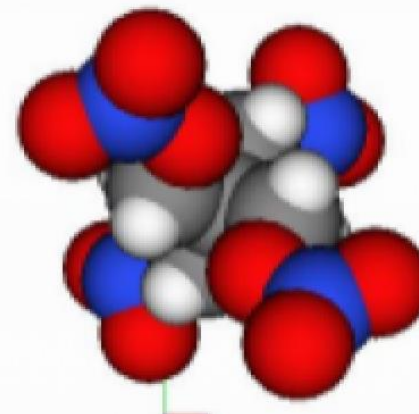


# THE RIETVELD REFINEMENT METHOD IN GSAS-II

# GSAS-2



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Acknowledgements: DOE/SC

# HISTORY – H.M. RIETVELD



Hugo Rietveld; neutron powder diffractometer,  
Petten, Netherlands

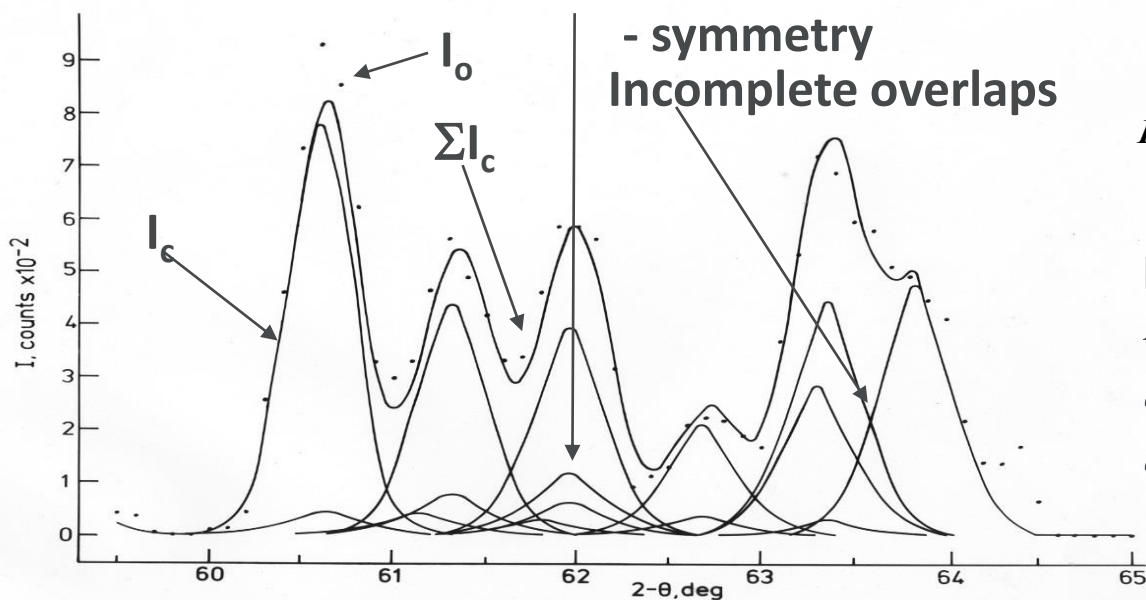
Papers: H.M. Rietveld, Acta Cryst. 22, 151-  
2(1967)

H.M. Rietveld, J. App. Cryst., 2, 65-71 (1969)

Multi-parameter, nonlinear LS curve fitting

Exact overlaps

- symmetry  
Incomplete overlaps



Residuals:

$$R_{wp} = \sqrt{\frac{\sum w(I_o - I_c)^2}{\sum wI_o^2}}$$

Rietveld Minimize  
 $M_R = \sum w(I_o - I_c)^2$

“chi-squared” or  
“goodness-of-fit”

$$\chi^2 = M_R/(n-p)$$

# LINEAR LEAST SQUARES THEORY

Given a set of observations  $I_{\text{obs}}$

and a function  $I_{\text{calc}} = f(p_1, p_2, p_3, \dots, p_n)$

then the best estimate of the values  $p_i$  is found by minimizing

$$M = \sum w(I_o - I_c)^2$$

This is done by setting the derivative to zero

$$\sum w(I_o - I_c) \frac{\partial I_c}{\partial p_j} = 0$$

Results in  $n$  “normal” equations (one for each variable) - solve for  $p_i$

# NON-LINEAR LEAST SQUARES THEORY

Problem -  $I(p_i)$  is nonlinear & transcendental (sin, cos, etc.)  
so can't solve directly

Expand  $I(p_i)$  as Taylor series & toss high order terms

$$I_c(p_i) = I_c(a_i) + \sum_i \frac{\partial I_c}{\partial p_i} \Delta p_i$$

$a_i$  - initial values of  $p_i$   
 $\Delta p_i = p_i - a_i$  (shift)

Normal equations - one for each  $\Delta p_i$

$$\sum w \left[ \Delta I - \sum_i \frac{\partial I_c}{\partial p_i} \Delta p_i \right] \frac{\partial I_c}{\partial p_j} = 0 \quad \Delta I = I_o - I_c(a_i)$$

Outer sum over observations

Solve for  $\Delta p_i$  - shifts of parameters, NOT values

# LEAST SQUARES THEORY - CONTINUED

Rearrange

$$\sum w \frac{\partial I_c}{\partial p_1} \left( \sum_{i=1}^n \frac{\partial I_c}{\partial p_i} \Delta p_i \right) = \sum w \Delta I \frac{\partial I_c}{\partial p_1}$$

⋮

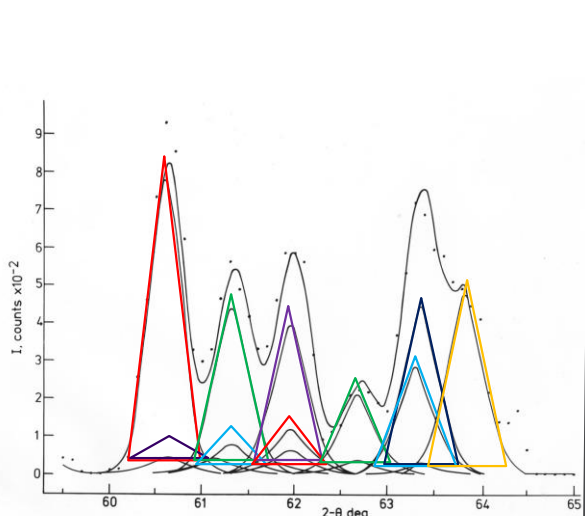
$$\sum w \frac{\partial I_c}{\partial p_n} \left( \sum_{i=1}^n \frac{\partial I_c}{\partial p_i} \Delta p_i \right) = \sum w \Delta I \frac{\partial I_c}{\partial p_n}$$

