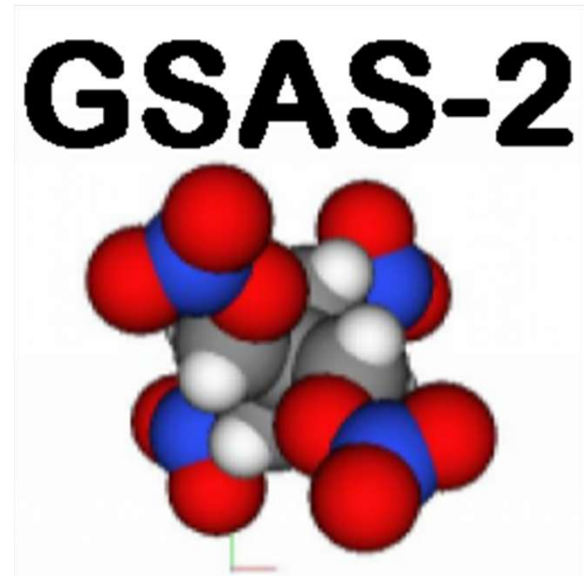


# GSAS-II BEYOND RIETVELD

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Saskatoon  
June, 2024



# 2D IMAGE PROCESSING – FORGOTTEN OLD MATH

# 2D IMAGE DATA

## Conic sections

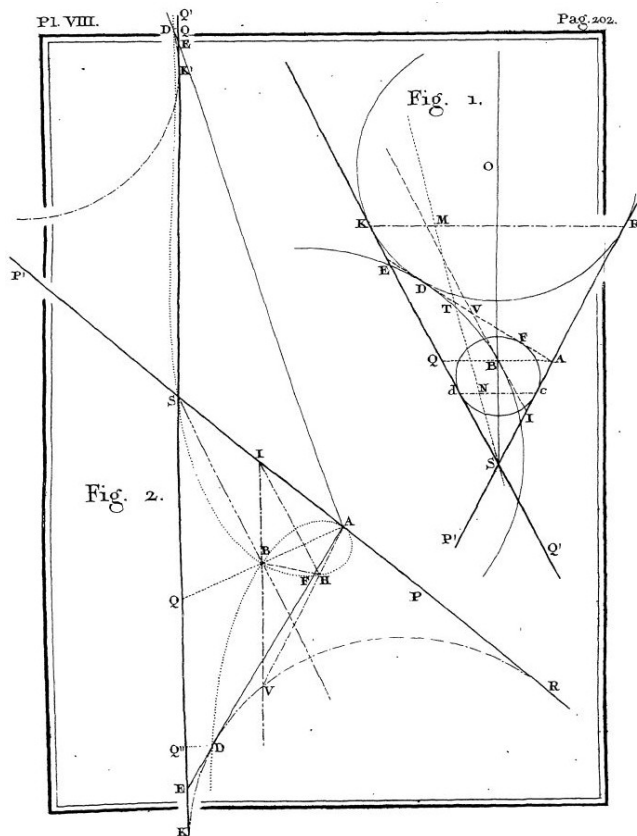
Where is the incident beam on the detector?

Fit2D (& DataSqueeze) – assumes center of the diffraction ellipse - **False**

Analysis – G.P. Dandelin,

Nouveaux memories de l'Academie royal de Bruxelles, 2, 171-202 (1822)

Drawing by Dandelin p.202



Taken from Dandelin's original paper  
Fig. 1: Shows the 2 spheres in contact with plane EA

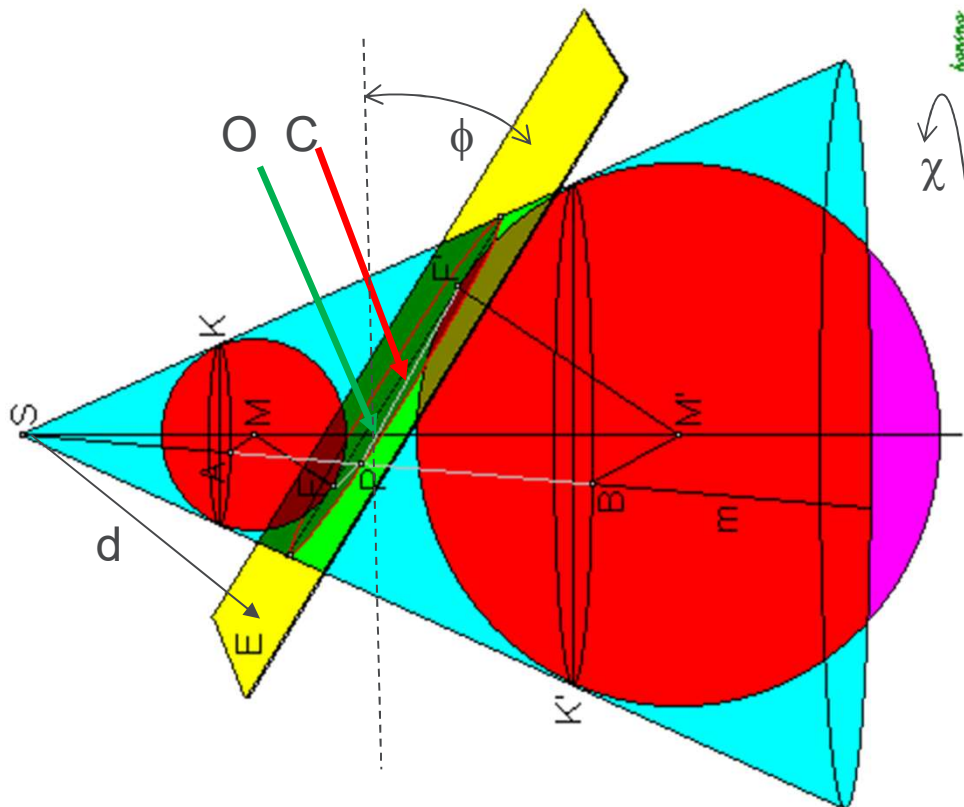
- line SO is cone axis
  - F&D are the ellipse foci on the plane
- He refers to a work by M. Quetlet as having previously made this construction - source?

This is not something new!

Dandelin sphere construction is used in GSAS-II for image plate orientation calibration

NB: Irena & pyFAI get this right

# GSAS-II IMAGE DETECTOR CALIBRATION VIA DANDELIN SPHERES

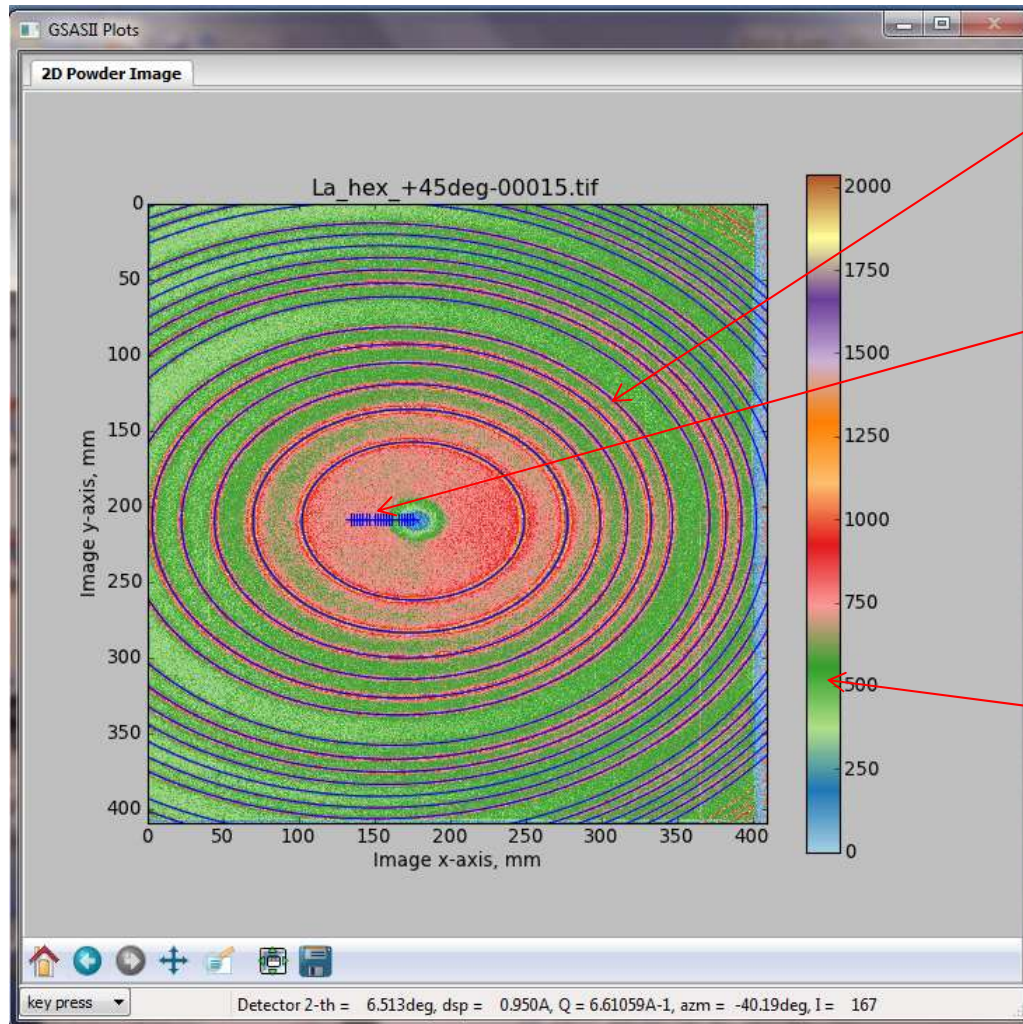


- Plane E is a tilted area detector
- The line SMM' is the Bragg cone axis – incident beam direction & passes through centers of both spheres
- Spheres touch plane at foci (F & F') of conic section (ellipse)
- Intersection of axis with plane (**O**) not at halfway point (**C**) between F & F' (ellipse center) – note similar triangles MFO & M'F'O of different sizes
- If plane is perpendicular to cone axis then conic section is a circle and O & C coincide
- GSAS-II parameters:
  - $d$  – sample-detector plane distance
  - $\phi$  – detector tilt angle ( $= 2\Theta_{\text{detector}}$ )
  - $\chi$  – tilt azimuth angle
  - $x_o, y_o$  – beam position @ **O** on detector

This is just geometry

## 2D IMAGES IN GSAS-II:

Calibration – tilted detector (e.g. 45° about vertical axis)



Ellipses – sections of Debye-Scherrer cones

Ellipse centers – not on beam center!

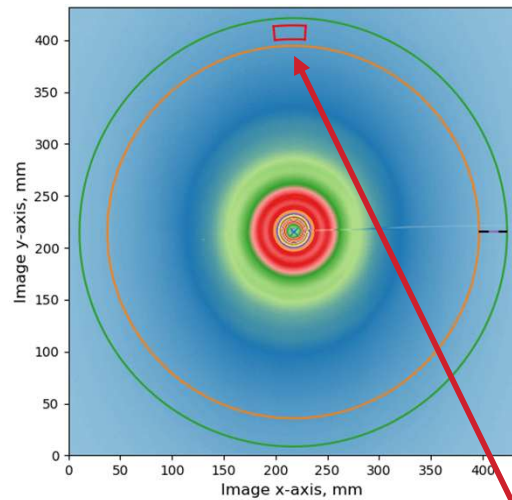
Fitting only requires material ( $\text{LaB}_6$ ) and  $\lambda$  (e.g. don't need to know distance – get that from fit)

Choice of color scheme – “Paired” is shown

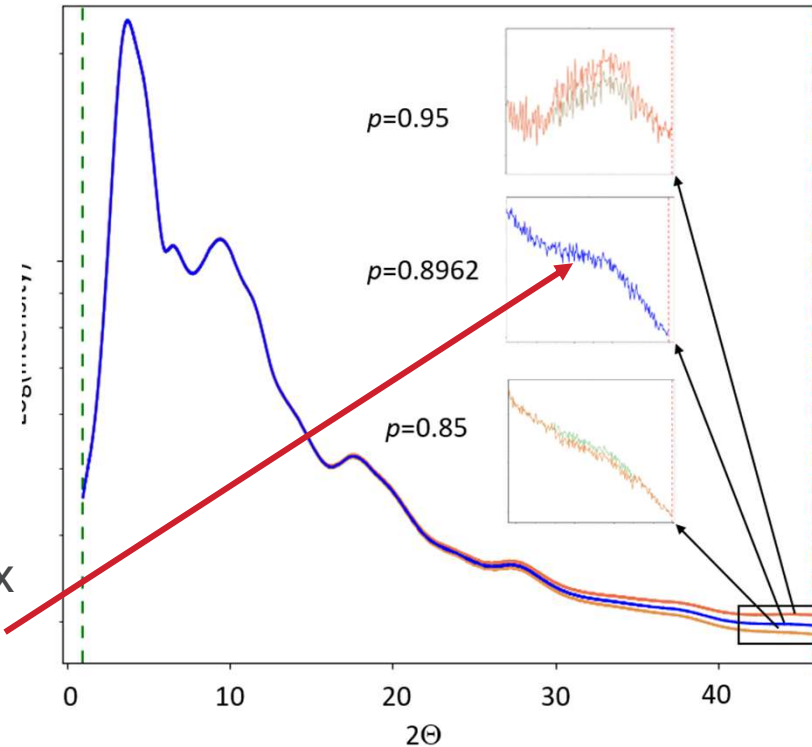
# 2D IMAGE POLARIZATION DETERMINATION

Sample – glass microscope slide – purely amorphous & isotropic  
Polarization correction: azimuth ( $\varphi$ ) dependent

$$P = [(1 - p)\cos^2\varphi + p\sin^2\varphi]\cos^2 2\Theta + (1 - p)\sin^2\varphi + p\cos^2\varphi$$

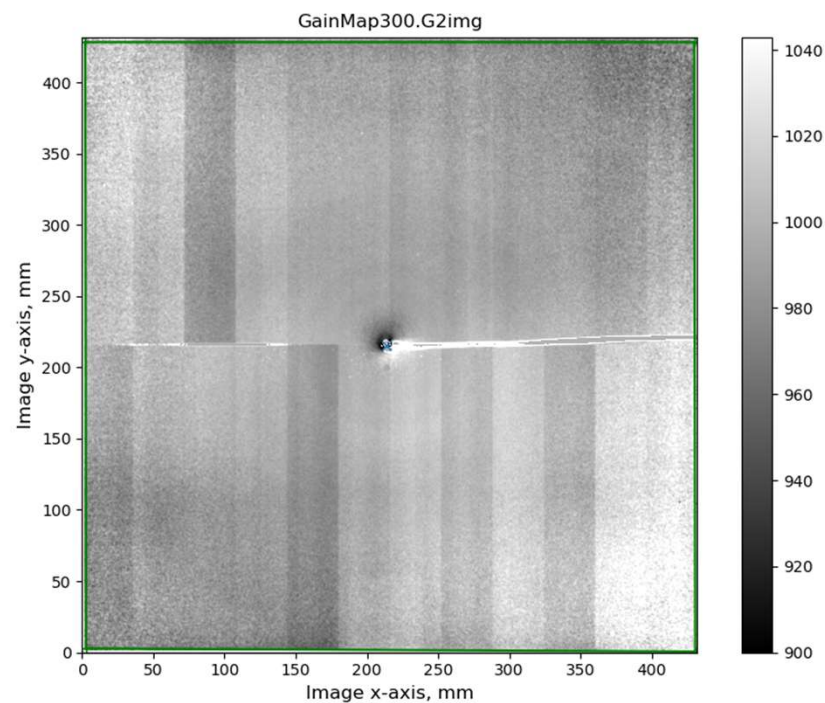
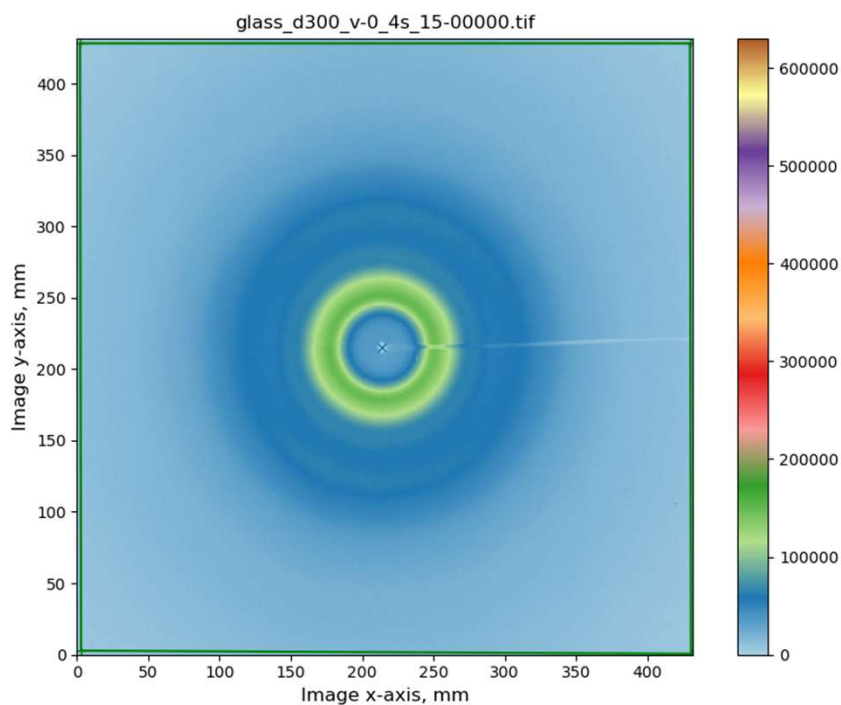


