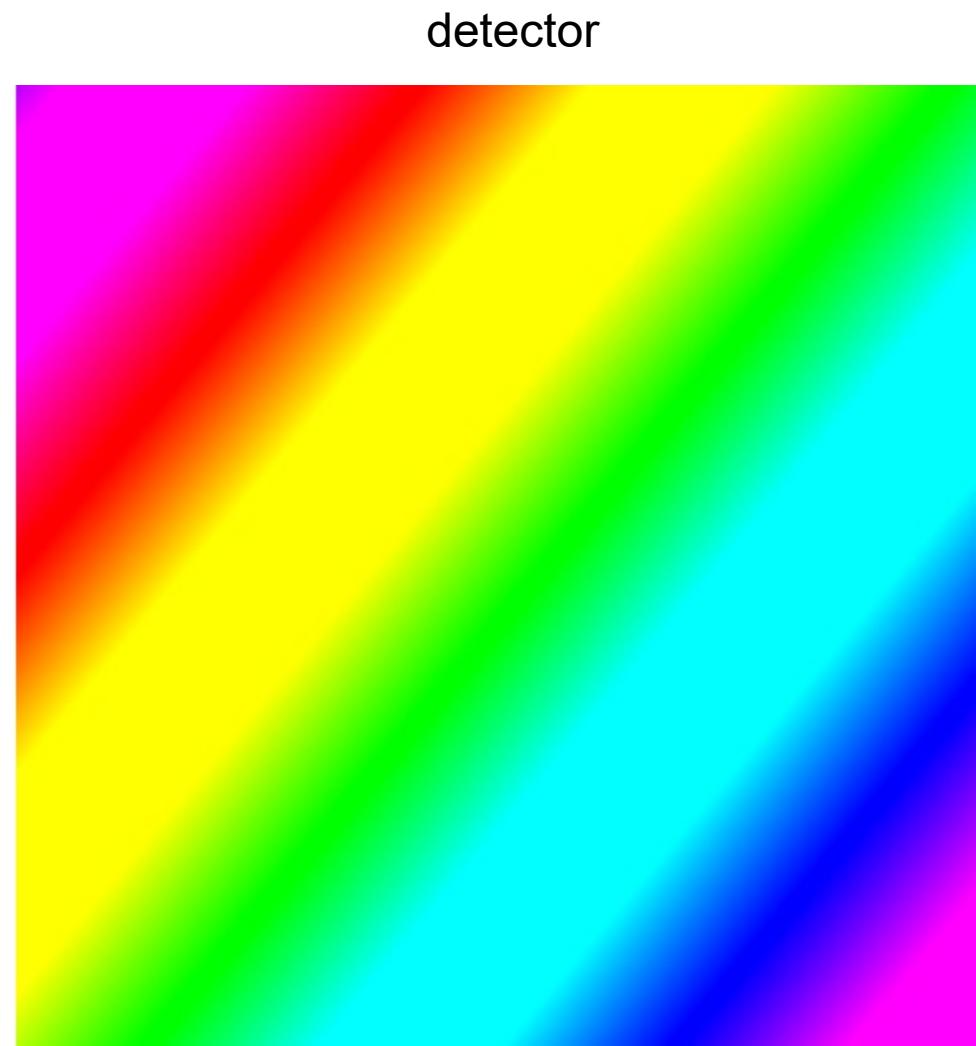
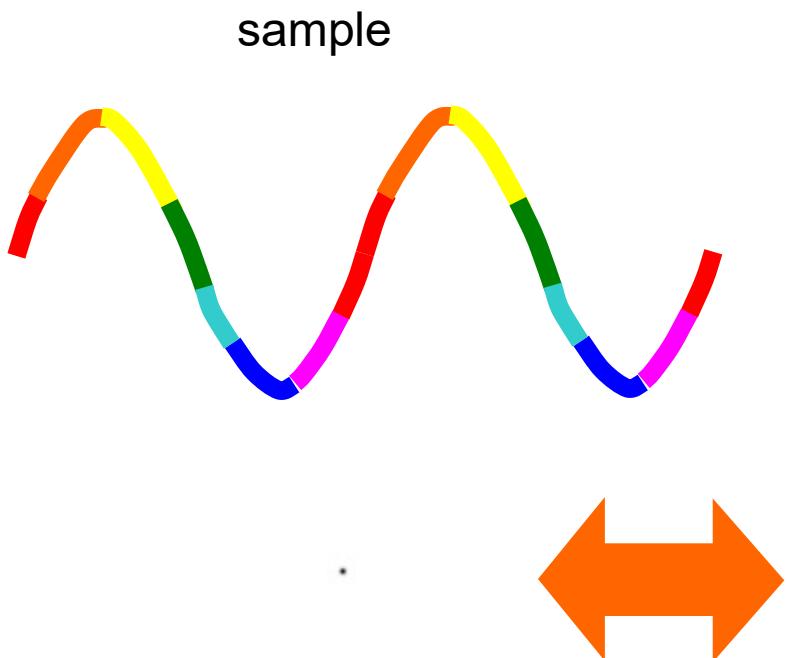
forward Fourier Transform