**Matrix form:  $\mathbf{Ax}=\mathbf{v}$**

$$a_{i,j} = \sum w \frac{\partial I_c}{\partial p_i} \frac{\partial I_c}{\partial p_j} \quad x_j = \Delta p_j \quad v_i = \sum w(\Delta I) \frac{\partial I_c}{\partial p_i}$$

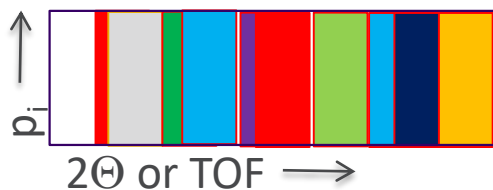
**Solve:  $\mathbf{x} = \mathbf{A}^{-1}\mathbf{v} = \mathbf{B}\mathbf{v}$ ;  $\mathbf{B} = \mathbf{A}^{-1}$  This gives set of  $\Delta p_i$  to apply to “old” set of  $a_i$ ; repeat until  $\Delta p_i$  small.**

# GSAS-II ALGORITHM

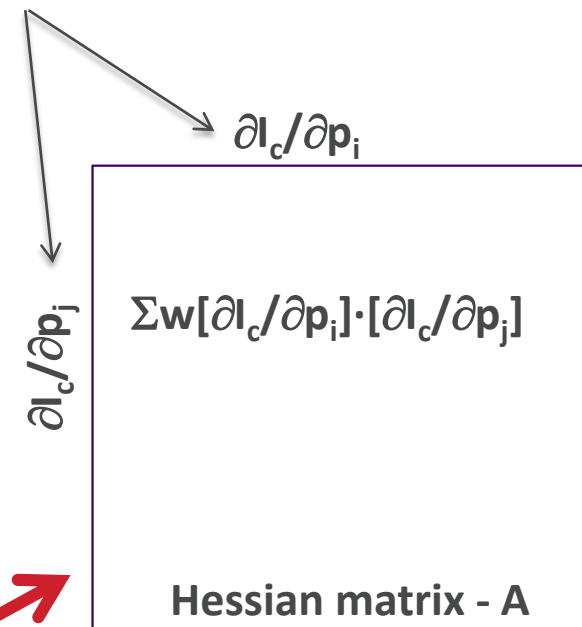
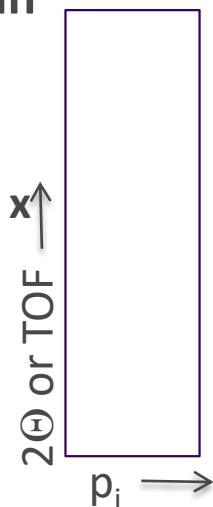


GSAS – process point-by-point to make  $I_c$  (value) &  $\partial I_c / \partial p_i$  (vector)

GSAS-II – process reflection-by-reflection to make  $I_c$  (vector) &  $\partial I_c / \partial p_i$  (Jacobian matrix)



Jacobian matrix - J



$$wJ^T J = A$$

**NB: GSAS-II – needs large memory!**

# REFINEMENT VIA MODIFIED LEVENBERG/MARQUARDT-SVD ALGORITHM

Steps:

1. Compute  $A_{ij} = \sum w \frac{\partial I_c}{\partial p_i} \frac{\partial I_c}{\partial p_j}$

**SLOW step**

2. Normalize  $A'_{ij} = A_{ij} / \sqrt{A_{ii}A_{jj}}$

3. compute  $\chi^2(p)$

4. Select  $\lambda$  (=0.001, “damping factor”)

5. Modify  $A''_{ii} = A'_{ii}(1 + \lambda)$

6. **Make SVD inversion of A''**

7. Solve for  $\delta p$  (unnormalized!) & compute  $\chi^2(p+\delta p)$

8. If  $\chi^2(p+\delta p) > \chi^2(p)$  then  $\lambda * 10$  go to 5

9. Else apply  $\delta p$  to  $p$  & go to 1 (new cycle)

10. Quit when  $\chi^2(p) - \chi^2(p+\delta p) / \chi^2(p) < 0.0001$

**FAST steps**

**NB: all in ~40 lines of python; all double precision**

**NB<sup>2</sup>: this thing is exceedingly robust – no user damping factors needed**

# SVD – SINGULAR VALUE DECOMPOSITION

**Singularities & near singularities – see Mathematical Recipes 2.9**

LS matrix: solve for  $x$   $Ax=b$  by  $x=A^{-1}b$ ;  $x$  are the parameter shifts

SVD: replace  $A = UwV$  where  $U$  &  $V$  are such that  $U^{-1} = U^T$  &  $V^{-1} = V^T$

&  $w$  – diagonal matrix; all same size as  $A$

Then:  $A^{-1} = V(1/w_{ii})U^T$

**The trick: what to do if  $w_{ii} \sim 0$ ? (singularity)  $\rightarrow$  make  $1/w_{ii} = 0!$  (instead of  $\infty$ )**

Then:  $x = V(1/w_{ii})U^Tb$  does away with ill-conditioned terms

Have to choose tolerance on  $w_{ii} \sim 0$  (typically  $10^{-6}$  but  $10^{-3}$  for proteins works well)

SVD is in python library as `numpy.linalg.svd`

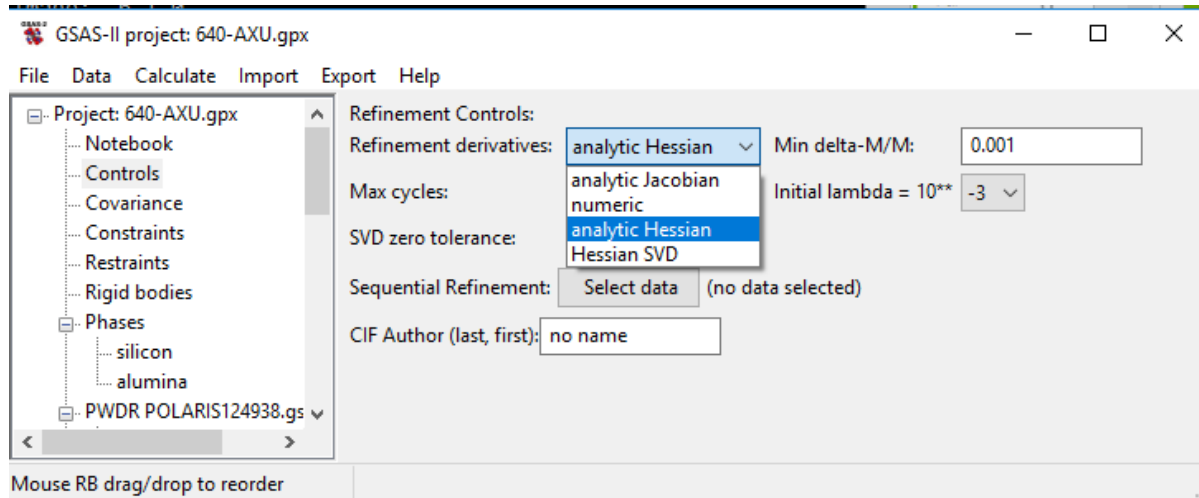
& uses LAPACK `_gesdd` routine (fortran – code in MR 2.9)

NB: all double precision in python; downside is  $w_{ii}$  not 1:1 to parameters so id of failures difficult.



