Modelling the PDF of Crystalline Materials with RMCProfile

Dr Helen Yvonne Playford

STFC ISIS Facility, Rutherford Appleton Laboratory, Didcot, UK

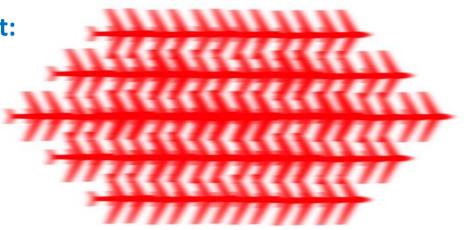
China Spallation Neutron Source

Institute of High Energy Physics, Dongguan, China 7th November 2016



Local and Average Viewpoints

Average viewpoint:

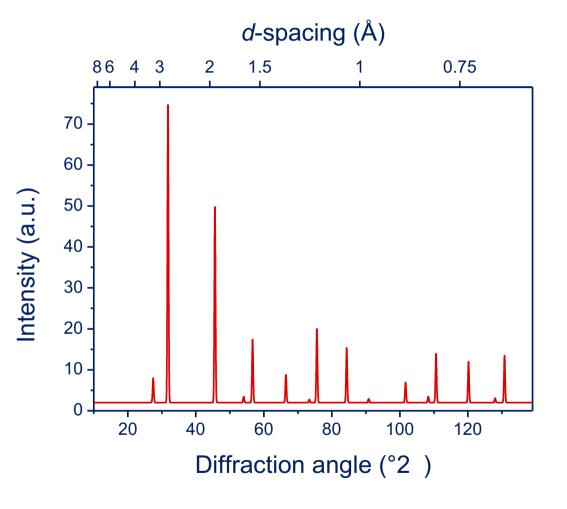




Local viewpoint:



Diffraction as a Structural Probe

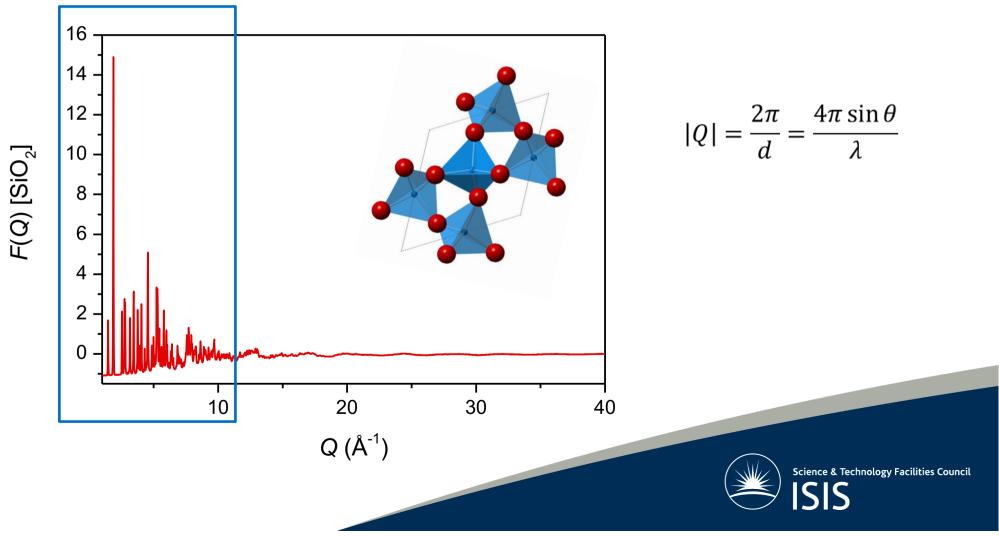


Information contained in a diffraction pattern:

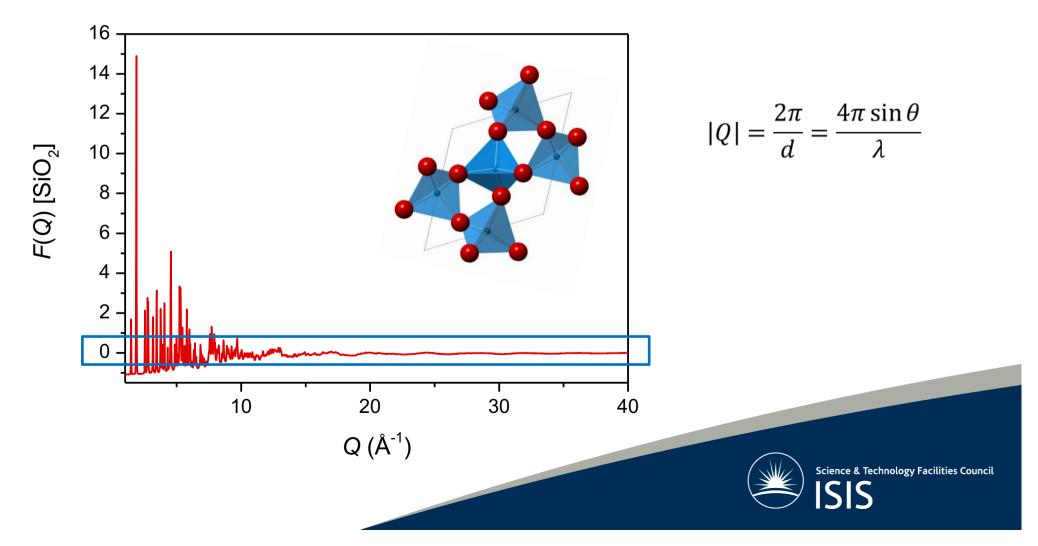
- Size and shape of unit cell (peak positions)
- Symmetry within the unit cell (absences)
- Contents of the unit cell (relative intensities)
- Thermal motion
- Particle size
- Strain
- Texture



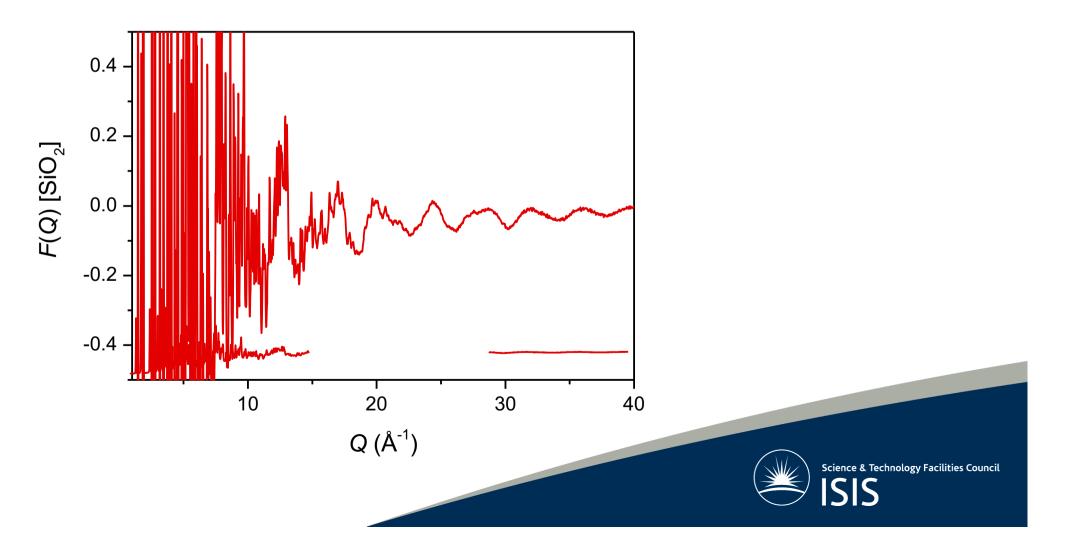
What is total scattering?