Integrate in band w/o mask box  
Match if polarization is correct



# 2D DETECTOR GAIN MAP

Sample – glass microscope slide – purely amorphous & isotropic  
Image corrected for polarization (automatic in GSAS-II)

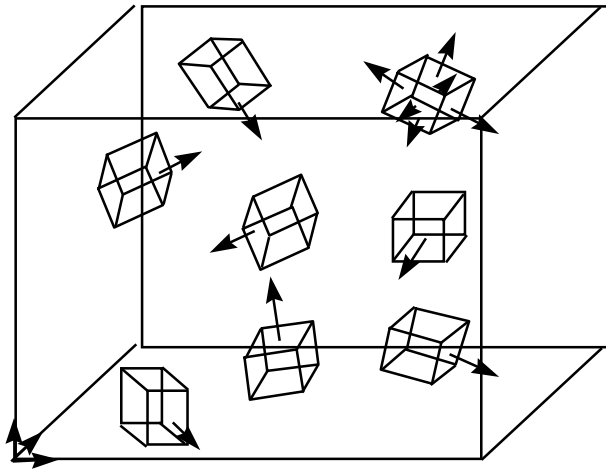


Integrate, compute ave image & subtract; residual is gain map (x1000)  
Better with 3 offset images – clean up center spot

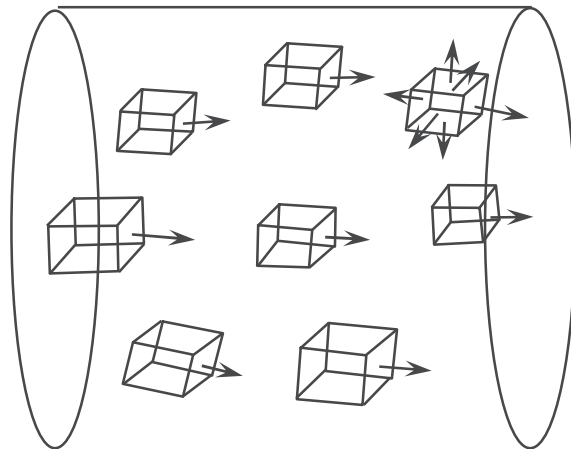
# TEXTURE ANALYSIS

# What is texture?

## Nonrandom crystallite grain orientations



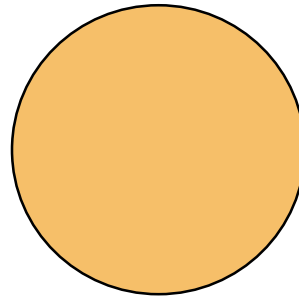
**Loose powder**



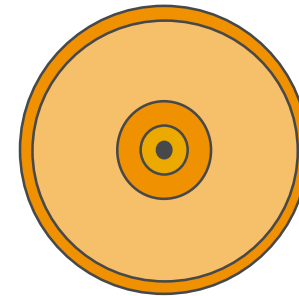
**Metal wire**

**Random powder - all crystallite orientations equally probable - flat pole figure**

**Pole figure - stereographic projection of a crystal axis down some sample direction**



**(100) random texture**



**(100) wire texture**

**Crystallites oriented along wire axis - pole figure peaked in center and at the rim (100's are 90° apart)**

**Orientation Distribution Function - probability function for texture**

# Texture - measurement by diffraction

**Non-random crystallite orientations in sample**

**Incident beam  
x-rays or neutrons**

**Sample**

**(220)**

**(200)**

**(111)**

**Debye-Scherrer cones**

- uneven intensity due to texture
- also different pattern of unevenness for different hkl's
- Intensity pattern changes as sample is turned

## Texture effect on reflection intensity – Sph. Harm. model

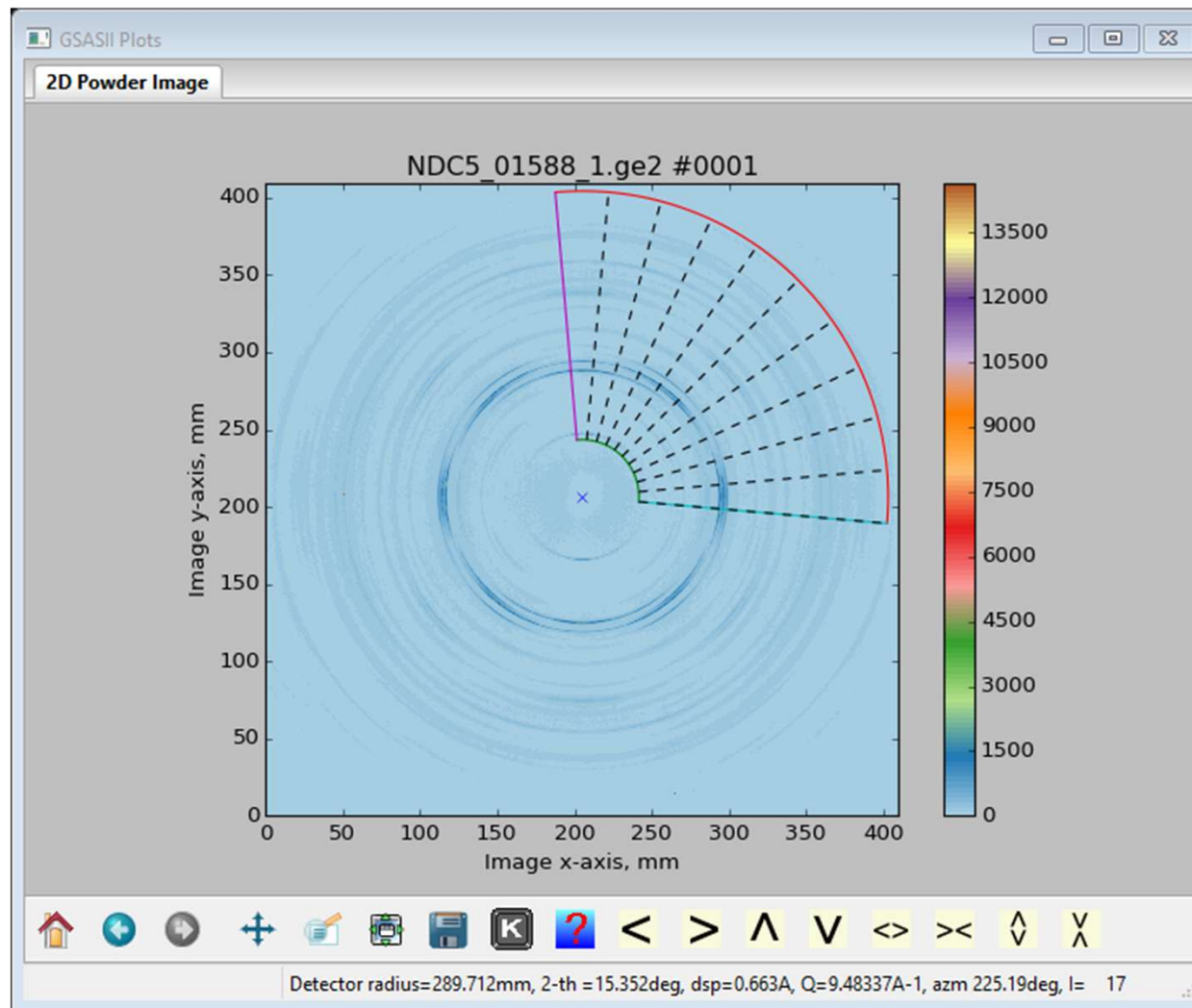
$$A(h, y) = \sum_{l=0}^{\infty} \frac{4\pi}{2l+1} \sum_{m=-l}^l \sum_{n=-l}^l C_l^{mn} K_l^m(h) K_l^n(y)$$

- **Projection of orientation distribution function for chosen reflection (h) and sample direction (y)**
- **$K$  - symmetrized spherical harmonics - account for sample & crystal symmetry**
- **“Pole figure” - variation of single reflection intensity as fxn. of sample orientation - fixed h**
- **“Inverse pole figure” - modification of all reflection intensities by sample texture - fixed y**
  - Ideally suited for neutron TOF diffraction
- **Rietveld refinement of coefficients,  $C_l^{mn}$ , and 3 orientation angles - sample alignment**

**NB: In GSAS-II as correction & texture analysis**

# 2D IMAGE

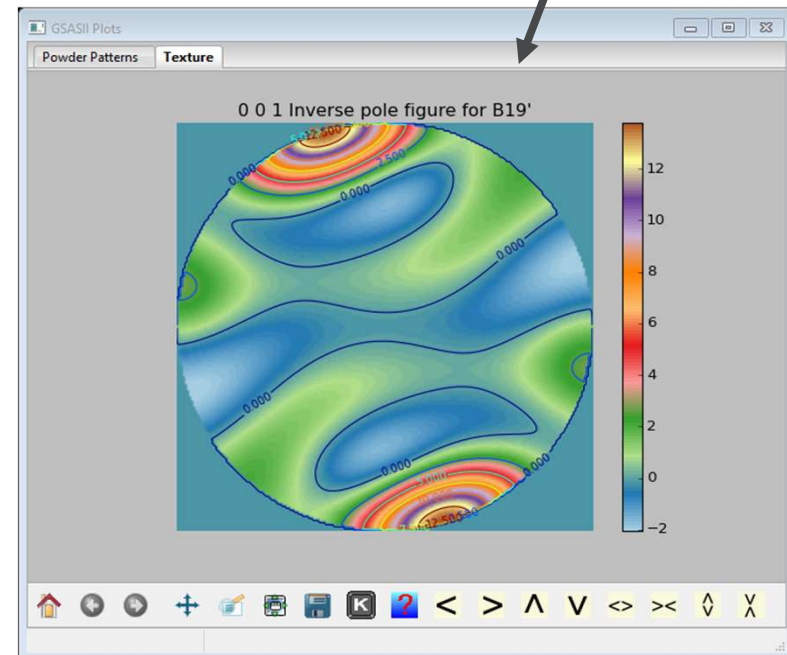
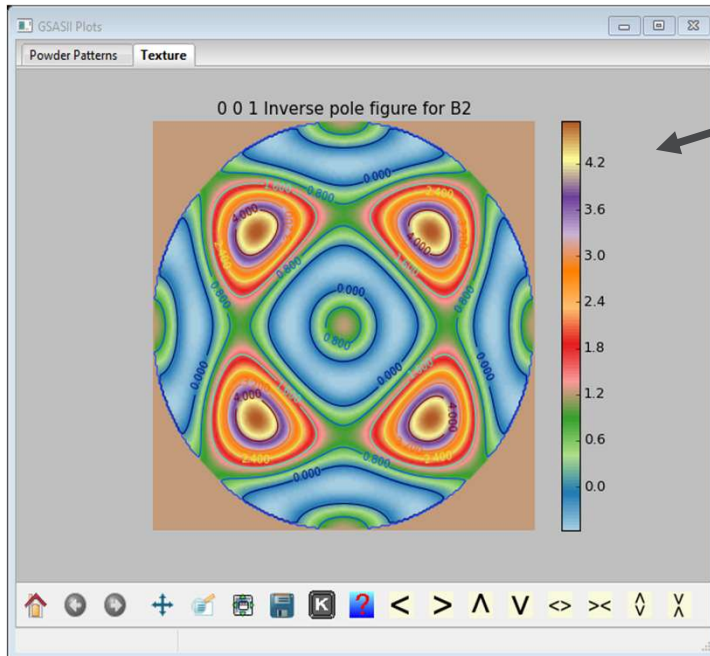
## NiTi shape memory alloy wire: B2 & B19' phases



Sample – wire  
symmetry  
Need only  $\frac{1}{4}$  of image  
Caked in  $10^\circ$   
increments  
Integration –  
PWDR patterns  
Analyze for texture

# GSAS-II TEXTURE ANALYSIS

Fit  $C_L^{mn}$  & crystal structure stuff – inverse pole figures B2 & B19'



Pole figures – bullseyes (boring)  
GSAS-II → 3 methods for texture

# RMCPROFILE IN GSAS-II

# RMCPROFILE “BIG BOX” SIMULATION

## GSAS-II interface development goals

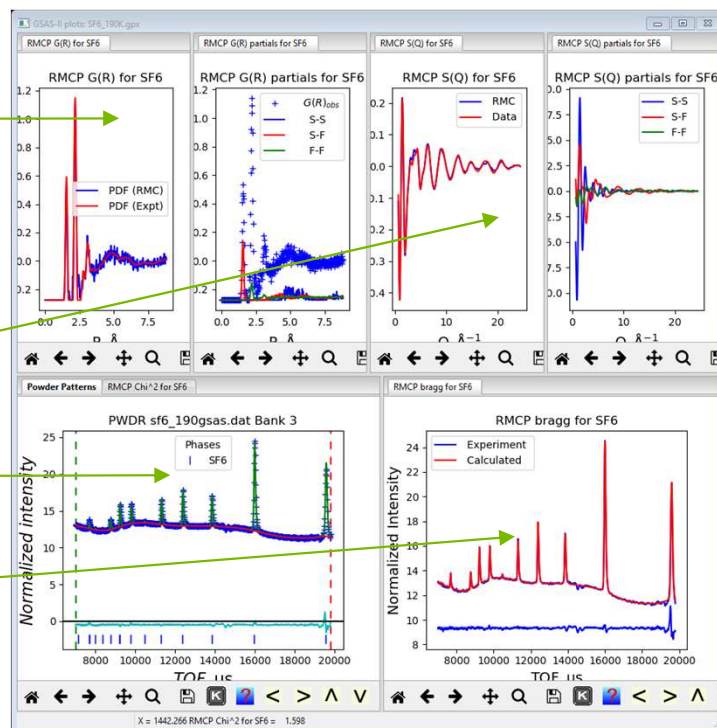
- Provide GUI interface to setup of RMCPProfile - save setup controls for reuse
- Initiate independent RMCPProfile execution – may run for hours
- Allow graphical display on intermediate results

