SAXS data reduction and analysis

Daniel Franke EMBL Hamburg



Outline

- SAXS experiment setup
- $3D \rightarrow 2D \rightarrow 1D$
- Background subtraction
- Concentration effects
- R_g, MM
- Volume
- Distance distribution function p(r)

SAXS experiment



SAXS experiment







$2D \rightarrow 1D$





 $|s| = 4\pi \sin\theta/\lambda$

s – scattering vector 2 θ – scattering angle λ – wavelength I(s) – intensity

Normalization

- Transmitted beam
- Exposure time



 λ – wavelength













s, nm⁻¹



s, nm⁻¹





s, nm⁻¹



s, nm⁻¹

Background subtraction Solution minus Solvent



Background subtraction Solution minus Solvent



Background subtraction



s, nm⁻¹

Background subtraction Solution minus Solvent



Data quality "Can I use this data for further analysis?"



s, nm⁻¹

Data quality Radiation damage



Data quality Radiation damage





Dilution series Low and High Concentration





Data range







Radius of gyration (R_g)

Measure for the overall size of a macromolecule

Average of square center-of-mass distances in the molecule weighted by the scattering length density

Radius of gyration (R_g)



 Estimate of the overall size of the particles

Guinier approximation:

 $l(s) = l(0) \exp(-s^2 R_g^2/3)$ $s R_a \leq 1.3$

- Quality of the data
 - aggregation
 - polydispersity
 - improper background substraction
 - Zero angle intensity I(0)
 - First point to use



Porod plot, volume

Excluded volume of the hydrated particle:





Kratky plot Patterns of globular and flexible proteins











Distance distribution function



Distance distribution function



Gnom



Data quality





Summary

- Exposure $3D \rightarrow 2D$
- Radial averaging \rightarrow 1D
- Normalization
- Background subtraction
- Analysis