no phase



scattering from a sample

colored by phase



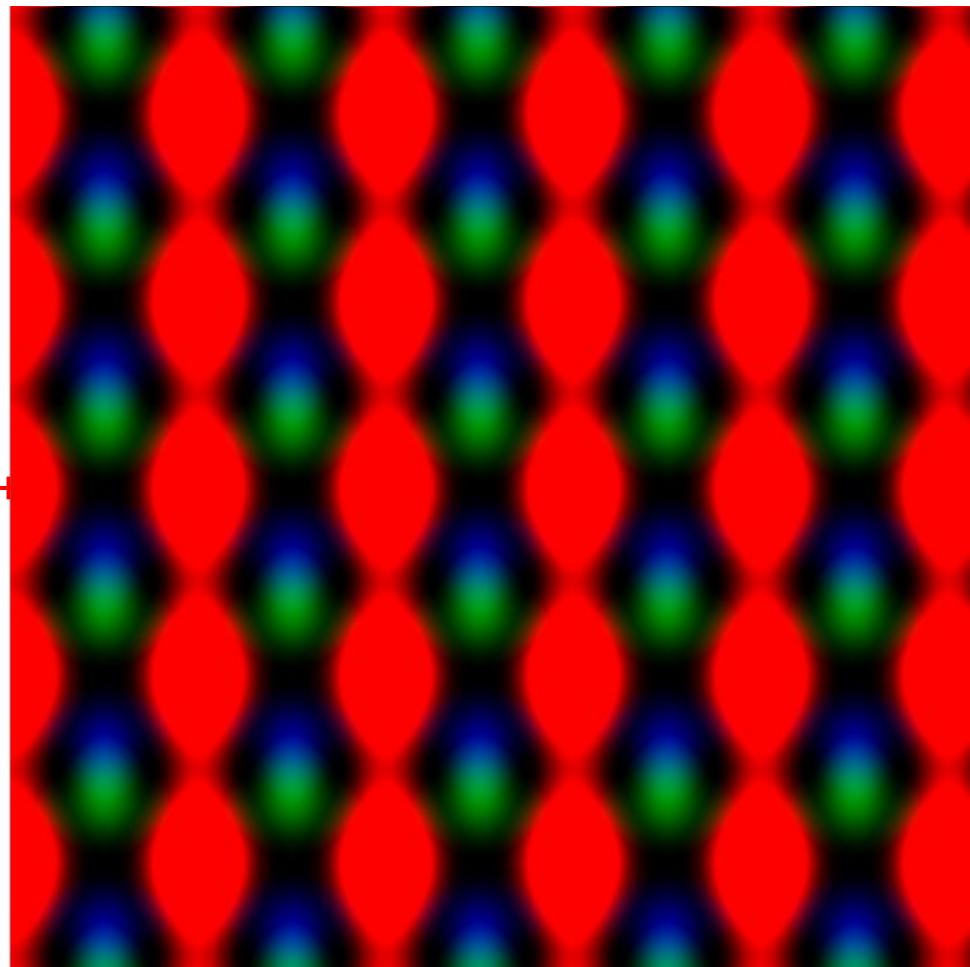
scattering from a lattice

colored by phase

sample

detector

beam center



scattering from a lattice

colored by phase

sample

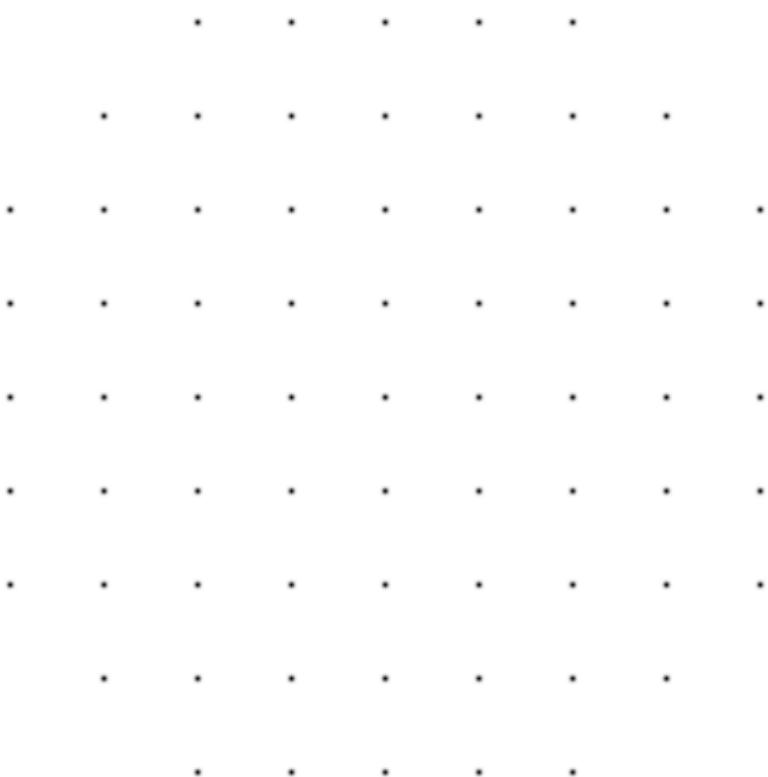
