

Durham
University

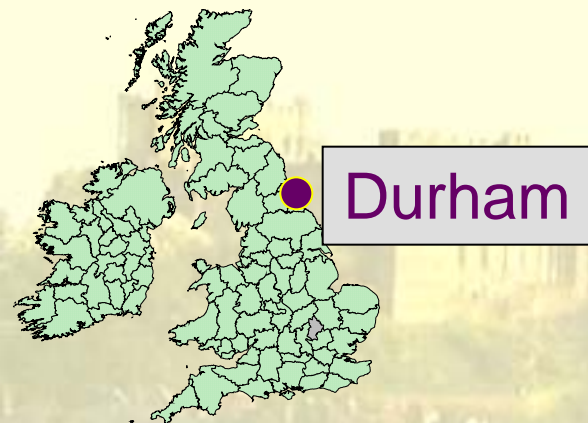
Chemistry
Department



Parametric Rietveld Refinement

Prof. John S.O. Evans

APD IV Gaithersburg, 2013



Durham



- What is parametric Rietveld refinement?
 - Should you do it?
 - How do you do it?
 - What can you parameterise?
- Examples
 - Cell parameter parameterisation
 - Subtle structural phase transitions
 - Background & amorphous content
 - Poor/low quality data
- Accuracy in Powder Diffraction
 - Accuracy – getting the answer right
 - Precision – better precision by more appropriate data analysis

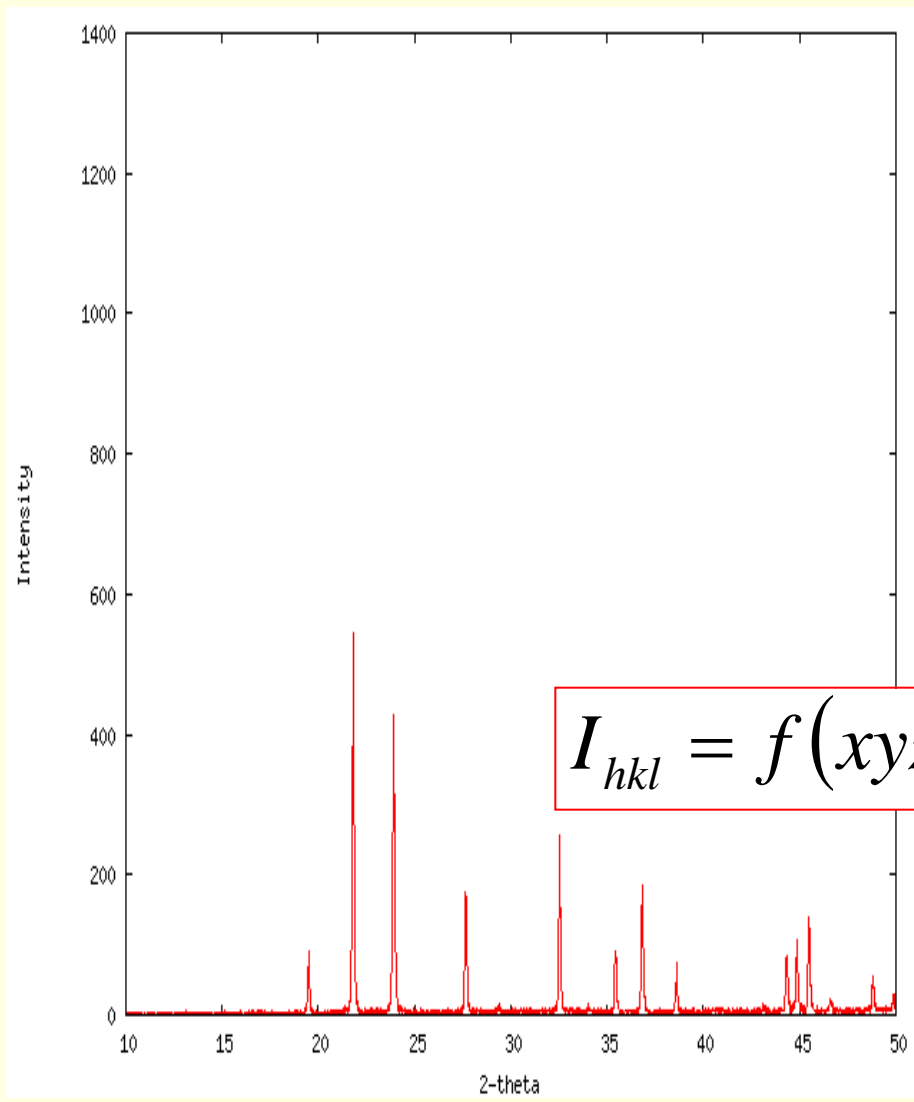
Evans/Stinton, *J. Appl. Cryst.*, **40**, 2007, 87

X+N refinements

Jean Francois Berar, XND

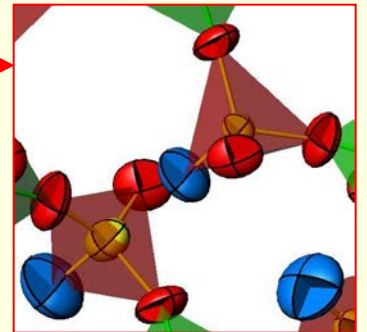


Diffraction = f(x)



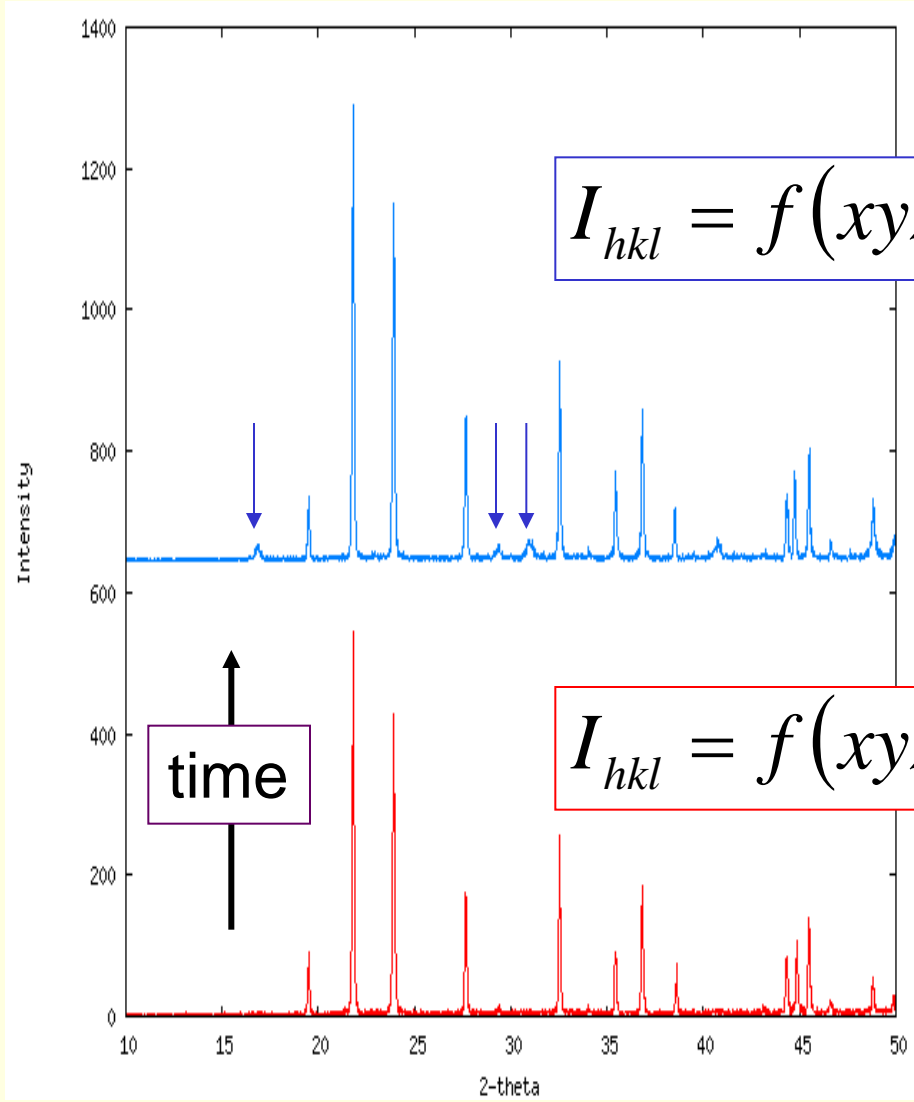
$$I \propto F_{hkl}^2; F_{hkl} = \sum_{j=1}^N f_j \exp [2\pi i(h x_j + k y_j + l z_j) -$$

$$8\pi^2 U_j \sin^2 \theta / \lambda^2]$$





Diffraction = $f(x)$

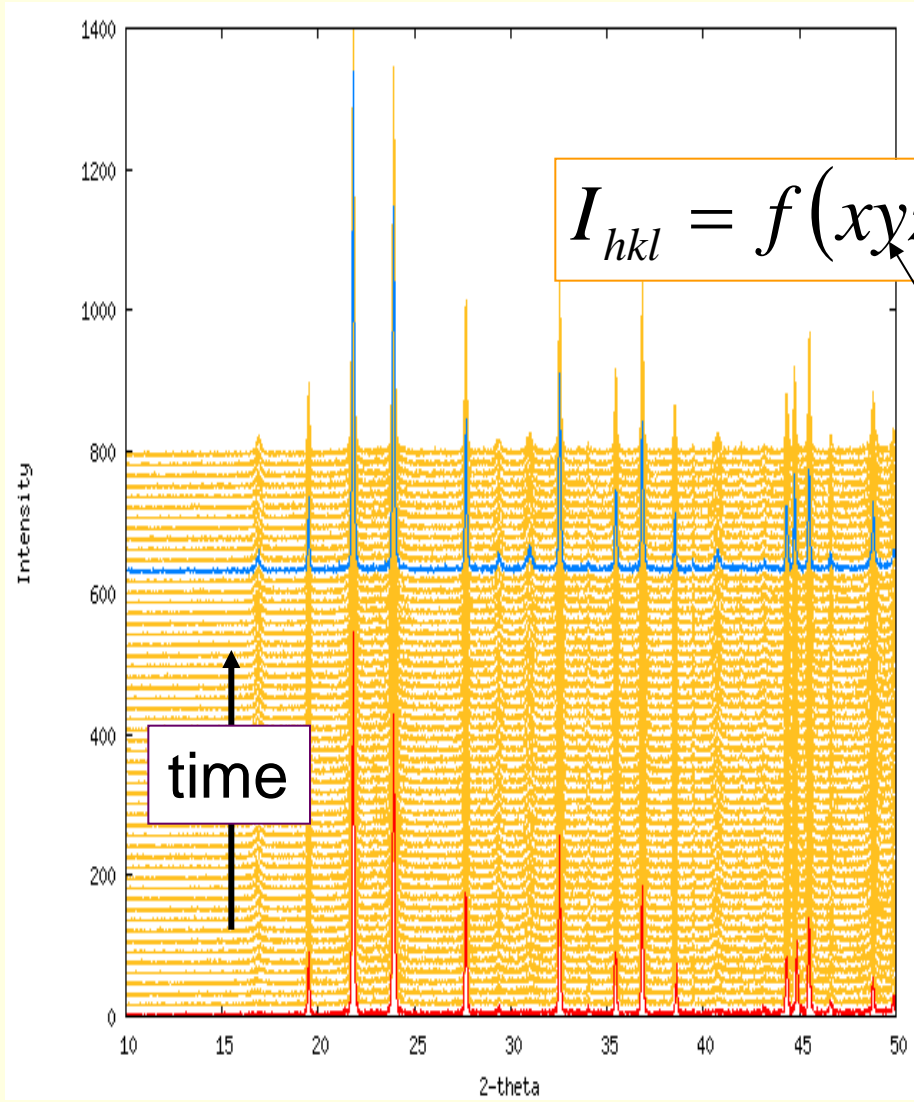


$$I_{hkl} = f(xyz(t = 2), occ(t = 2), adp(t = 2))$$

$$I_{hkl} = f(xyz(t = 1), occ(t = 1), adp(t = 1))$$



Diffraction = $f(x)$



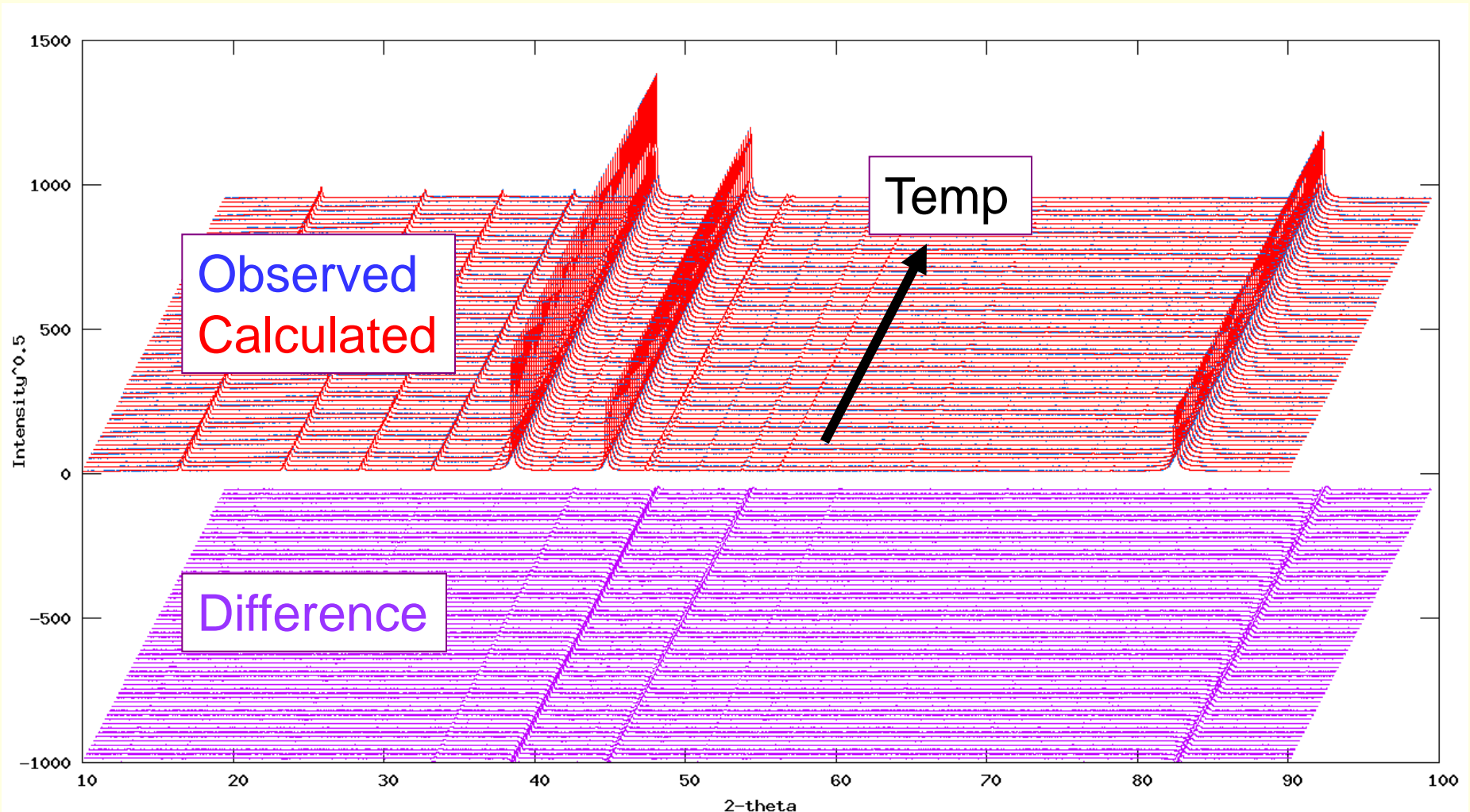
$$I_{hkl} = f(xyz, occ, adp)$$

$$adp = f(t)$$

$$occ = f(t)$$

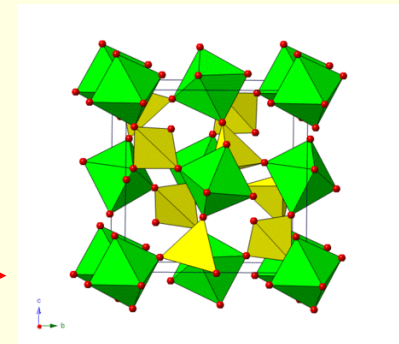
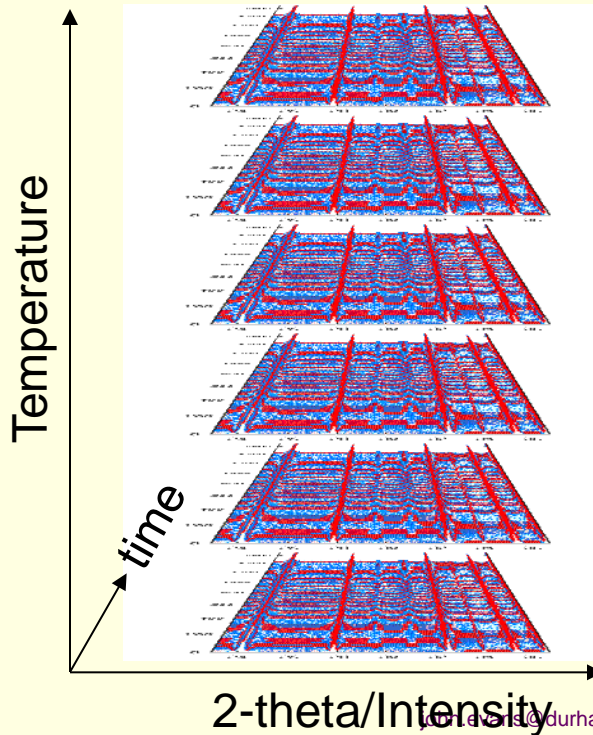
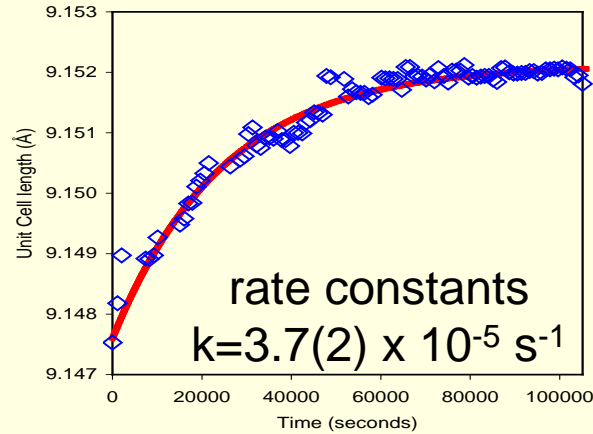
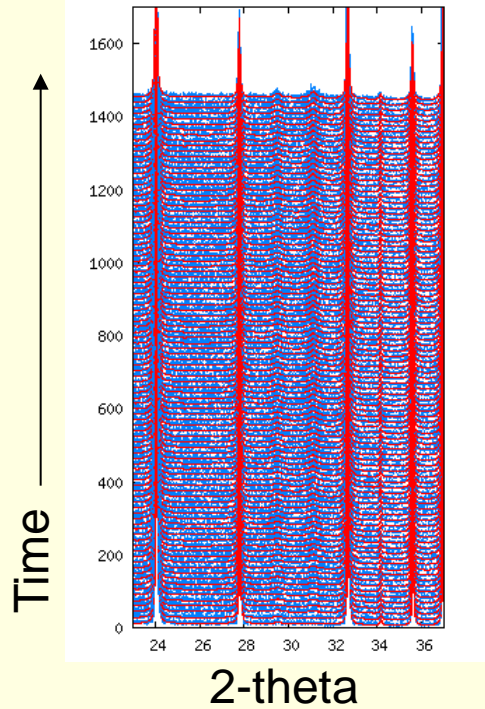
$$xyz = f(t)$$