G(R) & partials

S(Q) & partials

RR result

PWDR simulation

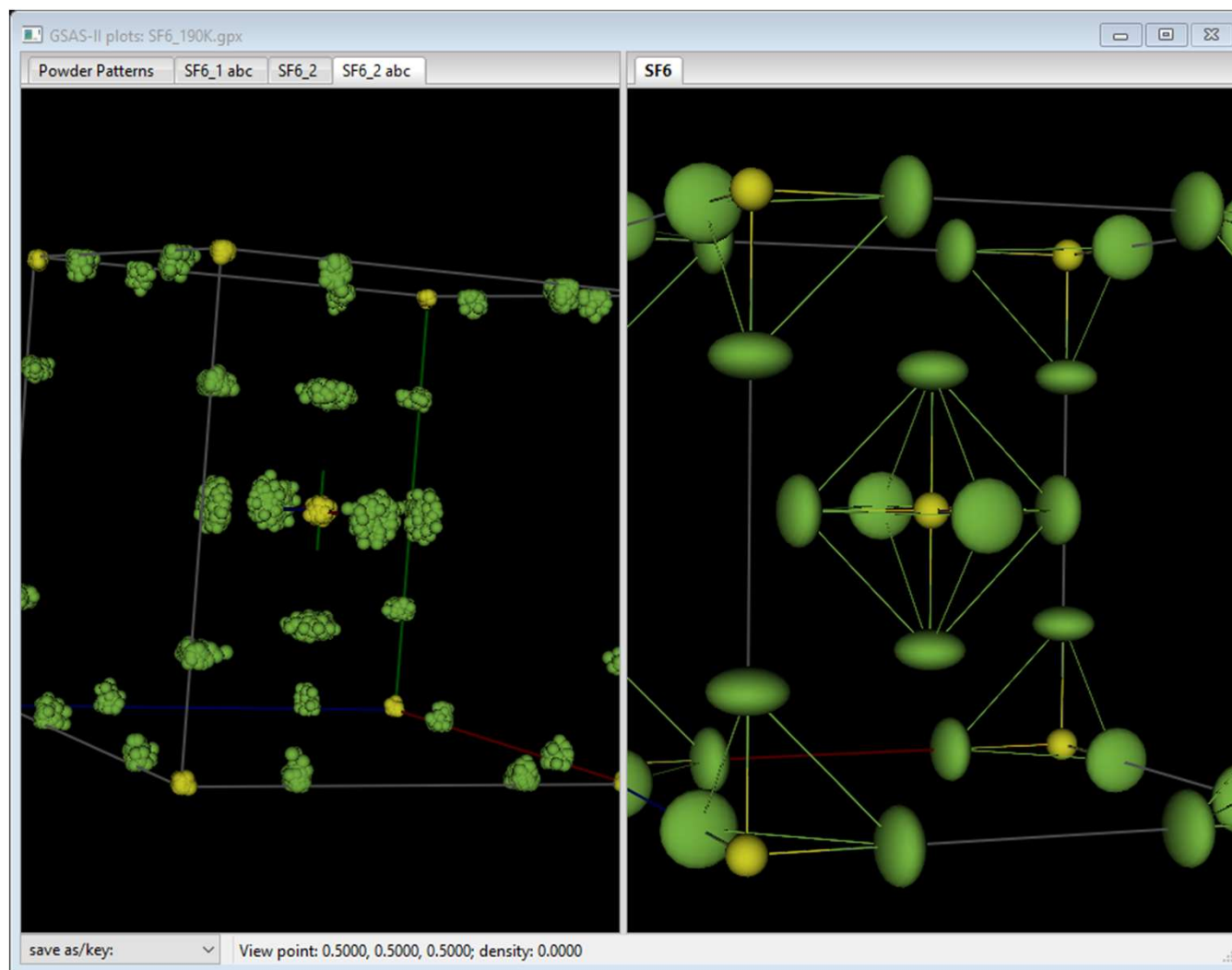


# RMCPROFILE RESULT FOR SF<sub>6</sub>

10x10x10 unit cell box – transform back to original

See disordered atom distribution

– compare to Rietveld  $U_{\text{aniso}}$  for F atom

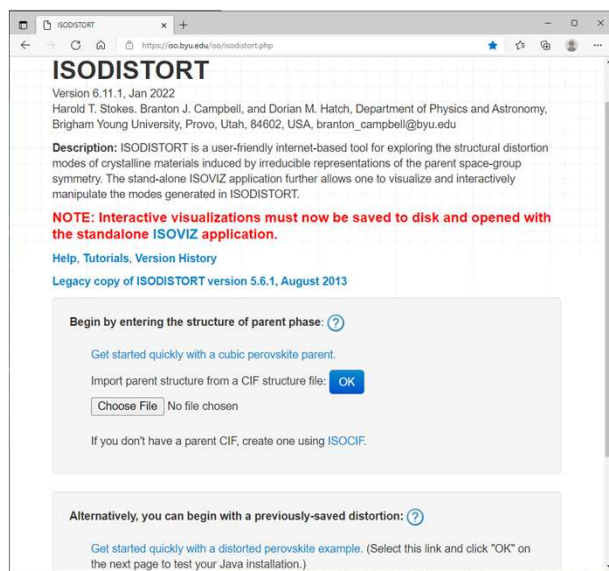


# PDFFIT & ISODISTORT

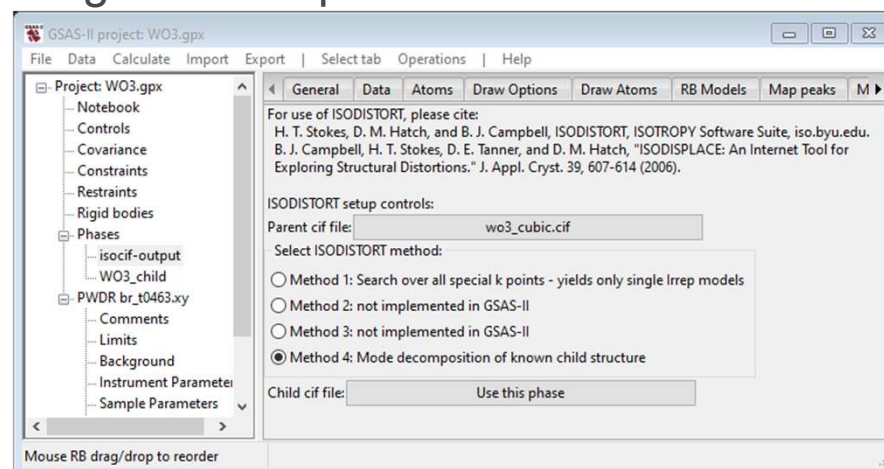
# ISODISTORT

## Implementation in GSAS-II

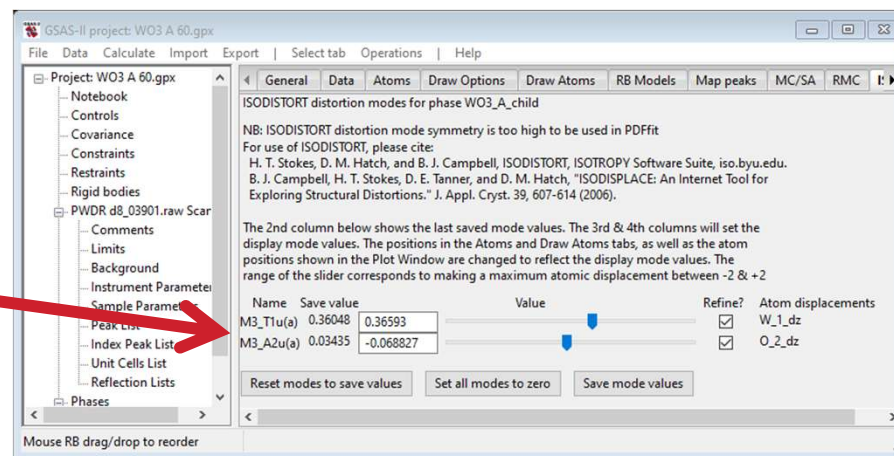
ISODISTORT: Web based tool for discerning mode displacements of atoms from an idealized parent structure



- To use: a multistep process → a cif file with modes; can be imported into GSAS-II with new variables for the modes.



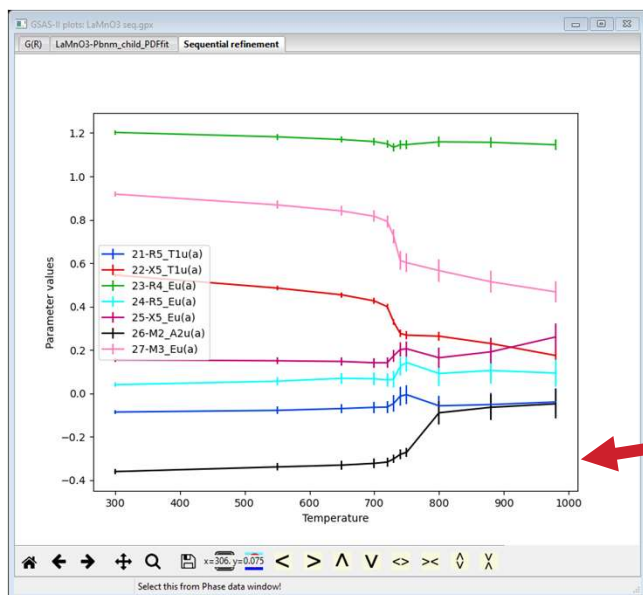
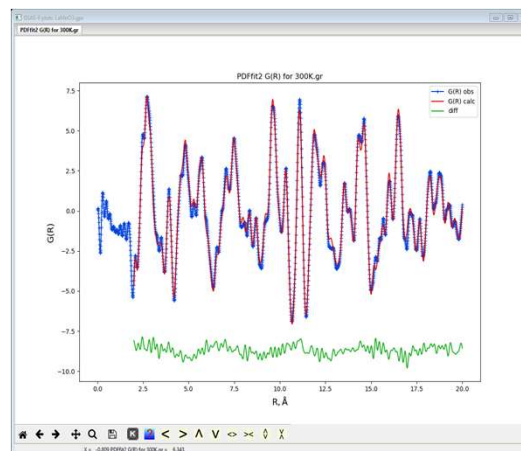
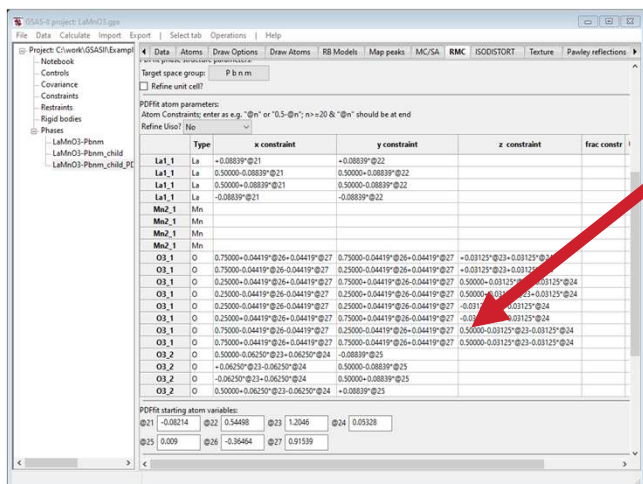
- New implementation – direct interaction between GSAS-II & ISODISTORT; simplified operation



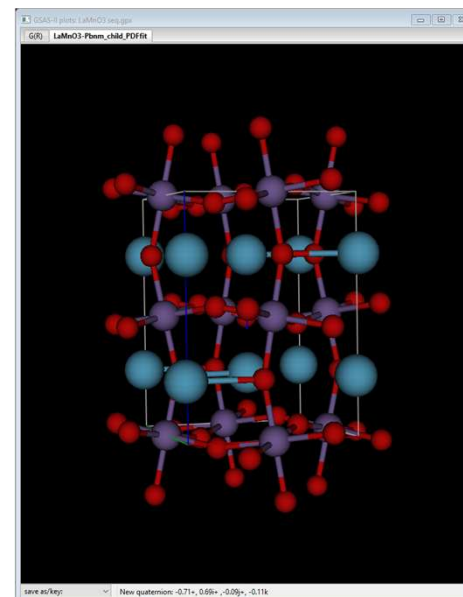
# PDFFIT2 = “PDFfit” IN GSAS-II

## “Small Box” modelling of pair distribution functions

Use ISODISTORT – create the atom position constraints in new interface to PDFfit2



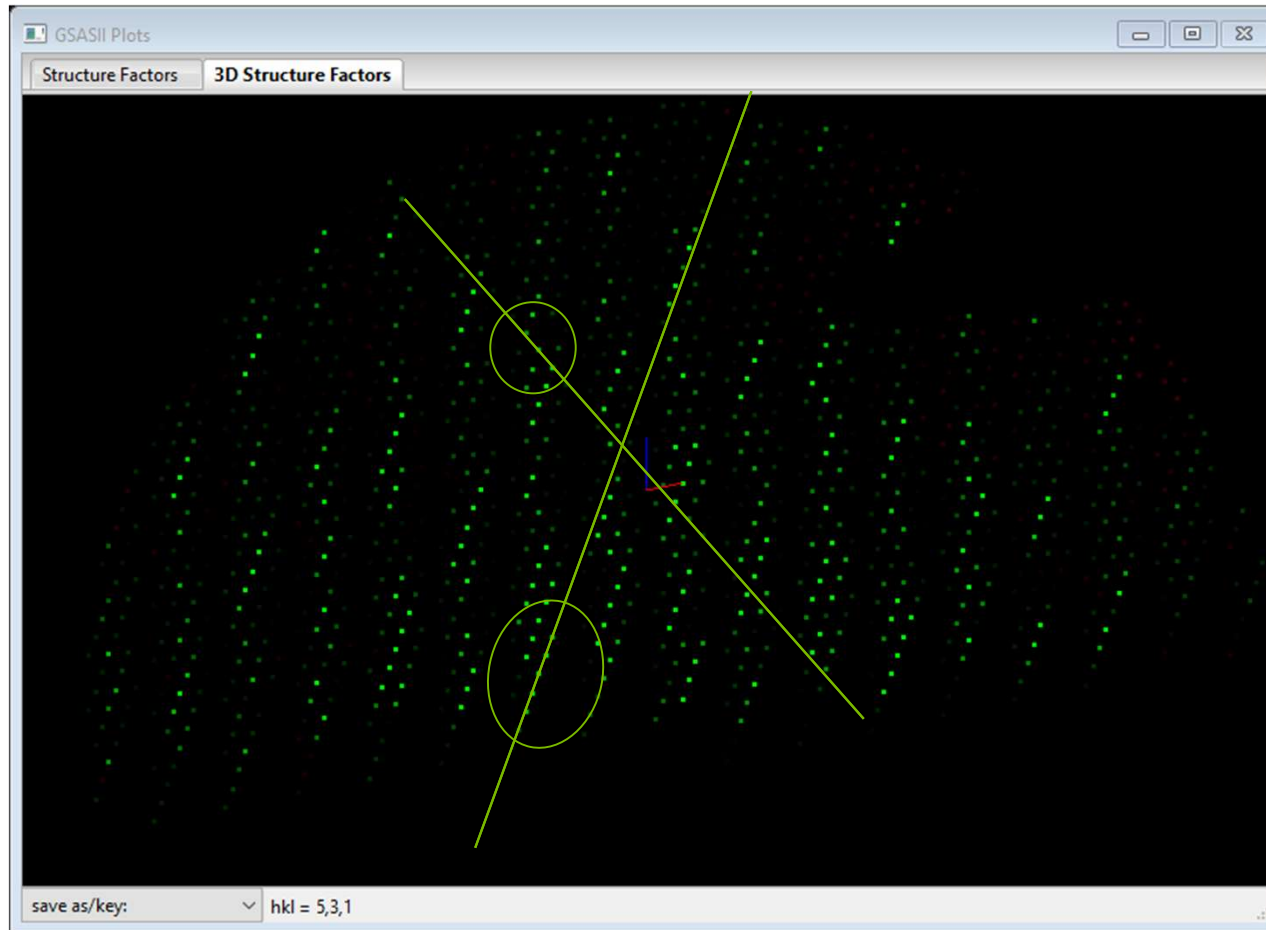
Parameters: mode displacements (Å)  
 Can be fit for sequence of T



# INCOMMENSURATE STRUCTURES IN GSAS-II

# INCOMMENSURATE STRUCTURES N GSAS-II

Book: “Incommensurate Crystallography” S. van Smaalen



$$H=G+mq$$

G: substructure hkl  
m: +/- small integers  
q: modulation vector

For  $\text{Na}_2\text{CO}_3$   
 $q = 0.183, 0, .319$

Each reflection: hklm  
m=0 sublattice  
m $\neq$ 0 superlattice

$\text{Na}_2\text{CO}_3$  – single crystal X-ray data – h0l zone  $\rightarrow$  rows of spots don't line up

# INCOMMENSURATE STRUCTURES

## Symmetry symbols – interpreted by GSAS-II (not lookup)

- Space group + super symmetry symbol

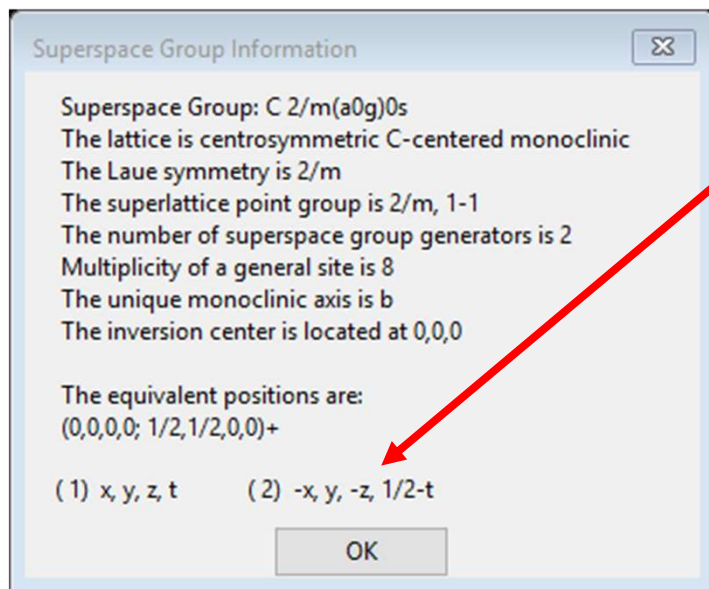
e.g.  $\text{Na}_2\text{CO}_3 - \text{C}2/m(\alpha 0 \gamma)0s$

Space group

Modulation vector

Translation component

Operators: conventional space group & 4<sup>th</sup> dim component



Possible modulation vectors:

e.g.  $\alpha\beta\gamma$ ,  $\alpha 0 \gamma$ ,  $0\beta 0$ ,  $\alpha^{1/2}\gamma$ ,  $1/2\beta 0$