# LEAST SQUARES ALGORITHMS IN GSAS-II

## Useful choices – found in Controls



Analytic Hessian – **default** Levenberg-Marquardt SVD from Hessian & computed derivatives  
Downside: hard singularities hard to find → “linear algebra errors” cause failures

Analytic Jacobian – uses Jacobian matrix (not Hessian) no SVD; identifies singularities & Removes them from LS refinement; always runs to convergence

Hessian SVD – no Levenberg-Marquardt (might be better for single crystal data)  
Same downside as Analytic Hessian

Numeric – no derivatives & slow – mostly for testing purposes.

# LEAST SQUARES THEORY - CONTINUED

Error estimates (mostly from W.C. Hamilton)

Given observations  $n > m$  parameters

with distributions that have finite 2nd moments

(no need to be “normal” although usually are for powders)

Then LS gives parameter estimates (shifts in our case)

with the minimum variance in any linear combination

The error estimates (“esd’s”) are

$$\sigma_i = \sqrt{\frac{b_{ii}}{\chi^2}} \quad \chi^2 = \frac{\sum w(I_o - I_c)^2}{n - m}$$

$b_{ii}$  - diagonal elements of the inverted A matrix

Note: There is little justification for additional scaling of

the  $\sigma_i$  **NB: systematic errors will bias results**

**beyond  $\sigma_i$ .**

# RIETVELD MODEL: $I_C = I_i \{ \sum K_p F_p^2 M_p L_p P(\Delta_p) + I_B \}$

$I_i$  - incident intensity - variable for fixed  $2\Theta$  (e.g. neutron TOF)

$k_p$  - scale factor for particular phase

$F_p^2$  - structure factor for particular reflection

$m_p$  - reflection multiplicity

$L_p$  - correction factors on intensity - texture, etc.

$P(\Delta_p)$  - peak shape function - size & microstrain, etc.

Sum over all reflections under a profile point (multiple phases)

$I_b$  – background function

**More complex model than for single crystal diffraction**

# PROFILE FUNCTIONS $P(\Delta_p)$ – BASICS

$$\Delta_p = T_{\text{reflection}} - T_{\text{profile}} \quad (T = 2\Theta \text{ or TOF})$$

**Gaussian profile - generally instrumental origin**

$$G(\Delta T, \Gamma) = \sqrt{\frac{4 \ln 2}{\pi \Gamma^2}} \exp\left[\frac{-4 \ln 2 (\Delta T)^2}{\Gamma^2}\right]$$

**Lorentzian profile - largely sample effect**

$$L(\Delta T, \gamma) = \frac{2}{\pi \gamma} \frac{1}{1 + \left(\frac{2\Delta T}{\gamma}\right)^2}$$

**Voigt – convolution =  $G \otimes L$**

**Pseudo-Voigt – linear combination =  $\eta L + (1-\eta)G$**

$\eta$  *via* Thompson, Cox & Hastings – pseudoVoigt = Voigt

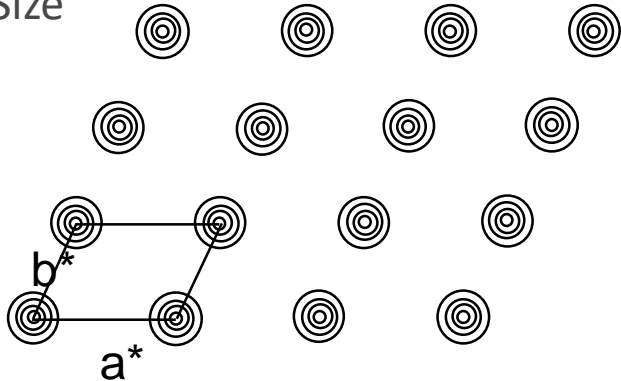
**CW Asymmetry from axial divergence – Finger, Cox & Jephcoat**

**NB: in g<sub>s</sub>as & GSAS-II, T is  $2\Theta$  in centideg or TOF in  $\mu\text{s}$**

# SAMPLE BROADENING

## Isotropic Crystallite size & $\mu$ strain broadening

Size



Small ( $<1\mu\text{m}$ ) crystals  $\rightarrow$  not  $\delta$ -functions

Size distribution  $\rightarrow$

superposition of sharp to broad spots

$\rightarrow$  Shape  $\sim$  Lorentzian

Width  $\Delta d^* = \text{constant} = \Delta d/d^2 = \Delta\Theta \cot\Theta/d$

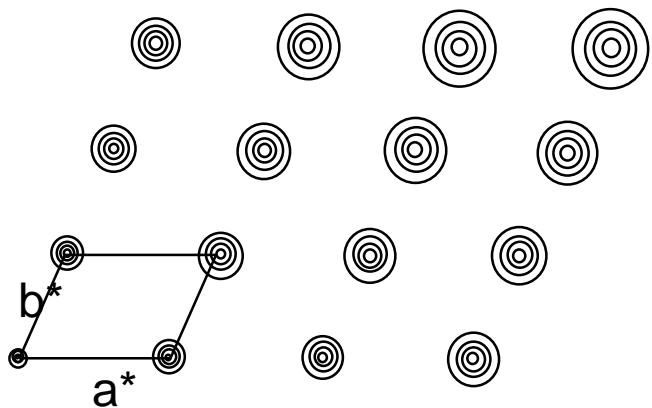
Bragg's Law:  $\Delta 2\Theta = \lambda \Delta d/d^2 \cos\Theta (= X/\cos\Theta)$

$\rightarrow$  Scherrer equation

$k=1, p = \text{size}$

$$S = \frac{180k\lambda}{\pi p \cos \Theta}$$

$\mu$ strain



Unit cell variation (defects??)