Parametric Rietveld Refinement





Parametric Rietveld Refinement

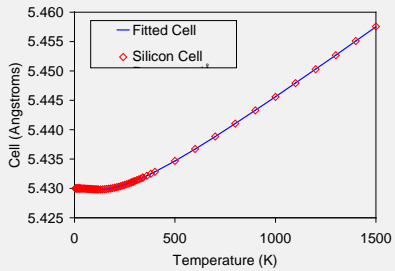


Activation
Energies

Evans/Stinton, *J. Appl. Cryst.*, **40**, 2007, 87



Things you Might Parameterise....



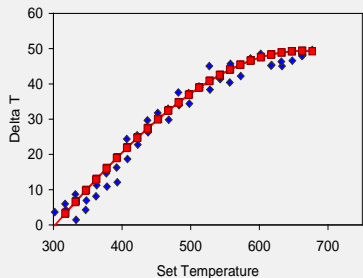
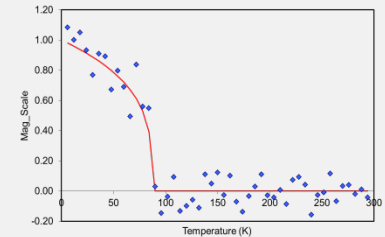
$$a(T) = \text{Exp} \left(\ln(a_0) + \frac{c_1 \theta_1}{\exp(\theta_1/T) - 1} \right)$$

$$x(T) = x_0 (1 + c_1 T + c_2 T^2 + c_3 T^3)$$

Structural variables

Critical behaviour

$$\text{Intensity}(T) = c_1 \left(1 - \frac{T}{T_C} \right)^\beta$$



$$\Delta T = c_0 + c_1 T_{set} + c_2 T_{set}^2$$

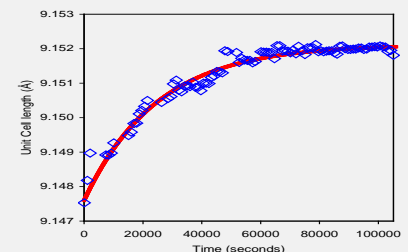
$$\text{height}(T) = h_0 (1 + c_1 T + c_2 T^2)$$

Instrumental effects

Kinetic parameters

$$\text{frac}(t) = c_1 [1 - \exp(-k_{frac} t)] + c_2$$

$$\text{cell}(t) = c_2 [1 - \exp(-k_{cell} t)] + c_3$$



Parametric/Surface vs Sequential

- Parametric fitting is a specialist beast
- Sequential fitting generally much easier, easily automated, fewer assumptions





EPDIC 2012 Software Discussion

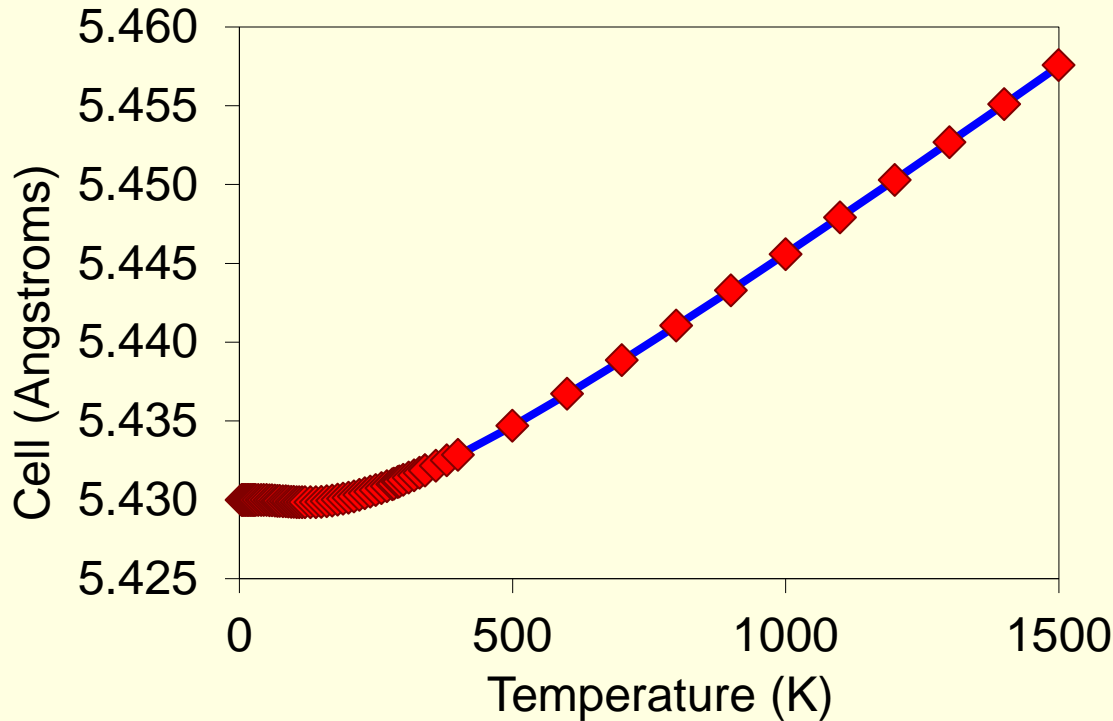
- Misquotes from “Profs F/G” EPDIC 2012:
 1. I don’t think we should be doing that.
 2. Why not just take all refined variables and variance-covariance matrices and analyse externally?
 3. What happens if you don’t choose the proper functional form?

- Misquotes in return:
 1. I agree with you 90% of the time.
 2. What piece of software do we have to do that (ANO); what if you’re in completely the wrong minimum.
 3. You learn a lot about your system.

 4. It’s really powerful when the wrong answer gives a better fit than the right answer



Unit Cell Parameterisation

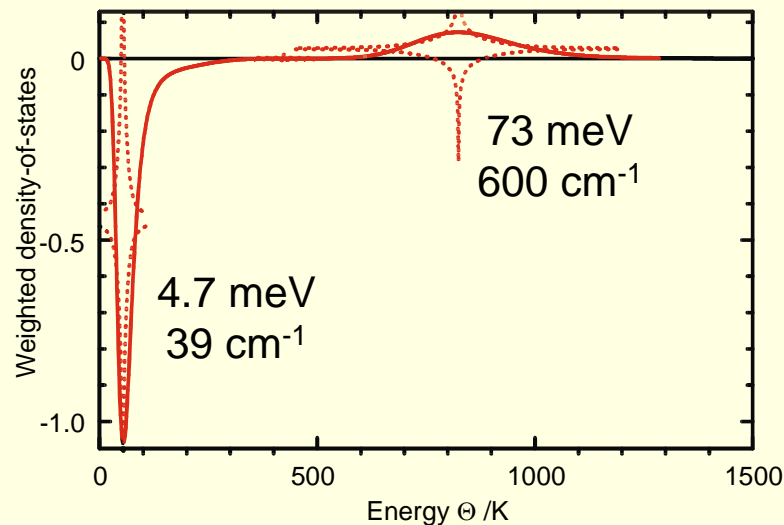
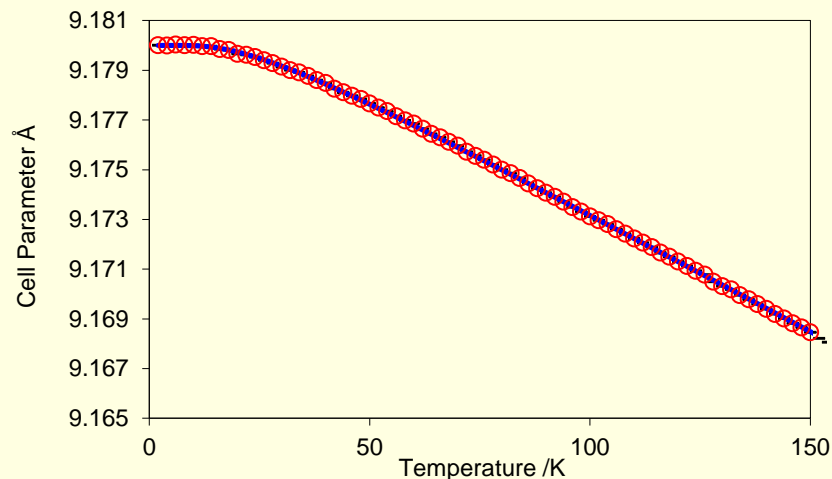
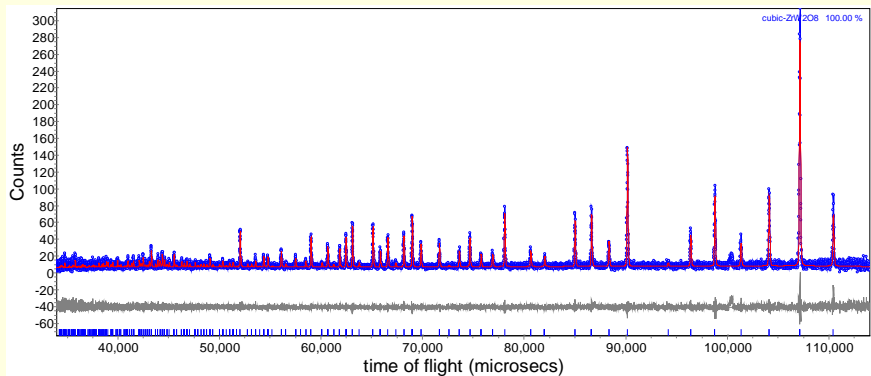


- Refine independently?
- Refine parametrically?

$$a(T) = \text{Exp} \left(\ln(a_0) + \frac{c_1 \theta_1}{\exp(\theta_1/T) - 1} + \frac{c_2 \theta_2}{\exp(\theta_2/T) - 1} + \dots \right)$$



ZrW₂O₈ Phonons – Don't Parameterise



260 relatively quick diffraction patterns



Cell Parameter at 260 temperatures

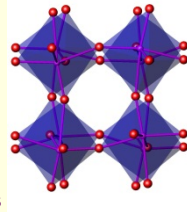
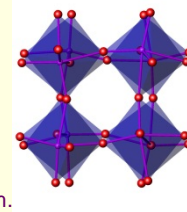
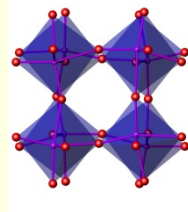
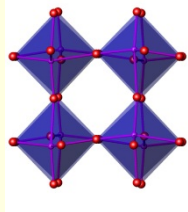
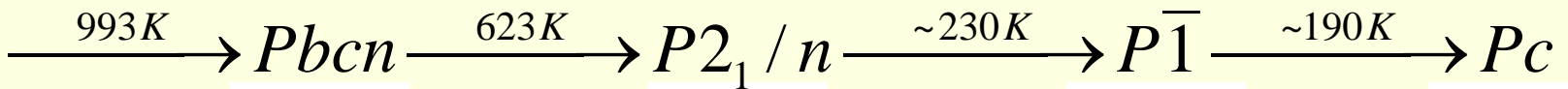
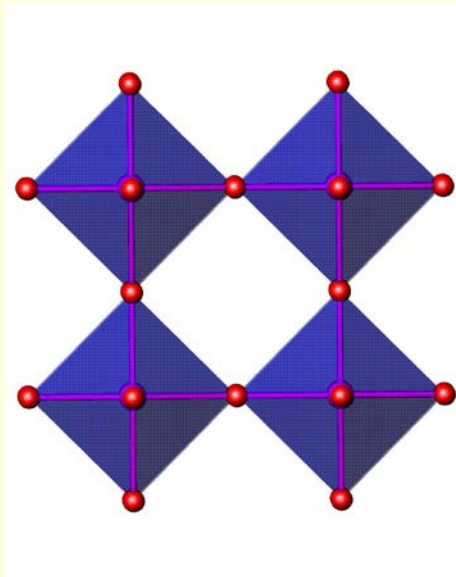
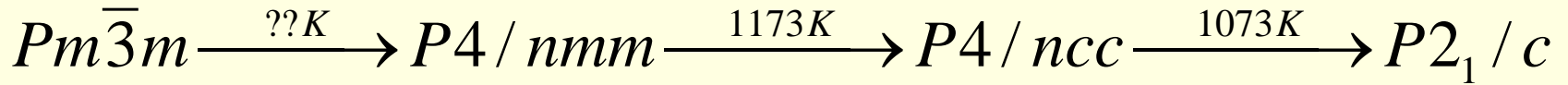
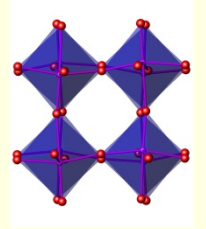
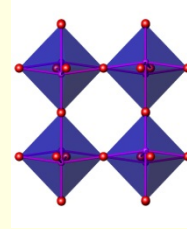
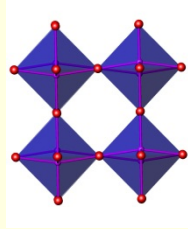
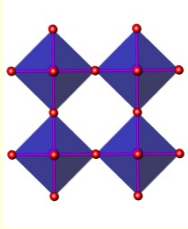


Complex physics

Bill David

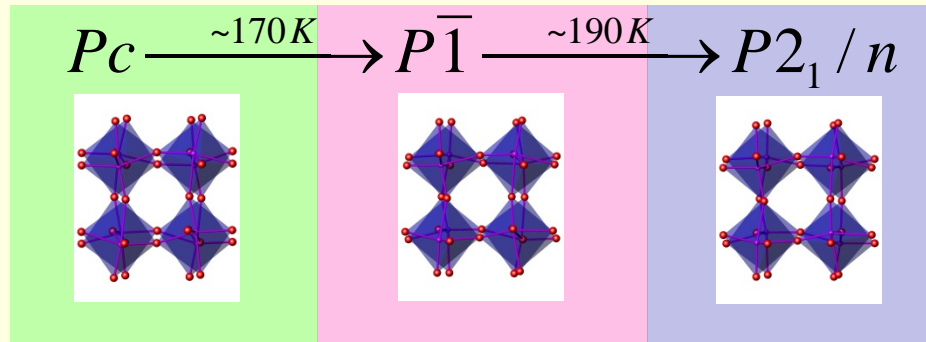
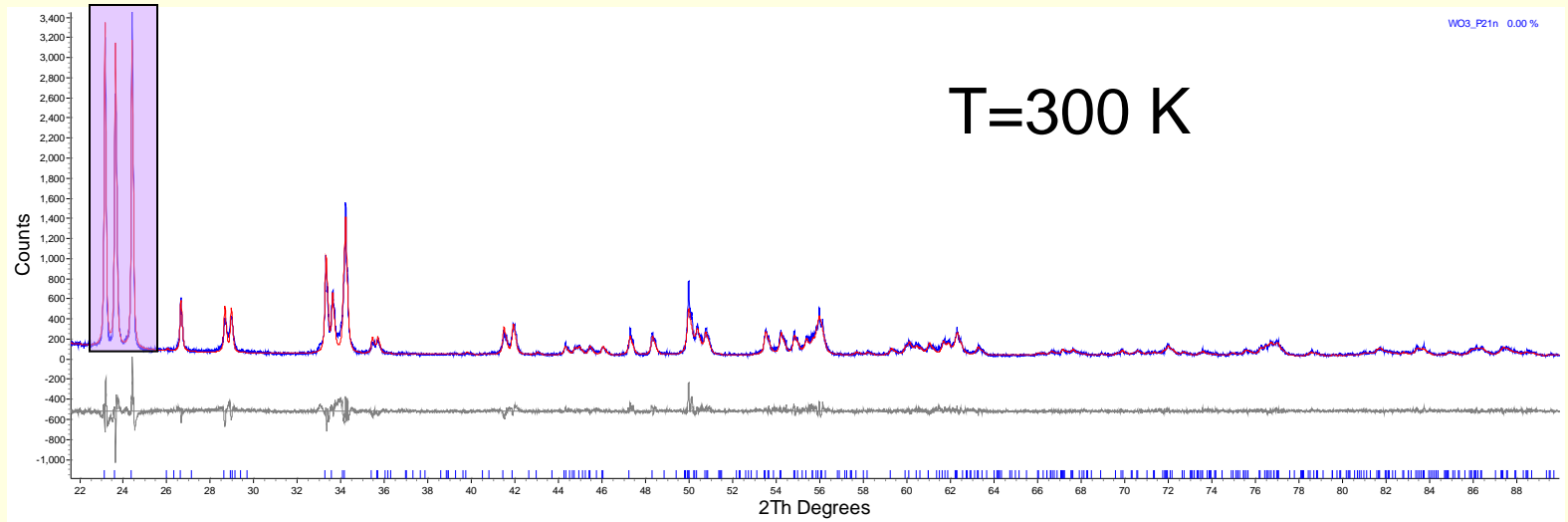


