

ISIS Neutron and Muon Source

#### Introduction to Disordered Materials Data Analysis Methods

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#### **1** Comparing Data to simulation

g(r), S(Q), F(Q), isotopic substitution.....

#### **2** Molecular simulation: key concepts

Interatomic potentials, Monte Carlo, Molecular Dynamics, Periodic Boundary Conditions.....

#### **3** Potential Refinement

Linking g(r) and V(r), "EPSR method"

#### 4 What next: Simulation analysis, Common pitfalls, Additional features





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#### **Comparing data to simulations**

# Total Structure Factor: From raw data....

Theory can link measured scattering intensities to real-space simulation data – but is **idealised. So we must**:

- Remove multiple scattering and beam attenuation effects
- Remove self-scattering Interference scattering only
- Remove inelastic scattering: Important (and difficult) for light H.
- Have a normalised intensity on an absolute scale (barns/atom/sr)
- For X-rays need to also take into account form factors of atoms Gudrun: .min01 (neutrons) and .int01 (X-rays) files



# **Total Structure Factor: Link to simulation**

 $F(Q) = \sum_{i,j} (2 - \delta_{ij}) c_i c_j b_i b_j S_{ij}(Q)$  (Experimental Observable)  $n_i$ 

$$c_i = \frac{n_i}{N}$$
  $b_i = scattering length$ 

$$S_{ij}(Q) = \rho \int_{0}^{\infty} 4\pi r^2 g_{ij}(r) \frac{\sin Qr}{Qr} dr$$

**Partial Structure Factor** 



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(Accessed *via* Simulation)

### **The Radial Distribution Function**

- A Radial Distribution Function (RDF) describes the average density of atoms of a given type *j* at a distance *r* from an atom of type *i*, compared to the bulk
- 'Sit' on an atom of type *i*, and count the number of atoms of type *j* that fall within a spherical shell of width Δ*r*, centred at *r*



# g(r) to S(Q) for water....



# **Isotopic Substitution**

$$F(Q) = \sum_{i,j} (2 - \delta_{ij}) c_i c_j \mathbf{b}_i \mathbf{b}_j S_{ij}(Q)$$
  
Scattering Lengths



- Change weightings of partials in the measured F(Q) by changing isotope
  - e.g. <sup>2</sup>H for H, <sup>15</sup>N for N, <sup>6</sup>Li for Li
- Key assumption: structure is independent of isotopes used
- Perform multiple measurements on the same system, with different isotopic substitutions









#### S(Q) to F(Q) for water....





### Aside: Exchangeable hydrogens

O-H and N-H hydrogens can exchange in solution and therefore isotopic substitutions will be mixed up.

1:1 H<sub>2</sub>O: D<sub>2</sub>O

1:1 H<sub>2</sub>O: d4-methanol

Mix of  $H_2O$ ,  $D_2O$  and HDO

Mix of H<sub>2</sub>O, D<sub>2</sub>O, HDO, CD<sub>3</sub>-OH and CD<sub>3</sub>-OD

EPSR and Dissolve deal with this for you, but you must tell the code which hydrogens are exchangeable and which aren't



$\left[F_{H_2O}(Q)\right]$		0.0374	-0.0964	0.0622	$\left[ S_{00}(Q) \right]$	
$F_{D_2O}(Q)$	=	0.0374	0.1722	0.1980	$S_{OH}(Q)$	$w_{ij} = (2 - \delta_{ij})c_ic_jb_ib_j$
$F_{HDO}(Q)$		0.0374	0.0378	-0.0277	$S_{HH}(Q)$	



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Direct extraction of individual S(Q) is possible for 'simple' systems

#### **Partial Pair Correlations**

- An "atom type" is a specific kind of atom in the system
  - Depends at least on the element. Can be split by chemical environment.
  - Does not depend on isotope.