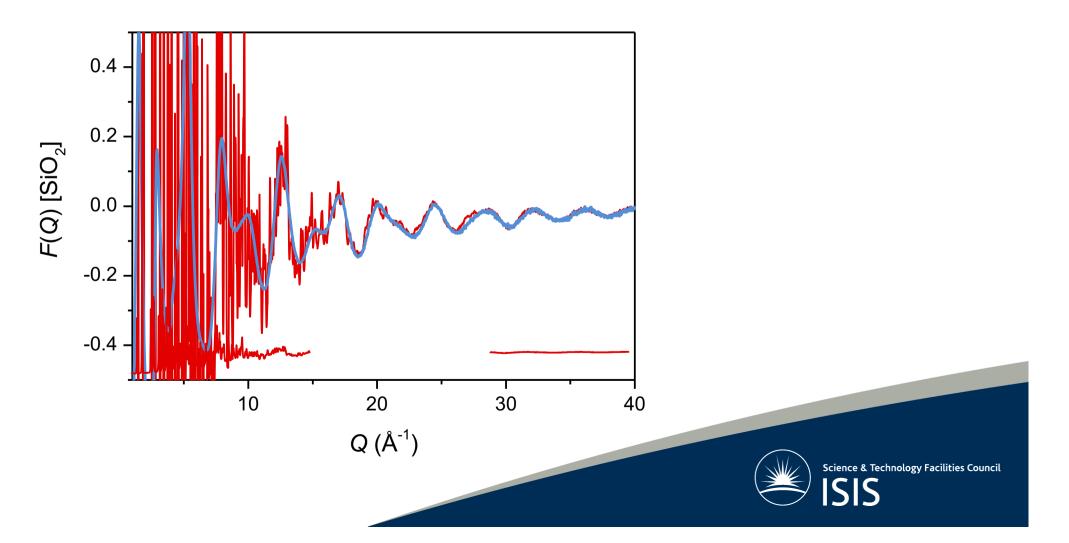
What is total scattering?



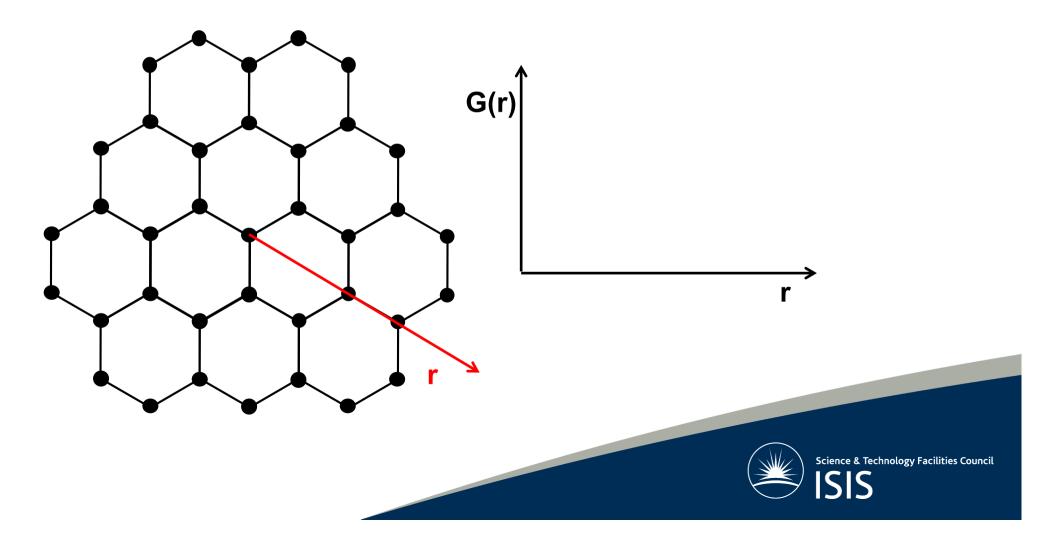
What is total scattering?



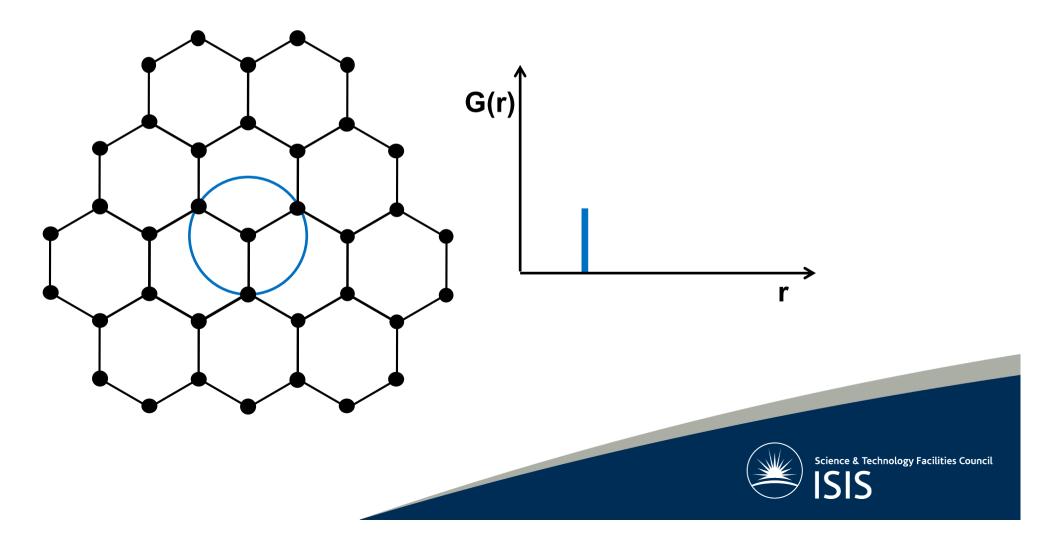
What is total scattering?



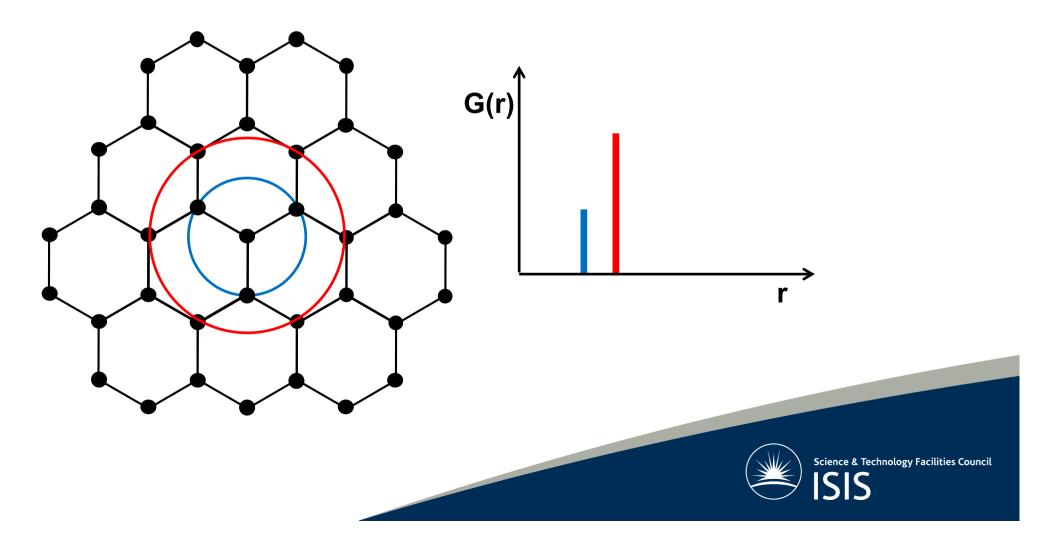
The pair distribution function (PDF)