WO₃ Phase Transitions – Do Parameterise





90 K



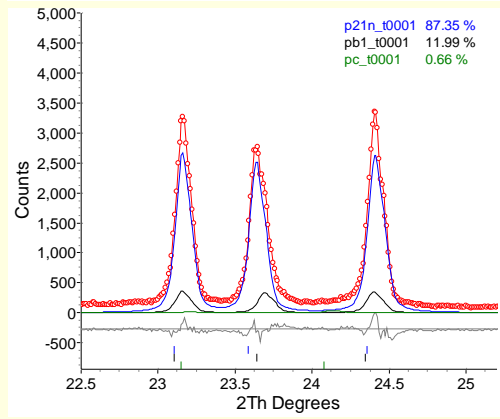
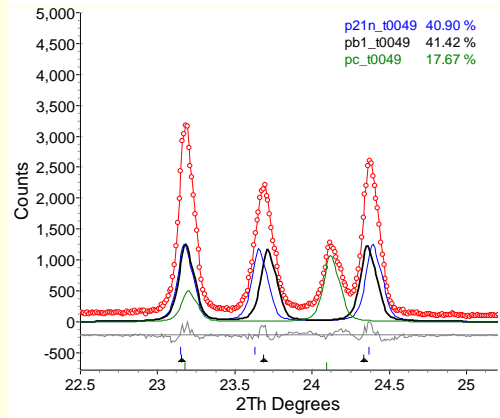
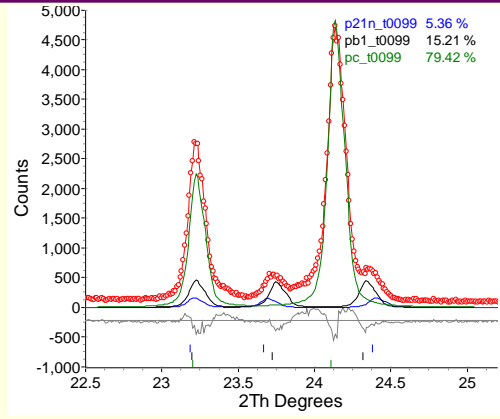
300 K



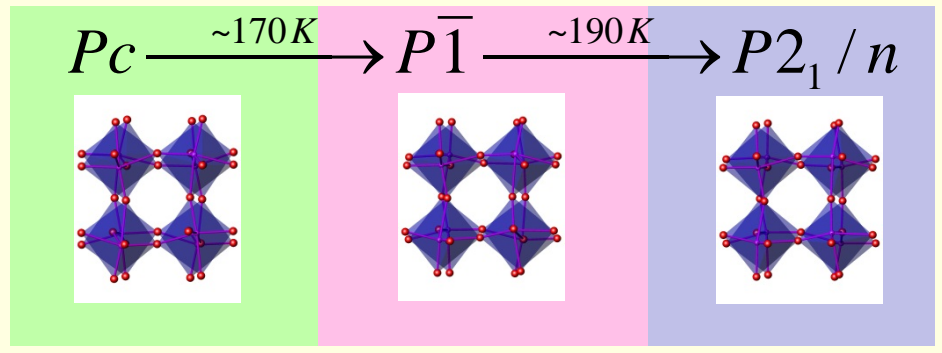
VT Lab Diffraction Data



90 K



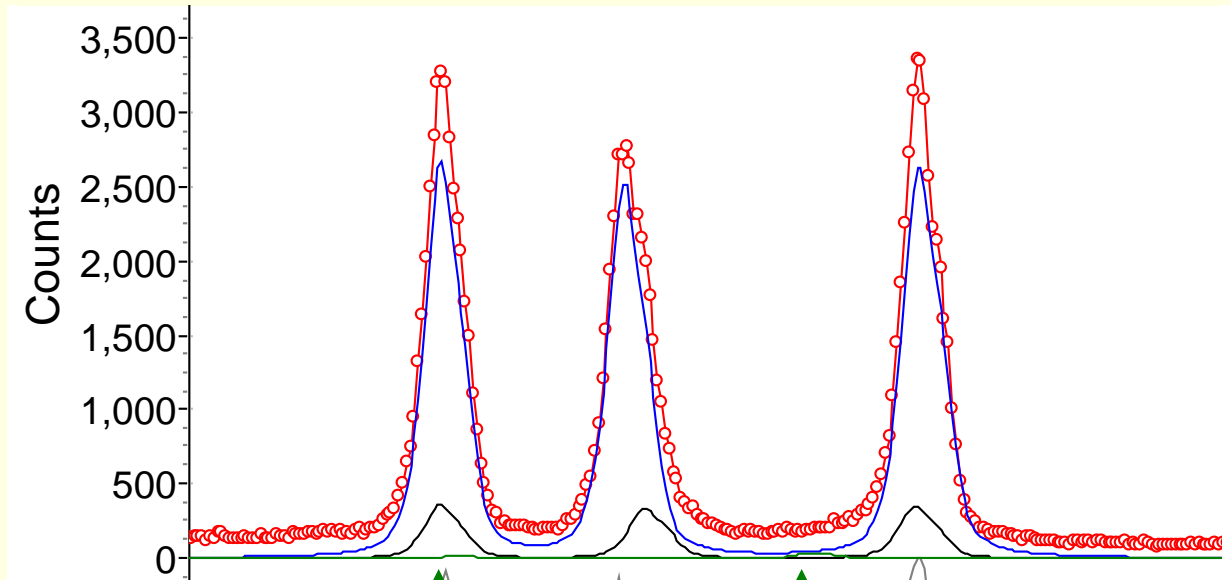
300 K





Peak Overlap/Structural Distortions

90 K



Pc

P-1

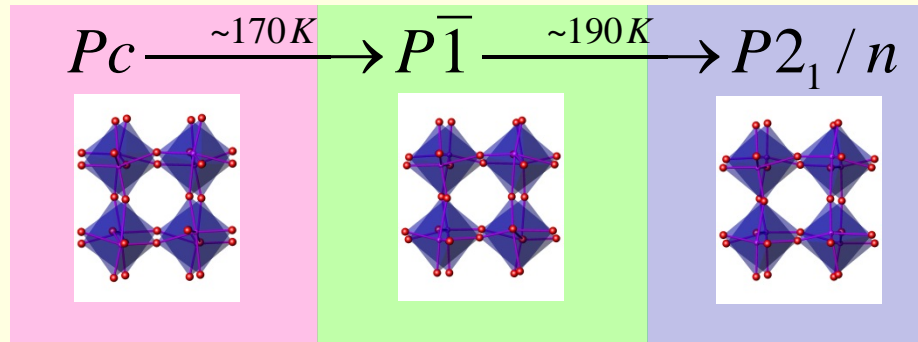
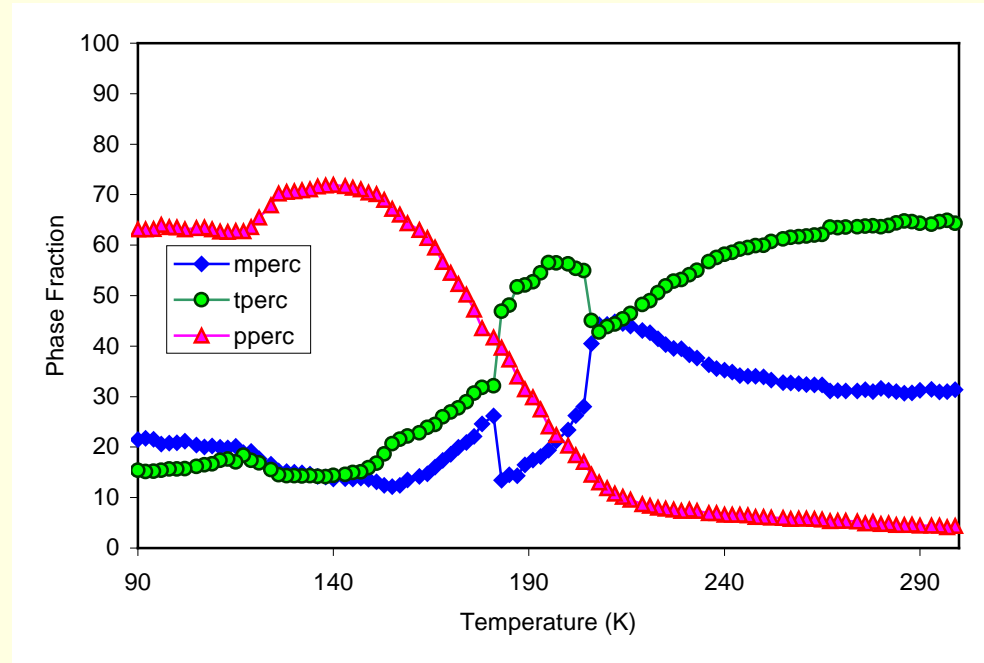
P2₁/n

P2₁/n (002)/(020)/(200) reflections

300 K

Sequential Phase Fractions

90 K



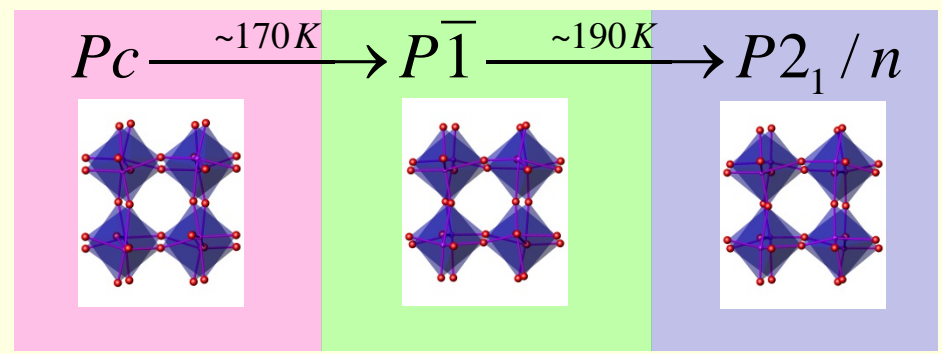
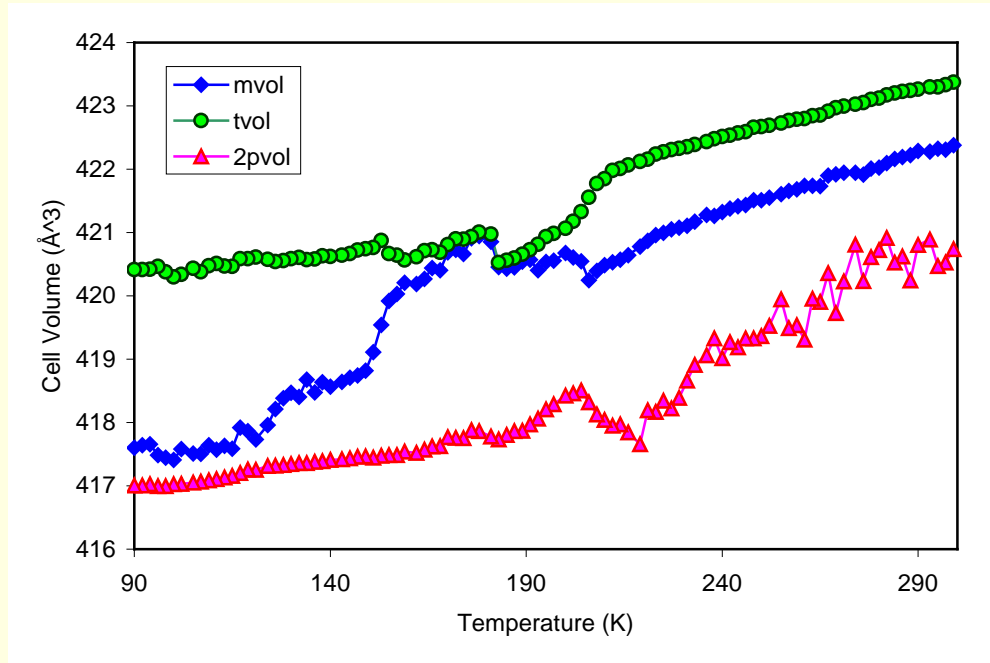
300 K



Sequential Cell Volumes



90 K



300 K



Parametric Assumptions



90 K

- Individual phases show smooth variations in $a/b/c$ and $\alpha/\beta/\gamma$ with temperature
- Temperature factors vary smoothly with temperature
- Peak shape for each phase derived from all data
- Einstein/polynomial type expressions
- 1102 parameters not 8100

300 K

Surface Fitting – Smooth Cell

Overall Refinable Parameters:

a0	5.42999
c1	4.86977×10^{-6}
θ1	570.1
.	
.	
.	

Refinement info for Temperature = 300 K

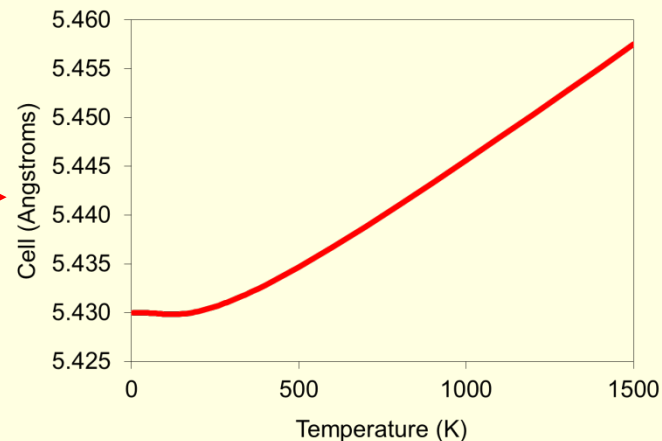
T = 300

$$a(T) = \text{Exp} \left(\ln(a_0) + \frac{c_1 \theta_1^*}{\exp(\theta_1/T) - 1} + \dots \right)$$

Refinement info for Temperature = 350 K

T = 350

$$a(T) = \text{Exp} \left(\ln(a_0) + \frac{c_1 \theta_1^*}{\exp(\theta_1/T) - 1} + \dots \right)$$



Surface Fitting – Smooth ADPs



Overall Refinable Parameters:

a0	5.42999
c1	4.86977*10 ⁻⁶
θ1	570.1
b0	0.113
c2	2.33*10 ⁻³
θ2	500

Refinement info for Temperature = 300 K

$$T = 300$$

$$a(T) = \text{Exp} \left(\ln(a_0) + \frac{c_1 \theta_1^*}{\exp(\theta_1/T) - 1} + \dots \right)$$

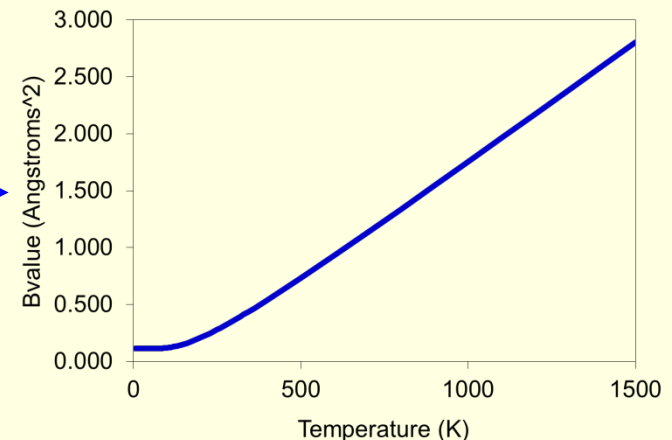
$$b(T) = b_0 + \frac{c_2 \theta_2^*}{\exp(\theta_2/T) - 1}$$