Translations: 0,s,t,q,h

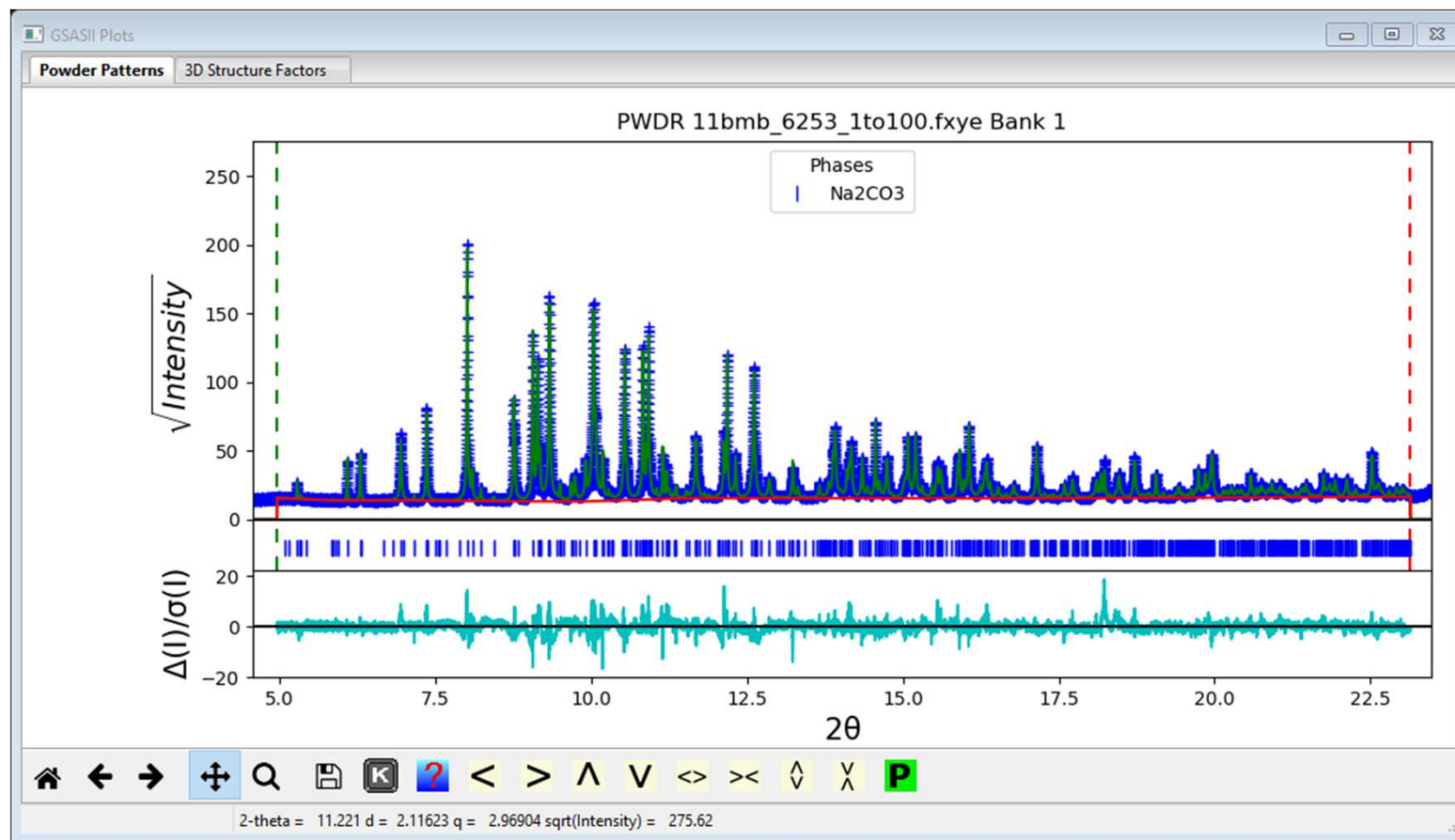
1-4 of these

Depend on space group

GSAS-II shows legal choices

# POWDER DIFFRACTION

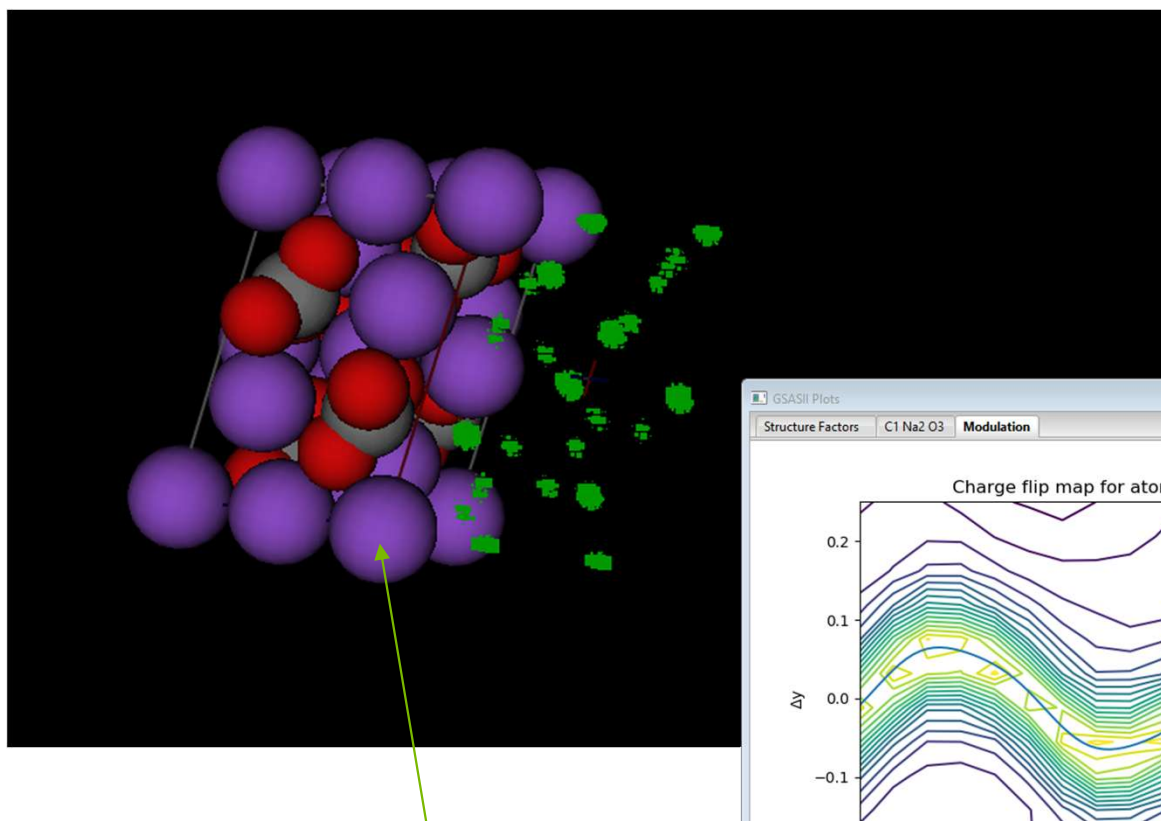
$\text{Na}_2\text{CO}_3$  – 11BM @ APS room temp.



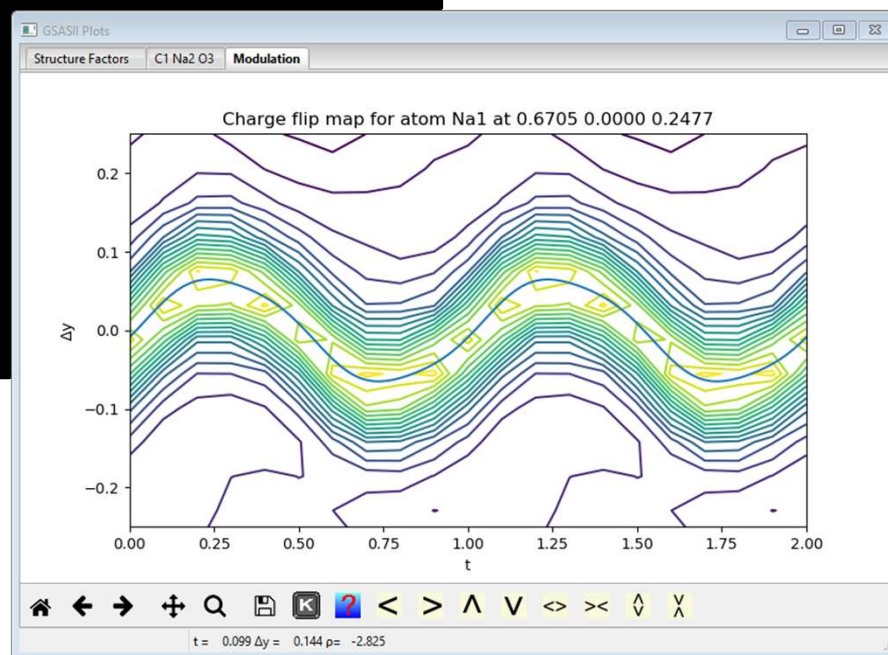
Includes  $m=-2,-1,1,2$  superlattice reflections; Rietveld refinement includes 1<sup>st</sup> & 2<sup>nd</sup> order harmonics on position depending on atom

# INCOMMENSURATE STRUCTURE SOLUTION

4D charge flipping; single crystal & powders (e.g. Pawley refinement)

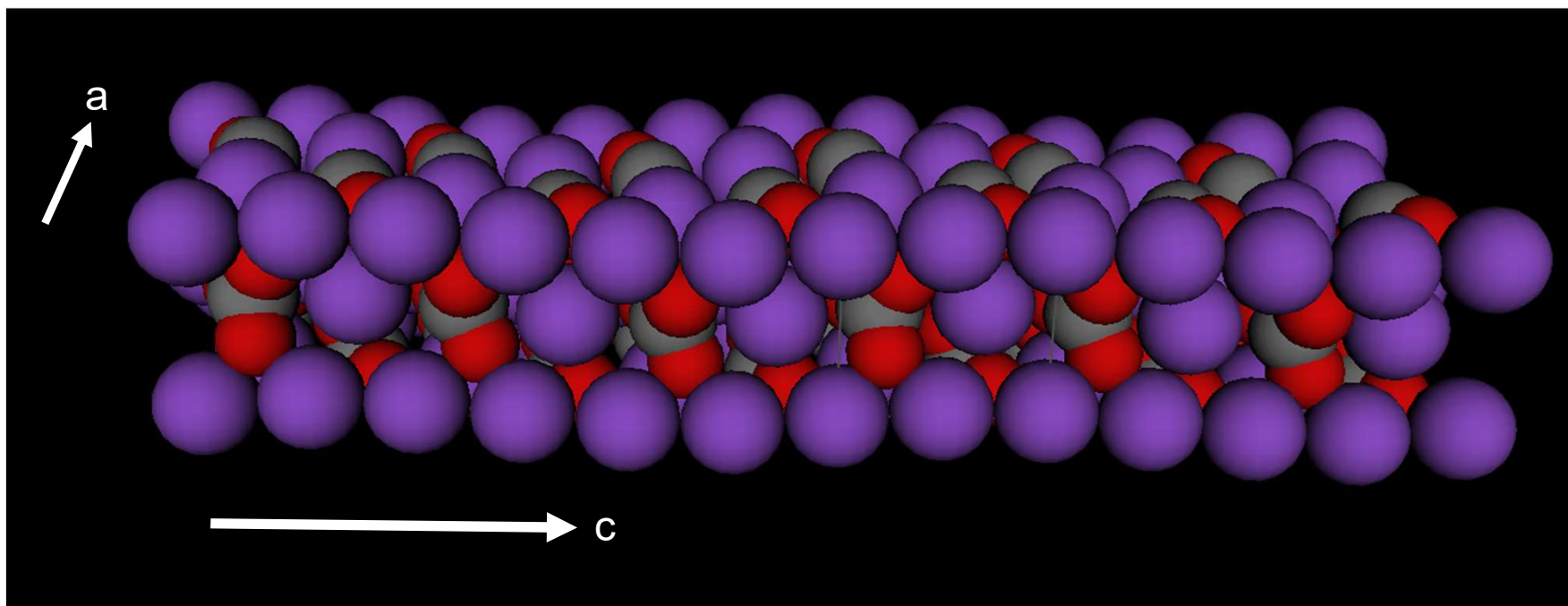


Modulation of atom positions ( $\text{Na}1-y$ )  
Fit function – fourier series in  $\tau$



# LATTICE MODULATION

$\text{Na}_2\text{CO}_3$  – single crystal data



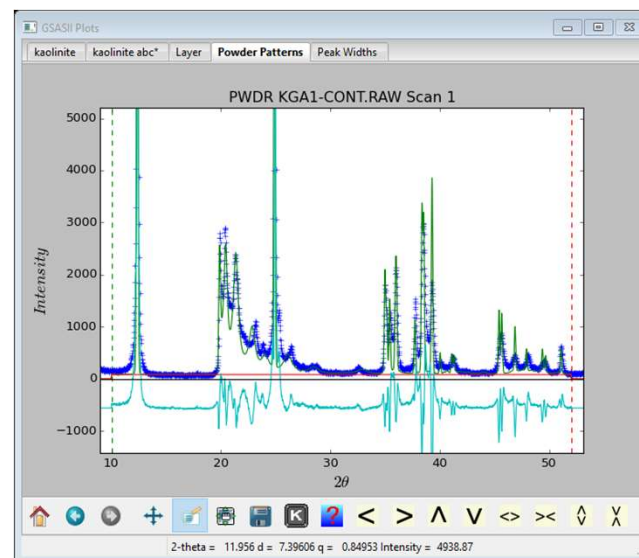
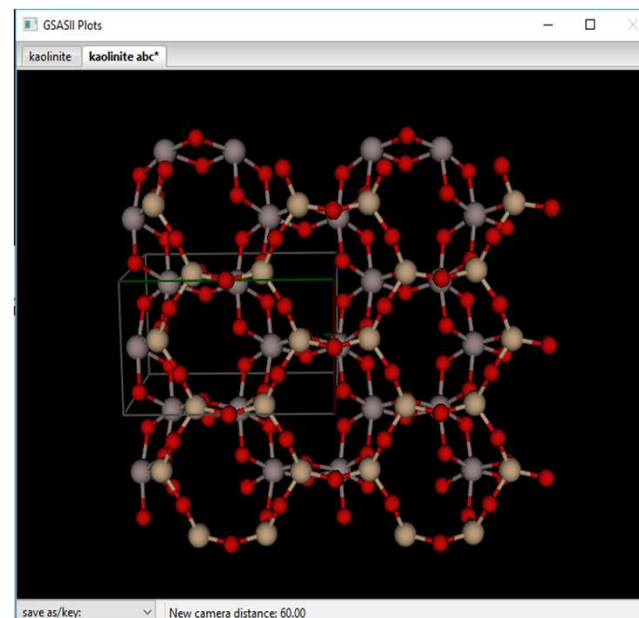
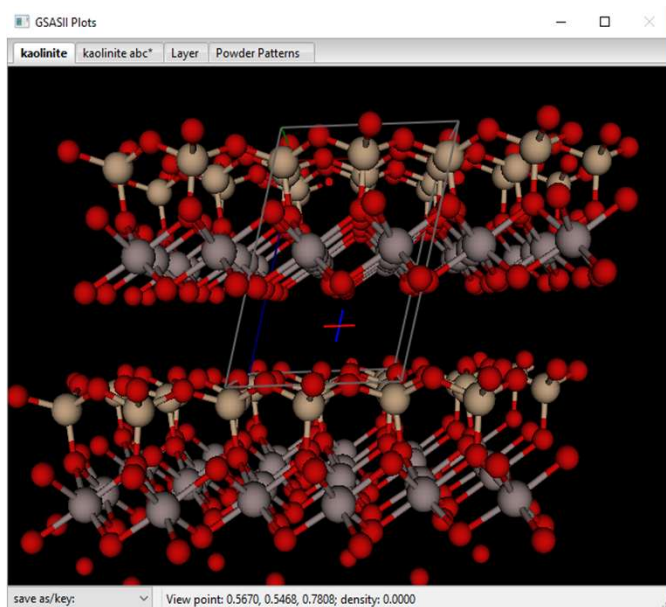
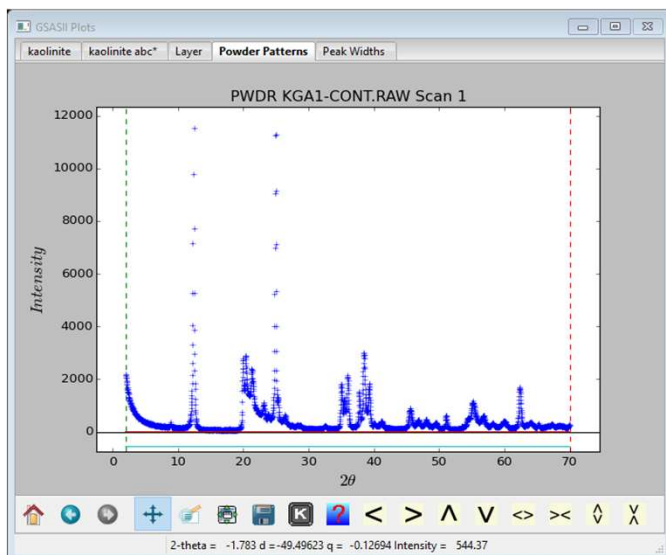
Coordinated wave motion – Na lattice y motion/  $\text{CO}_3$  rocking motion

Recall  $q = 0.183, 0, 319$  so period  $\sim 6-7$  on x &  $\sim 3$  on z

Possible modulations: positions, thermal parameters, site fractions  
(& magnetic moments)