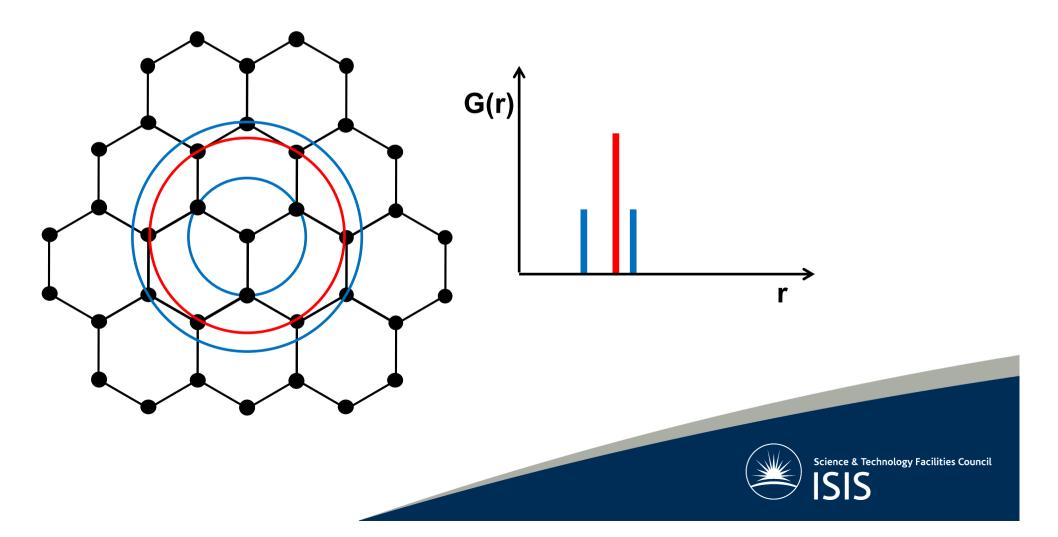
The pair distribution function (PDF)



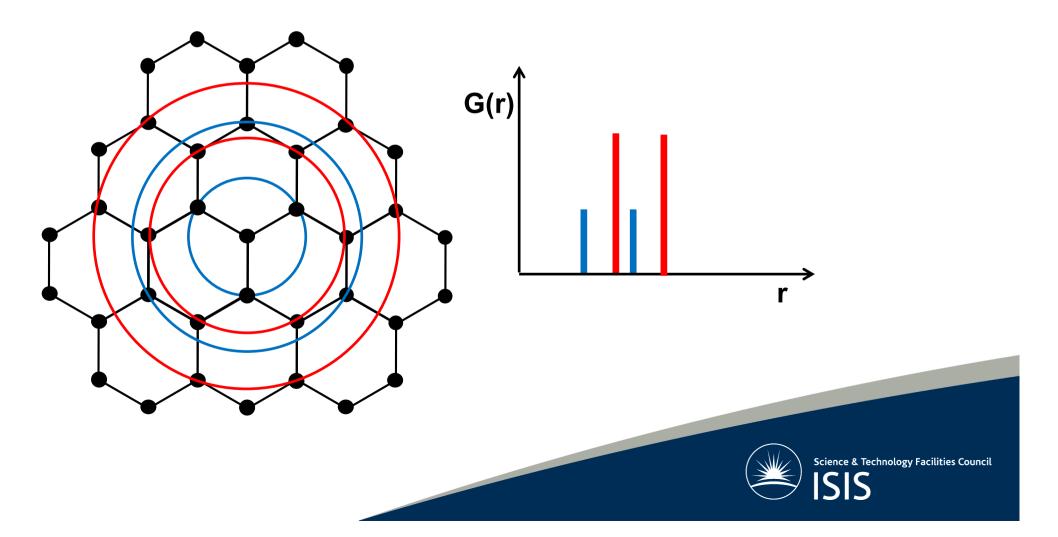
The pair distribution function (PDF)



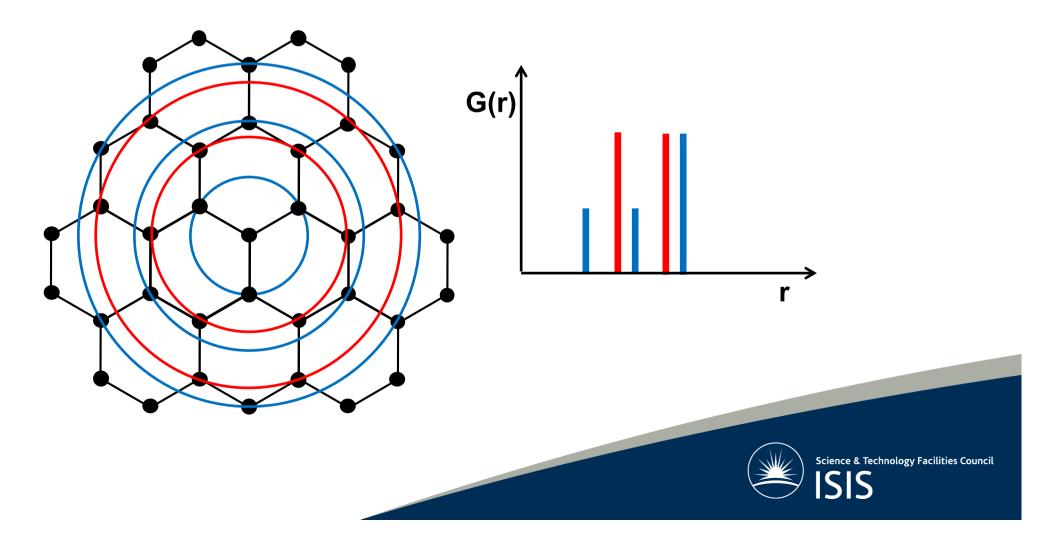
The pair distribution function (PDF)