Refinement info for Temperature = 350 K

$$T = 350$$

$$a(T) = \text{Exp} \left(\ln(a_0) + \frac{c_1 \theta_1^*}{\exp(\theta_1/T) - 1} + \dots \right)$$

$$b(T) = b_0 + \frac{c_2 \theta_2^*}{\exp(\theta_2/T) - 1}$$





.inp file format/implementation

- Topas input file

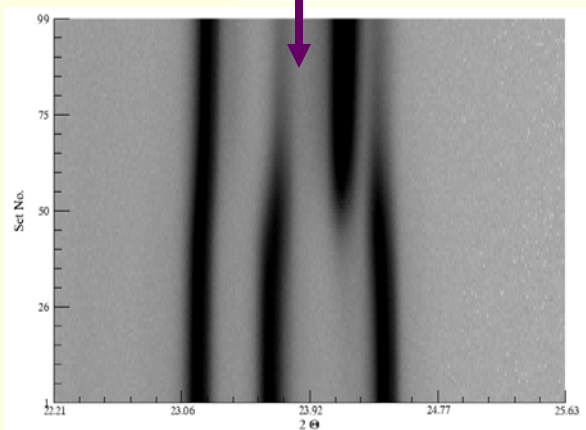
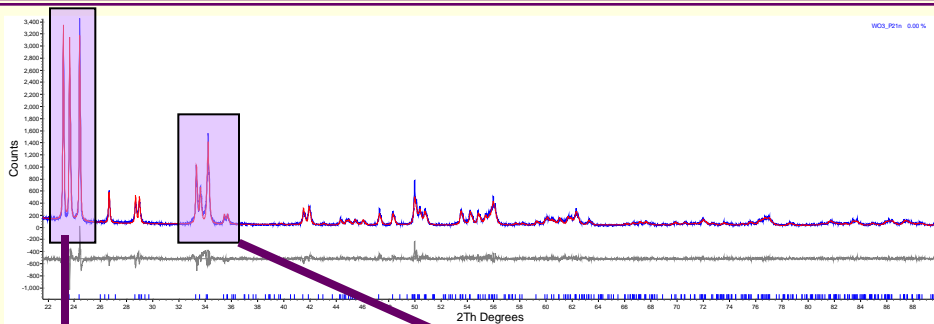
```
`a bit of the input file
prm zero_ma 7.2900
prm theta_ma 150
prm grad_ma 1.02e-5

str
  phase_name p21n_t0001
#ifdef param_cell
  prm mlpa_t_0001 = zero_ma + (grad_ma/(Exp(theta_ma/t_0001)-1));:7.30037
  a =mlpa_t_0001;:7.30037`
  ....
#else
  a mlpa_t_0001 7.30735 mlpaminmax
  ....
#endif
```

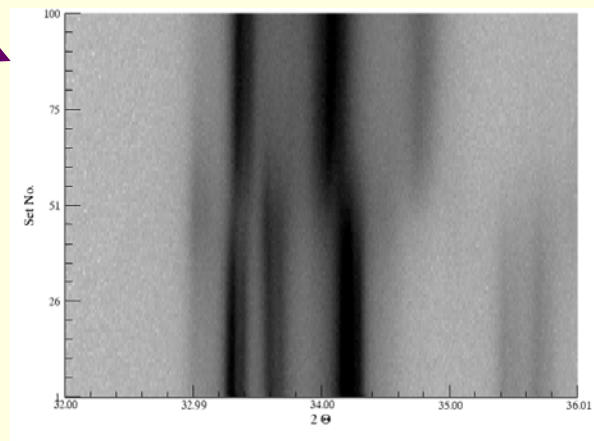



Surface Fit

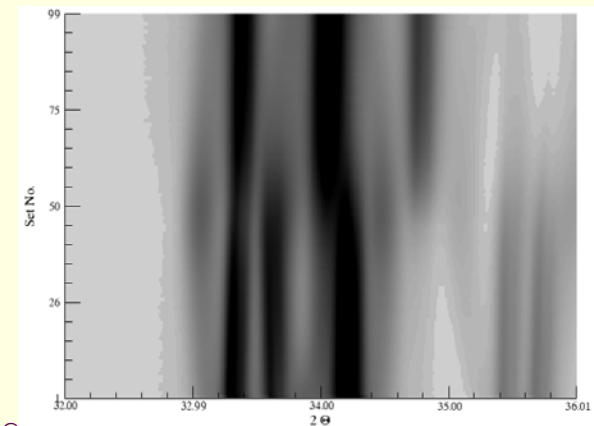
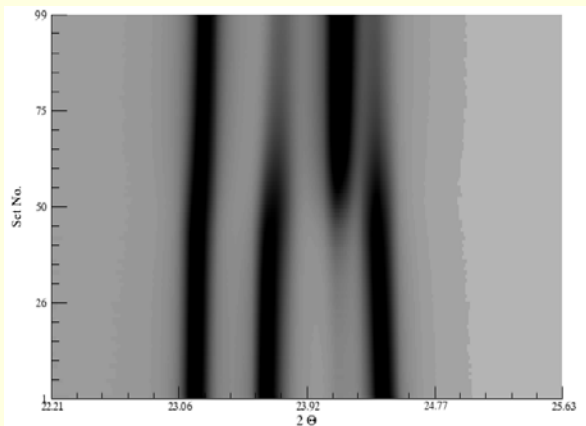
90 K



obs



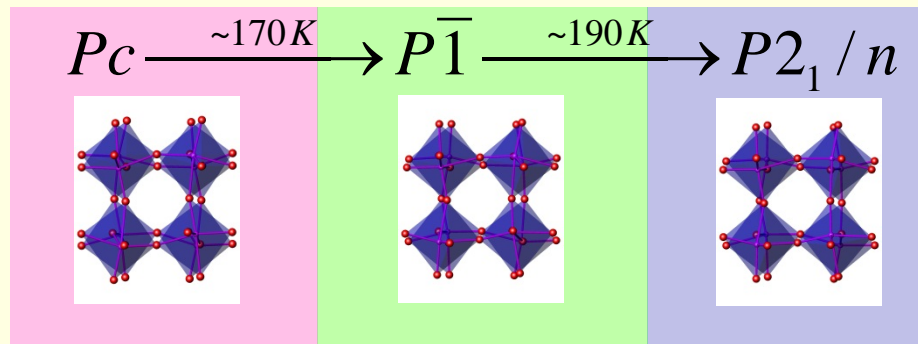
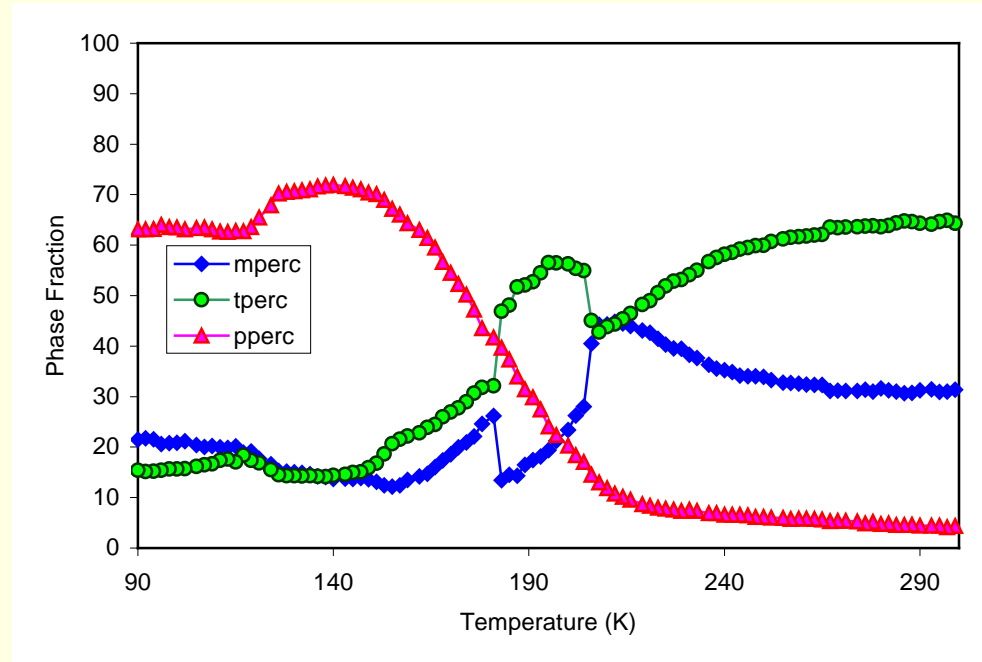
calc



300 K

Sequential Phase Fractions

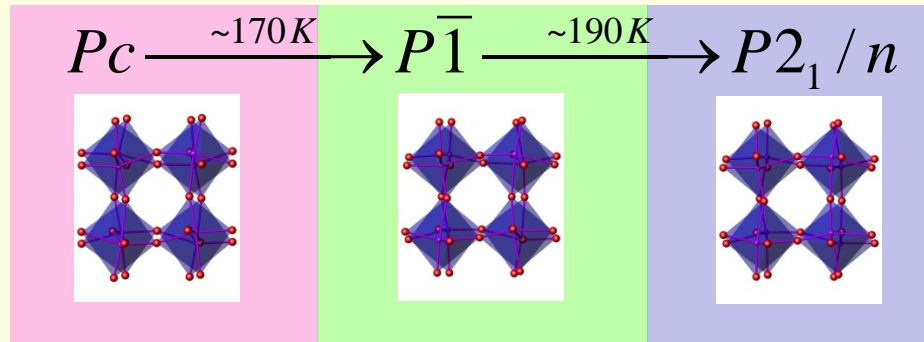
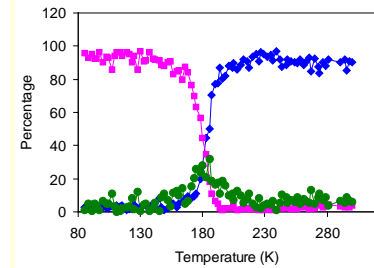
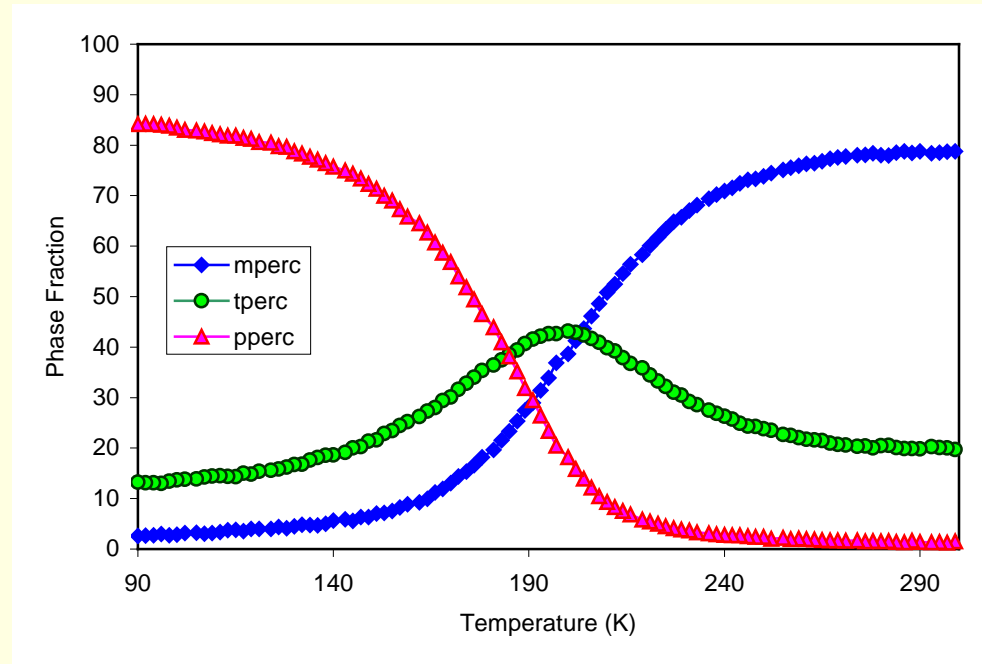
90 K



300 K

Parametric Phase Fractions

90 K



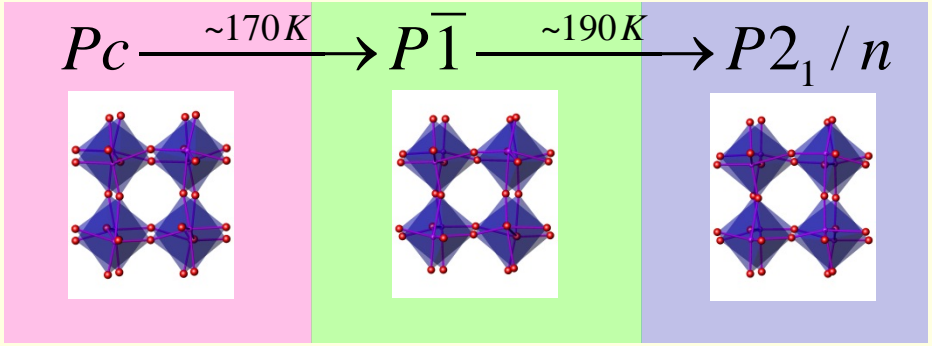
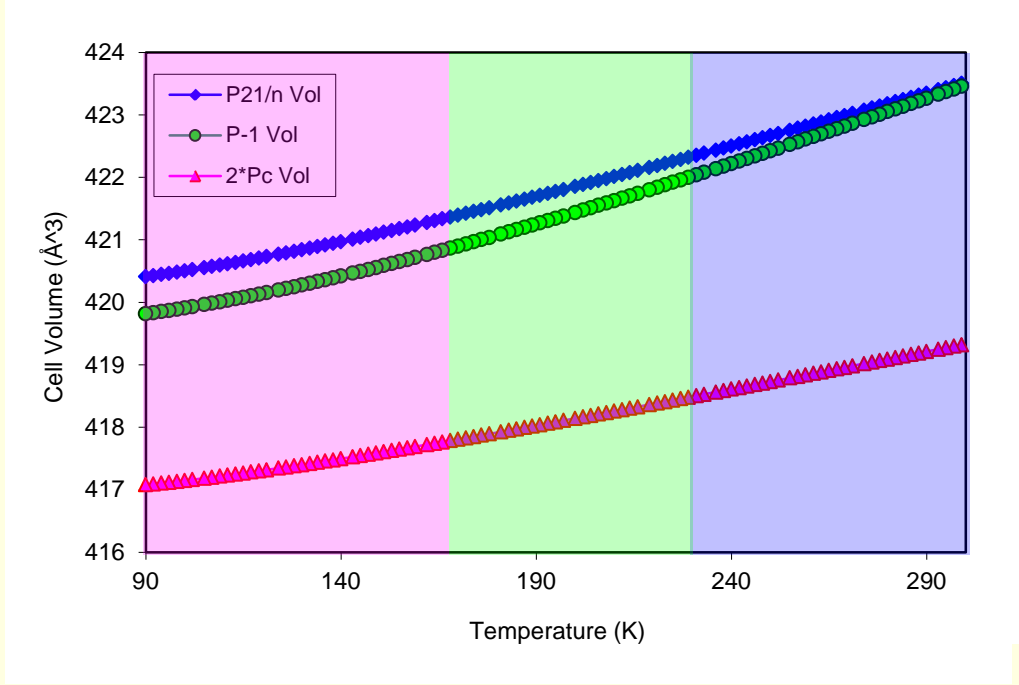
300 K



Parametric Cell Volumes



90 K



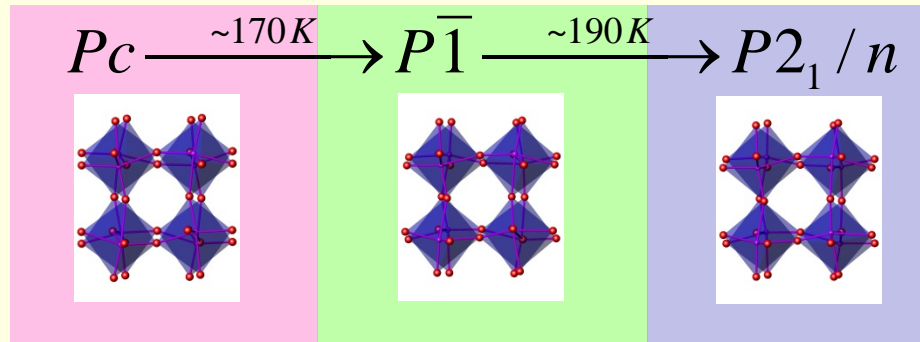
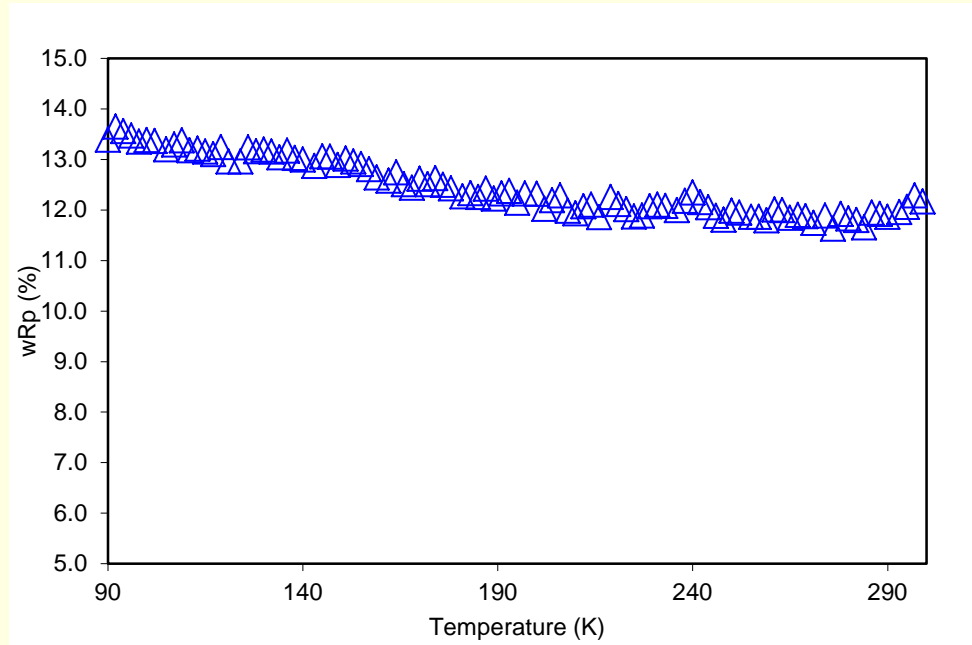
300 K