detector



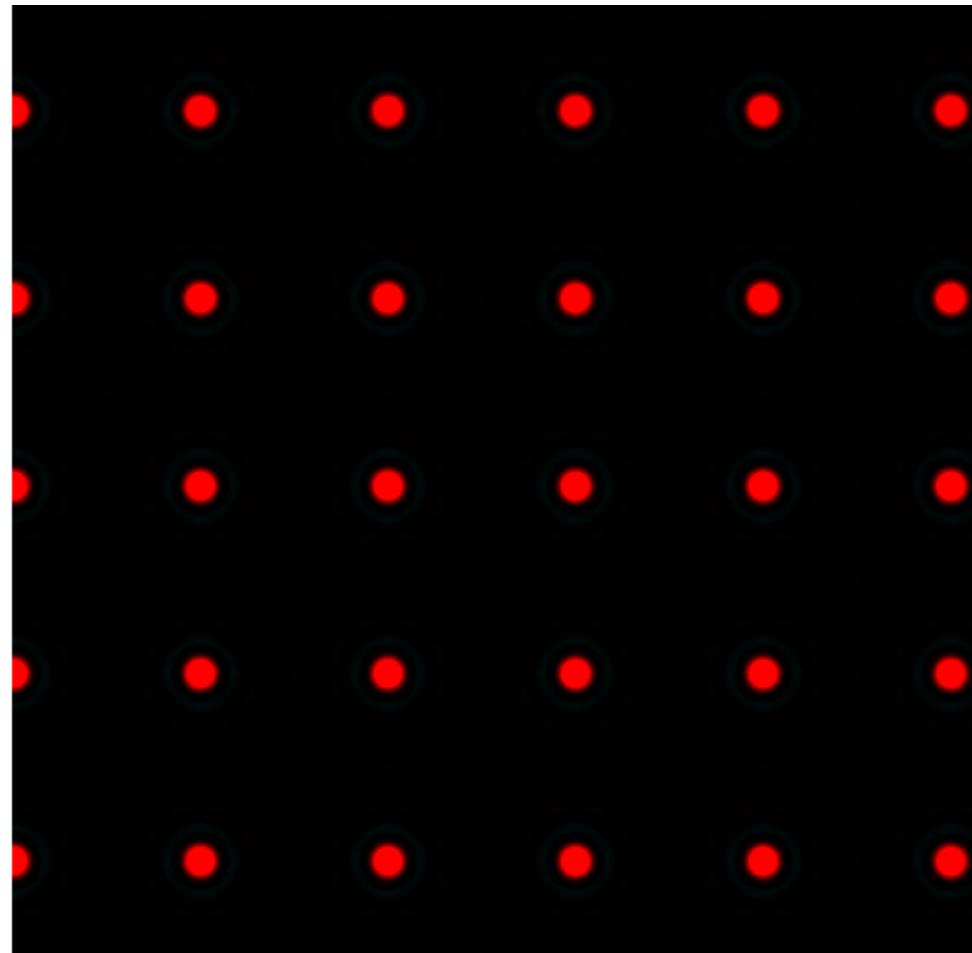
scattering from a lattice

colored by phase

sample



detector

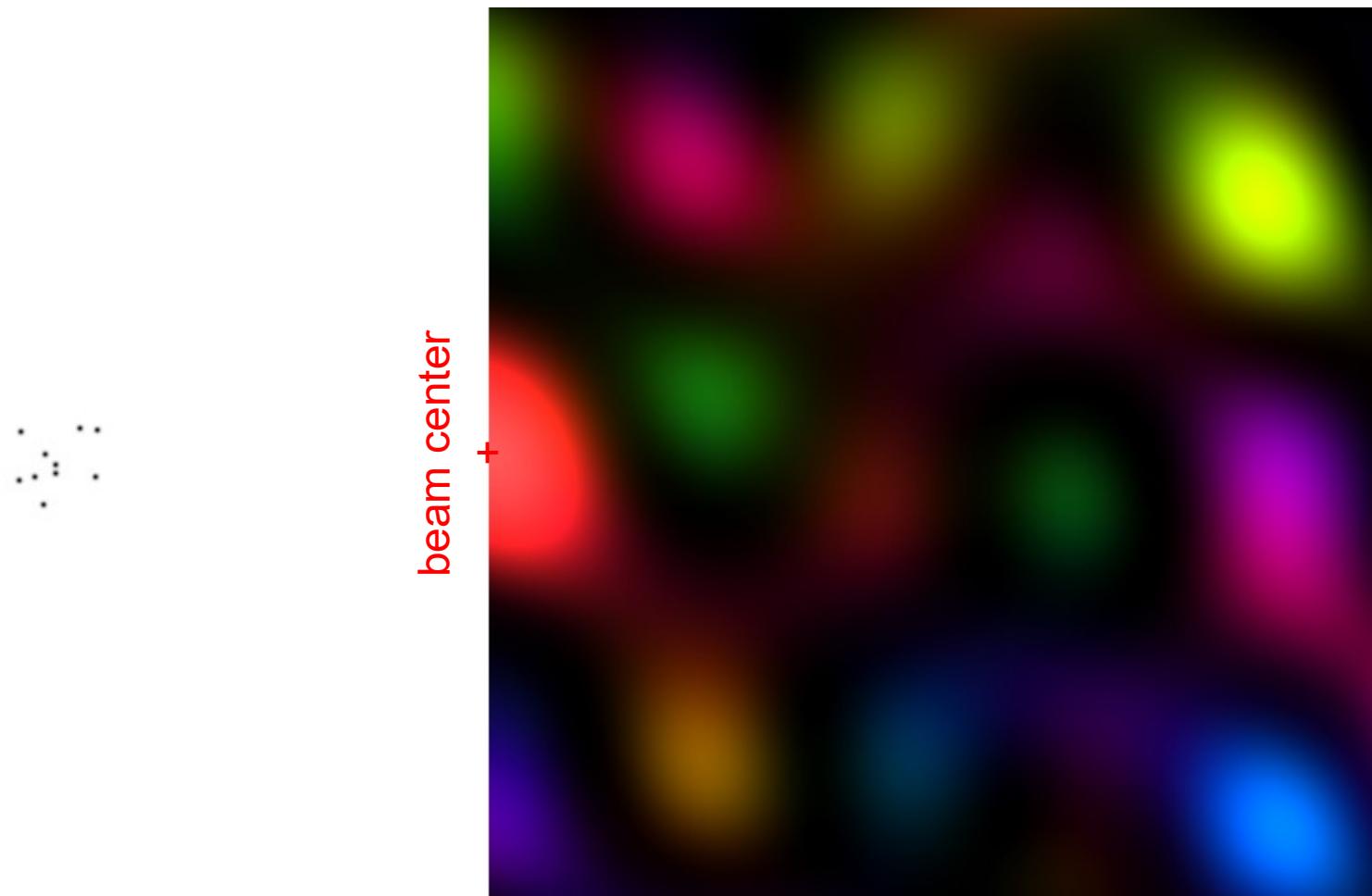


scattering from a crystal structure

colored by phase

sample

detector

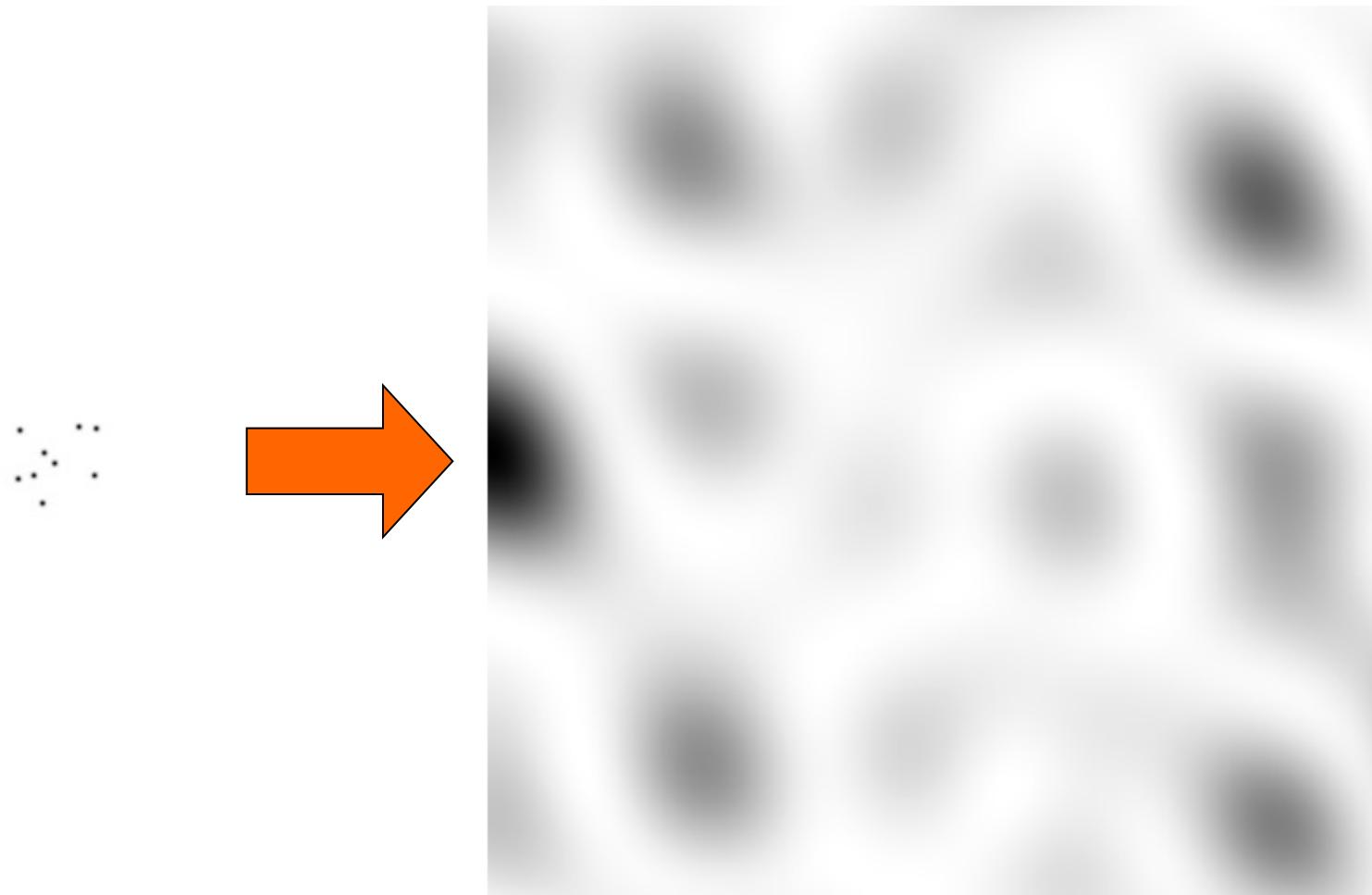


Major Phasing techniques

- Molecular Replacement
- Multiple Isomorphous Replacement
- Multiwavelength Anomalous Diffraction
- Single-wavelength Anomalous Diffraction

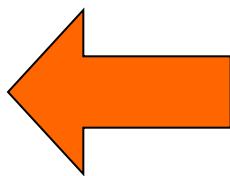
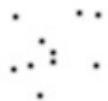
inverse Fourier Transform