Lorentzian distribution  $\rightarrow$  shape

$\Delta d/d = \text{constant} = \Delta d^*/d^* = \Delta\Theta \cot\Theta$

Or:  $\Delta 2\Theta = 2\Delta d \tan\Theta/d (= Y \tan\Theta)$

$$M = 180\mu \tan \Theta/\pi$$

$\mu$  –  $\mu$ strain ( $\times 10^6$ ) parameter

# CW PROFILE COEFFICIENTS

## Lorentzian vs Gaussian sample broadening?

▪ Size:  $S = \frac{180k\lambda}{\pi p \cos \Theta}$        $\mu$ strain:  $M = 180\mu \tan \Theta / \pi$

- Need:  $S_\Gamma$  (Gauss) &  $S_\gamma$  (Lorentzian) sample broadening (2 slides back)

$$\Gamma_g^2 = 8\ln 2(U \tan^2 \Theta + V \tan \Theta + W + S_\Gamma)$$

$$\gamma = \frac{X}{\cos \Theta} + Y \tan \Theta + Z + S_\gamma$$

- Mixing coeff for each;  $m_s$  &  $m_\mu$  (NB: called 'mx' in GSAS-II; range 0-1)

$$S_\gamma = m_s S + m_\mu M$$

$$S_\Gamma = [(1 - m_s)^2 S^2 + (1 - m_\mu)^2 M^2] / 8\ln 2$$

- Normally  $m_s$  &  $m_\mu = 1$  (all Lorentzian sample broadening) so:

$$S_\gamma = S + M$$

$$S_\Gamma = 0 \quad (\text{no Gaussian sample broadening})$$

- $X, Y, Z = 0$  (no Lorentzian instrument broadening)

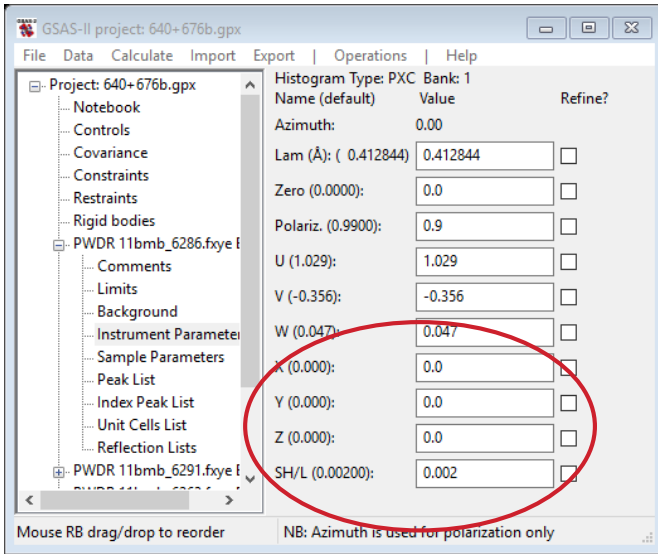
# CW PROFILE PEAK BROADENING IN GSAS-II

## The split of sample broadening from instrumental contribution

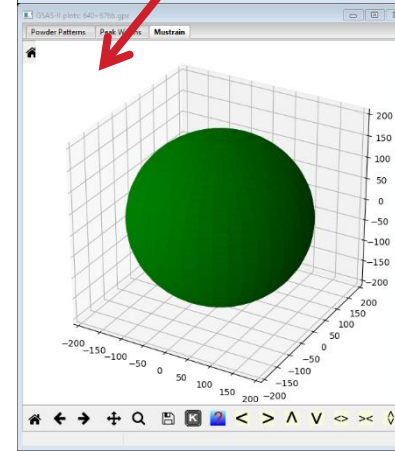
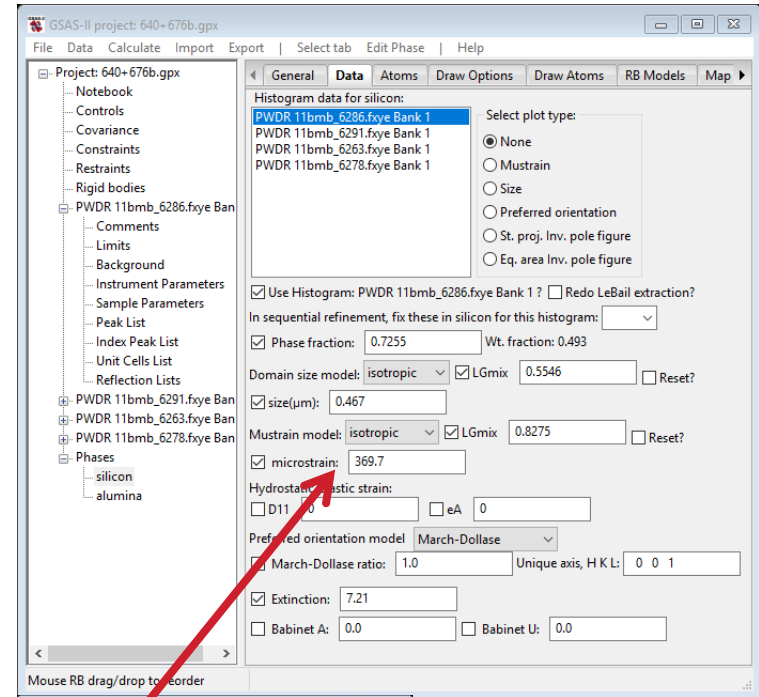
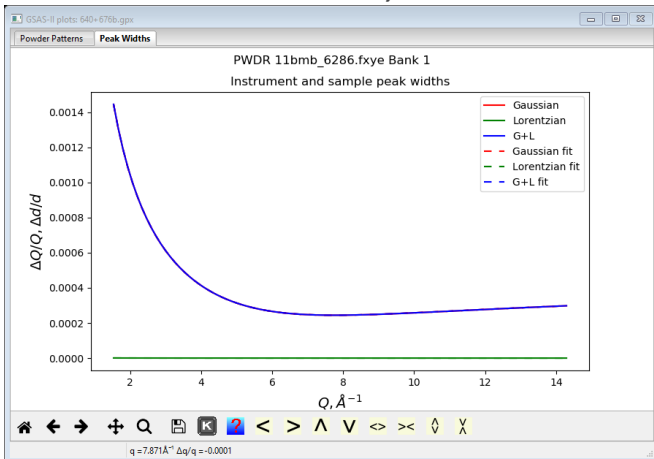
Instrument – fixed from calibration

Sample – phase & histogram dependent

Refined & constrained as needed



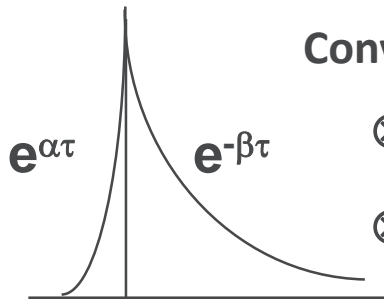
NB: for APS 11BM X,Y & Z = 0



Sample:  
New NIST SRMS  
640f & 676b

# TOF PROFILE FUNCTION IN GSAS-II

The best of gas fxns 1, 3, 4 & 5 combined (2 is not implemented)