Parametric R-factors



90 K

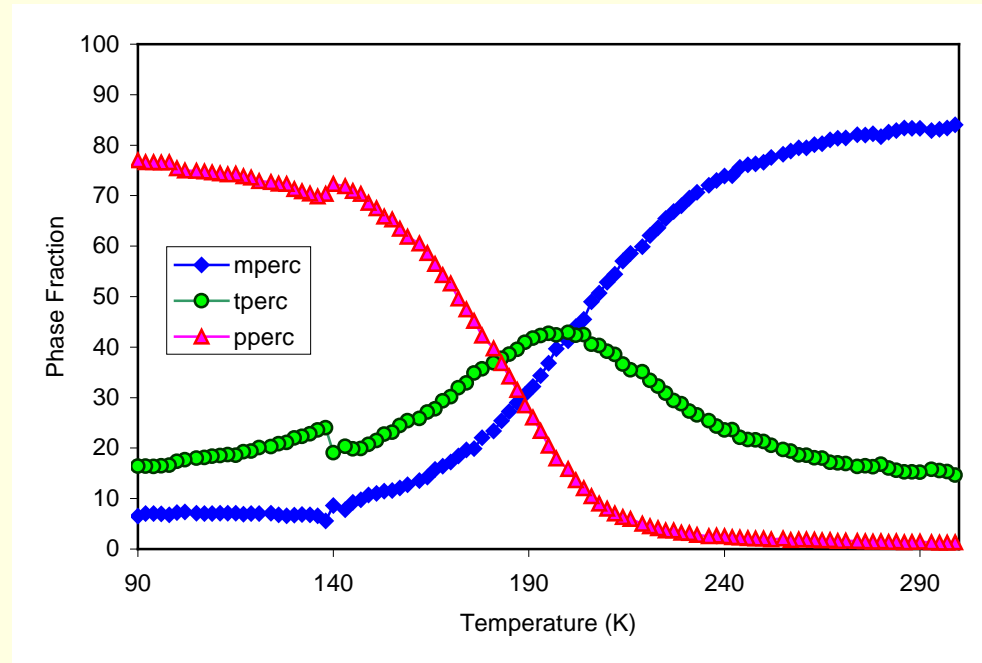


300 K



“Best Possible” Independent Fitting?

90 K



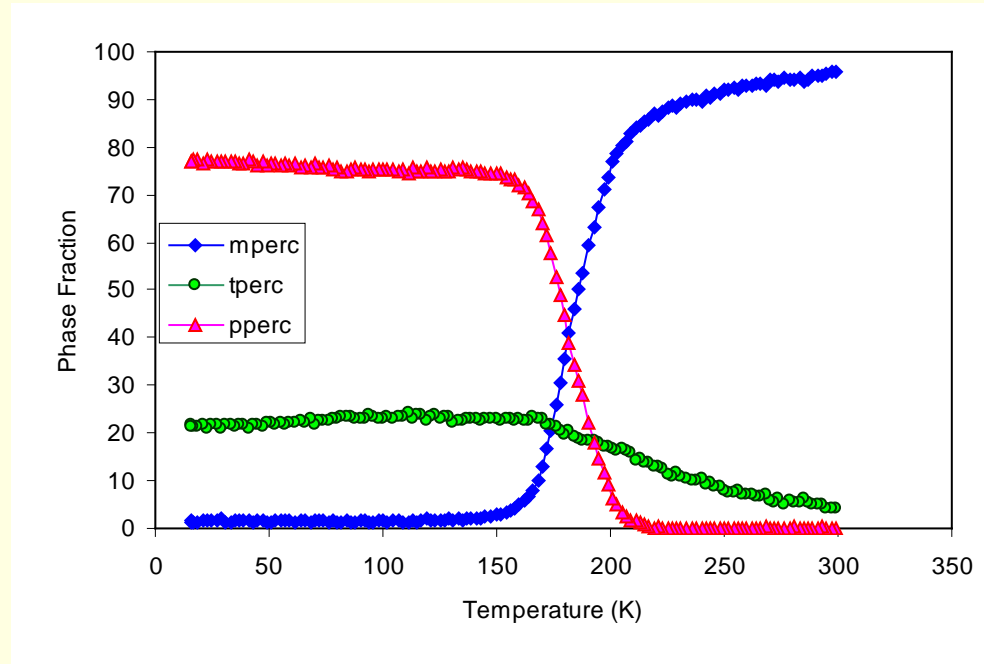
- Start all refinements at “perfect” cell parameters from parametric fit
- Minimum number of parameters (identical peak shapes etc)
- Perform limited simulated annealing at each T
- “Wrong” answer can have lower R-factor

300 K

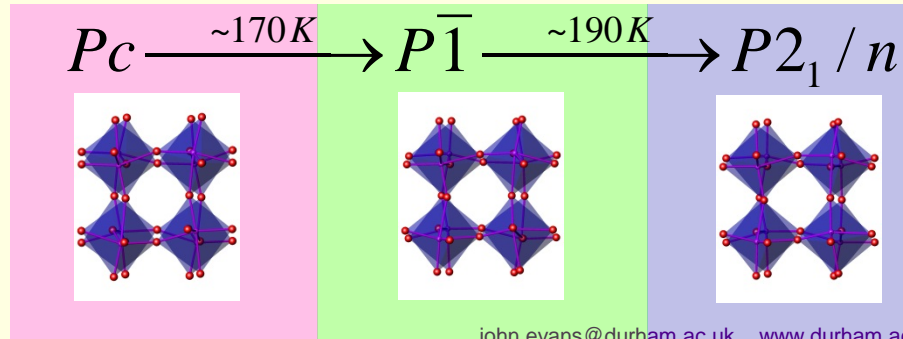
Wrong Model?

90 K

- Different sample
- Equivalent X-ray experiment



300 K

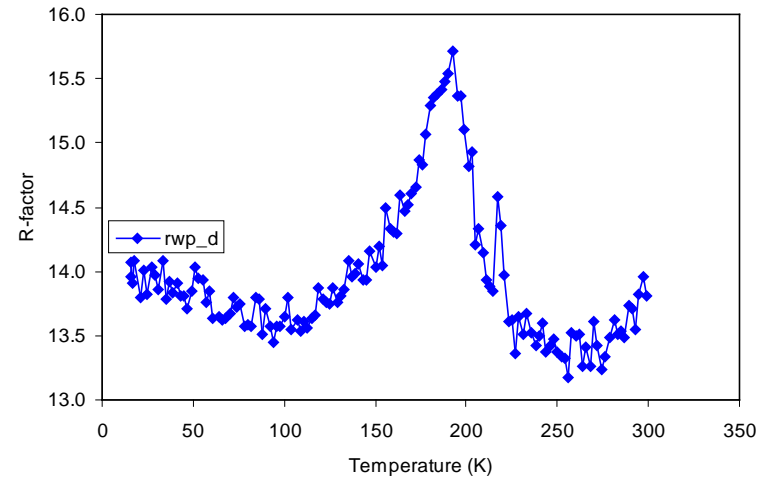
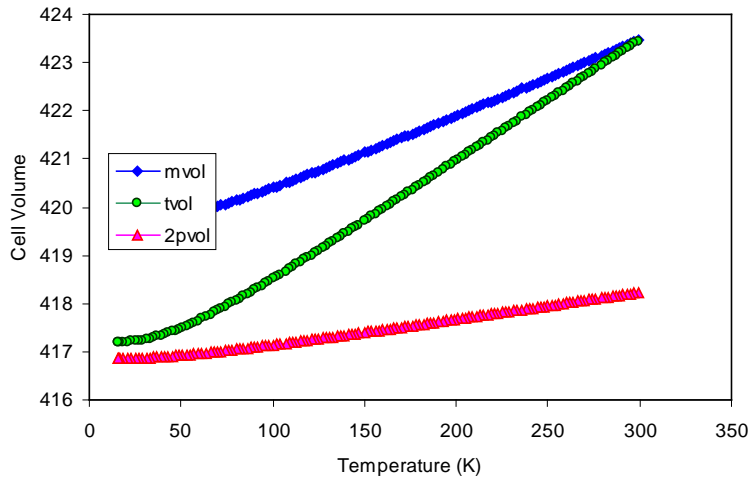




Cell volumes and R-factor



90 K

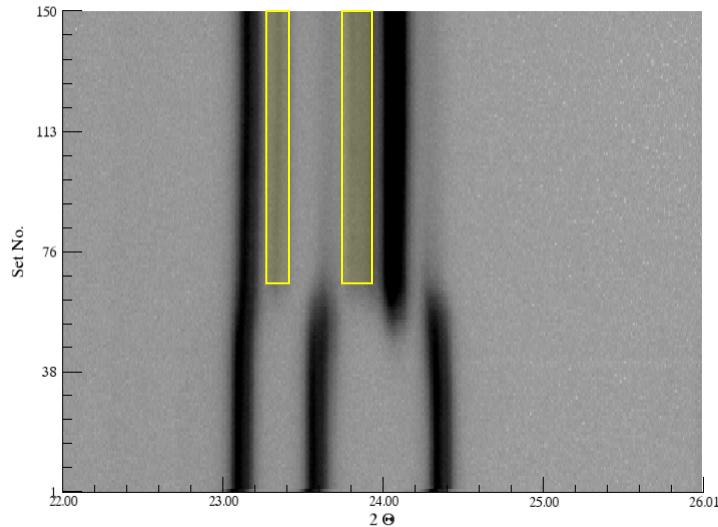


- Cell volumes with temperature very suspicious
- R-factors very suspicious
- Unusual trends suggest something wrong

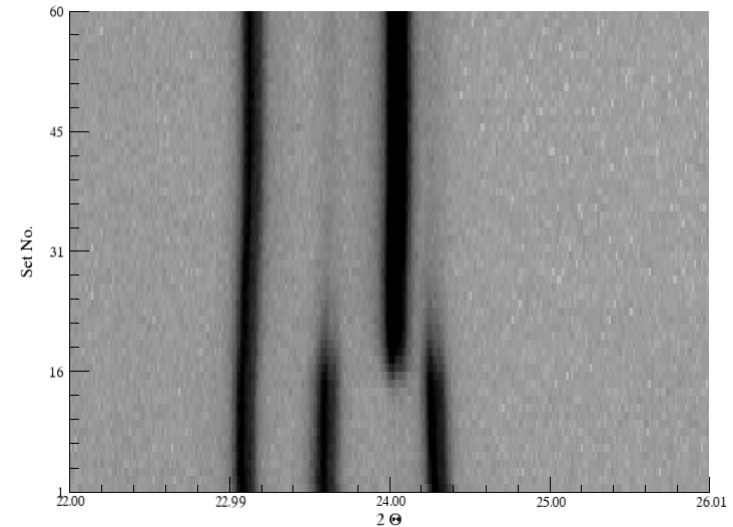
300 K

Raw data – additional peaks

90 K



d9_03124



d9_03125

- Extra low temperature phase
- Without surface fitting these peaks get “mopped up” by P-1 phase
- Phase transitions very dependent on thermal history

300 K



Quantitative Analysis – Advantages

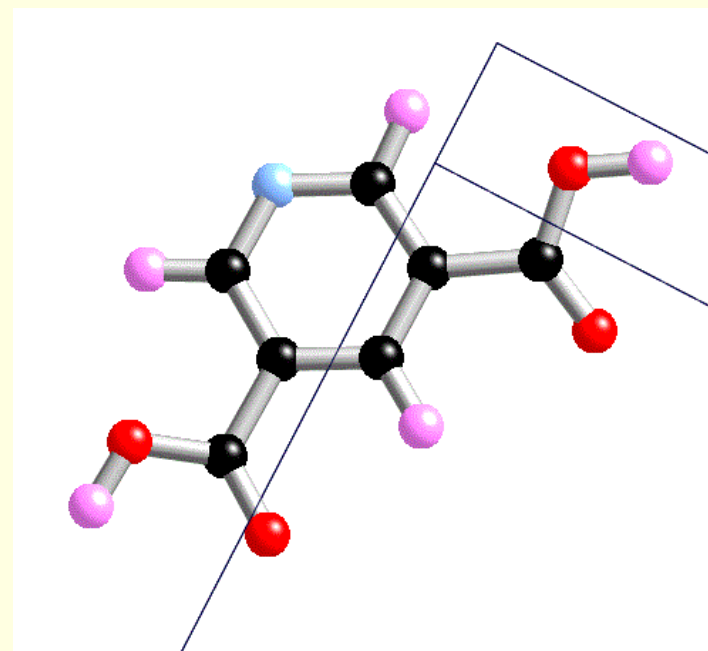
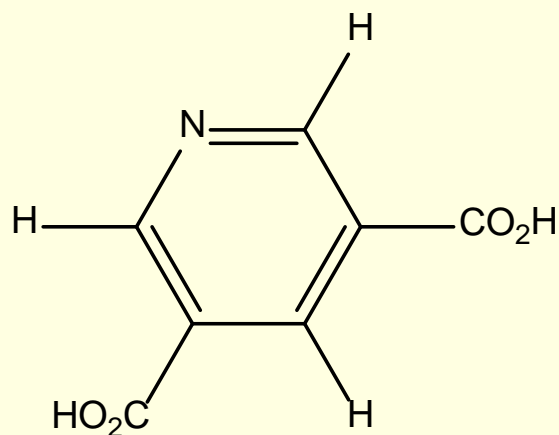
- Impose “physically sensible model” on well understood quantities
- Prevent “wrong solutions” fitting data
- Prevent peaks becoming infinitely broad and correlating with background
- Unbiased way to refine data?



Example 2 – Proton Migration

285 K

- Subtle structural change in the organic solid state
- 3,5 pyridine dicarboxylic acid (3,5 PDCA)

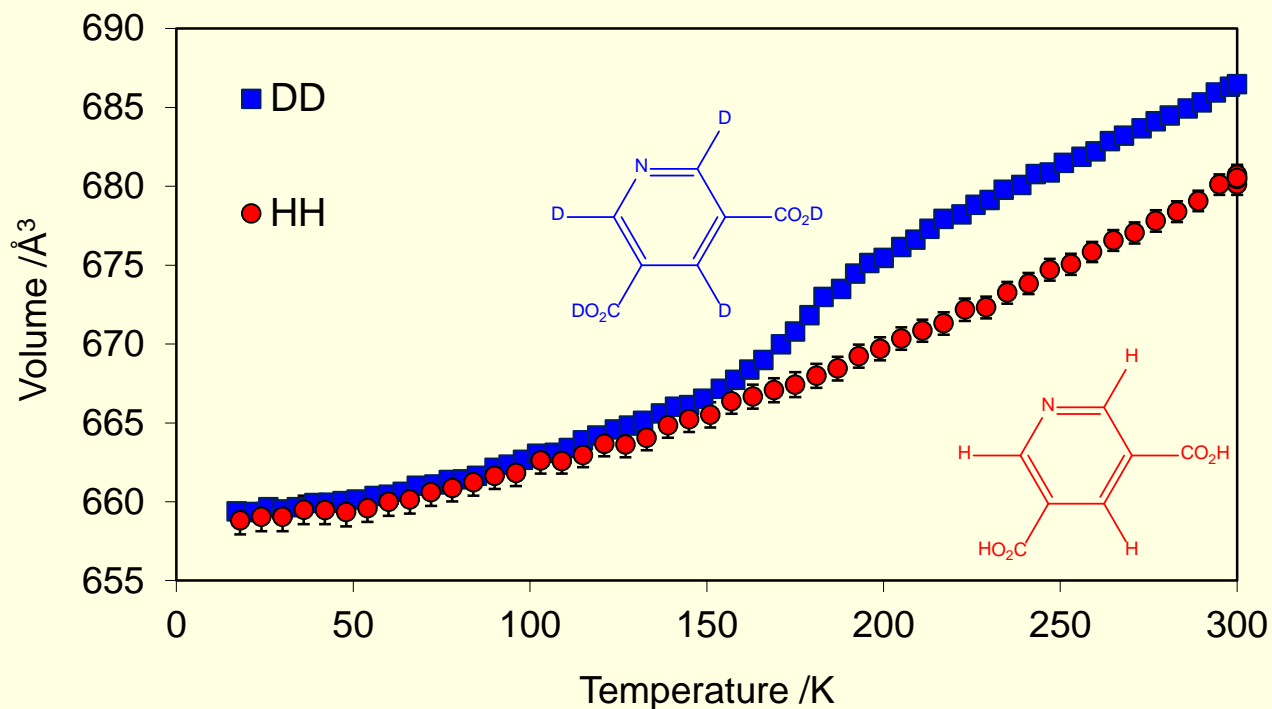


15 K



285 K

- 3,5 pyridine dicarboxylic acid
- Unusual difference between cell volumes of H and D isotopologues

