SAXS Studies of Ion-Nucleic Acid Interactions

Written by Lois Pollack
Presented by Yang Wu
Content

• SAXS Background

• Application on Ion-Nucleic Acid Interactions
Scattering Detail

- Scattering amplitude

\[ F(q) = \sum_{n=1}^{N} e^{i q \cdot r_n} f_n(q) \]

- Intensity

\[ \langle I(q) \rangle \propto \sum_{n=1}^{N} \sum_{m=1}^{N} f_n(q) f_m(q) \frac{\sin qr_{nm}}{qr_{nm}} \]

- Momentum transfer

\[ q = 4\pi \sin \theta / \lambda \]
Scattering Detail

- Scattering amplitude

\[ F(q) = \sum_{n=1}^{N} e^{i\mathbf{q} \cdot \mathbf{r}_n} f_n(q) \]

\[ F(Q) = \frac{1}{V_p} \int_{0}^{R} \int_{0}^{2\pi} \int_{0}^{\pi} \frac{e^{iQr\cos\theta}}{r^2} \sin\theta d\theta d\phi dr = \frac{1}{V_p} \int_{0}^{R} 4\pi \frac{\sin(Qr)}{Qr} r^2 dr \]

\[ \langle I(q) \rangle \propto \sum_{n=1}^{\infty} \sum_{m=1}^{\infty} f_n(q) f_m(q) \frac{q r_{nm}}{q r_{nm}} \]

- Momentum transfer

\[ q = 4\pi \sin \theta / \lambda \]
Scattering Detail

- Scattering amplitude
  \[ F(q) = \sum_{n=1}^{N} e^{iq\cdot r_n} f_n(q) \]

- Intensity
  \[ \langle I(q) \rangle \propto \sum_{n=1}^{N} \sum_{m=1}^{N} f_n(q)f_m(q) \frac{3J_1(QR)}{QR} \frac{r_{nm}^3}{qr_{nm}} \]

- Momentum transfer
  \[ q = 4\pi \sin \theta / \lambda \]
Guinier Approximation

- Long wavelength limit $q \to 0$

\[
\mathcal{F}(Q) \approx \frac{3}{Q^3 R^3} \left[ Q R - \frac{Q^3 R^3}{6} + \frac{Q^5 R^5}{120} - \cdots - Q R \left( 1 - \frac{Q^2 R^2}{2} + \frac{Q^4 R^4}{24} - \cdots \right) \right]
\]

- Radius of gyration

\[
R_g^2 = \frac{1}{V} \int r^2 \, dV, \text{ uniform sphere case } R_g^2 = \frac{3}{5} R^2
\]

- Approximated intensity

\[
I_{\text{SAXS}}(Q) \approx \Delta \rho^2 V_p^2 e^{-Q^2 R_g^2 / 3}
\]

- Where $I_0$ stands for $I(q = 0)$
Guinier Approximation

- Long wavelength limit $q \to 0$
  \[ F(Q) \approx 1 - \frac{Q^2 R^2}{10} \]

- Radius of gyration
  \[ R_g^2 = \frac{1}{V} \int r^2 \, dV, \text{ uniform sphere case } R_g^2 = \frac{3}{5} R^2 \]

- Approximated intensity
  \[ I_{1}^{\text{SAXS}}(Q) \approx \Delta \rho^2 V_p^2 e^{-Q^2 R_g^2 / 3} \]

- Where $I_0$ stands for $I(q = 0)$
Guinier Approximation

- Long wavelength limit $q \to 0$
  \[
  I_{1}^{SAXS}(Q) \approx \Delta \rho^2 V_p^2 \left[ 1 - \frac{Q^2 R^2}{10} \right]^2 \approx \Delta \rho^2 V_p^2 \left[ 1 - \frac{Q^2 R^2}{5} \right]
  \]

- Radius of gyration
  \[
  R_g^2 = \frac{1}{V} \int r^2 \, dV, \text{ uniform sphere case } R_g^2 = \frac{3}{5} R^2
  \]

- Approximated intensity
  \[
  I_{1}^{SAXS}(Q) \approx \Delta \rho^2 V_p^2 e^{-Q^2 R_g^2/3}
  \]

- Where $I_0$ stands for $I(q = 0)$
Guinier Approximation

- Long wavelength limit \( q \rightarrow 0 \)

\[ I_{1SAXS}^{SAXS}(Q) \approx \Delta \rho^2 V_p^2 e^{-Q^2 R_g^2 / 5} \]

- Radius of gyration

\[ R_g^2 = \frac{1}{V} \int r^2 dV, \text{ uniform sphere case } R_g^2 = \frac{3}{5} R^2 \]

- Approximated intensity

\[ I_{1SAXS}^{SAXS}(Q) \approx \Delta \rho^2 V_p^2 e^{-Q^2 R_g^2 / 3} \]

- Where \( I_0 \) stands for \( I(q = 0) \)
Guinier Approximation

- Long wavelength limit \( q \to 0 \)

\[
I_1^{SAXS}(Q) \approx \Delta \rho^2 V_p^2 e^{-Q^2 R_g^2/5}
\]