Convolution of paired exponentials and a pseudoVoigt

$$\otimes (1-\eta)G(\Delta T, \Gamma)$$

$$\otimes \eta L(\Delta T, \gamma)$$

$$T = Cd + Ad^2 + B/d + Z$$

$$H(\Delta T) = (1-\eta)N[e^u \operatorname{erfc} y + e^v \operatorname{erfc} z] - \frac{2N\eta}{\pi} \{ \operatorname{Im}[\exp(p)E_1(p)] + \operatorname{Im}[\exp(q)E_1(q)] \}$$

N, p, q, u, v, x & y functions of  $\alpha$ ,  $\beta$ ,  $\sigma$  &  $\gamma$

Empirical relationships to d-spacing

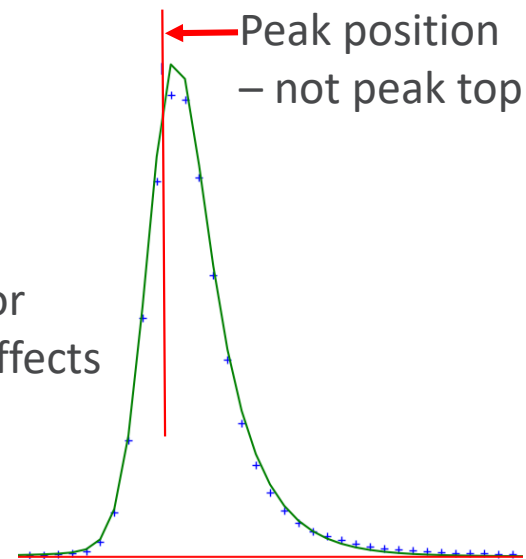
$$\alpha = \alpha_0/d; \beta = \beta_0 + \beta_1/d^4 + \beta_q/d^2$$

$$\sigma^2 = s_0 + s_1d^2 + s_2d^4 + S_qd + S_\Gamma$$

$$\gamma = Xd + Yd^2 + Z + S_\gamma$$

Sample broadening terms  
- earlier slide; may be hkl  
dependent

New terms for  
epithermal effects





# MIXING

## Lorentzian vs Gaussian sample broadening?

- Size:  $S = \frac{180k\lambda}{\pi p \cos \Theta}$        $\mu$ strain:  $M = 180\mu \tan \Theta / \pi$

- Need:  $S_\Gamma$  (Gauss) &  $S_\gamma$  (Lorentzian) sample broadening (2 slides back)

$$\Gamma_g^2 = 8\ln 2(U \tan^2 \Theta + V \tan \Theta + W + S_\Gamma)$$

$$\gamma = \frac{X}{\cos \Theta} + Y \tan \Theta + Z + S_\gamma$$

- Mixing coeff for each;  $m_s$  &  $m_\mu$  (NB: called 'mx' in GSAS-II; range 0-1)

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- Normally  $m_s$  &  $m_\mu = 1$  (all Lorentzian sample broadening) so:

$$S_\gamma = S + M$$

$$S_\Gamma = 0 \quad (\text{no Gaussian sample broadening})$$

- $X, Y, Z = 0$  (no Lorentzian instrument broadening)

# TOF PROFILE PEAK BROADENING IN GSAS-II

## The split of sample broadening from instrumental contribution

Instrument – fixed from calibration

Sample – phase & histogram dependent

Independent of experiment (e.g. CW or TOF)

GSAS-II project: 640-AXU.gpx

File Data Calculate Import Export | Operations | Help

Project: 640-AXU.gpx

Histogram Type: PNT Bank: 3

Flight path: 17.453 2-theta: 52.21

Name (default)	Value	Refine?
difC (3376.505):	3374.293	<input type="checkbox"/>
difA (-1.009):	-1.009	<input type="checkbox"/>
difB (2.131):	2.131	<input type="checkbox"/>
Zero (-3.697):	-3.697	<input type="checkbox"/>
alpha (0.122):	0.122	<input type="checkbox"/>
beta-0 (0.034467):	0.034467	<input type="checkbox"/>
beta-1 (0.015018):	0.015018	<input type="checkbox"/>
beta-q (0.019362):	0.019362	<input type="checkbox"/>
sig-0 (10.496):	10.496	<input type="checkbox"/>
sig-1 (99.229):	99.229	<input type="checkbox"/>
sig-2 (6.984):	6.984	<input type="checkbox"/>
sig-q (1.703):	1.703	<input type="checkbox"/>
X (1.287):	1.287	<input type="checkbox"/>
Y (-0.142):	-0.142	<input type="checkbox"/>
Z (0.000):	0.0	<input type="checkbox"/>

Mouse RB drag/drop to reorder NB: Azimuth is used for polarization only

GSAS-II project: 640-AXU.gpx

File Data Calculate Import Export | Select tab Edit Phase | Help

Project: 640-AXU.gpx

General Data Atoms Draw Options Draw Atoms RB Models Map pe

Histogram data for alumina:

- PWDR POLARIS124938.gsas Bank 3
- PWDR POLARIS124941.gsas Bank 3
- PWDR POLARIS124946.gsas Bank 3
- PWDR POLARIS124947.gsas Bank 3
- PWDR POLARIS124950.gsas Bank 3
- PWDR POLARIS124938.gsas Bank 4
- PWDR POLARIS124941.gsas Bank 4
- PWDR POLARIS124946.gsas Bank 4
- PWDR POLARIS124947.gsas Bank 4
- PWDR POLARIS124950.gsas Bank 4

Select plot type:

- None
- Mustrain
- Size
- Preferred orientation
- St. proj. Inv. pole figure
- Eq. area Inv. pole figure

Use Histogram: PWDR POLARIS124938.gsas Bank 3?  Do new LeBail extraction?

In sequential refinement, fix these in alumina for this histogram:

Phase fraction: 0.2705 Wt. fraction: 0.502

Domain size model: isotropic  LGmix: 1.0000  Reset?

size( $\mu\text{m}$ ): 0.746

Mustrain model: isotropic  LGmix: 1.0000  Reset?

microstrain: 314.7

Hydrostatic/elastic strain:

D11 0  D33 0

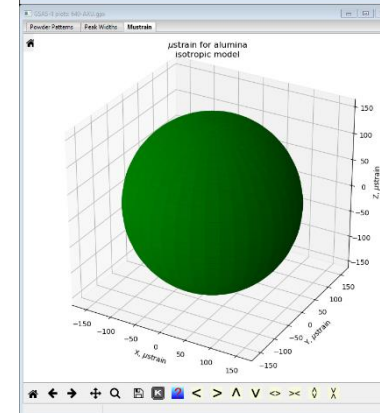
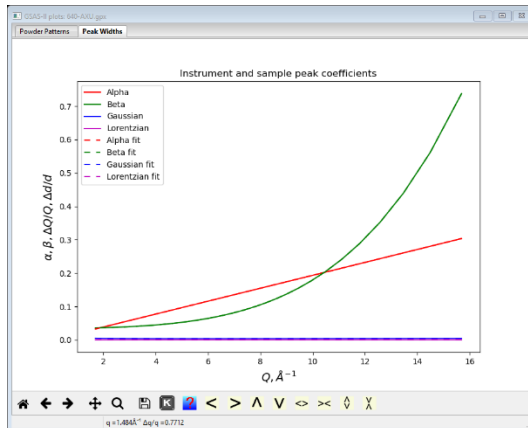
Preferred orientation model: March-Dollase