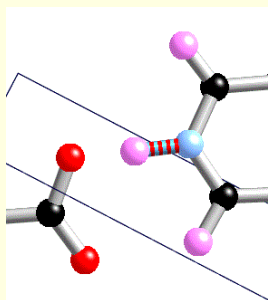
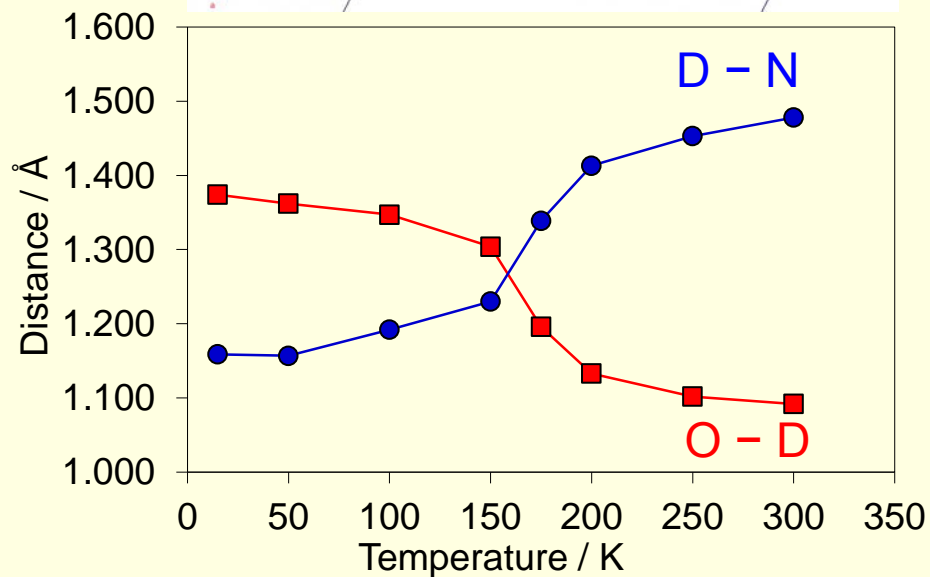
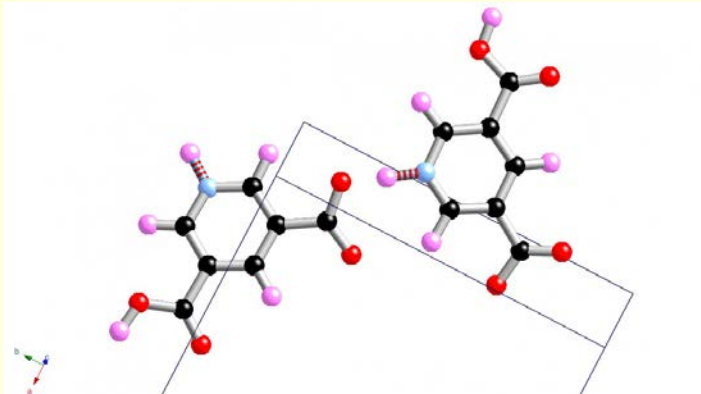


15 K

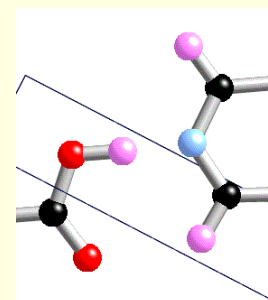


Single Crystal neutron diffraction

285 K



O D - N

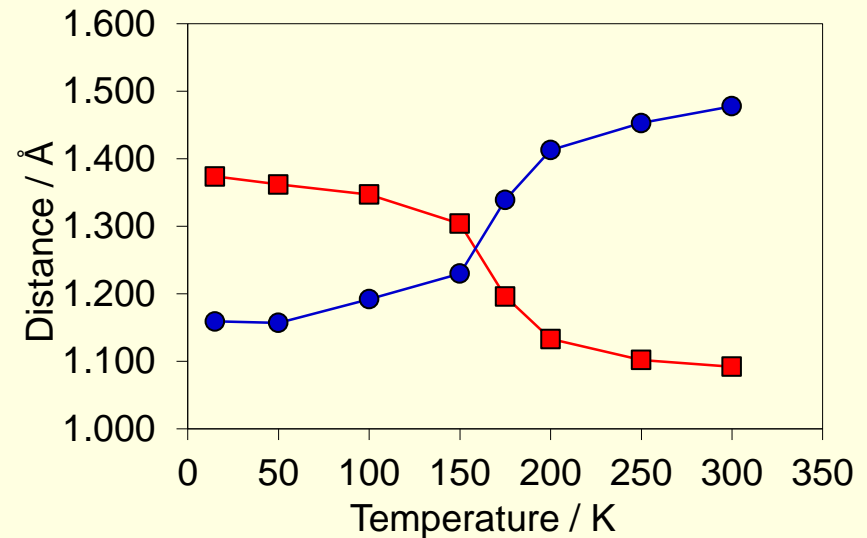
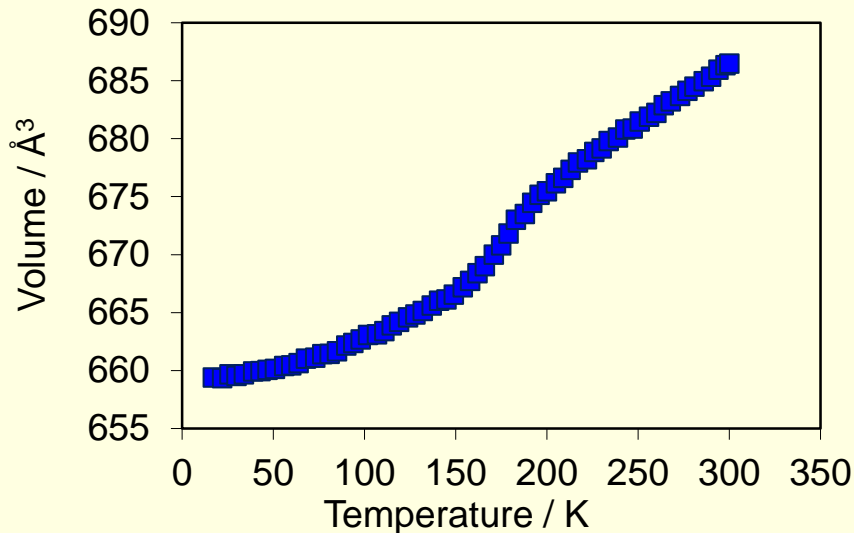


O - D N

15 K



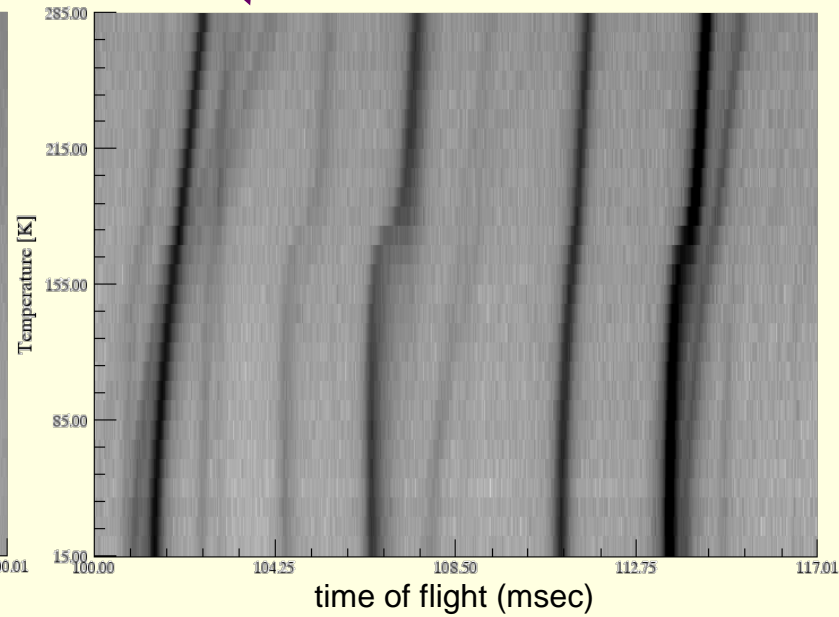
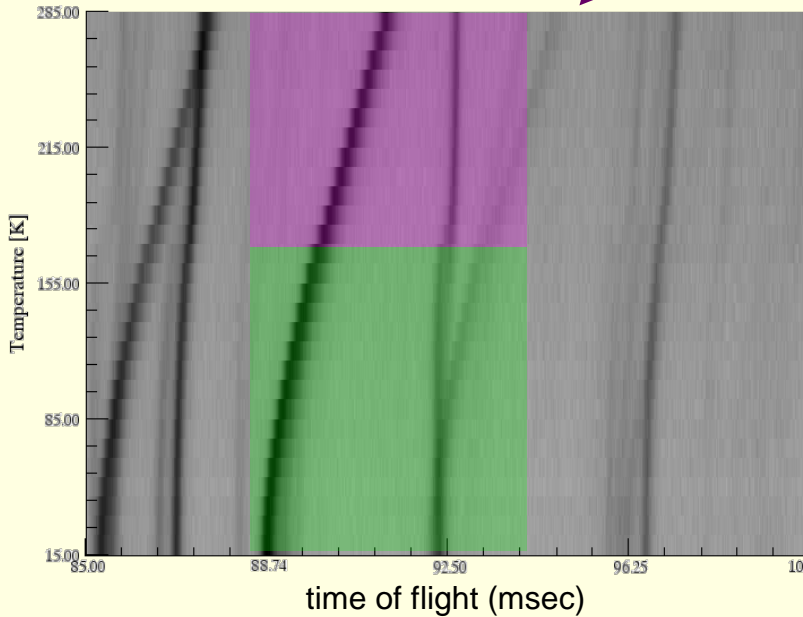
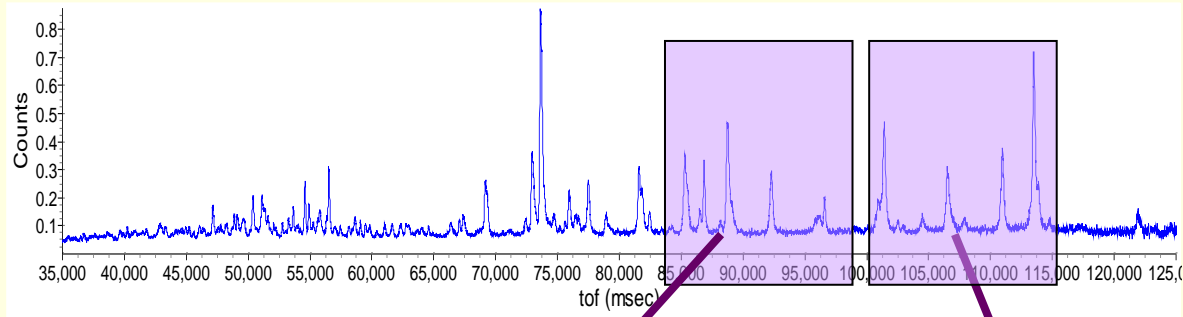
- Smooth effect or sharp phase transition?
- 1st or 2nd order?
- Isosymmetric phase transition



HRPD Observed Powder Data



285 K

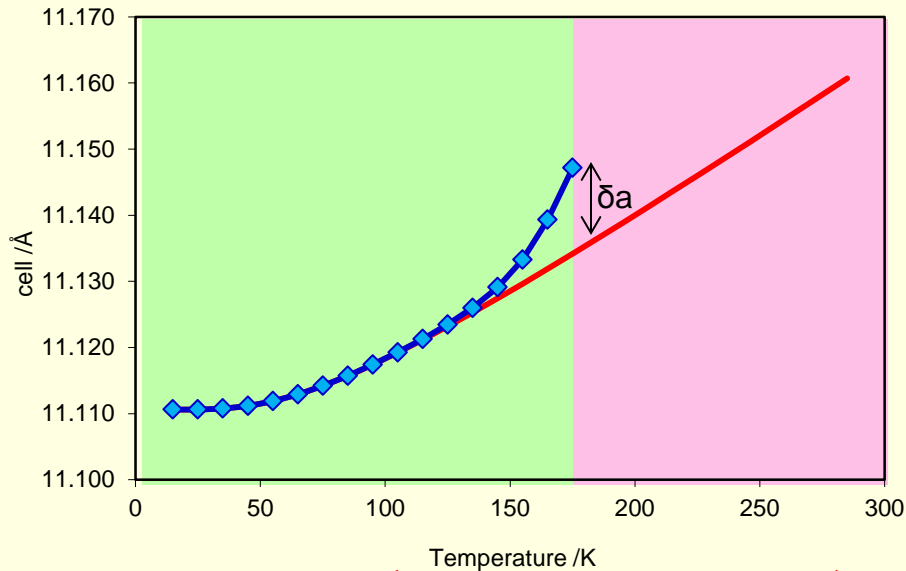


15 K



285 K

- 2 phase Rietveld refinement
- Assume each phase has a smooth evolution of cell parameters away from T_c
- Allow a critical excess cell close to T_c



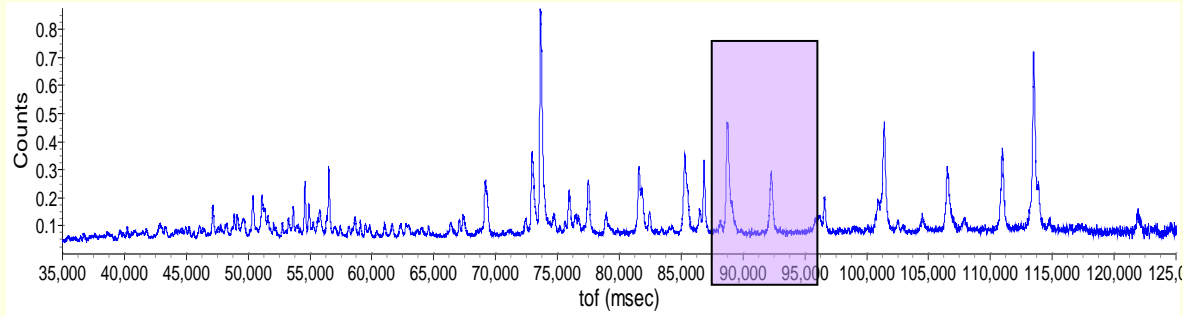
$$a(T) = \text{Exp} \left(\ln(a_0) + \frac{c_1 \theta_1}{\exp(\theta_1/T) - 1} \right) + c_2 \exp(-c_3 |T - T_c|^\beta)$$

