

### Chemical Crystallography and Structural Chemistry (VO 270287) Lecture 6 7<sup>th</sup> May 2020

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# **Previous Lecture**

- 1. Overview: from data to structure
- 2. Integration: strong and weak reflections
- 3. Scaling: independence of the data from the experiment



# **Today's Lecture**

- 1. Phasing: Solving a crystal structure
- 2. direct methods
- 3. Patterson map

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# Solving the Structure: Phasing



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### Detour before Phasing: The Structure factor F(hkl)

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# The Structure Factor F(hkl)

- Context between atoms and diffraction intensities
- Describing the electron density with the independent atom model ("IAM")
- Form factor and the "fudge factor" ADP



# The Structure Factor

The structure factor F(hkl) is related to the **electron density**  $\rho(x, y, z)$ , i.e. the distribution of electrons inside the unit cell:

$$F(hkl) = \int_{\text{unit cell}} \rho(x, y, z) e^{2\pi i (hx + ky + lz)} d^3x$$
(1)

This equation is the Fourier transformation of the electron density. *Note:* The term "Fourier transformation" is important mainly because computers are very fast in calculating Fourier transformations.



# The Structure Factor

The Independent Atom Model (IAM, alias isolated atom model) is a powerful method to calculate the atomic structure factor F(hkl)

$$F(hkl) = \sum_{\text{in u.c.}}^{\text{atoms } j} f_j(\theta) e^{-8\pi^2 U_j(\theta,\lambda)} e^{2\pi i (hx_j + ky_j + lz_j)}$$
(2)

- $f_j$  atomic form factor. Dependent on atom element, decreases with decreasing scattering angle  $\theta=\theta(hkl)$
- $U_j(\theta,\lambda)$  atomic displacement parameter (ADP, alias Debye-Waller factor): models thermal vibration of atoms

 $e^{2\pi i (h x_j + k y_j + l z_j)}$  phase shift of the atom relative to the origin of the unit cell



# The form factor $f_j(\theta)$

The intensity of spots decreases at increasing scattering angle  $\boldsymbol{\theta}$ 



The wavelength  $\lambda$  is of the same order of magnitude as the size of the atoms: photons "see" the shape of atoms.

Note: hydrogen atoms do not contribute to data higher than 1 Å

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# The atomic displacement parameter $U_j(\theta, \lambda)$

- Atoms vibrate at T > 0K
- Vibration leads to reduction of spot intensities, but not to change in spot shape
- At medium resolution: 1 parameter
- At high resolution: anisotropic description with 6 parameters as ellipsoids

 $\begin{array}{c|c} \textbf{Isotropic} \\ U_j(\theta, \lambda) = 4U_{\text{iso}} \frac{\sin^2 \theta}{\lambda^2} \\ 1 \text{ parameter per atom} \end{array} \begin{array}{c} \textbf{Anisotropic} \\ U_{11} & U_{12} & U_{13} \\ U_{12} & U_{22} & U_{23} \\ U_{13} & U_{23} & U_{33} \\ \end{array} \begin{array}{c} a^* \\ b^* \\ c^* \\ \end{array} \right)$ 

• Name : ADP = isotropic or anisotropic *atomic displacement parameter* 



# Example images for ADP



Refinement with isotropic ADPs



### Refinement with anisotropic ADPs



# The ADP U: a fudge factor



- Sharp drop-off with resolution: can make wrongly placed atoms disappear.
- Similarity with form factor: confusion of atom types
- Risk of overfitting

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# Solving the Structure: Phasing



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# Phasing *alias* Solving the structure

- Ideally, we would measure data, run a single calculation, and get the molecular structure as result.
- our data: thousands of measured intensities I(hkl).
- Previous lecture:

$$\begin{split} I(hkl) &= c |F(hkl)|^2 \\ &= c \left| \int_{\text{unit cell}} \rho(x,y,z) e^{2\pi i (hx+ky+lz)} d^3x \right|^2 \end{split}$$

• If we could invert this equation, we could calculate the coordinates x, y, z in one go. But we cannot ...

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## The phase problem

The inverse of the Fourier transformation

$$F(hkl) = \int_{\rm unit \ cell} \rho(x,y,z) e^{2\pi i (hx+ky+lz)} d^3x$$

reads

$$\rho(x, y, z) = \sum_{(h,k,l)} F(hkl)e^{-2\pi i(hx+ky+lz)}$$



## The phase problem

The structure factor F(hkl) is a complex number. Therefore, it has

an amplitude  $|F(hkl)| = \sqrt{I(hkl)/c}$ 

a phase  $\phi(hkl) =???$ 

 $F(hkl) = \sqrt{I(hkl)/c} \times e^{-i\phi(hkl)}$ 

We can measure the amplitudes  $|F(hkl)| = \sqrt{I(hkl)/c}$ , but we cannot measure the phase angles  $\phi(hkl)$ . This is known as the **phase problem of crystallography**.