# STACKING FAULTS – DIFFAX IN GSAS-II

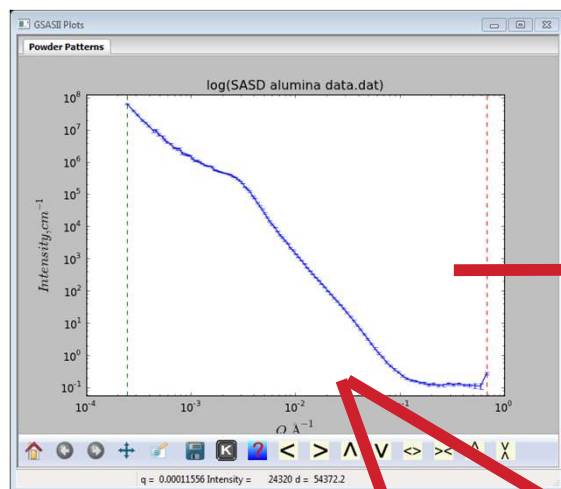
# STACKING FAULTS IN KAOLINITE $\text{Al}_2\text{Si}_2\text{O}_5(\text{OH})_4$



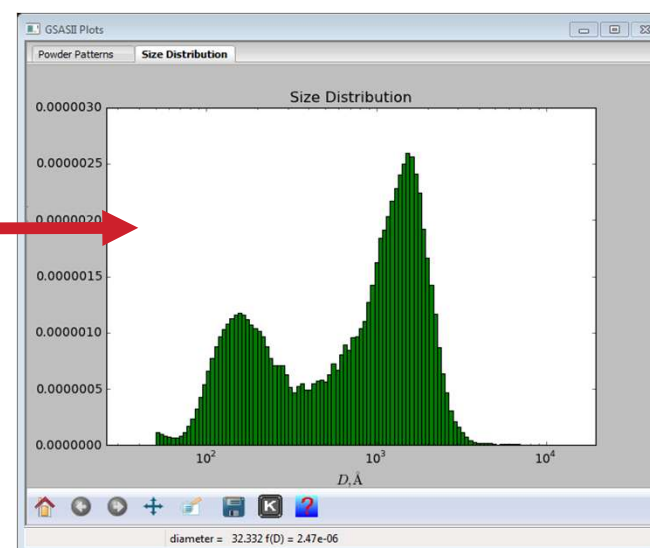
# SMALL ANGLE DATA ANALYSIS IN GSAS-II

# SMALL ANGLE SCATTERING

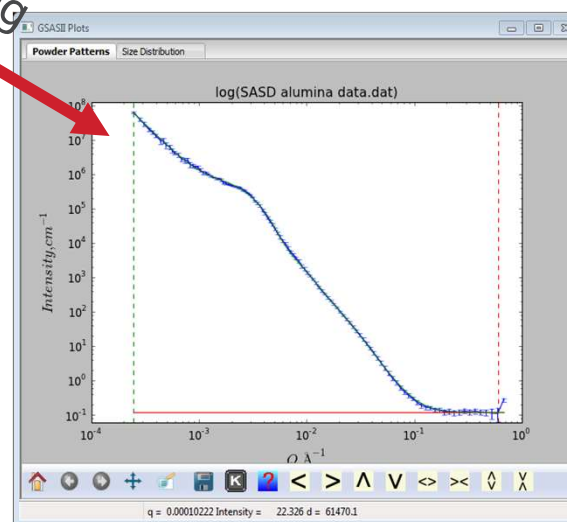
## Range of tools



Size  
Distribution  
by MaxEnt

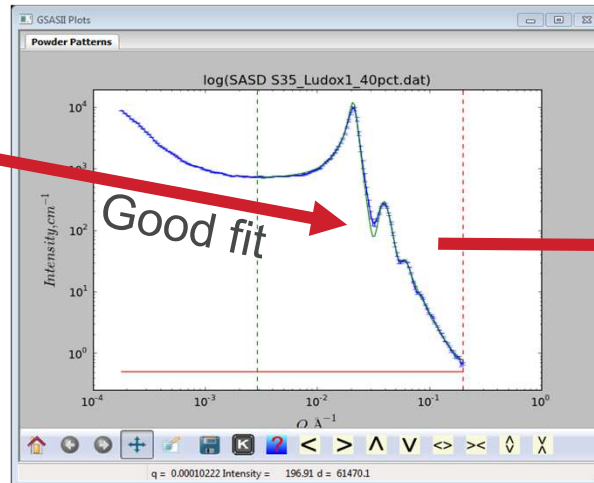
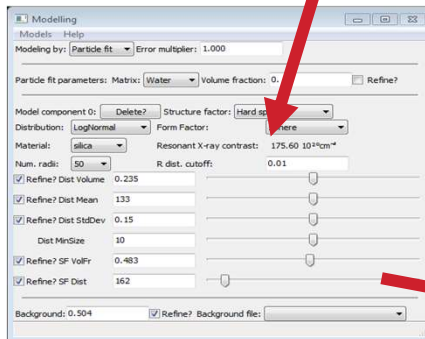
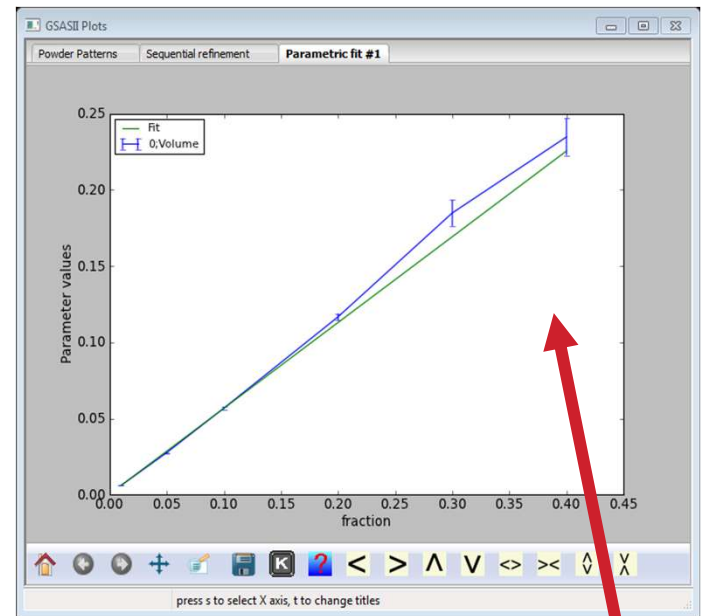
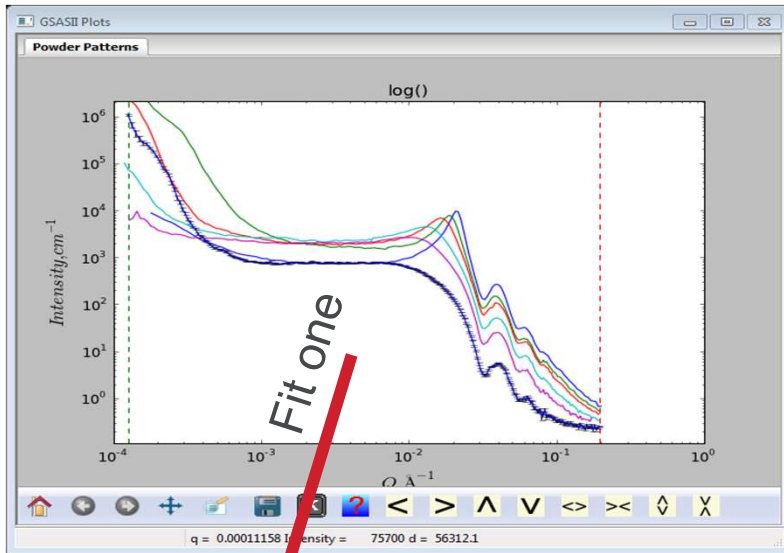


Modelling  
LSQ fitting



# SEQUENTIAL ANALYSIS

Series of experiments vs independent variable (e.g. composition)



Plot coeff. & fit to equation

Sequential refinement results

Columns Pseudo Vars Parametric Fit Help

|                           | Use                                 | Rwp   | fraction | Back     | Q,Dist     | Q,VolFr  | Q,Volume | Q,Mean     | Q,StdDev |
|---------------------------|-------------------------------------|-------|----------|----------|------------|----------|----------|------------|----------|
| SASD S35_Ludox1_40pct.dat | <input checked="" type="checkbox"/> | 3.553 | 0.400000 | 0.503530 | 162.350116 | 0.483169 | 0.234723 | 133.307516 | 0.149627 |
| SASD S40_Ludox2_30pct.dat | <input checked="" type="checkbox"/> | 8.673 | 0.300000 | 0.403854 | 160.490330 | 0.365993 | 0.184833 | 136.794497 | 0.180324 |
| SASD S41_Ludox3_20pct.dat | <input checked="" type="checkbox"/> | 3.626 | 0.200000 | 0.371692 | 173.447835 | 0.300004 | 0.116669 | 134.278946 | 0.152560 |
| SASD S42_Ludox4_10pct.dat | <input checked="" type="checkbox"/> | 2.424 | 0.100000 | 0.305805 | 196.221060 | 0.190653 | 0.056749 | 134.199202 | 0.149174 |
| SASD S47_Ludox5_5pct.dat  | <input checked="" type="checkbox"/> | 2.142 | 0.050000 | 0.300112 | 223.312205 | 0.110934 | 0.027559 | 134.221218 | 0.152267 |
| SASD S49_Ludox6_1pct.dat  | <input checked="" type="checkbox"/> | 2.639 | 0.010000 | 0.240443 | 311.082692 | 0.030708 | 0.006053 | 134.205294 | 0.154655 |

# Do rest in sequence

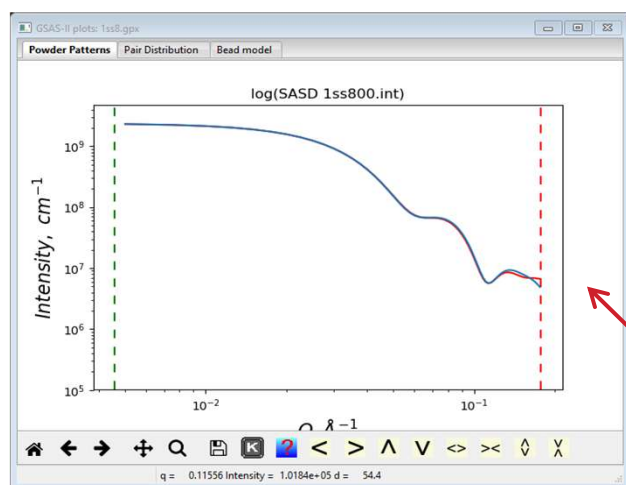
Select column to export; Double click on column to plot data; on row for Covariance

Do rest in sequence

All inside GSAS-II

# PROTEIN SMALL ANGLE MODELING IN GSAS-II

## Bead models via SHAPES (alternative to DAMMIN in python)

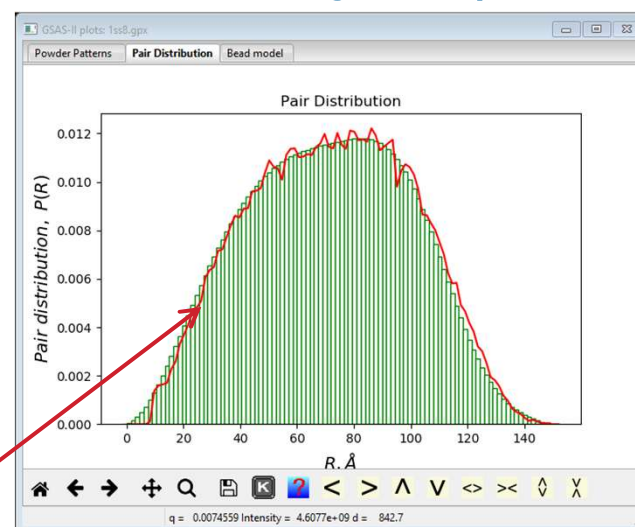


Data (simulated) from PDB 1ss8  
3668 AA, 7-fold rot. symm.  
E. Coli chaperonin GroEL

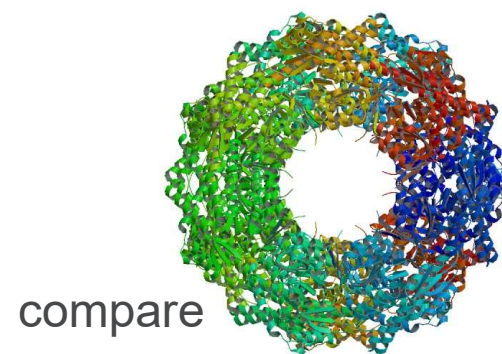
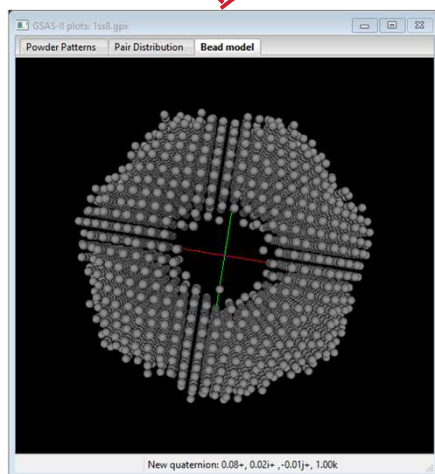
Direct fit?  
(In development)

Make  $P(R)$

calc



Run SHAPES  
Make bead model



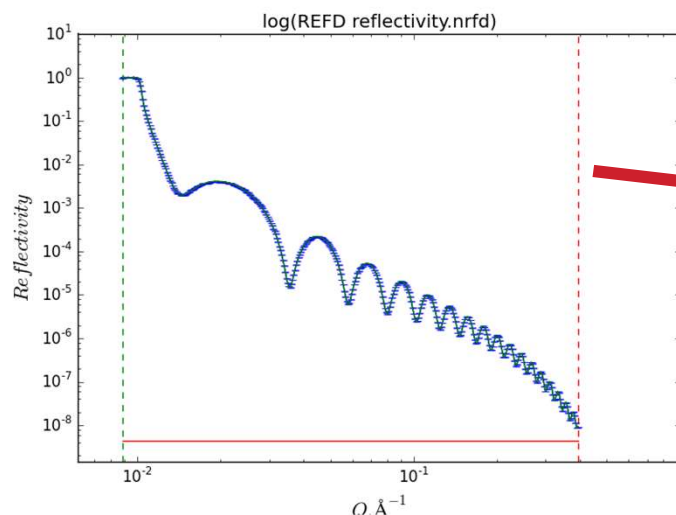
compare

“SHAPES”, J. Badger, J. Appl. Cryst 52, 937-944 (2019)

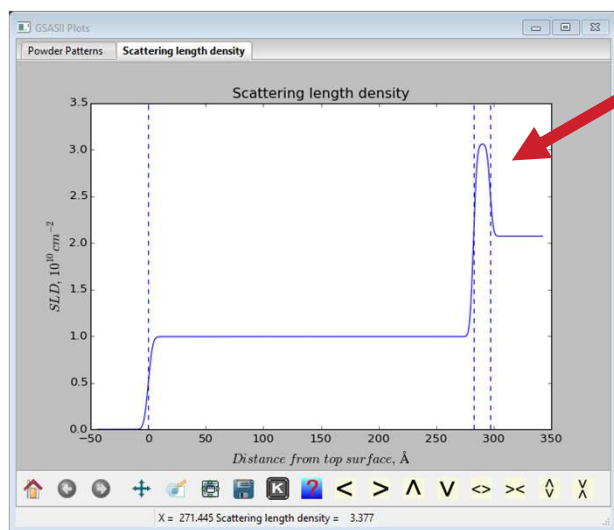
# REFLECTOMETRY

# REFLECTOMETRY ANALYSIS IN GSAS-II

## X-rays & Neutrons (CW at least)



Multilayer model  
Scattering density



Modelling

Models Help

Reflectometry fitting for: REFD reflectivity.nrfd

Controls:

Instrument resolution type: ☐ None ☒ const  $\Delta Q/Q$  (FWHM %): 3.0

Minimizer: LMLS Bounds factor: 0.85 ☐ Use 2% sig. weights

Plot controls: ☐ Plot SLD? Zero position location: Top

Global parameters:

Scale: 1.0 ☐ Refine? Flat bkg: 4.4e-09 ☒ Refine?

Layer sequence: 1 2

Use sequence nos. from: 1: Alumina 2: Alumina

NB: Repeat sequence by e.g. 6\*(1 2)

Layers: scatt. densities are  $10^{10} \text{ cm}^{-2} = 10^{-4} \text{\AA}^{-2}$

Top layer (superphase):

Substance: vacuum ☐ air or gas

Insert Delete

Layer no. 1

Substance: Alumina Den. Mult.: 0.1737 ☒ Refine? Real scat. den.: 0.9943 Imag scat. den.: 0

Magnetic SLD: 0.0 ☐ Refine? Real+mag scat. den.: 0.9943

Upper surface Roughness,  $\text{\AA}$ : 3.0 ☒ Refine? Layer Thickness,  $\text{\AA}$ : 282.63 ☒ Refine?