March-Dollase ratio: 1.0 Unique axis, H K L: 0 0 1

Extinction: 0.0

Cabinet A: 0.0  Cabinet U: 0.0

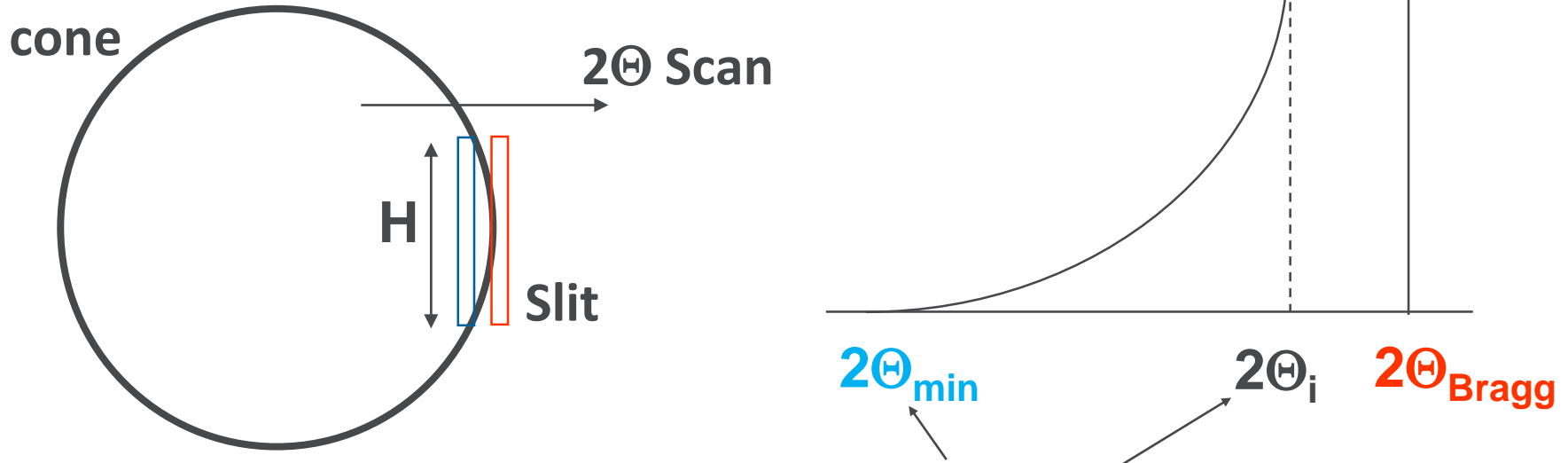
Mouse RB drag/drop to reorder



Sample:  
New NIST SRMS  
640f & 676b

# AXIAL BROADENING FUNCTION – CONST. WAVELENGTH

Finger, Cox & Jephcoat based on van Laar & Yelon  
Debye-Scherrer



Depend on slit & sample “heights” wrt diffr. radius  
 $H/L$  &  $S/L$  - parameters in function; combined as  $H+S/L$  in GSAS-II  
(typically 0.005 - 0.020)

⊗ Pseudo-Voigt  
= profile function

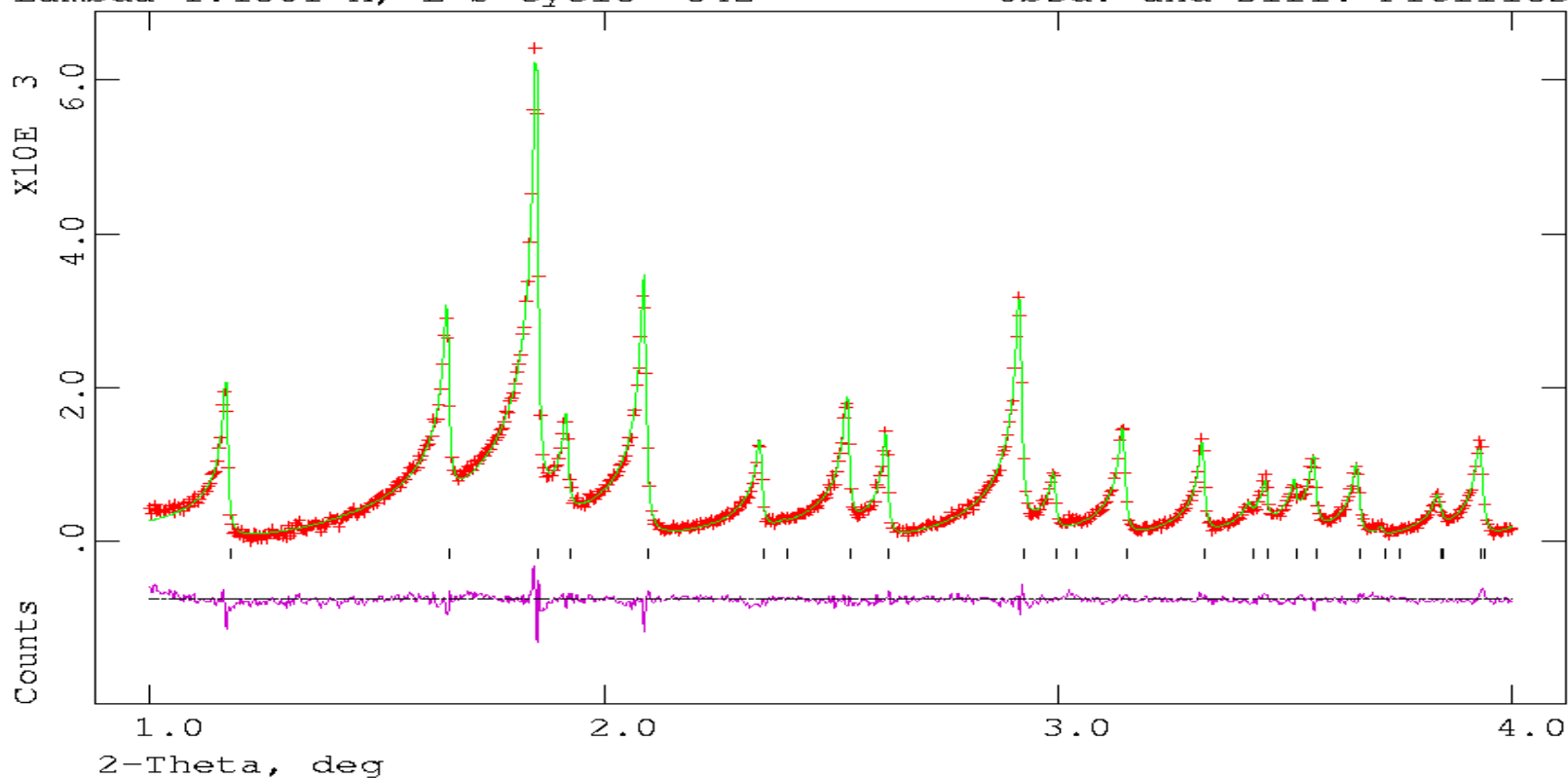
# HOW GOOD IS THIS FUNCTION?