Each atoms contributes to F(430)

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Contributions per atom to F(430)

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Contributions per atom to F(430)

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Same coordinates, *different* contributions per atom to F(840)

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# Phases $\phi(hkl)$ - Summary

- The length  $f_j$  for each atom is independent of (hkl).
- The phase contribution  $e^{2\pi i(hx_j+ky_j+lz_j)}$  varies for each reflection.
- The total phase  $\phi(hkl)$  contains convoluted information from each atom



# Solving the structure = Solving the phase problem

- The phase problem prevents us from calculating the electron density map directly from our data
- Phases can be calculated from a chemical model (its coordinates)
- "Phasing" means to find a model close enough to the proper model
- Once a good enough molecule has been found, it needs to be improved: "model building" and "refinement"





# Phasing methods

Phasing in small molecule crystallography uses primarily one of two methods:

- 1. Patterson map
- 2. Direct methods



## The Patterson map

- since 1934, Arthur Lindo Patterson (1902–1966)
- good for very small structures with some heavy elements
- direct determination of atom positions



# Calculation of the Patterson map

The Patterson map ignores phases and calculates the Fourier transformation from the intensities:

$$P(uvw) = \sum_{(hkl)} I(hkl)e^{-2\pi i(hu+kv+lw)}$$

This can be calculated without knowing the phases  $\phi(hkl),$  only from the measured intensities.

It turns out this map is the "auto-convolution" of the electron density with itself ( $(uvw) = \vec{u}$ ):

$$\begin{split} P(uvw) &= \rho(\vec{x}) \star \rho(\vec{x} - \vec{u}) \\ &= \int_{\text{unit cell}} \rho(\vec{x}) \rho(\vec{x} - \vec{u}) d^3x \end{split}$$



# Meaning of the Patterson map

It can be shown that the Patterson map

$$\begin{split} P(uvw) &= \rho(\vec{x}) \star \rho(\vec{x} - \vec{u}) \\ &= \int_{\text{unit cell}} \rho(\vec{x}) \rho(\vec{x} - \vec{u}) d^3x \end{split}$$

has its peaks at vector (positions)  $\vec{u}$  that corresponds to the connecting vector between two atoms in the molecule in the unit cell.





"2D molecule, 5 atoms"

peaks of Patterson map







"2D molecule, 5 atoms"

peaks of Patterson map

















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### Patterson map observations

- heavy elements have stronger peaks (high density  $\rho(x, y, z)$ )
- with too many atoms: origin peak overwhelms: non-interpretable
- Patterson map always centro-symmetric (peak at  $(x,y,z)\Leftrightarrow$  peak at (-x,-y,-z))



# Patterson map for $La[Au(CN)_2]_3 \cdot 3H_2O$



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# Summary Patterson map

- Patterson map calculated from intensities, without phases
- Patterson map corresponds to convolution of density  $\rho(x,y,z)$
- Peaks correspond to connecting vectors between atoms
- Peak height corresponds to product of number of electrons
- Atom coordinates can be deduced from map in case of few atoms, or few heavy atoms
- The more atoms (of similar weight), the harder to interpret



# **Direct methods**



# **Direct methods**

- Well suited with molecules of similar atom types (organic compounds with  $C, N, O, \ldots$ )
- Can work with thousands of atoms
- Requires atomic resolution, better than 1.2 Å (Sheldrick's rule) (Morris & Bricogne, "Sheldrick's 1.2 Å rule and beyond" Acta Cryst. (2003), D59, 615–617)



# **Concept of direct methods**

- 1. Generate roughly the number of expected atoms at arbitrary positions
- 2. Calculate phases of this pseudo-molecule
- 3. Improve phases based on tangent formula
- 4. Improved phases produce an improved electron density map
- 5. Peak picking from improved map
- 6. Repeat
- 7. Best solution: assign atom types



# Direct methods: the tangent formula

Tangent formula<sup>1</sup> was derived by H. A. Hauptman and J. Karle — chemistry Nobel prize 1985

$$\tan(\phi_{\mathbf{h}}) \approx \frac{\sum_{\mathbf{h}'} |E_{\mathbf{h}'} E_{\mathbf{h}-\mathbf{h}'}| \sin(\phi_{\mathbf{h}'} + \phi_{\mathbf{h}-\mathbf{h}'})}{\sum_{\mathbf{h}'} |E_{\mathbf{h}'} E_{\mathbf{h}-\mathbf{h}'}| \cos(\phi_{\mathbf{h}'} + \phi_{\mathbf{h}-\mathbf{h}'})}$$

"entangles" phases with one another. Historically based on Sayre-Equation (1952)

$$F(hkl) = q(\sin\theta/\lambda) \sum_{(h'k'l')} F(h'k'l') * F(h-h', k-k', l-l')$$

Sayre equation is exact for cases of only one atom type in crystal (diamond, silicon, *etc*). That is why the tangent formula works best for similar-atoms-compounds.

 $<sup>^1</sup>E(hkl):$  normalised structure factors, derived from measured F(hkl)



# Direct methods: dual space recycling







# **Structure Refinement**



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# End of lecture