no phase



inverse Fourier Transform

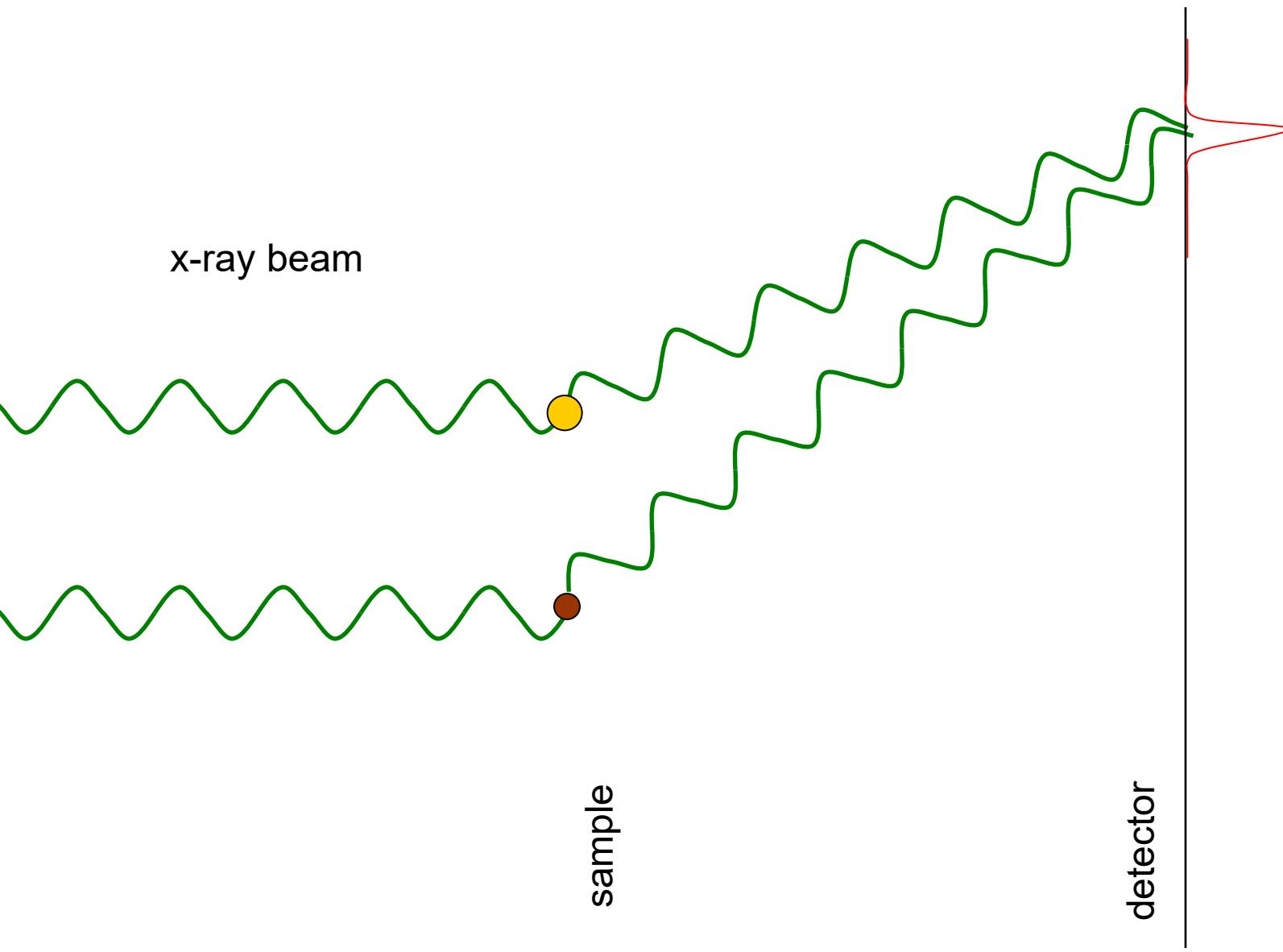
no phase



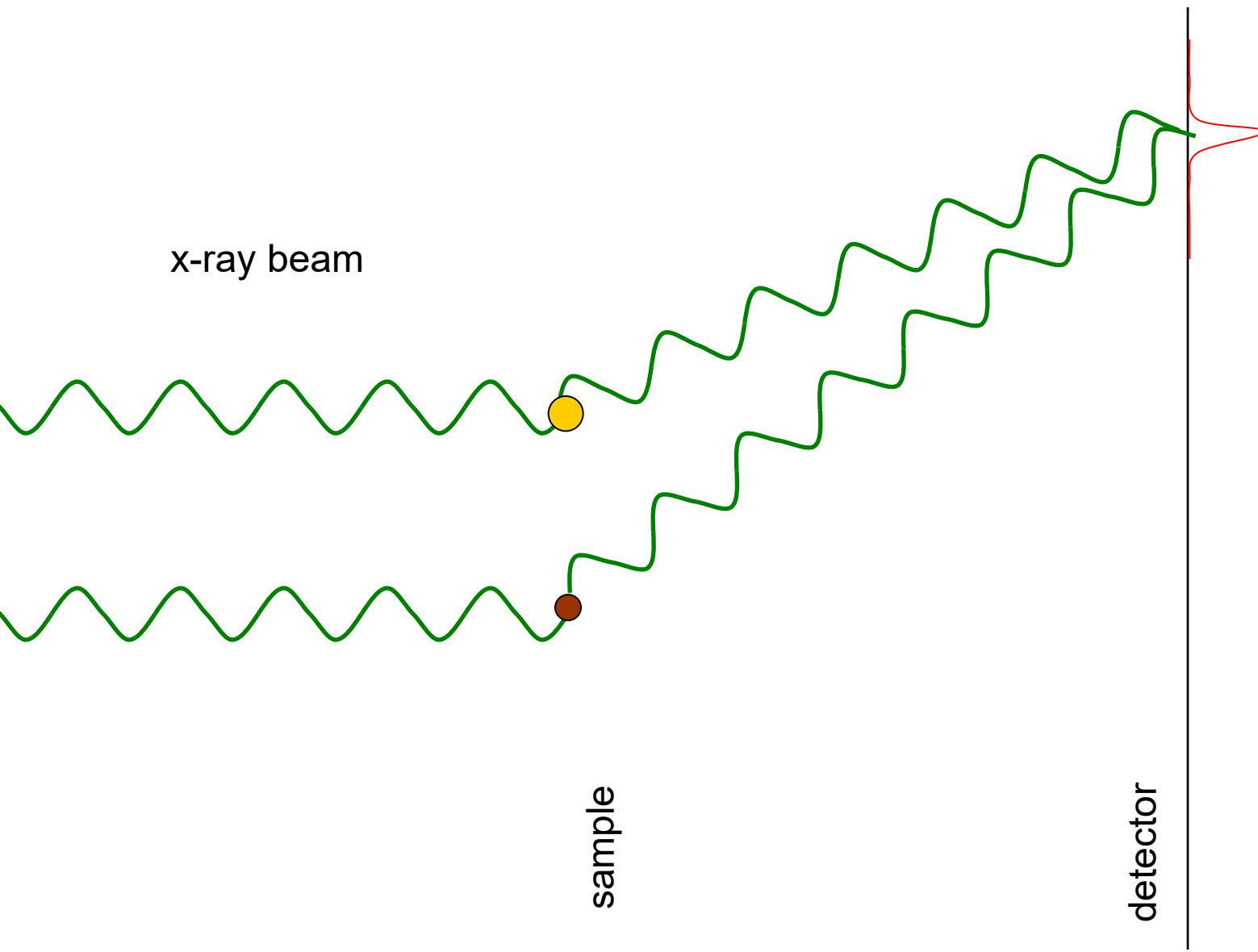
Major Phasing techniques

- Molecular Replacement
- Multiple Isomorphous Replacement
- Multiwavelength Anomalous Diffraction
- Single-wavelength Anomalous Diffraction

