































> $\mathbf{F}(\mathbf{r^*}) = \Sigma^{N}_{j=1} f_{at,j}(Z, \mathbf{r^*}, U) \exp 2\pi i \mathbf{r^*} \cdot \mathbf{r}_{j}$

- $rac{f_{at}}{=}$ atomic scattering factor = 33 isolated atom (later):
- > Depends on # electrons, thermal vibration.
- Tabulated theoretical or experimental values.
- > Can be approximated roughly by spherically symmetric Gaussian.
- \succ Scattering = $\mathcal{F}\mathcal{F}(molecule)$

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Scattering by elements of electron density

- \succ **F(r*)** = $\Sigma^{N}_{i=1} \mathbf{A}_{i} \exp 2\pi i \mathbf{r} \cdot \mathbf{r}_{i}$
- > Let \mathbf{r}_i be small element of electron density, ρ .
- > Consider total scattering:
- **F(r*)** = ∫_V ρ(r)exp 2π*i*r*·r dr
- > Right-hand side = $\mathcal{F}\mathcal{T}(\rho)$.
- > Structure determination:
- measure amplitude
- determine phase throughout (continuous) function, F(r*)
- compute inverse $\mathcal{F}\mathcal{T} \rightarrow$ electron density:
- > $\rho(\mathbf{r}) = T^{-1}[\mathbf{F}(\mathbf{r}^*)] = V^* \int_{V^*} \mathbf{F}(\mathbf{r}^*) \exp -2\pi i \mathbf{r}^* \mathbf{r} d\mathbf{r}^*$

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Infinite 1-D lattice -- Lessons

- $> \mathcal{FT}(lattice) = (lattice)$, in reciprocal space.
- Spacing of reciprocal lattice inversely proportional to real lattice.
- >Diffraction of crystals → relatively strong diffraction spots and insignificant intensity between spots.
- Need only use lattice points --> discrete transform.

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Structure amplitudes from partials

- Measured intensity = F²/partiality
- Partiality depends on experiment, not structure
- Need to correct
- Make equivalent to full reflection
 Partiality = 1
- Two approaches
- 1. Series of contiguous oscillations
- Add intensities from successive images
- Errors changing beam intensity etc..
- 2. Estimate partiality → mathematical correction
 Errors Requires accurate understanding of crystal orientation
- Partial reflections less accurate

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- Center zones from still images
- Computer-auto-indexing (details later)
- From 1 to 3 still images
- No longer necessary to precisely orient before data collection
- Some use the American Method
- Shoot first ask questions later
- When crystal lifetime in beam is short

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Prolonging Lifetime w/ Cryocrystallography Radiation damage

Reduced at 100 K

- Caused by:
- Crystal heating
- Ionizing radiation → roaming free radicals
- Changing covalent structure
- Abated by reducing diffusion in ice

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Detectors		
Туре	Advantages	Disadvantages
Scintillation counter	Most precise	One spot at a time (small unit cells)
Film	Spatial resolution < 50 µm	Background, dynamic range, turnaround time
Multiwire	Precise	Spatial resolution, expense
TV detector		Unstable, calibration, expense
Image plate	Size, Medium precision	Scan-time
CCD's	Precise, dynamic range	Large ones very expensive
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Data Processing - Overview

 \succ Determine which region contains each reflection

- "Indexing"
- Orientational refinement
- > Integrate intensity near reflection center
- > Subtract background

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> Scaling:

- Correct for factors that don't depend on structure, but
 - Geometry of data collection
 - Shape and absorption of crystal
- > Merging symmetry equivalent measurements
- Calculate quality statistics

Scaling - Introduction

- Calculate image scale constant
- Intensities agree w/ symmetry equivalents
- > Approx. correction for many factors:
- Crystal Absorption:
 Depends on path length
 Depends on crystal orientation and individual reflection.
- Other absorption: capillary, solvent varies slowly, can be minimized.
- Volume of crystal in beam:
 depends on \u00f6, therefore image #
- Decay due to radiation damage:
 depends on resolution and time (→ φ, image #).
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Quality of Scaling

- > Quality of data is now assessable with a scaling
- R-factor. $R_i = \Sigma_h \Sigma_i |\langle I_h \rangle K_{hi} I_{hi}| / h\langle I_h \rangle$
- > Compare this R-factor to the least-squares residual (or corresponding variance):
- Both depend on magnitude of difference.
- Residual is squared, so more sensitive to large differences.
- R-factor is normalized, and expressed as decimal fraction or %.
- $> R_i (R_{sym})$ is calculated from intensities.
- Most other R-factors are calculated from |F| = √I.

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Quality of Data

- $> R_i$ is used as a measure of data quality:
 - $R_i \leq 3\%$: excellent.
 - R_i ≤ 5%: typical average protein.
 - R_i ≤ 9%: typical large protein.
- R_i ≤ 13%: typical virus capsid.
- > Partial reflections are usually excluded
 - \rightarrow underestimate of error, especially for large molecules (small $\Delta \phi,$ many partials).
 - Inclusion of partials for virus $\rightarrow R_i = 18\%$.

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