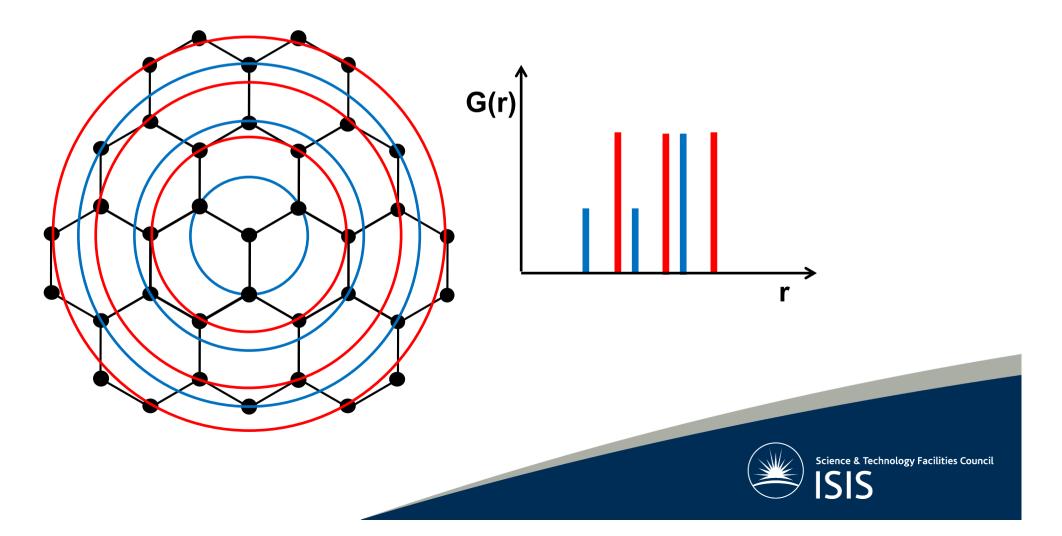
The pair distribution function (PDF)



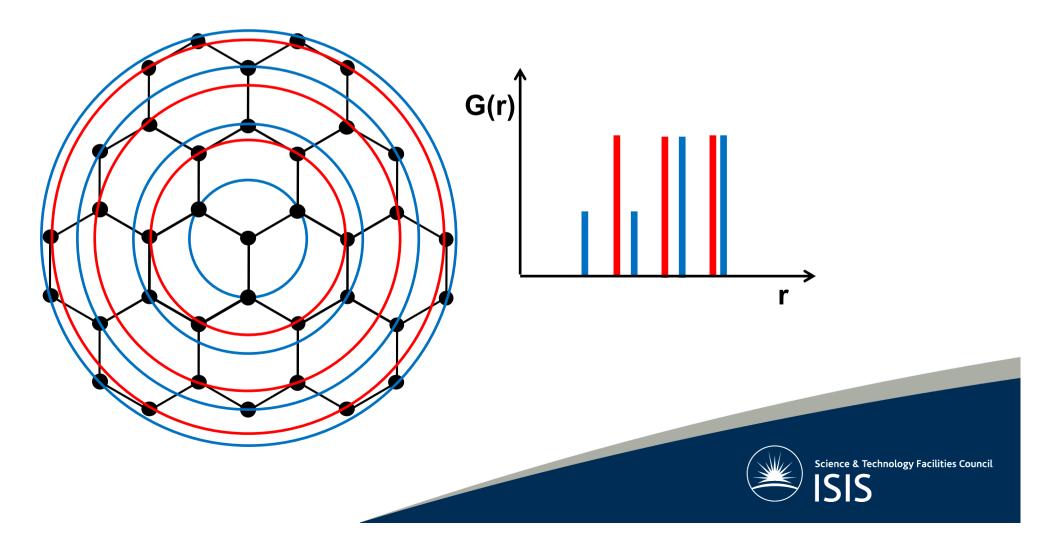
The pair distribution function (PDF)

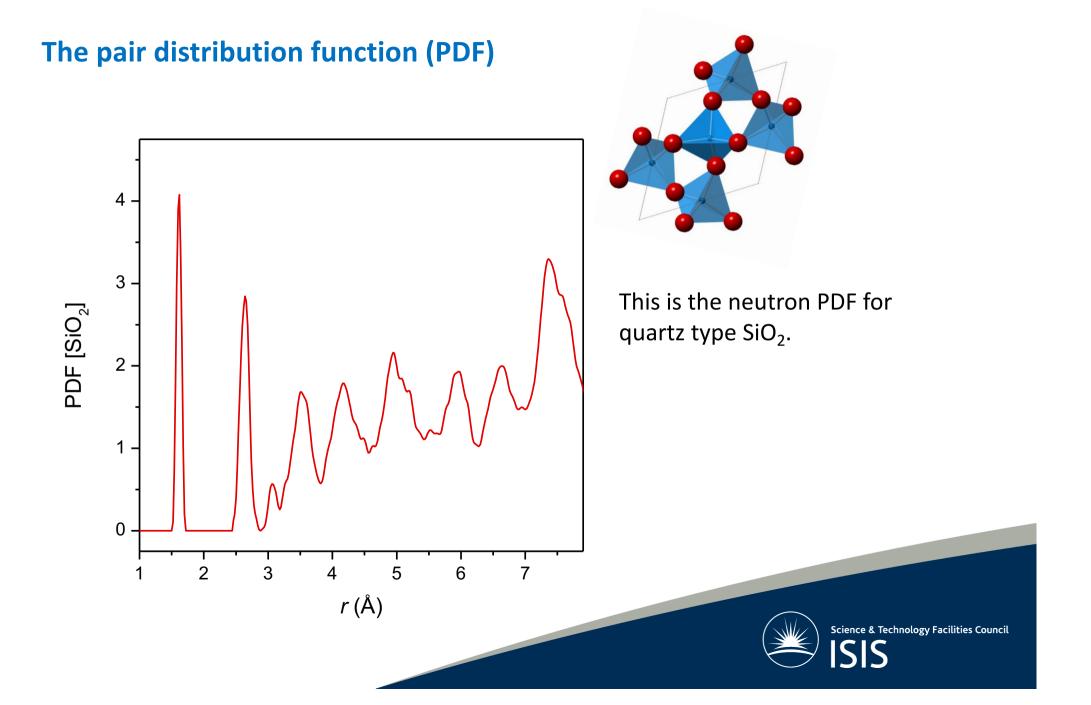


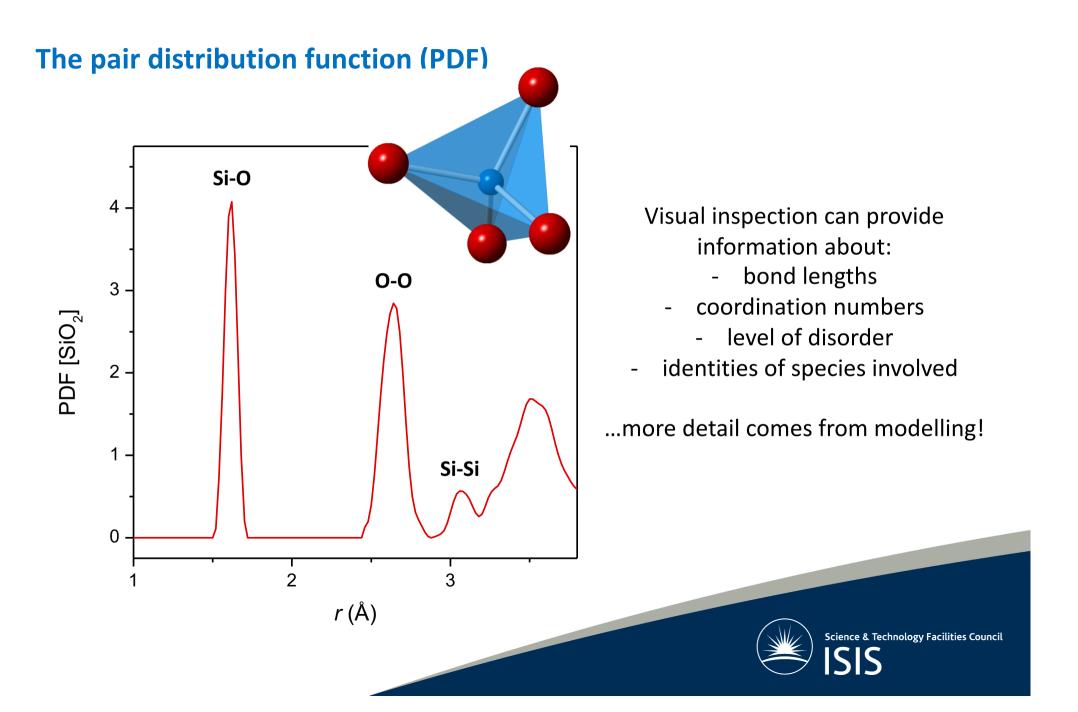
The pair distribution function (PDF)