Insert Delete

Layer no. 2

Substance: Alumina Den. Mult.: 0.5352 ☒ Refine? Real scat. den.: 3.063 Imag scat. den.: 0

Magnetic SLD: 0.0 ☐ Refine? Real+mag scat. den.: 3.063

Upper surface Roughness,  $\text{\AA}$ : 2.4 ☒ Refine? Layer Thickness,  $\text{\AA}$ : 14.41 ☒ Refine?

Insert Delete

Bottom layer (substrate):

Substance: Silicon Den. Mult.: 1.0 ☐ Refine? Real scat. den.: 2.073 Imag scat. den.: 0

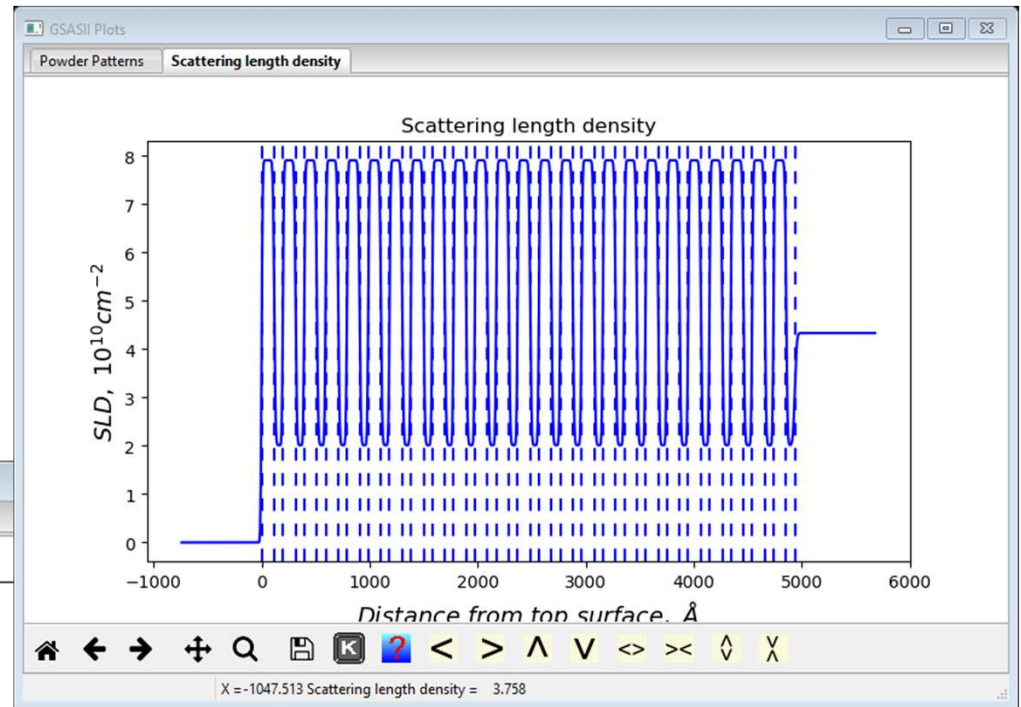
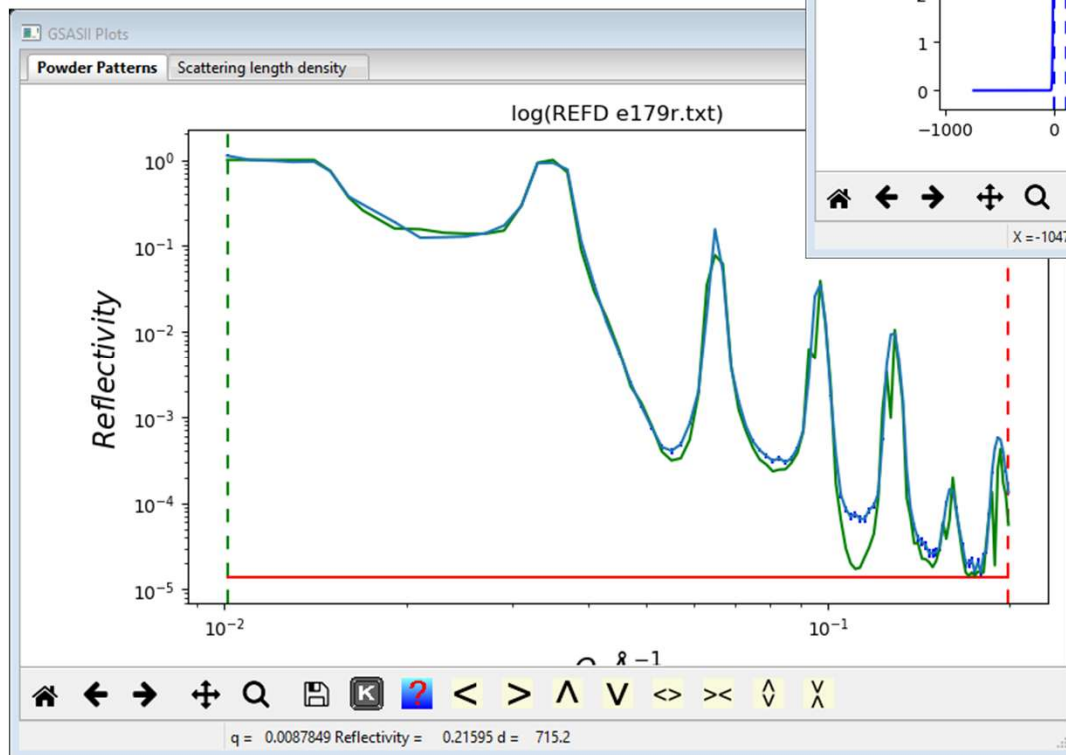
Magnetic SLD: 0.0 ☐ Refine? Real+mag scat. den.: 2.073

Upper surface Roughness,  $\text{\AA}$ : 2.2 ☒ Refine?

Define components, stacking sequence  
(can be repeated), thickness & "roughness"  
Fit by LSQ, MC/SA & "basinhopping"  
(under development)

# MULTILAYER REFLECTIVITY

25 layers on a substrate  
Common thickness & contrast



# CLUSTER ANALYSIS

# CLUSTER ANALYSIS?

**“Unsupervised Machine Learning”, “Pattern Recognition”, etc.**

**Faced with (say) 1000 powder patterns collected as a survey of some object**

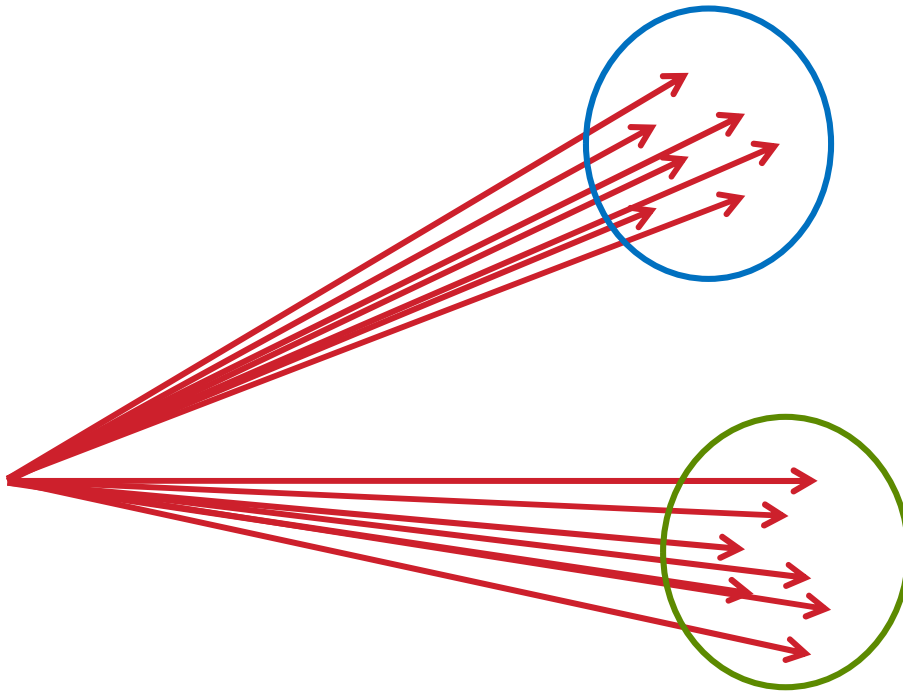
**What to do?**

- Group “similar” data
- Somehow different from other data
  - May be other clusters each with own “similar” data
  - Some may be “outliers” (“bad” data?)
- Start knowing “nothing” about the entire suite of data (no preconceived notions)
- Not a single method! Iterative exploration to find useful result.
- Fast – can do 100’s-1000’s of data sets in few seconds
- GSAS-II – will do cluster analysis on powder patterns & pair distribution functions (PDF); NB: not images
- Some requirements:
  - Don’t want to compare “apples & oranges” so data collections (e.g. powder data) must all be done the same way (span, #steps, radiation wavelength, etc.)
  - Don’t mix x-rays & neutrons.
  - Otherwise, cluster analysis will pick out these differences first (& not what you’re after).

# PROCESS

## Comparison method?

- Each pattern – vector (1000's of dimensions)
- Cluster similar vectors (data sets) by “distance”



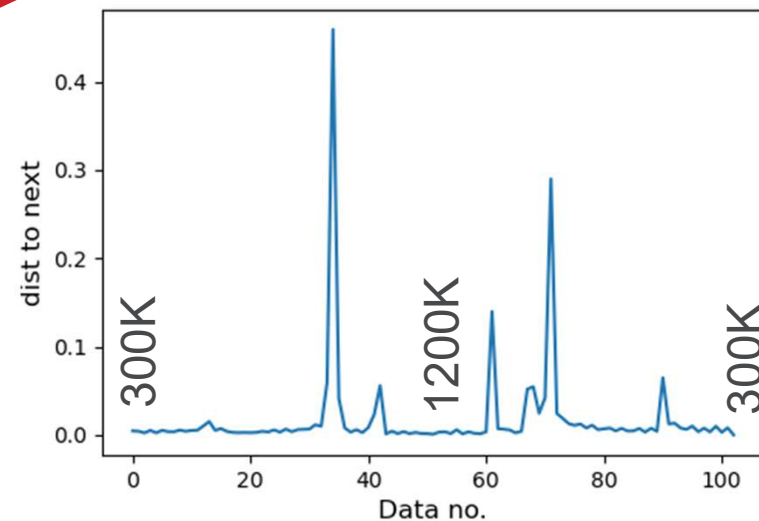
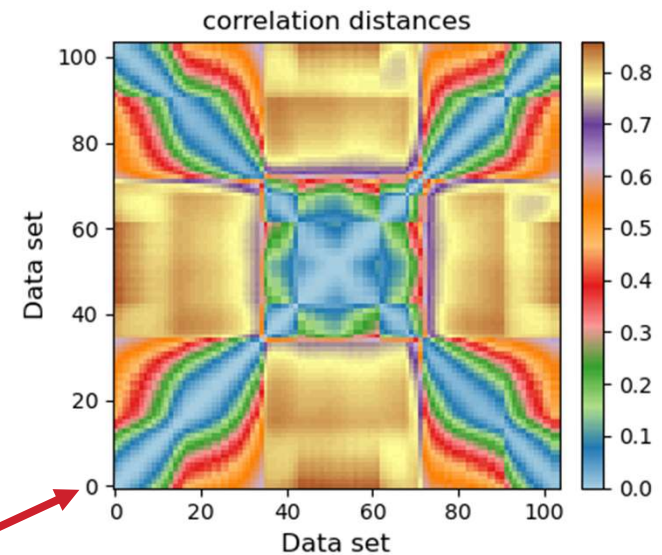
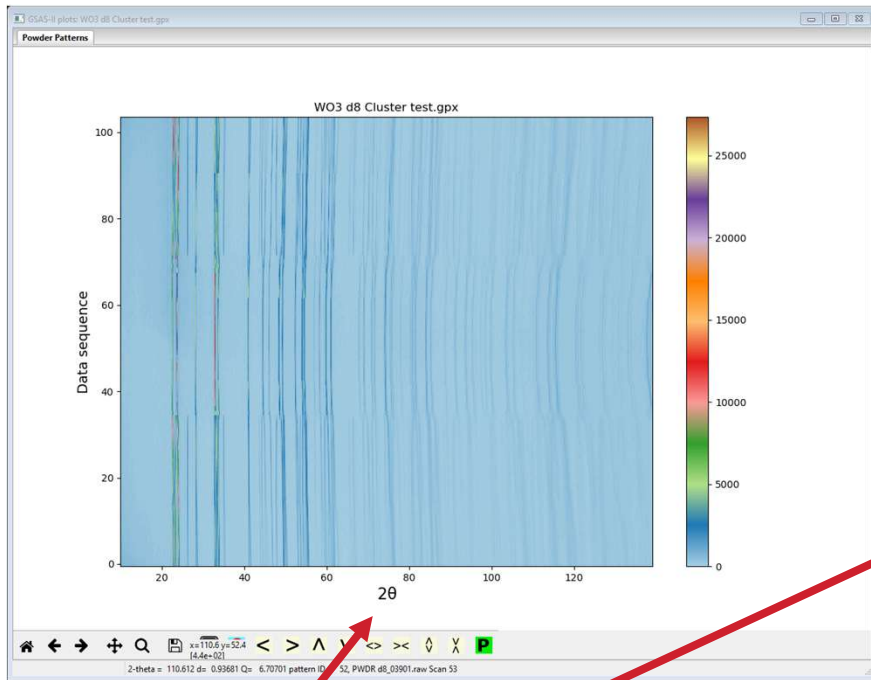
### “Distance” in GSAS-II

- Euclidian - shortest
- City block – steps along each axis (longer)
- Cosine – of angle between
- Correlation – coefficient
- Etc... - 11 methods; take your pick. Some are more contrasty than others

# DISTANCES

## Preliminary results – distance matrix & serial distances

- Example –  $\text{WO}_3$  x-ray data 300-1200K & back; 108 powder patterns (integrated from images).