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# G(r): FT of data F(Q)

 The total pair distribution function, obtained as a FT of the data, can also be useful to compare to simulation – particularly for local intramolecular structure (bonds, angles etc) that are **not** refined to the data

From data

$$G(r) = \frac{1}{(2\pi)^{3}\rho_{0}} \int_{0}^{\infty} 4\pi Q^{2} F(Q) \frac{\sin Qr}{Qr} \, \mathrm{d}Q.$$

From Simulation  $G(r) = \sum_{i,j=1}^{n} c_i c_j \bar{b}_i \bar{b}_j [g_{ij}(r) - 1],$ 





# **Bragg Scattering**

- By usual method scattering calculation limited to local structure only (i.e. half the box length)
- Can calculated by different method for low Q which then includes periodic structure based on boundary conditions
- Calculation is more computationally expensive at higher Q, so need to set sensible upper Q limit.
- Peak widths are another adjustable parameter (based on crystalinity of sample)





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# Molecular Simulation: Key concepts

# VERY quick background on molecular simulation

We need:

- 1. A force-field that describes the energy/force on an atom as function of position w.r.t. other atoms
- 2. A way evolving the system that correctly represents thermodynamic state point
  - a) Molecular dynamics: essentially iteratively evolving Newton's equations of Motion

#### **b)** Monte Carlo simulation:

- 1. Make a "move"
- 2. Calculate new energy, U, based on FF
- 3. If U<0 accept move.
- 4. If U>0 accept move with probability

$$eta = exp\left(rac{-\Delta U}{k_BT}
ight)$$



# Forcefields: Intermolecular\* (through space)





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Coulomb:

$$U_{Coul} = \frac{1}{4\pi\varepsilon_0} \frac{q_i q_j}{r_{ij}^2}$$

Three terms (per atom type):

 $\epsilon$  – LJ energy term

 $\sigma$  – LJ distance term

q – (partial) charge

### Forcefields: Intramolecular



NOTE: EPSR and *Dissolve* treat intermolecular potentials in different ways



ISIS Neutron and Muon Source EPSR defines the strength of the bond/angle/dihedral with an effective potential for **all atoms** weighted by the reduced mass of the pair – This is "floppier" than standard bonded potentials to account for zero point energy – meaning neutron "sees" a more disordered atom locations.

## **Periodic Boundary Conditions**

- We need to represent the bulk with a small box of atoms (3-10nm)
- Achieve this with periodic boundary conditions
- Potential is calculated between atom and the nearest version of another atom within these conditions.
- Potentials must therefore be limited "cutoff" at a distance shorter than half the box length





### Starting and running a simulation

- Define your atoms/molecules: Bonding and FF
- Fill a box of an appropriate size, density and composition - this can be random placement





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Iteration number

# Starting and running a simulation

- 1. Define your atoms/molecules: Bonding and FF
- Fill a box of an appropriate size, density and composition this can be random placement
- 3. Evolve the system to reach equilibrium
- 4. Accumulate and calculate



#### **Basic Simulation**

• Published forcefield parameters describing many systems, so...





# Improving on a Basic Simulation

- Need to have a forcefield-based simulation to interpret data in vast majority of cases – literature parameters exist for a variety of systems
- How are these forcefield parameters obtained?
  - Reproduction of thermodynamic properties
  - Extrapolated / inferred from other systems
  - Chosen to reproduce experimental structural data? NO!
- Change these somehow to improve the agreement between simulation experiment?
  - Tweaking by hand almost impossible
  - Fitting algorithm could work, but parameter space is large





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#### **Potential Refinement**

1) Take differences between experimental and simulated F(Q) to get  $\Delta F(Q)$ 



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2) Enter these  $\Delta F(Q)$  into the inverse scattering matrix to generate  $\Delta S(Q)$ 

$\left[\Delta S_{OO}(Q)\right]$	4.8238	-2.7037	24.6061	$\Delta F_{H_2O}(Q)$
$\Delta S_{OH}(Q) =$	-5.8227	1.6265	4.1962	$\Delta F_{D_2O}(Q)$
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3) Fourier transform the  $\Delta S(Q)$  into  $\Delta g(r)$  and use these to form an additional, empirical potential for each atom type pair

$$\Delta S_{ij}(Q) = \rho \int_{0}^{\infty} 4\pi r^2 \Delta g_{ij}(r) \frac{\sin Qr}{Qr} dr$$

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### Aside: Linking g(r) and potential U(r)

Potential of mean force:



 $U(r) = -kT\ln g(r)$ 

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- 3) Fourier transform the  $\Delta S(Q)$  into  $\Delta g(r)$  and use these to form an additional, empirical potential for each atom type pair
- 4) Repeatedly run the simulation and generate <u>additional potentials</u> until the experimental and simulated F(Q) 'match'



#### **Potential Refinement: EPSR results**





# ereq: Maximum energy of the empirical potential

- This parameter is set in EPSR or *Dissolve* software to provide a maximum limit for the empirical potential energy
- You may need to try a few values to get the best fit to the data
- Too low: empirical potential energy not sufficient to reach a good level of fit
- Too high: "weird stuff can happen". The empirical potential is meant to be a perturbation on the seed potential. For example it can make the system too cohesive – leading to voids.



#### "Enhanced" Simulation



Experimental datasets actively used to derive new pair potentials



#### **Isotope Availability & Access**

- For many systems, there are too few isotopic sample possibilities available
  - Elements for which there are no suitable isotope pairs
  - Isotopic exchange prohibited by difficulty in synthesising target compounds
  - System complexity means there may be too many measurements to make in the timescale of a reasonable experiment

For instance, silica:  

$$\begin{bmatrix} F_{SiO_2}(Q) \end{bmatrix} = \begin{bmatrix} 0.0191 & 0.1070 & 0.1497 \end{bmatrix} \begin{bmatrix} S_{SiSi}(Q) \\ S_{SiO}(Q) \\ S_{OO}(Q) \end{bmatrix}$$
No inversion possible, so no access to partial  $S(Q)$ 



## Generalisation

• What is a general method to allow inversion of the underdetermined case?

$$\begin{bmatrix} F_{Si_{2}}(Q) \end{bmatrix} = \begin{bmatrix} 0.0191 & 0.1070 & 0.1497 \end{bmatrix} \begin{bmatrix} S_{SiSi}(Q) \\ S_{SiO}(Q) \\ S_{00}(Q) \end{bmatrix}$$

- Use the simulation? It has all the partials we need, which are hopefully a good "guess" for the experimental ones
- Define a feedback factor, 0 < f < 1 (typically 0.7-0.9), and write new weights factors...</li>

$$w_{ij} = f(2 - \delta_{ij})c_ic_jb_ib_j$$
$$x_{ij} = (1 - f)$$



# **The Augmented Scattering Matrix**

- For each partial in the simulation, add a row to the scattering matrix weighted by x<sub>ij</sub>
- Typically, *f*~0.9



Now have an overdetermined matrix for which we can find a (pseudo) inverse





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#### What next: Simulation analysis, Common pitfalls, Additional features

# Got a good fit? Now what?

- Run simulation for a large number of iterations (or time steps) for good statistics
- You can analyse the save ensemble/trajectory for any structural information you want
- Tools are available in EPSR and Dissolve
- Or the atomistic coordinates can be saved and analysed using external software







# **Options for analysis:**

1D g(r)'s – not necessarily from atom sites





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2D angular radial distribution functions

#### 3D spatial density functions



# **Options for analysis:**

Cylindrical distribution functions



### Garbage in, garbage out

- Double check input parameters for forcefields – automation of this process can help (as long as that process works!)
- Check all output functions are behaving as expected e.g. g(r)'s – have in mind what the expected behaviour is



#### Finite size effects

- Is the size of the simulation box large enough to accurately represent the system of interest?
- Check for finite size effects: Increase box size, any change in structure?
- Is the cut-off long enough to represent structure in the system?
- If the box is too large, this can make the simulation too slow.



# **Reaching equilibrium**

- Simulation can get stuck in a local (high energy) minimum
- Simulations of mesoscale systems (e.g. surfactants in solution) may take a long time to reach equilibrium - may need build the simulation box close to the "solution" rather than randomly
- Recommend checking the output coordinate files to check for appropriate sampling





#### **Additional features**

- Bragg scattering calculation: For crystalline and mixed phase systems (e.g. confined fluids in porous media) – *Dissolve* and EPSR
- X-ray scattering calculation: Allows use of HEXRD data as additional contrast - *Dissolve* and EPSR



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