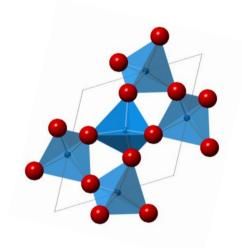


The pair distribution function (PDF)





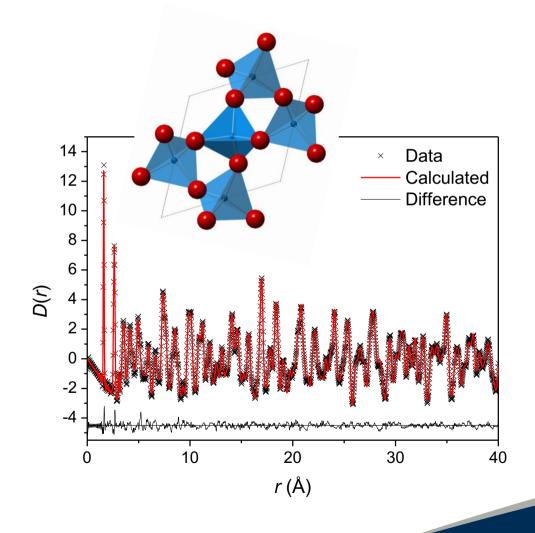






Modelling techniques

There are two main ways in which detailed structural information can be extracted from total scattering data: <u>small box</u> and big box modelling.



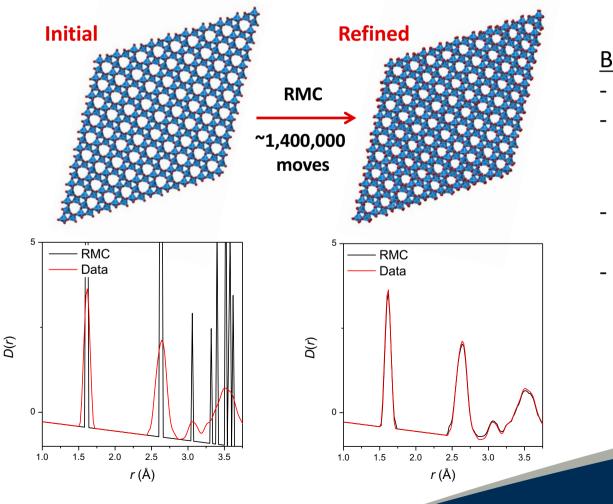
Small box modelling:

- Crystal structure refined to fit the PDF: "real-space Rietveld".
- Limited to crystallographic descriptions of structural parameters.
- Identify discrepancies between average and local structure.



Modelling techniques

There are two main ways in which detailed structural information can be extracted from total scattering data: small box and <u>big box</u> modelling.



Big box modelling:

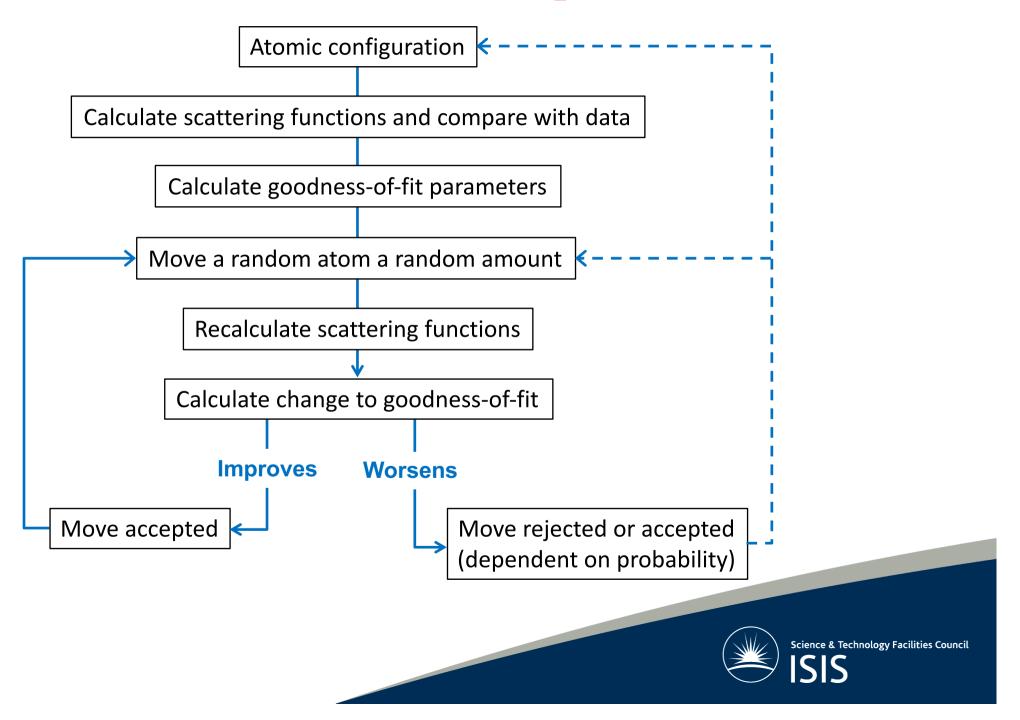
- Reverse Monte Carlo (RMC).
- Supercell of >10,000 atoms, moved at random to obtain best possible agreement with all data.
- Atomistic model that is consistent with average and local structure.

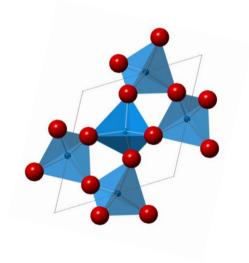
Science & Technology Facilities Council

SIS

- Not constrained by symmetry.