- Radius of gyration

\[
R_g^2 = \frac{1}{V} \int r^2 \, dV, \text{ uniform sphere case } R_g^2 = \frac{3}{5} R^2
\]

- Approximated intensity

\[
\langle I(q) \rangle = I_0 e^{-q^2 R_g^2/3}
\]

- Where \( I_0 \) stands for \( I(q = 0) \)
Form Factor

- For a DNA duplex plus associated ions

\[ F_{\text{DNA-ion}}(q) : F(q) = \sum_{n=1}^{N} e^{iq \cdot r_n} f_n(q) f_{\text{IONS}} F_{\text{IONS}}(q) \]

- For the ions

\[ f_{\text{IONS}} = N_{\text{ions}} \times f_{\text{ions}} \]

- By definition \( F(0) \) \( f(Q) = \int \rho(r) e^{iQ \cdot r} d^3r \) to \( I(q) \) determined by \( f_{\text{DNA}} \) and \( f_{\text{IONS}} \). Intensity \( I(q) = |F_{\text{DNA-ion}}|^2 \)
Form Factor

- For a DNA duplex plus associated ions
  \[ F_{\text{DNA\text{--}ion}}(q) = f_{\text{DNA}} F_{\text{DNA}}(q) + f_{\text{IONS}} F_{\text{IONS}}(q) \]

- For the ions
  \[ f_{\text{IONS}} = N_{\text{ions}} \times f_{\text{ions}} \]

- By definition \( f(0) = \int \rho(r) e^{iQ \cdot r} d^3r \) transforms \( I(q) \) determined by \( f_{\text{DNA}} \) and \( f_{\text{IONS}} \). Intensity \( I(q) = |F_{\text{DNA\text{--}ion}}|^2 \)
Form Factor

- For a DNA duplex plus associated ions

\[ F_{\text{DNA-ion}}(q) = f_{\text{DNA}}F_{\text{DNA}}(q) + f_{\text{IONS}}F_{\text{IONS}}(q) \]

- For the ions

\[ f_{\text{IONS}} = N_{\text{ions}} \times f_{\text{ions}} \]

- By definition \( F(0) = 1 \), thus contribution to \( I(q) \) determined by \( f_{\text{DNA}} \) and \( f_{\text{IONS}} \). Intensity \( I(q) = |F_{\text{DNA-ion}}|^2 \)
Anomalous Scattering (ASAXS)

- Scattering strength changes near binding energies
- Measure scattering profiles at two selected energies
- Different in intensity

\[ \Delta I(q) \propto f_{DNA}F_{DNA}F_{IONS} + f_{IONS}F_{IONS}^2 \]

- Data analyzed by comparison with models
Structure Factor

(a) Particles repel → Particles do not interact → Particles associate

(b) Form factor
- Repulsion
- Weak repulsion
- No interaction
- Association

Increasing magnesium concentration
Structure Factor

- Two ways to interpret information provided
  1) computed effective structure factor compares with potentials

  decoupling approximation

  \[ S_M(q) = \left(1 + \frac{\langle F(q) \rangle^2}{\langle F(q)^2 \rangle} (S(q) - 1)\right) \]

  isotropic structure factor \( S(q) \) computed assuming particles interact via a distance-depending potential

  2) \( S_M(0) \) yield second viral coefficient

\[
\frac{P(q = 0)}{I(c, q = 0)} = \frac{1}{S_M(q = 0)} = 1 + (2MA_2)c
\]

\[ A_2 > 0 \text{ repulsive; } A_2 < 0 \text{ attractive} \]
Structure Factor

1. Two ways to interpret information provided
   - Computed effective structure factor compares with potentials
   - Decoupling approximation

\[ S_M(q) = \left(1 + \frac{\langle F(q) \rangle^2}{\langle F(q) \rangle^2} (S(q) - 1) \right) \]

2. \( S_M(0) \) yields second virial coefficient

\[ \frac{P(q = 0)}{I(c, q = 0)} = \frac{1}{S_M(q = 0)} = 1 + (2MA_2)c \]

\[ A_2 > 0 \text{ repulsive; } A_2 < 0 \text{ attractive} \]
Reconstructions

- SAXS also study ion-induced folding providing information about molecules global structure at all time

1) Analyze RNA conformation
   measuring radius of gyration;
   computing Fourier transform of $I(q)$;
   using Kratky plots to assess molecular compaction;
   employing singular value decomposition (SVD) methods to determine the number of independent states;

2) Analyze DNA conformation (liquid crystalline forms)
   standard diffraction techniques
Content

• SAXS Background

• Application on Ion-Nucleic Acid Interactions
Probing Ions Atmosphere with ASAXS
Ion-Mediated Interactions

[Graph showing the relationship between DNA concentration, Mg²⁺ concentration, and the interaction parameter A₂. The graph distinguishes between DNA and RNA with different colored markers. The interactions are categorized into attraction and repulsion zones based on the A₂ parameter.]
Thank you!

April 30, 2012