lysozyme RT 0.70A

Hist 1

Lambda 1.1501 A, L-S cycle 542

Obsd. and Diff. Profiles



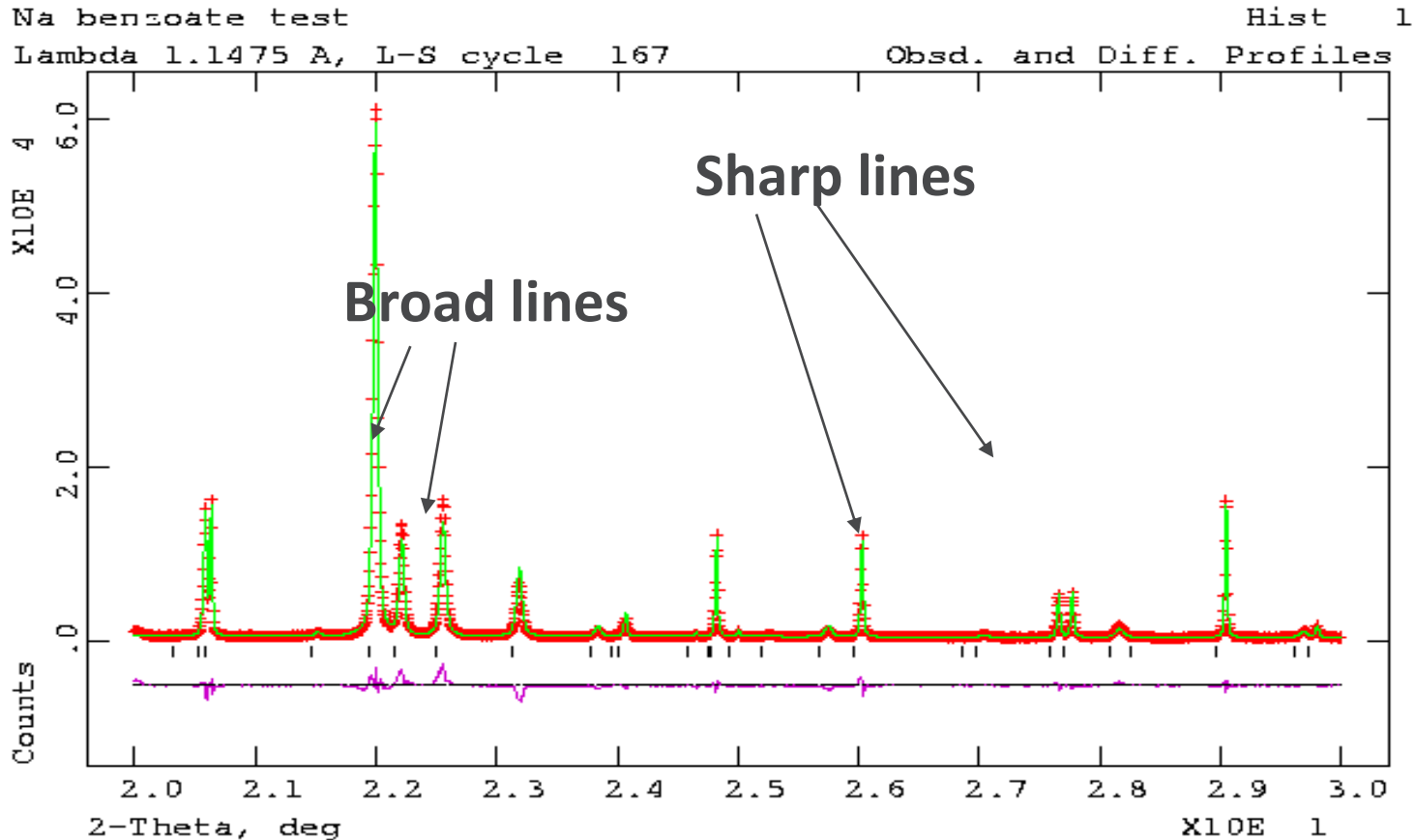
**Protein Rietveld refinement - Very low angle fit**

**1.0-4.0° peaks - strong asymmetry**

**“perfect” fit to shape**

# PROFILE FUNCTION – COMPLEXITIES

## AN EXAMPLE – UNUSUAL LINE BROADENING



Seeming inconsistency in line broadening - hkl dependent

# MICROSTRAIN BROADENING – PHYSICAL MODEL

Model – elastic deformation of crystallites

Stephens, P.W. (1999). *J. Appl. Cryst.* 32, 281-289.

Also see Popa, N. (1998). *J. Appl. Cryst.* 31, 176-180.