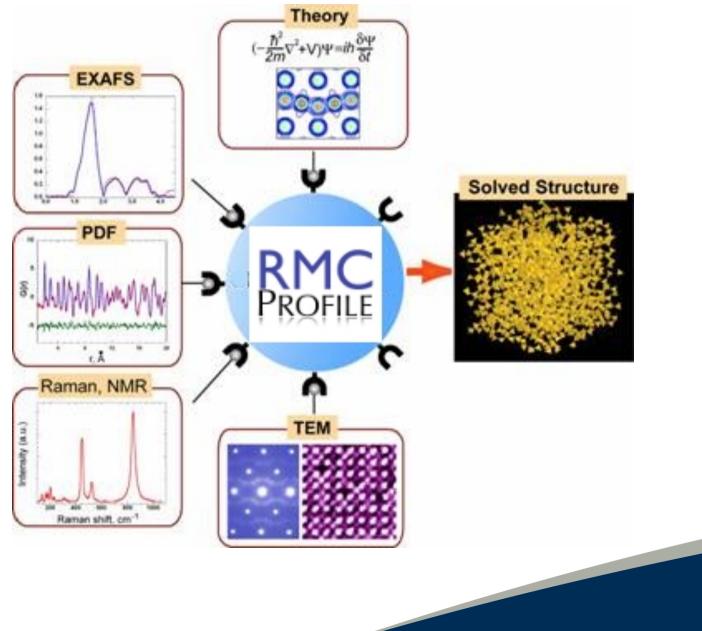
The Reverse Monte Carlo Technique





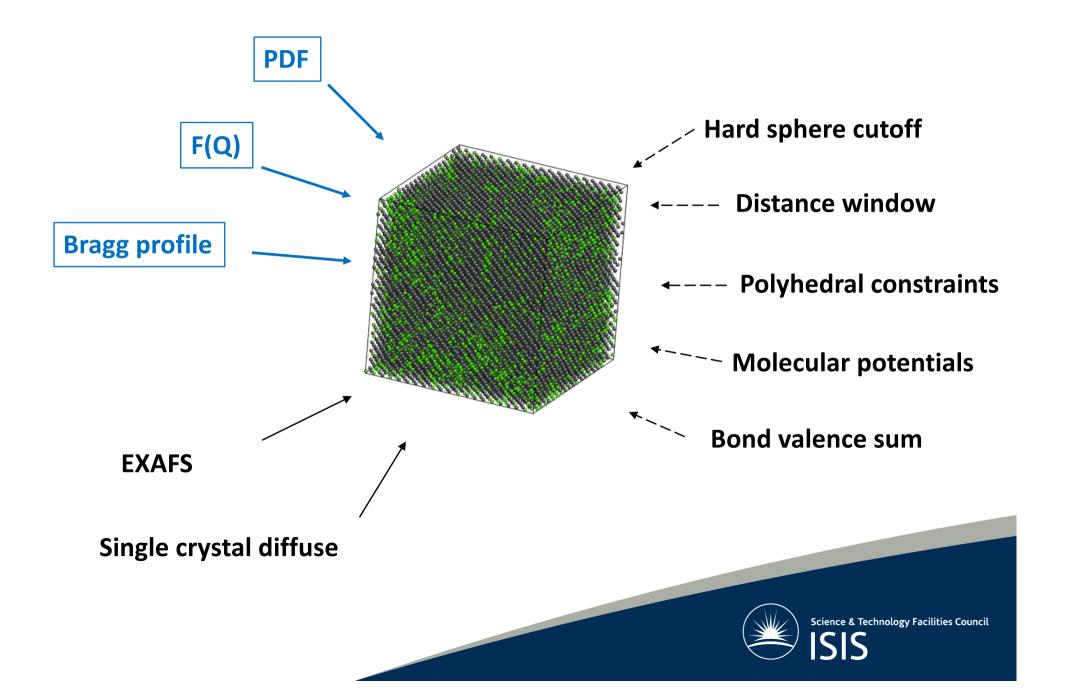
- Implementation of the RMC algorithm particularly suited to crystalline materials.
- "Profile" refers to the Bragg profile a very important constraint for average structure.
- Based on the original RMCA code of McGreevy and Puzstai, extended by Matt Tucker (now at ORNL).
- Developers: Dave Keen (ISIS), Martin Dove (QMUL), Andrew Goodwin (Oxford), Helen Playford (ISIS), Wojciech Slawinski (ISIS), and many others.
- The program is available online at <u>www.rmcprofile.org</u>
- It can fit multiple datasets (X-ray and neutron PDF, F(Q), Bragg)...
- ...and use "chemical sense" in the application of appropriate constraints.





Adapted from: S. J. L. Billinge and I. Levin, *Science*, 2007, **316**, 561–565.





Requirements for successful RMCProfile refinement:

- Quality data
- Multiple datasets
- Single phase sample*
- Good powder average**
- Average structure well-characterised
- Understanding of structural chemistry
- Targeted analysis of refined configurations



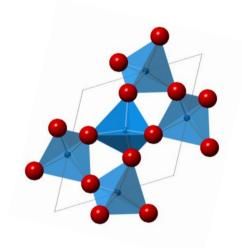
• RMCProfile 6.6

- developed at ISIS by Wojciech Slawinski
- arbitrary scattering length inputs
- multiple atom swapping
- bugfixes
- usability improvements
- release date: ASAP

• RMCProfile 7.0 *

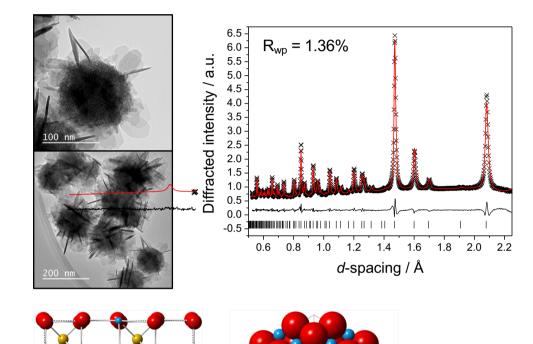
- being developed at ISIS by Wojciech Slawinski
- big news: multiphase RMC (multiple 'boxes' of atoms)
- currently in need of input from users and colleagues
- (beta) release date: February 2017
- RMCProfile 7.1 and later **
 - incorporation of small-box modelling (with colleagues at SNS)
 - developments for nanoparticles, low-dimensional systems & networks (with QMUL and University of Oxford)
 - release date: future







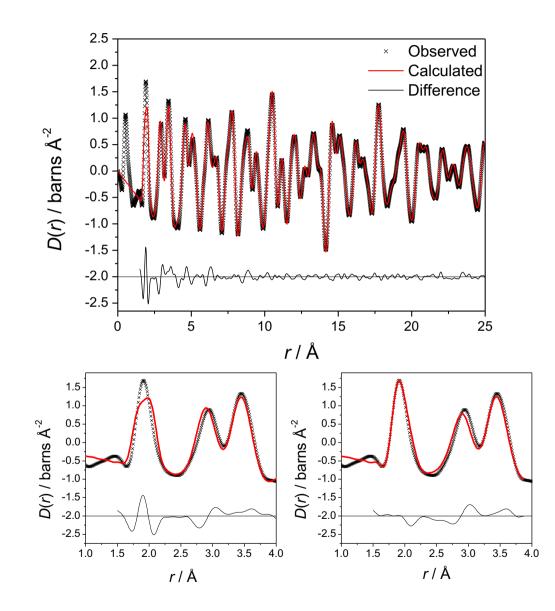
A disordered polymorph of Ga₂O₃



- Potential photocatalyst and catalyst support
- Structure poorly understood
- Cubic spinel structure
- Rietveld refinement reveals four partially occupied Ga sites
- Nanocrystalline