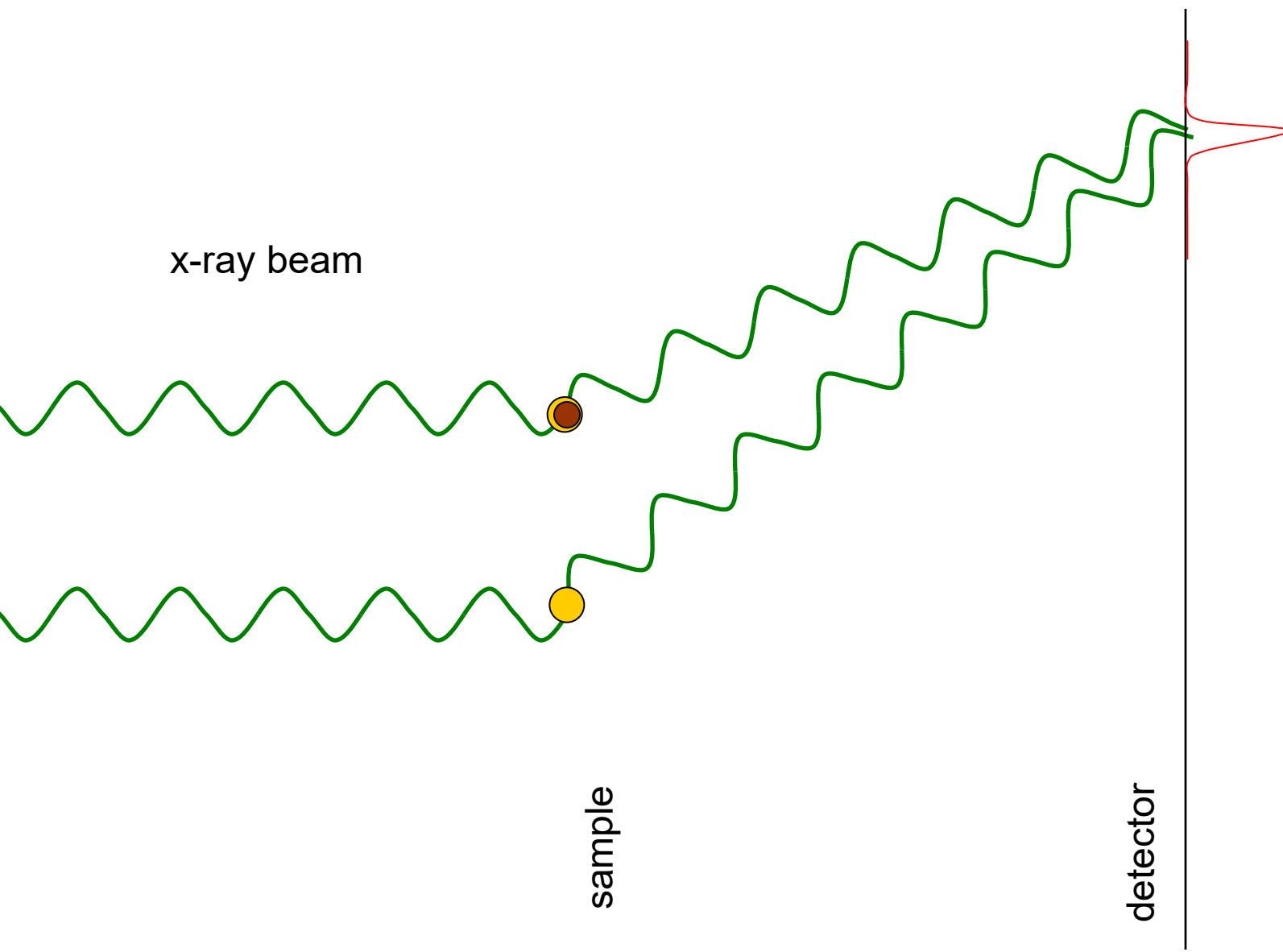
anomalous scattering



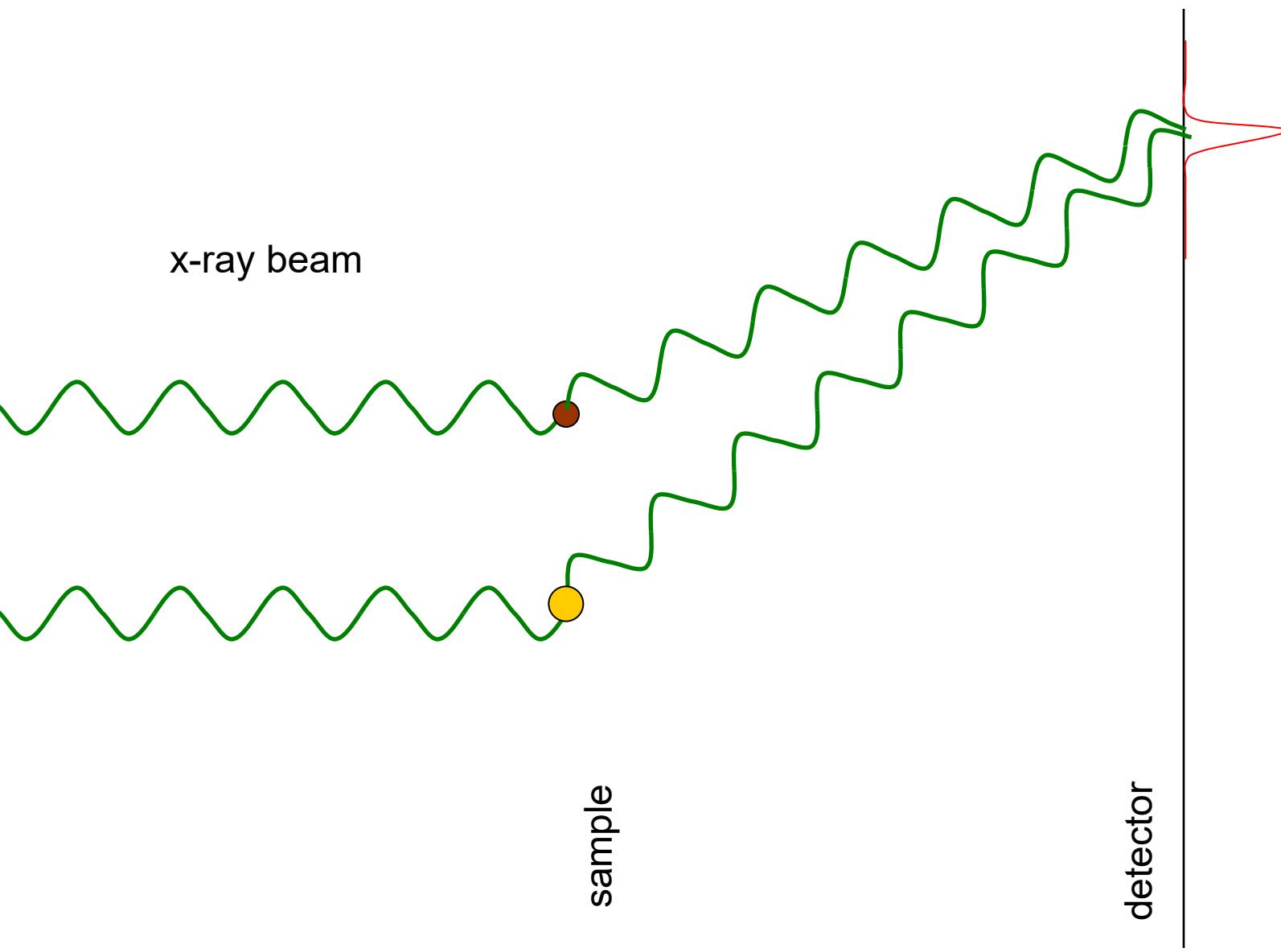
anomalous scattering



anomalous scattering



anomalous scattering



anomalous scattering