15 K

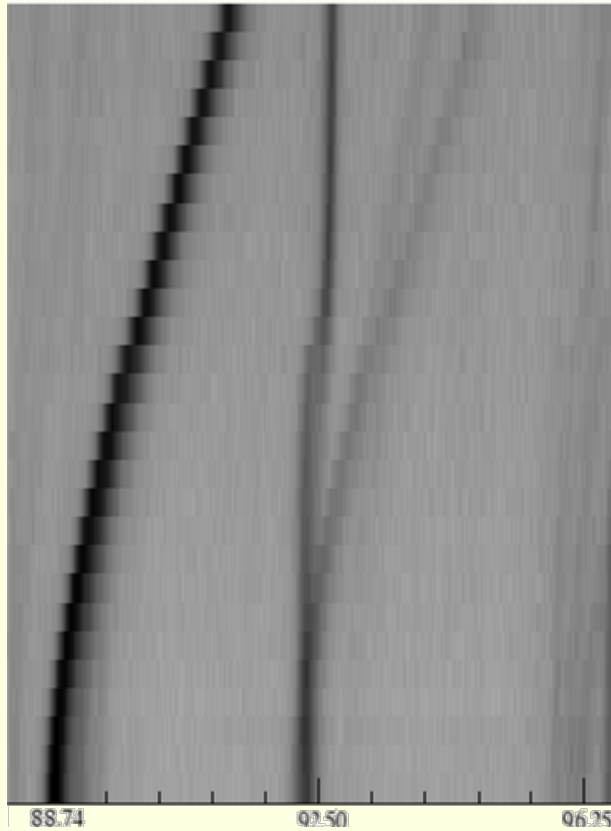
Surface Rietveld



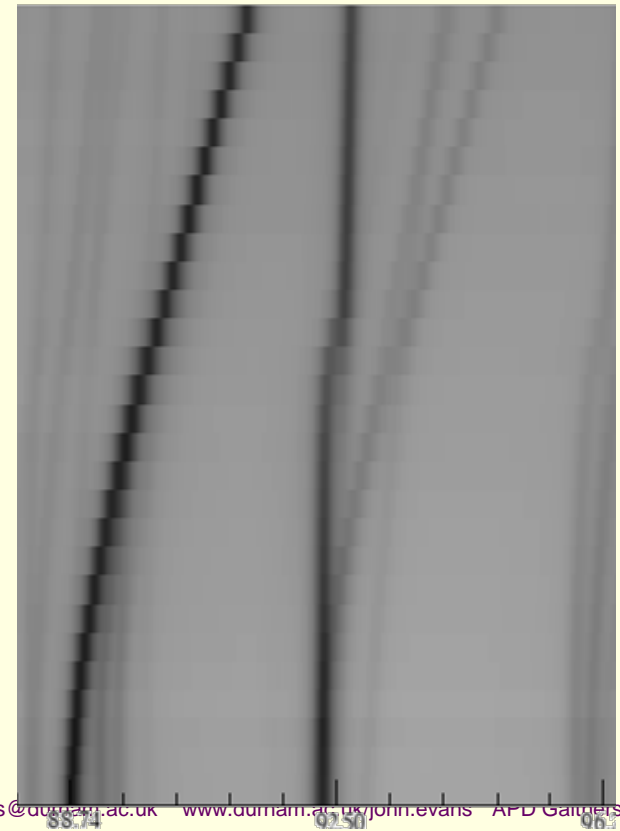
285 K



observed



calculated



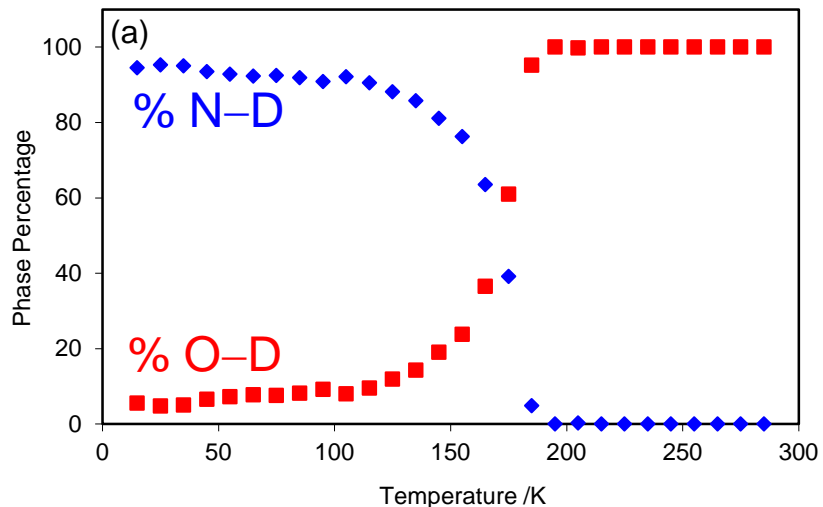
15 K



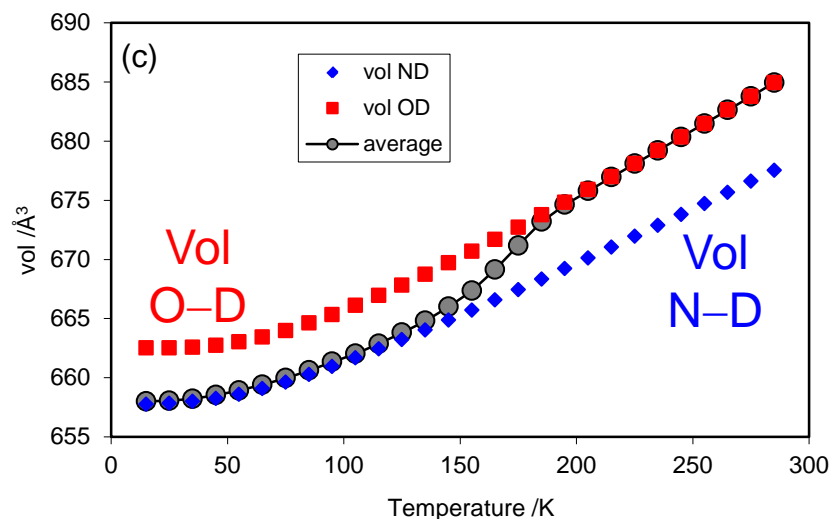
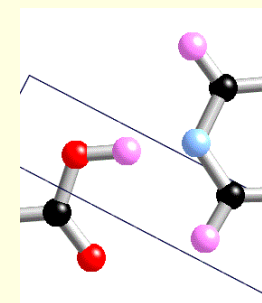
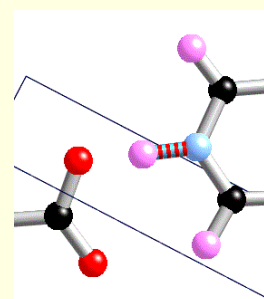
Results - 1



285 K



Phase Fractions

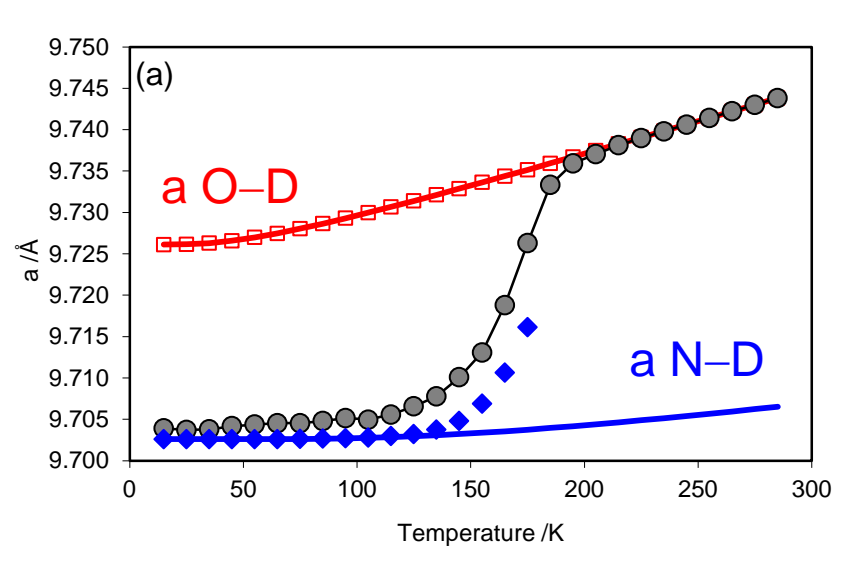


Cell Volumes

15 K

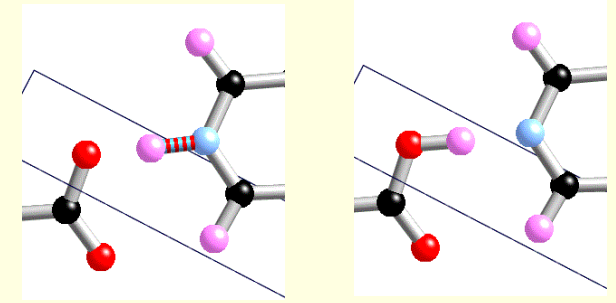
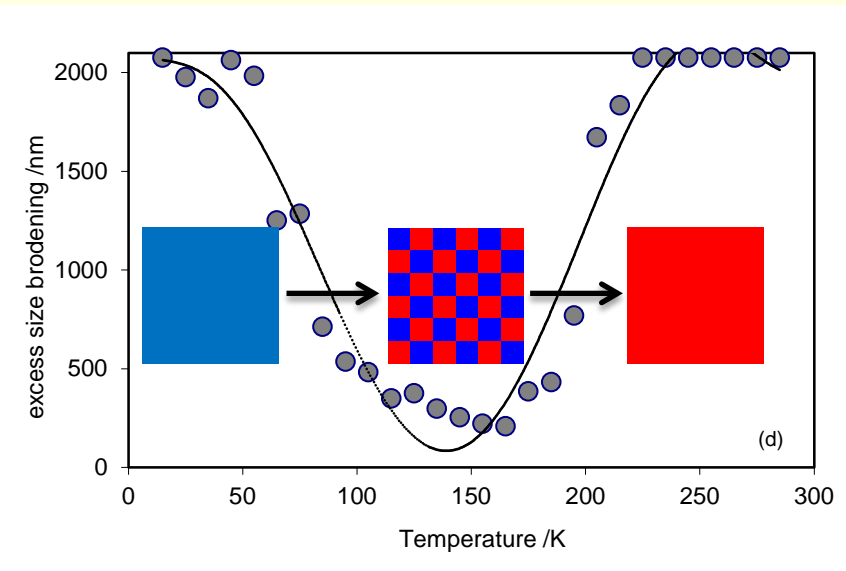


285 K



Unit cell param a

15 K



N-D

O-D

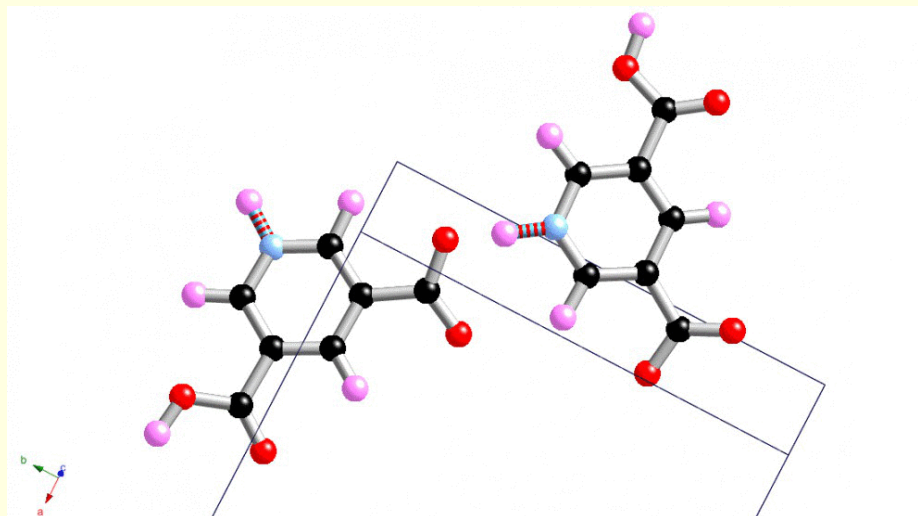
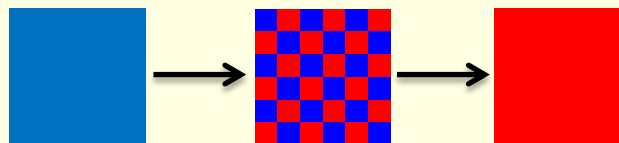
Size broadening



3,5-PDCA Summary

285 K

- 3,5 pyridine carboxylic acid
- Unusual proton migration
- Unusual isotopologue polymorphism



15 K



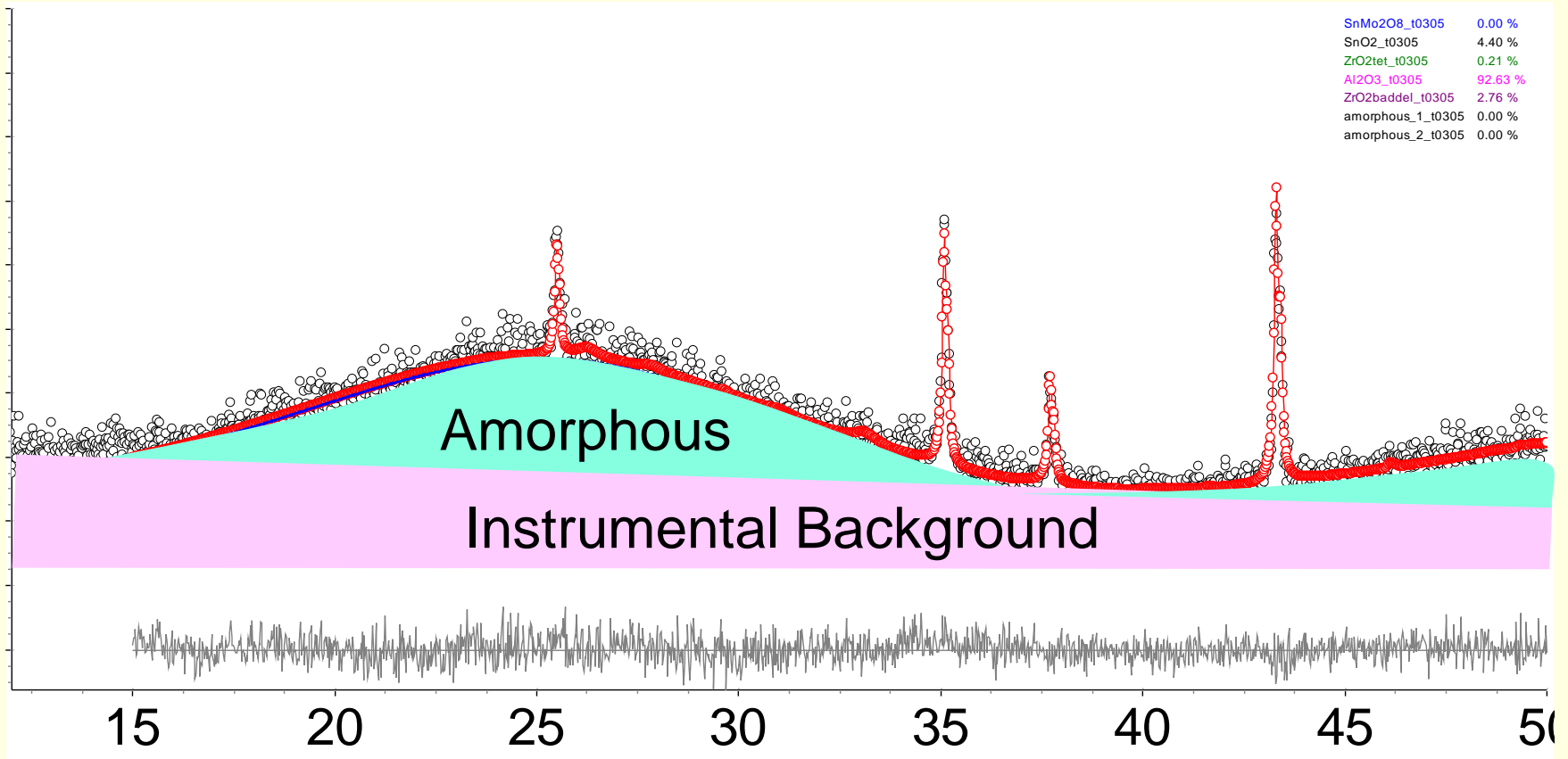
Example 3 – in situ synthesis



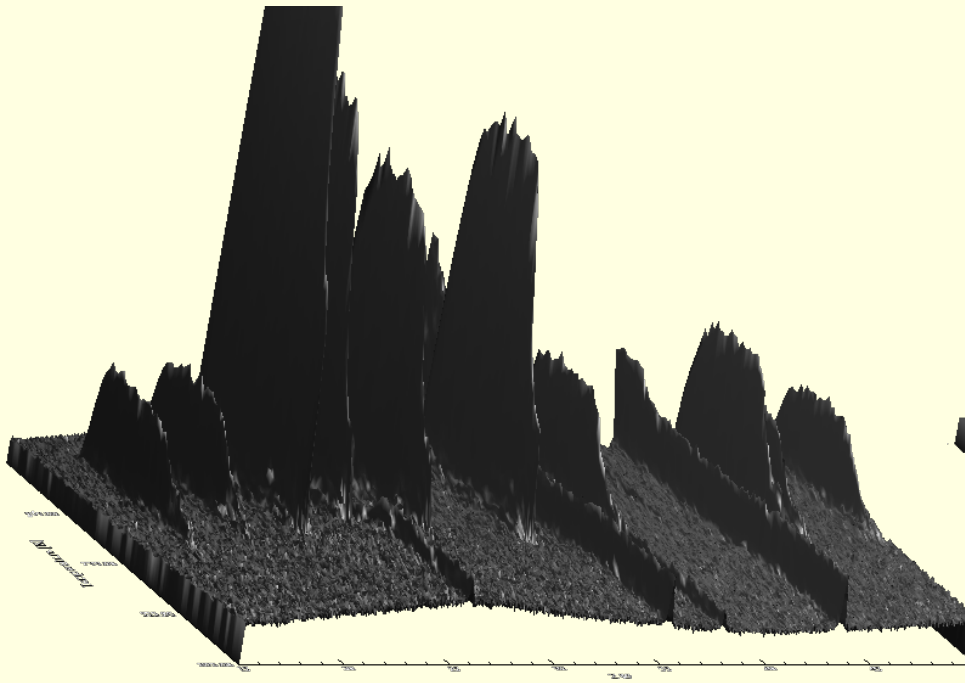
- Lab data following in situ synthesis
- Short 2-theta range
- Relatively quick data collections
- Several hundred data sets on each of 10 compositions
- Need to quantify several crystalline phases
- Need to quantify amorphous content



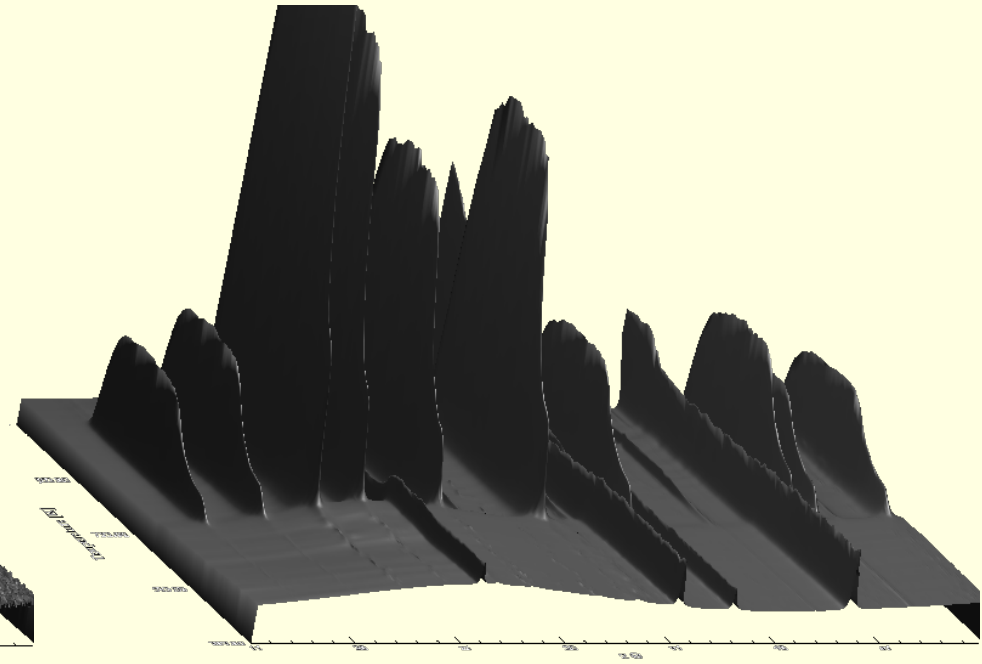
Quantify Amorphous Background?