Powder data

Distance matrix

Serial distances

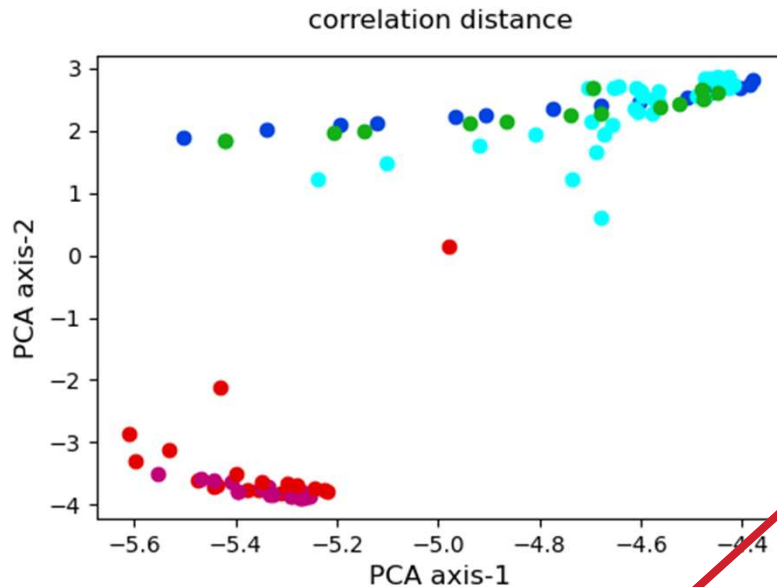
n+1 vs n

Peaks = Phase changes

Not useful for random data

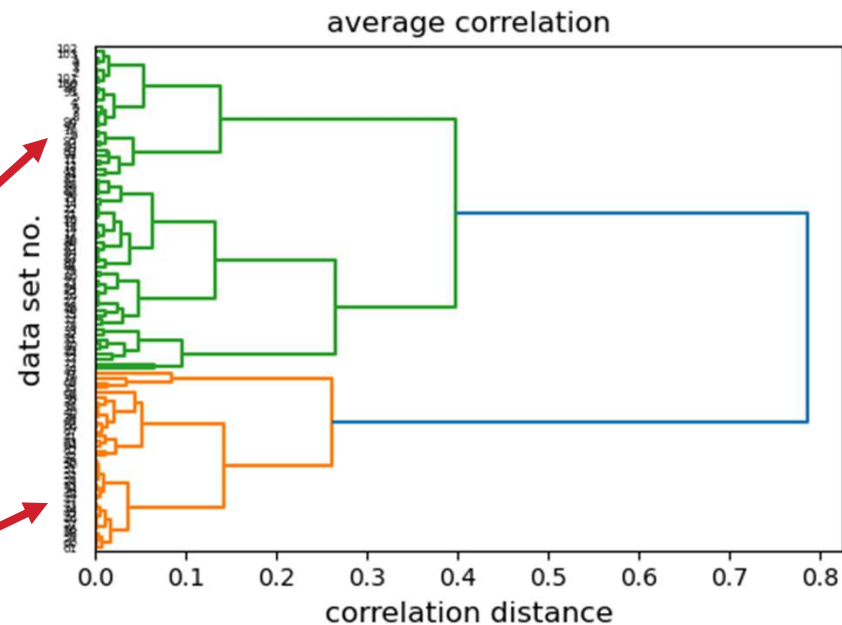
# DISTANCES – PRINCIPAL COMPONENT ANALYSIS & DENDOGRAM

Most significant 2-3 dimensions – cluster analysis



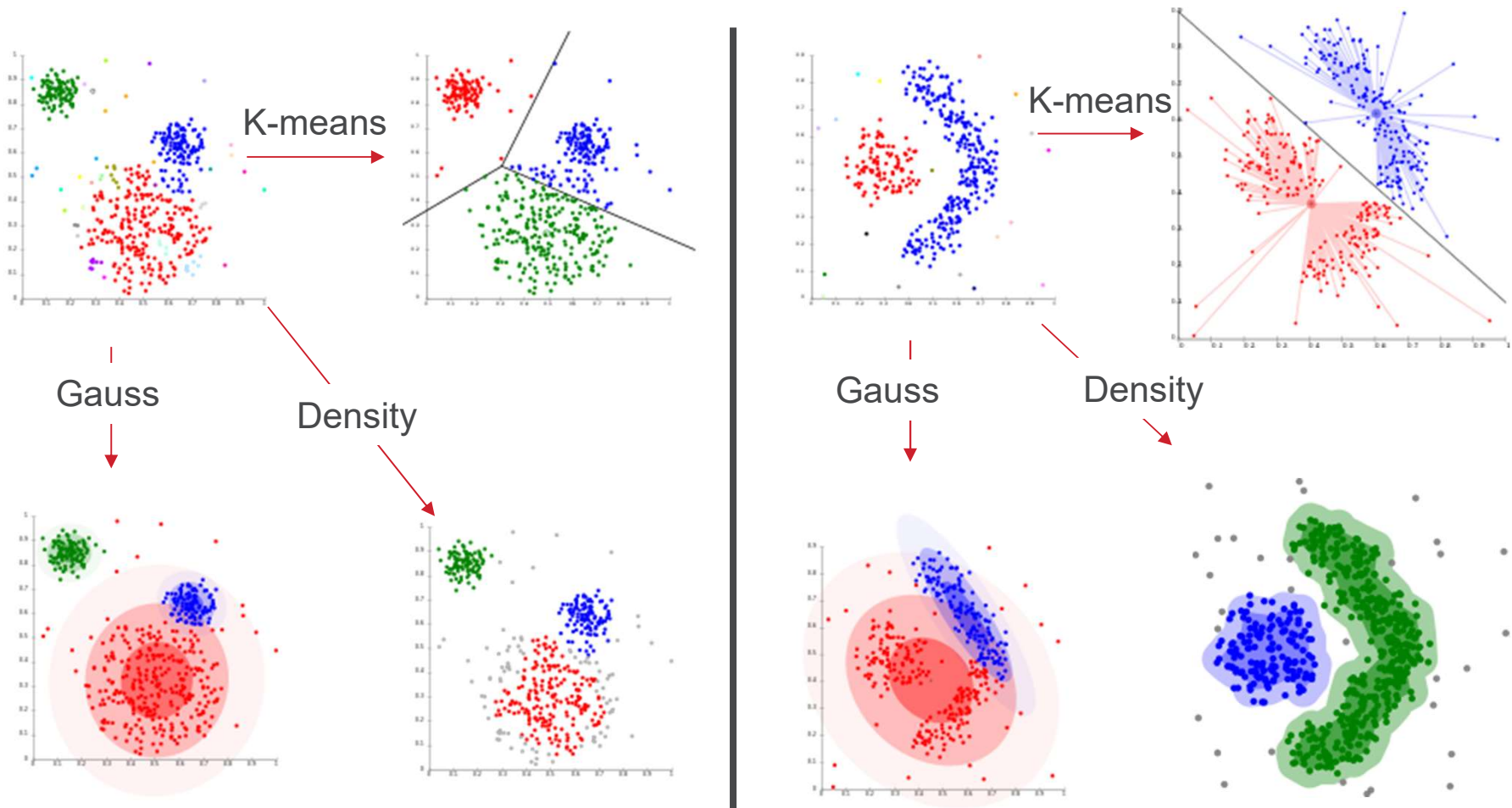
Temp variation – trails in PCA  
→ Clusters ill defined in this case  
Colored by “cluster”

Dendrogram  
– hierarchy in data?  
Low T phase  
Intermediate T phases  
High T phase



# THE CLUSTERING PROBLEM

Wide variations possible – 2 example PCAs & cluster algorithms

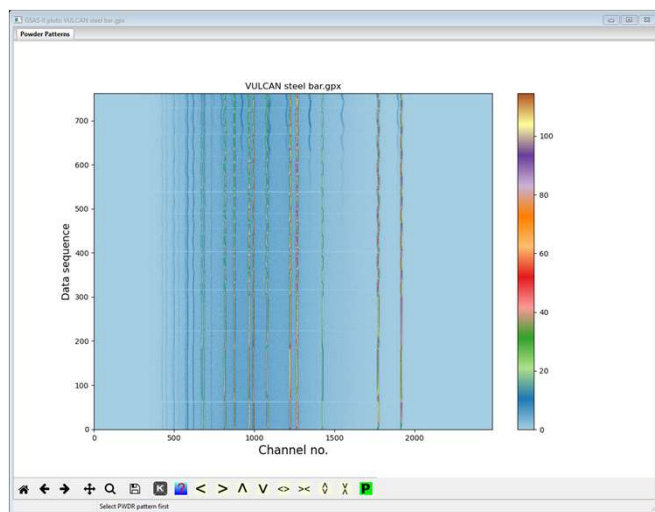


GSAS-II has 6 clustering algorithms – some require # of clusters

Taken from Wikipedia

# OUTLIER ANALYSIS IN GSAS-II

Find “bad data”: Steel bar – repeated stress (TOF neutron)



800 patterns

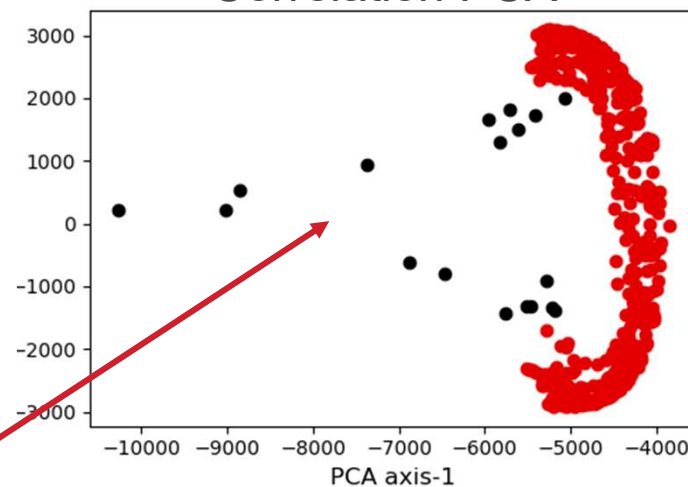
There were beam dropouts!

3 outlier algorithms in GSAS-II

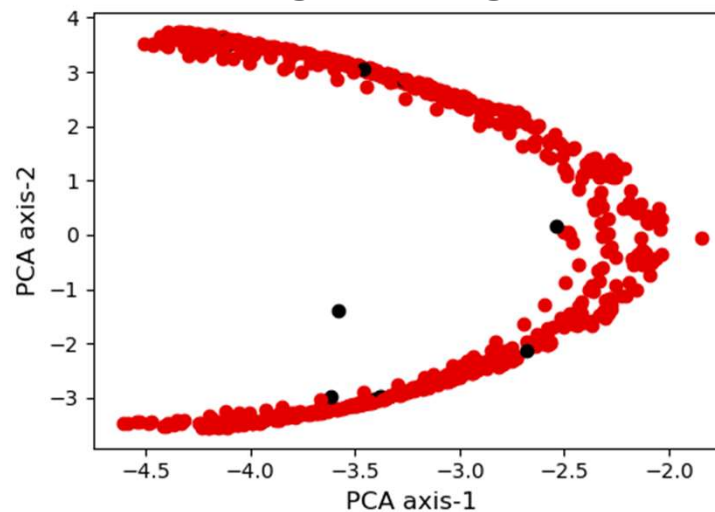
Depends on distance algorithm

GUI will show list of bad data

Correlation PCA



Cosine PCA

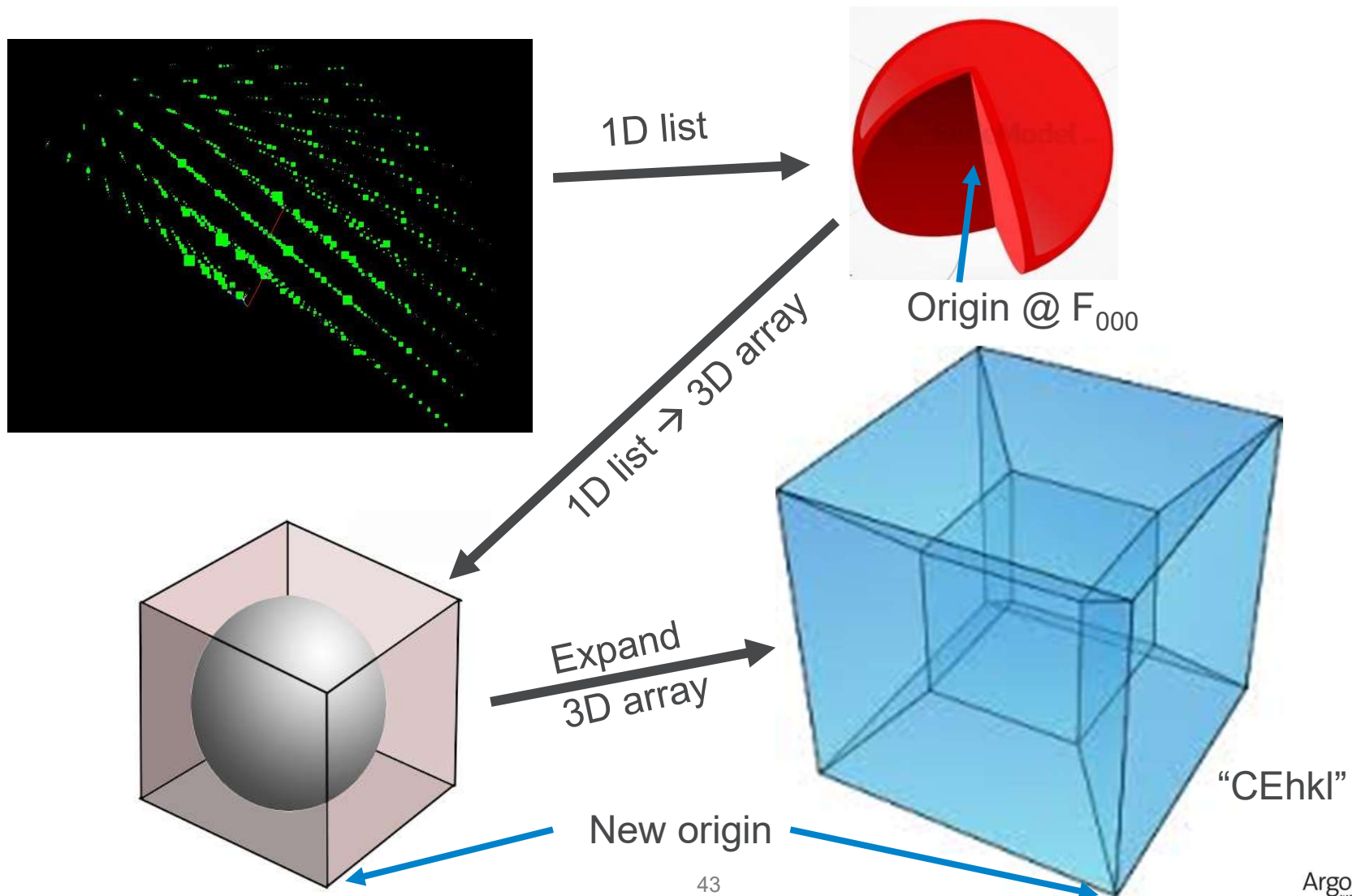


# CHARGE FLIPPING

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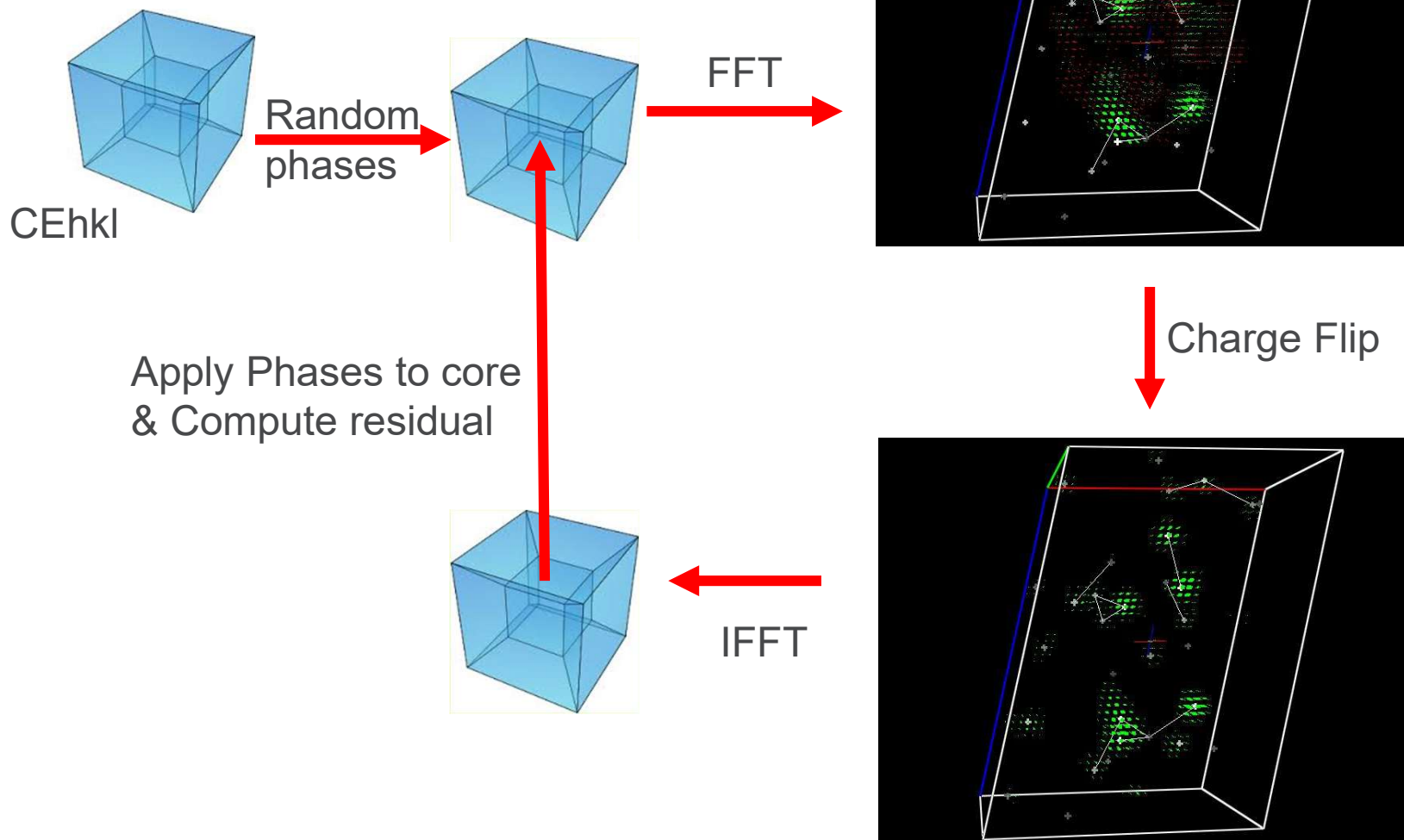
The algorithm set up:

~1Å unique reflections → sphere → box → 0.5Å box



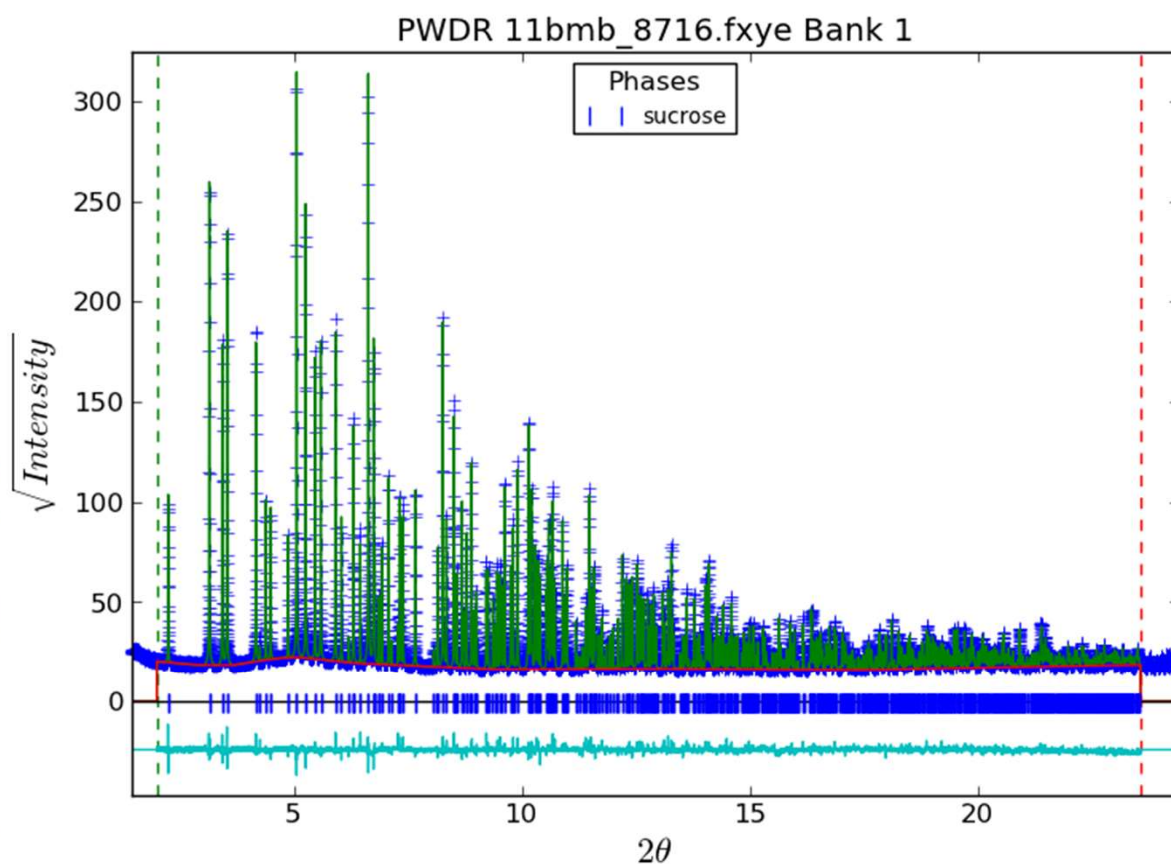
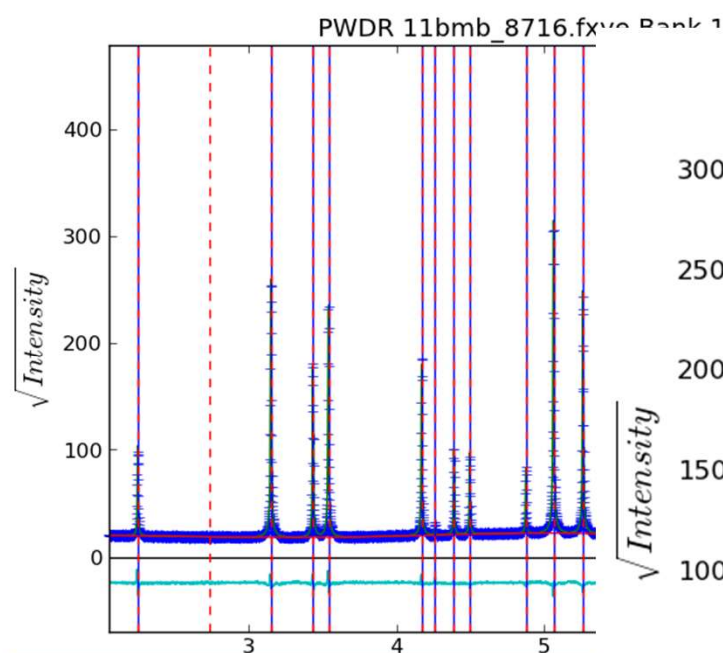
# CHARGE FLIPPING

## The Algorithm



# EXAMPLE – SUCROSE POWDER

11BM @ APS - 1<sup>st</sup> steps – peak fitting/indexing/Pawley refinement



Unit Cells List

Cell Index/Refine Help

Indexing controls:

Max Nc/Nobs 4 Start Volume 25 ☒ Use M20/(X20+1)?

Select Bravais Lattices for indexing:

☐ Cubic-F ☐ Cubic-I ☐ Cubic-P ☐ Trigonal-R ☐ Trigonal/Hexago  
☐ Orthorhombic-F ☐ Orthorhombic-I ☐ Orthorhombic-C ☐ Orthorhombic-P ☐ Monoclinic-C

Cell Test Refinement:

Bravais lattice **P2/m** Space group **P 21** Zero offset 0.0007 ☒ Refine?

Unit cell: a = 7.71525 b = 8.66389 c = 10.80965

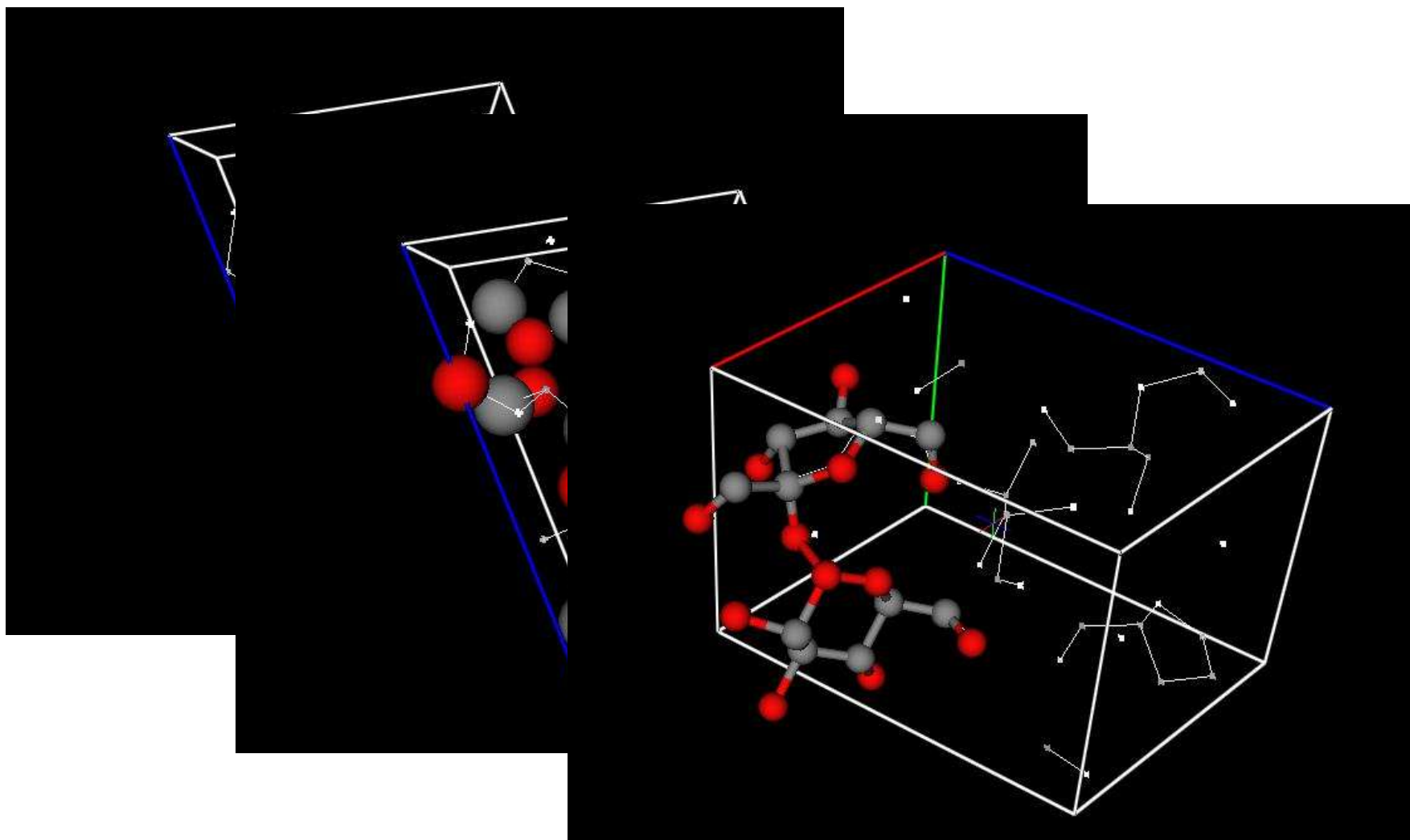
Indexing Result:

| M20     | X20 | use                                 | Bravais | a       | b        | c        | alpha  | beta    | gamma  | Volume  | Keep                     |
|---------|-----|-------------------------------------|---------|---------|----------|----------|--------|---------|--------|---------|--------------------------|
| 1312.84 | 0   | <input checked="" type="checkbox"/> | P2/m    | 7.71525 | 8.66389  | 10.80965 | 90.000 | 102.983 | 90.000 | 704.09  | <input type="checkbox"/> |
| 907.76  | 0   | <input type="checkbox"/>            | P2/m    | 7.71412 | 8.66281  | 10.80843 | 90.000 | 102.982 | 90.000 | 703.82  | <input type="checkbox"/> |
| 15.05   | 0   | <input type="checkbox"/>            | P2/m    | 7.69200 | 8.66511  | 10.79433 | 90.000 | 102.664 | 90.000 | 701.96  | <input type="checkbox"/> |
| 2.38    | 1   | <input type="checkbox"/>            | P2/m    | 6.78185 | 10.56374 | 15.20797 | 90.000 | 98.621  | 90.000 | 1077.21 | <input type="checkbox"/> |
| 2.38    | 1   | <input type="checkbox"/>            | P2/m    | 6.78185 | 10.56374 | 15.20797 | 90.000 | 98.621  | 90.000 | 1077.21 | <input type="checkbox"/> |

781 unique hkl's  
CF with 61440

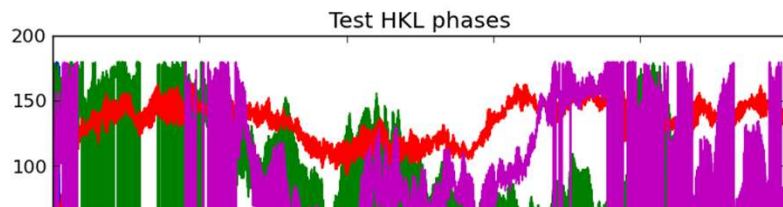
# CHARGE FLIPPING SOLUTION

Residual ~45% → ~17% & 46 peaks in cell (NB: sucrose  $C_{12}H_{22}O_{11}$ )  
Map peaks – unique set & select – identify atoms – make molecule

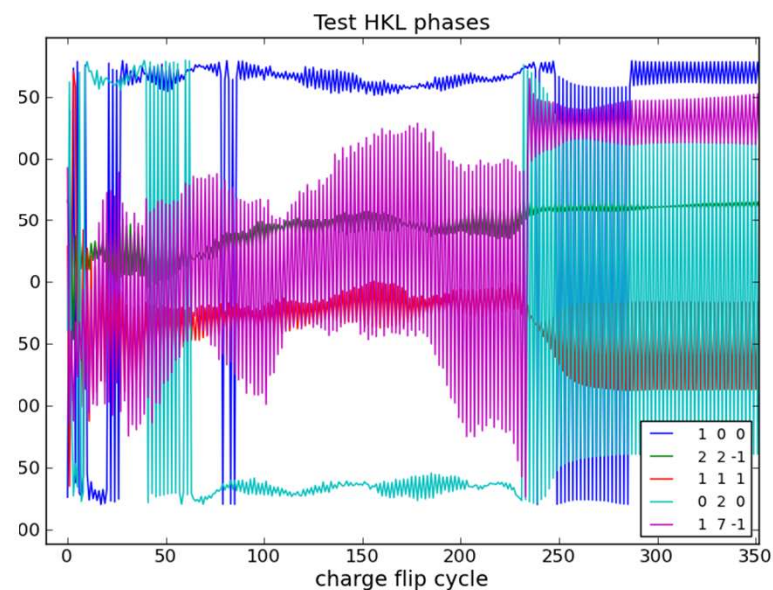
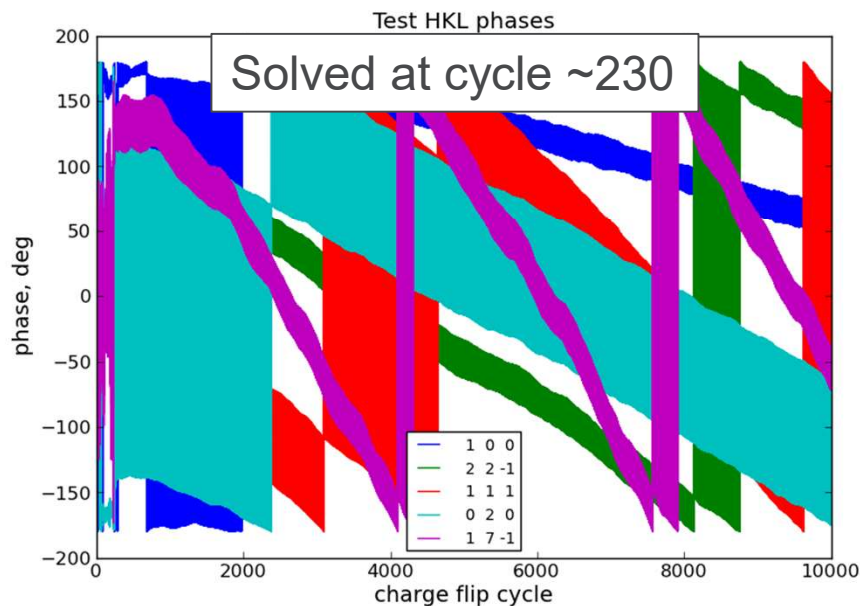
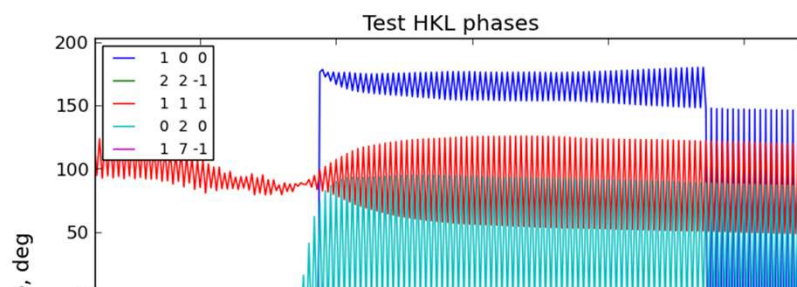
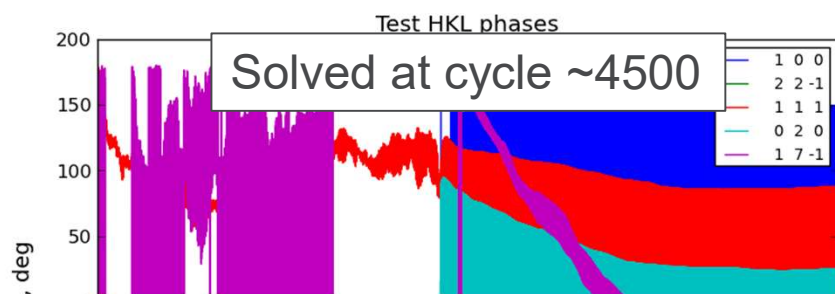


# CHARGE FLIPPING – PHASES?

Track phases of 5 reflections – 10000 CF cycles



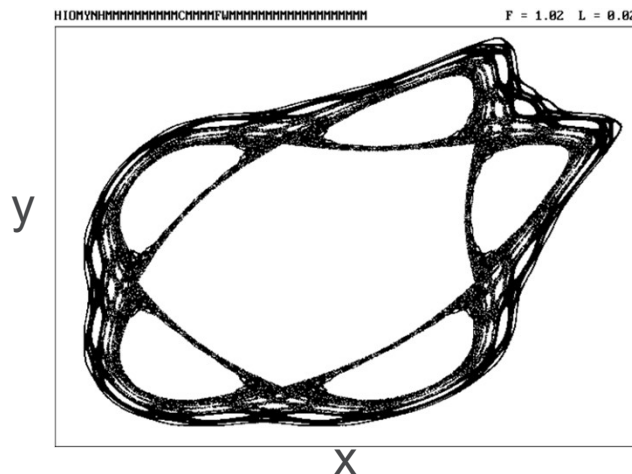
Not solved in 10000 cycles



# CHARGE FLIPPING – CHAOS MATHEMATICS?

## Strange attractors? Cantor dust? Butterfly effect? Basin of attraction?

- Cyclic algorithm – successive iteration – stable solution (apparently?)
- Chaotic phase behavior – but deterministic (Butterfly effect?)
- Hyper dimensionality ~7680-D for sucrose example (NB: no symmetry used)
- Infinite phase possibilities >> Infinite phase sets for recognizable atoms (Cantor dust?)



- Phase oscillation & drift – “symplectic” or “non-symplectic” strange attractors?
- Is there a “basin of attraction”?
- Does this really matter?

(picture from “Strange Attractors: Creating Patterns in Chaos” by J. C. Sprott)



**THANK YOU**

[www.anl.gov](http://www.anl.gov)