H. Y. Playford, A. C. Hannon, E. R. Barney, and R. I. Walton, *Chem. Eur. J.*, 2013, **19**, 2803–2813.

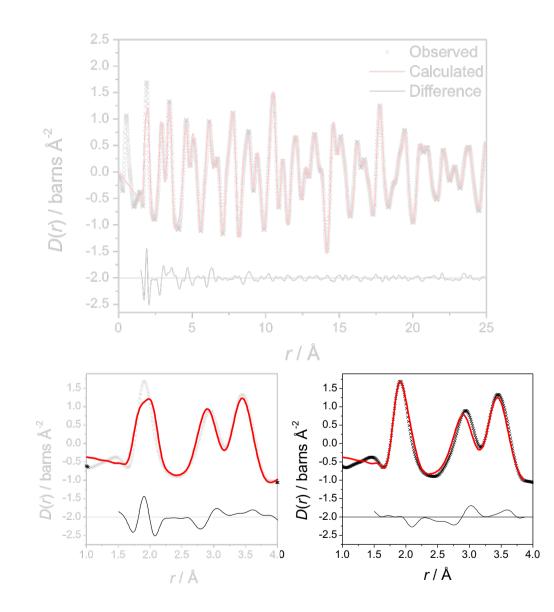




- Small-box modelling of the PDF
- Medium-to-high r agrees well with average crystal structure
- Large discrepancies in local structure
- Improved fit when lower symmetry model is used, but it is a purely local effect

H. Y. Playford, et al., J. Phys. Chem. C, 2014, 118, 16188-16198.

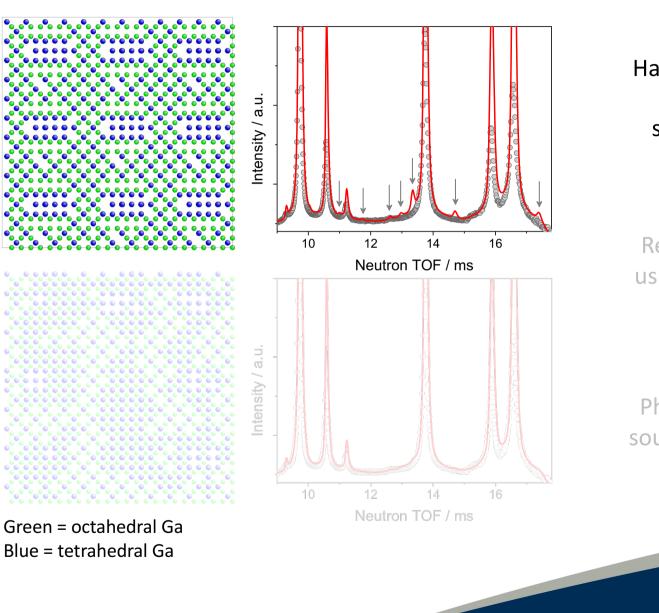




- Small-box modelling of the PDF
- Medium-to-high *r* agrees well with average crystal structure
- Large discrepancies in local structure
- Improved fit when lower symmetry model is used, but it is a purely local effect

H. Y. Playford, *et al., J. Phys. Chem. C*, 2014, **118**, 16188–16198.

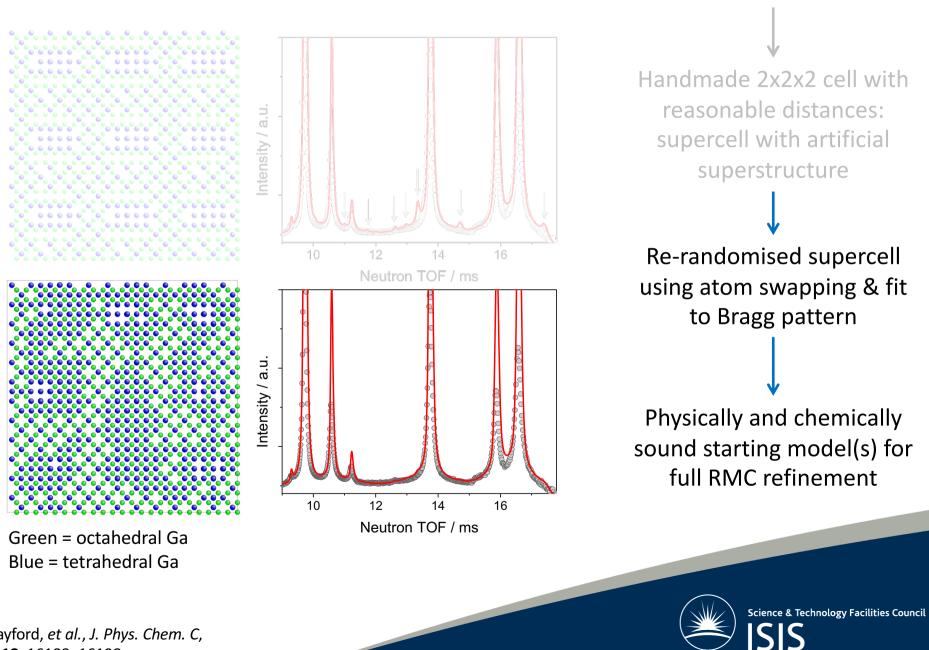




Random starting model: Ga-Ga < 1Å Handmade 2x2x2 cell with reasonable distances: supercell with artificial superstructure Re-randomised supercell using atom swapping & fit to Bragg pattern Physically and chemically sound starting model(s) for full RMC refinement

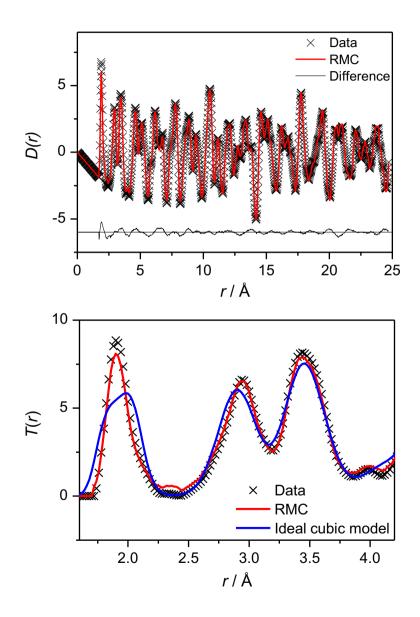


Science & Technology Facilities Council



Random starting model:

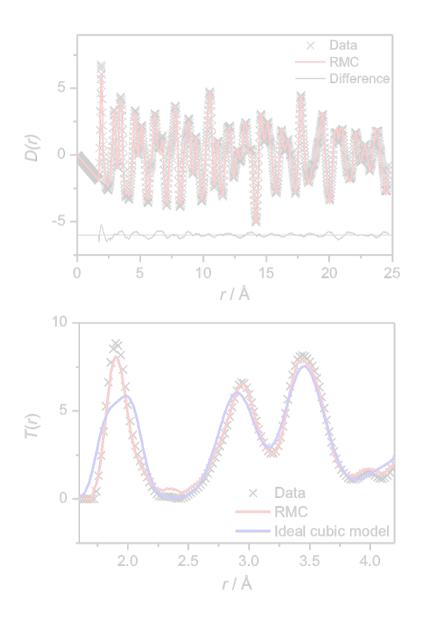
Ga-Ga < 1Å



RMC refinement using 6x6x6 supercell

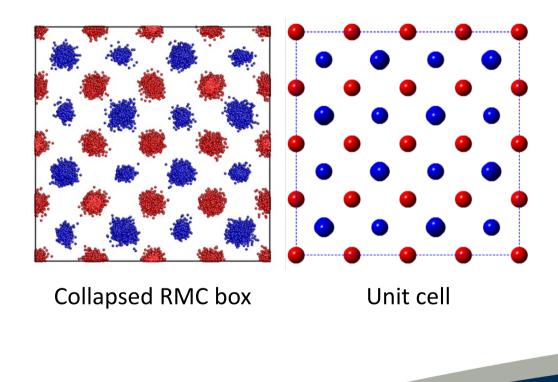
- vastly improved fit to local structure