d-spacing expression

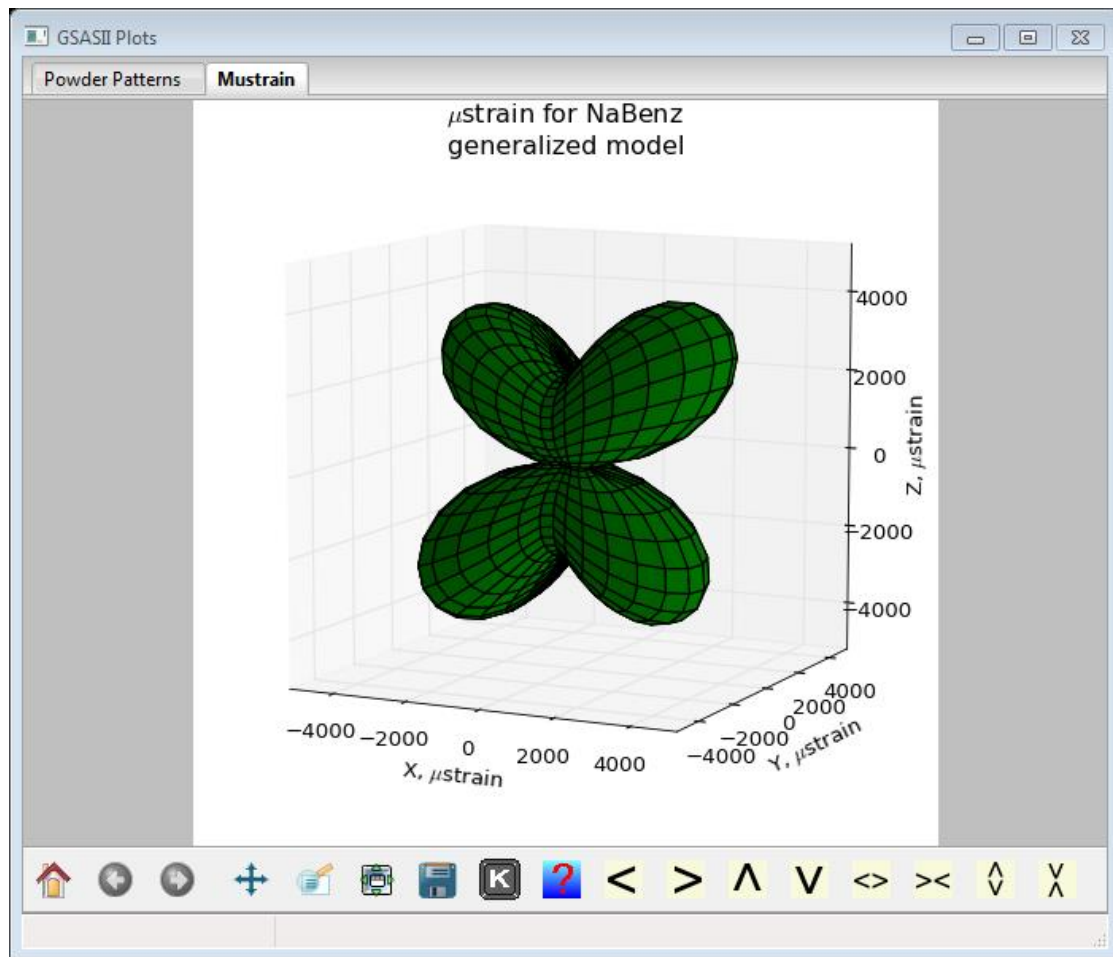
$$\frac{1}{d_{hkl}^2} = M_{hkl} = \alpha_1 h^2 + \alpha_2 k^2 + \alpha_3 l^2 + \alpha_4 kl + \alpha_5 hl + \alpha_6 hk$$

Broadening – variance in  $M_{hkl}$ ; refine  $C_{ij}$

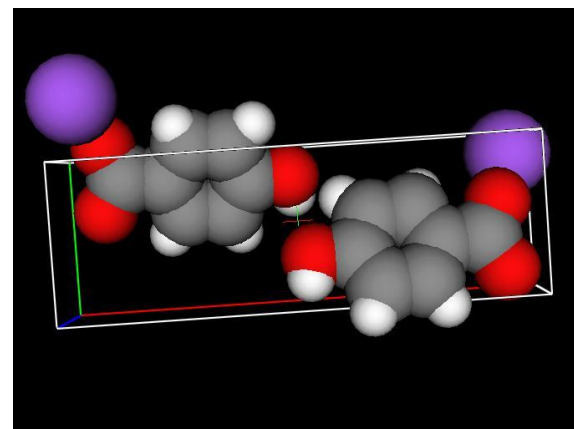
$$\sigma^2(M_{hkl}) = \sum_{i,j} C_{ij} \frac{\partial M}{\partial \alpha_i} \frac{\partial M}{\partial \alpha_j}$$

# NA PARAHYDROXYBENZOATE

## *Unusual microstrain effects - peak broadening*

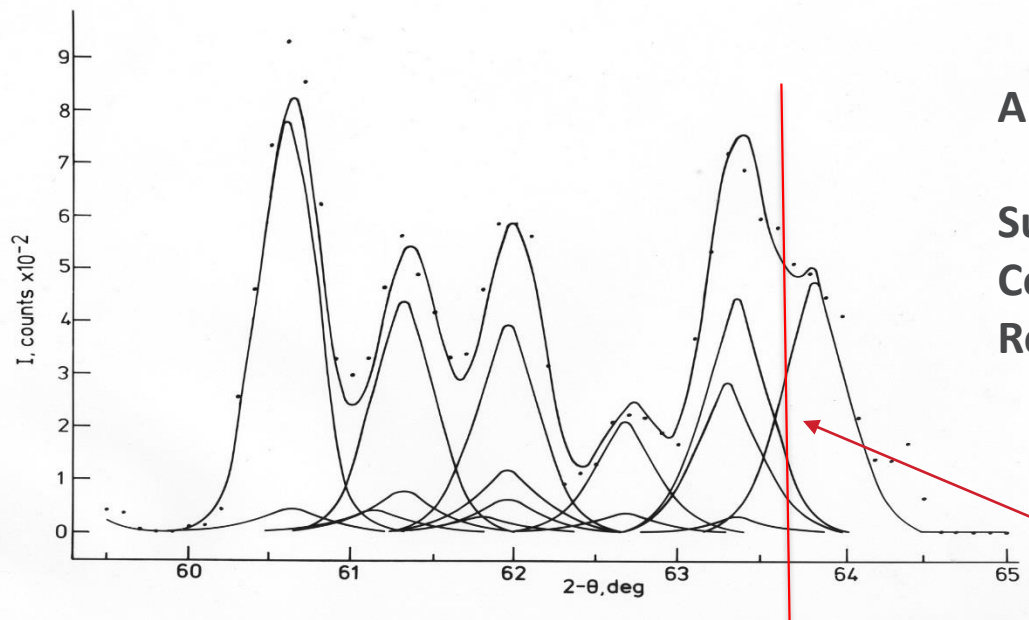


**Directional dependence -  
Lattice defects?  
Inclusion allowed  
OH atom  
placement from  $\Delta F$   
map**



# INTENSITY EXTRACTION

Structure factors from powder patterns? → structure solution



Apportion  $I_o$  by ratios of  $I_c(H)$   
for contributing reflections →  
Sum over all under peak profile  
Correct for multiplicity &  $L_p$ , etc.  
Result is  $F^2(H)$

Here 4 reflections contribute

LeBail algorithm – extracted  $F^2_o$  → new  $F^2_c$  then next cycle;  
refine only background, peak shapes & positions – few parameters  
No constraints needed for overlaps – Simple

Pawley refinement –  $F^2_o$  are parameters  
+ background, peak shapes & positions – many parameters  
Constraints & restraints required for overlaps - Complex



**THANK YOU**