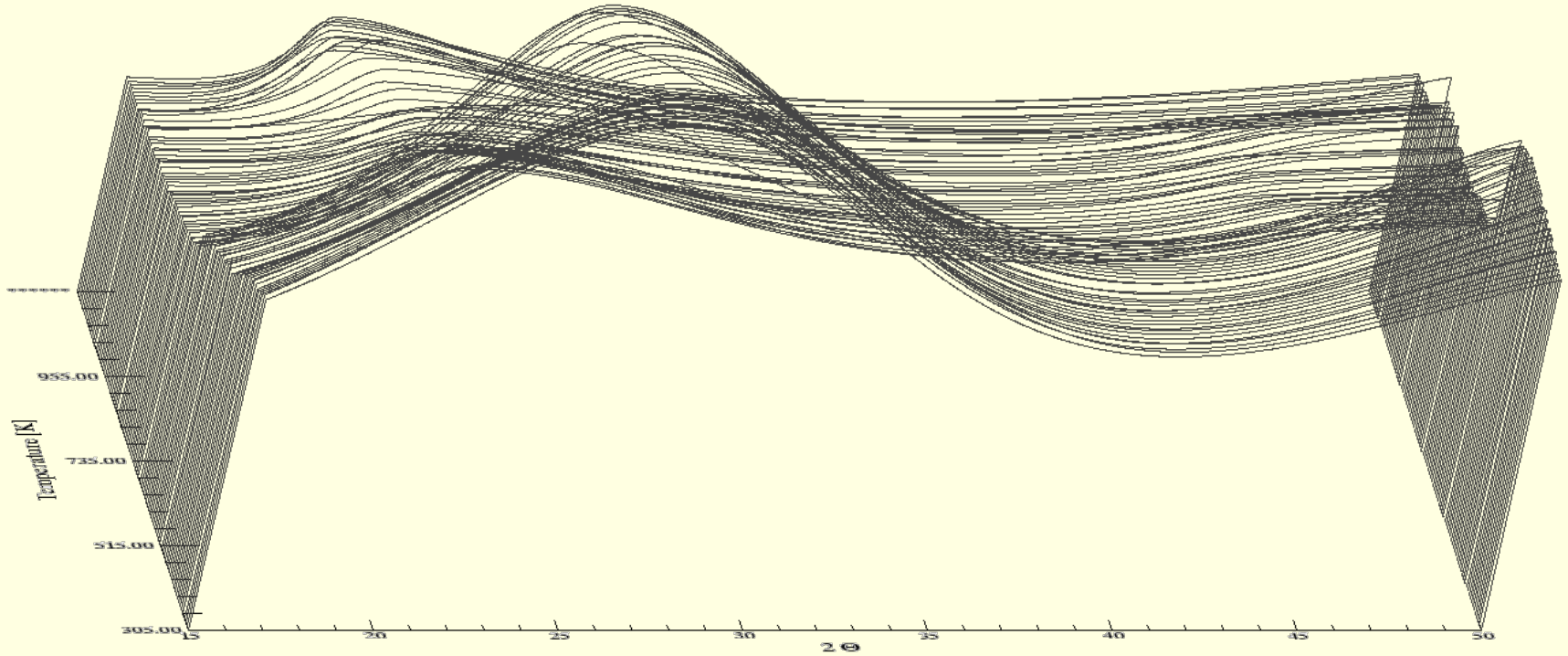
- Separate instrumental and amorphous (sample + diffuse) contributions to background?



observed



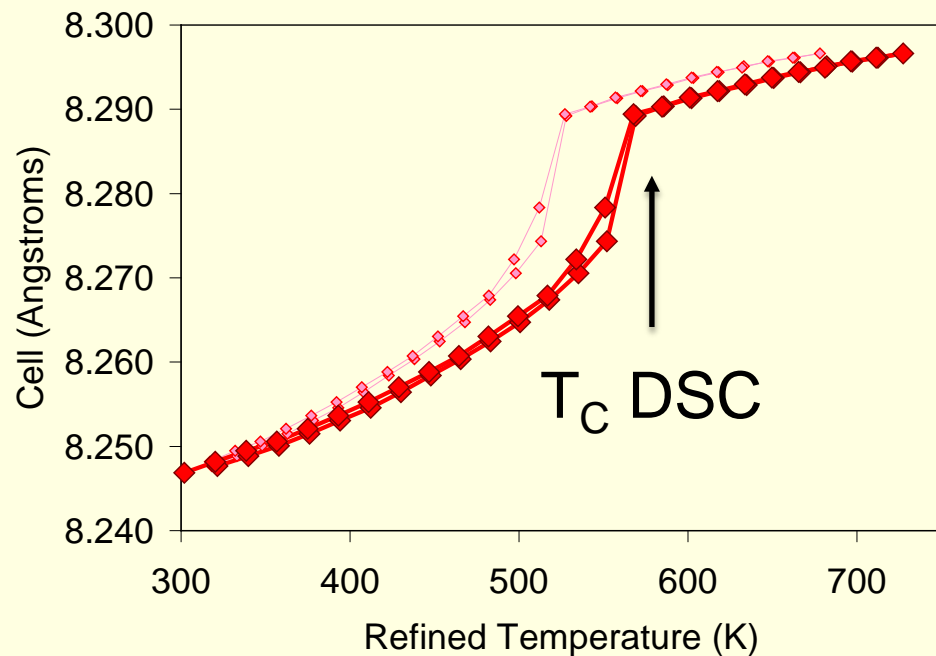
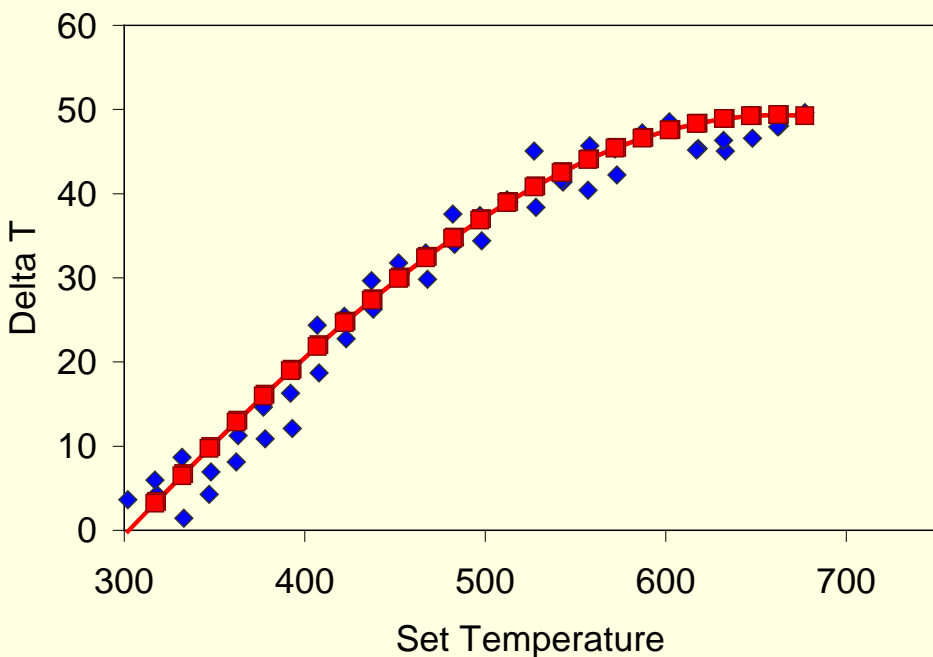
calculated



Overall + Individually refined background



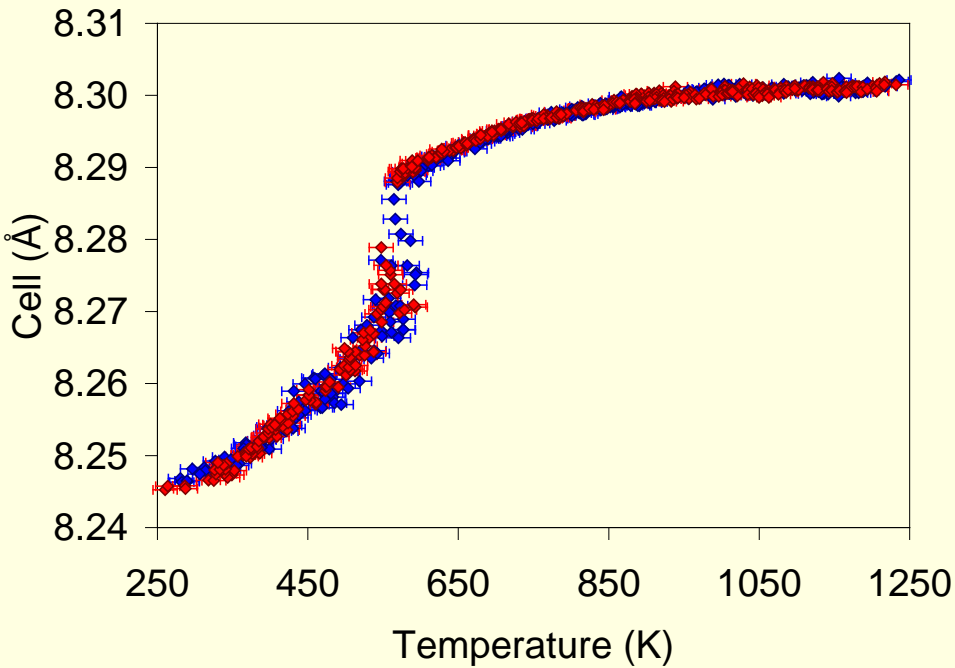
Temperature Calibration/Internal Standards



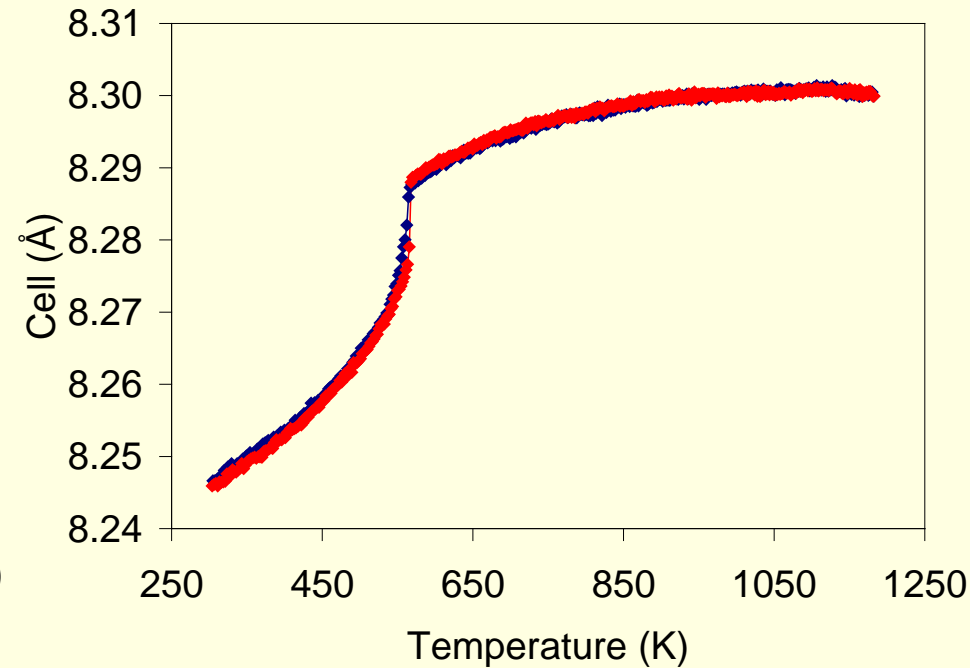
ΔT fit all data sets
 ΔT individual data sets

X-ray $T_C < 567$ K
DSC $T_C = 565$ K

Better Precision from Bad Data”



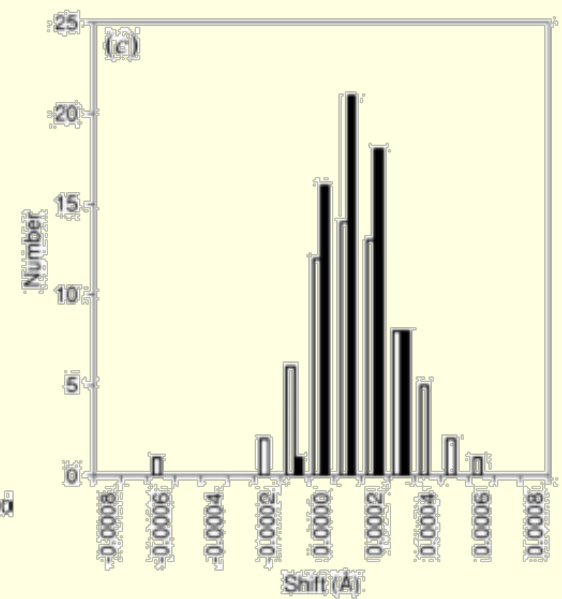
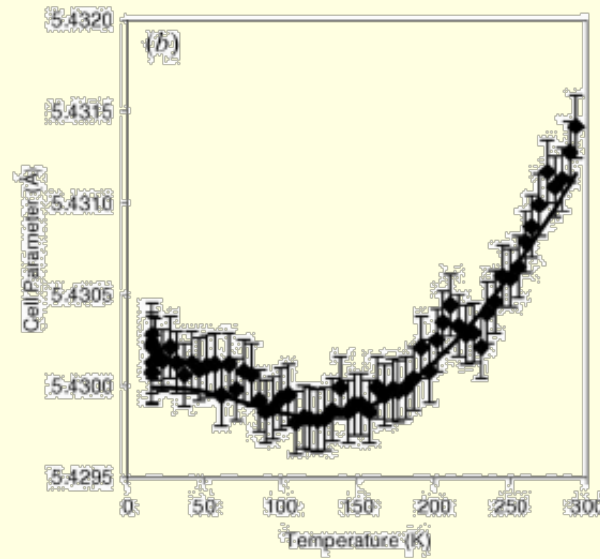
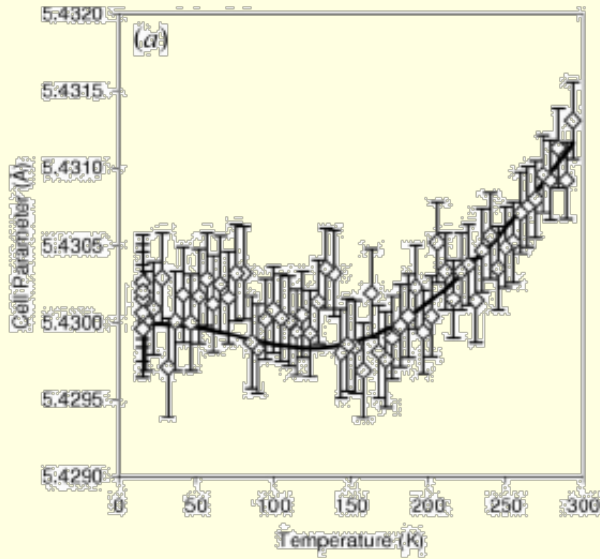
Individual Fitting
4.75 minutes



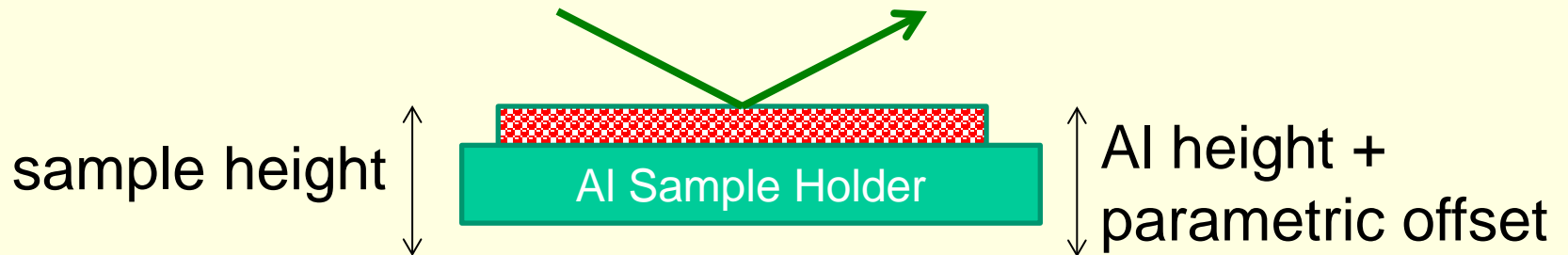
Surface Fitting
871*4.75 minutes
(~3 days)



Better Precision from Data



Parameterising sample height offset improves precision
Average esd 0.00028 to 0.00017 Å





When/What Should you Parameterise?

- When should you parameterise?
 - Rarely.....5-10% of systems?
 - When you have poor data
 - When you have significant correlations
 - When you know the wrong answer
 - When you want to quickly test a model against 1000s of data sets
 - When you want to test if you're assumption is right/wrong
- What should you parameterise?
 - Information you're not particularly interested in
 - Information for which you're sure of model to apply



Acknowledgements!



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