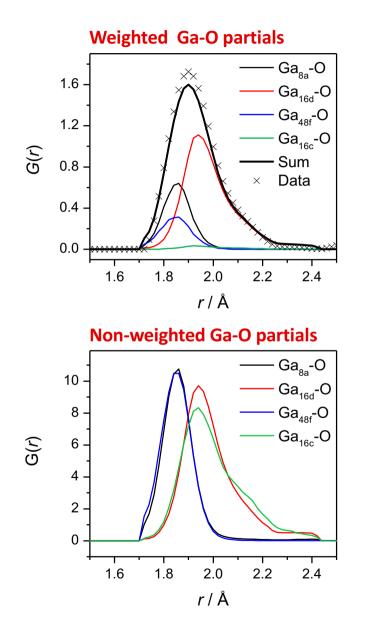
RMC refinement using 6x6x6 supercell

- vastly improved fit to local structure
- maintains correct average



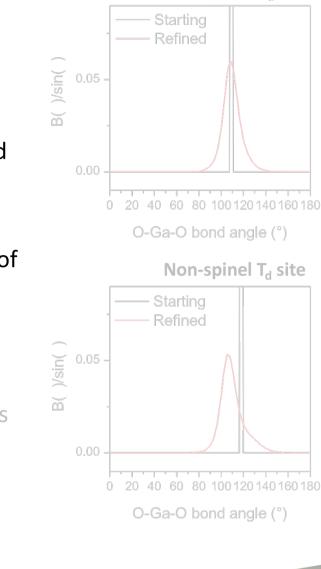


Science & Technology Facilities Council



RMC provides bond length and angle distributions:

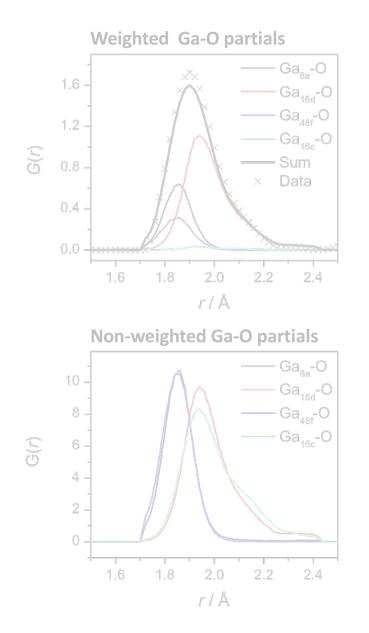
- these distributions are the sum of 200 refined "boxes of atoms"
- the O_h sites are highly distorted
- the crystal structure defines two very different T_d sites
- but locally these sites are very similar



Spinel T_d site

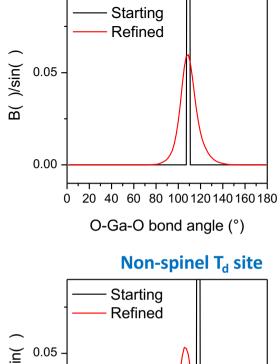


Science & Technology Facilities Council

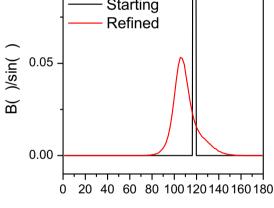


RMC provides bond length and angle distributions:

- these distributions are the sum of 200 refined "boxes of atoms"
- the O_h sites are highly distorted
- the crystal structure defines two very different T_d sites
- but locally these sites are very similar



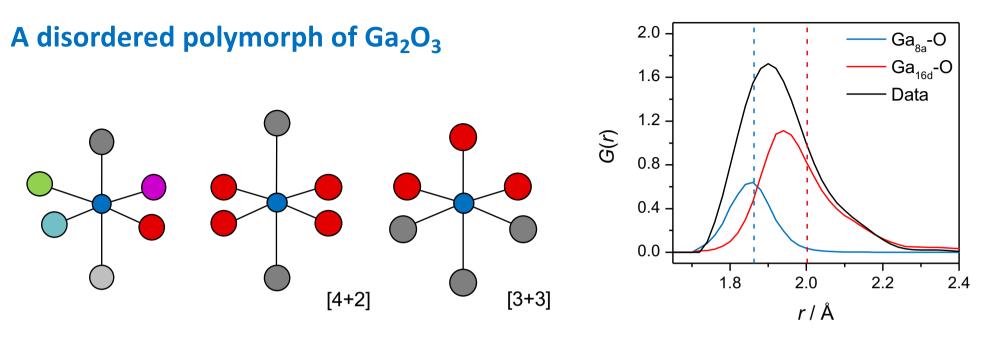
Spinel T_d site



O-Ga-O bond angle (°)



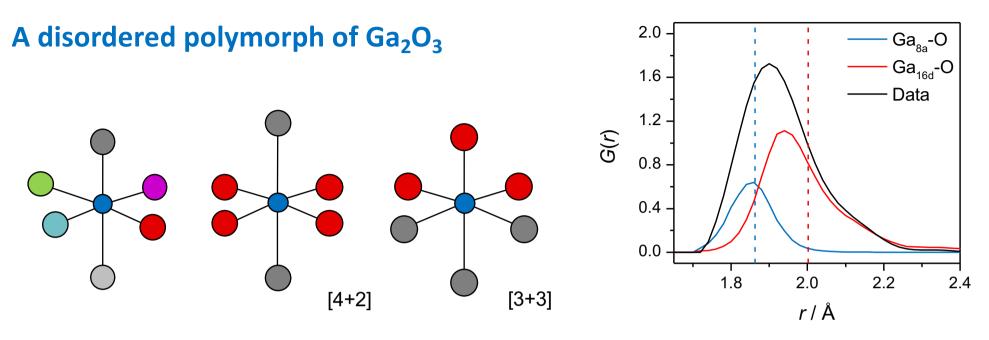
Science & Technology Facilities Council



The data clearly show the octahedra are distorted, but what do they actually look like?

- multiple RMC runs provide ensemble of >700,000 polyhedra to analyse!
- 50% all 6 bonds shorter than the mean bond length
- 40% [3+3] type





The data clearly show the octahedra are distorted, but what do they actually look like?

- multiple RMC runs provide ensemble of >700,000 polyhedra to analyse!
- 50% all 6 bonds shorter than the mean bond length
- 40% [3+3] type

Thermodynamically stable β -Ga₂O₃ has [3+3] type...

Locally, cubic γ -Ga₂O₃ = monoclinic β -Ga₂O₃

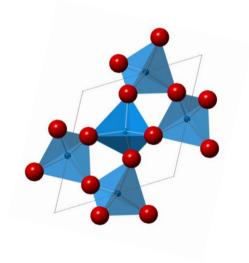


Why was the Case Study successful?

Requirements for successful RMCProfile refinement:

- Quality data 🗸
- Multiple datasets
- Single phase sample[∗] ✓
- Good powder average^{**} ✓
- Average structure well-characterised
- Understanding of structural chemistry \checkmark
- Targeted analysis of refined configurations





Conclusions

- Total scattering is an extension of powder diffraction that changes the viewpoint from average to local.
- Reverse Monte Carlo refinements using RMCProfile produce atomistic models that are consistent with all available data
- Requirements for success include prior characterisation and an understanding of what you want to know about your structure!
- The program is always being developed and we always want to hear from you!
- <u>www.rmcprofile.org</u>



Thank you!



