

Calculating Label Distances Within Biomolecules Using **Anomalous Small Angle X-ray** Scattering

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Distances in Biomolecules

- Interaction between proteins is important
- Learning how proteins interact helps us learn their function and can lead to medicines for diseases



- Proteins and nucleic acids are dynamic
- Many possible structures, an ensemble
- Distances are dynamic as well







SASSIE / SASSIE-web

- Provides simulation and modeling tools
- Program process:



A

0.01

SANS data interpolated data

(b) 0.001





Use of Anomalous Small Angle X-ray Scattering (ASAXS)

- Used in materials science for determining distances
- Uncommon for biological systems
 - Limited by sample preparation labeling methods
 - Lack of adequate tools to generate and evaluate ensembles and their theoretical ASAXS data

OPEN CACCESS Freely available online

PLOS ONE

Anomalous Small Angle X-Ray Scattering Simulations: Proof of Concept for Distance Measurements for Nanoparticle-Labelled Biomacromolecules in Solution

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https://doi.org/10.1371/journal.pone.0095664

Program to calculate the intramolecular distance of a single labeled biomolecule by simulating ASAXS But, biological systems are dynamic and often flexible.

Accounting ensembles and direct comparisons to experiments are needed.

Our goal: extend these ideas and use the simulation and experimental comparison tools of SASSIE-web toward Ensemble-ASAXS





Small Angle X-ray Scattering (SAXS)



What is measured?







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Anomalous Small Angle X-ray Scattering (ASAXS)

• Fluorescence X-ray photon emitted at very specific energy (absorption edge).



 Scattering length now has new energydependent terms near the absorption edge.

 $f = f_0 + f'(E) + if''(E)$



Gruzinov et al. (2021). J. Synchrotron Rad. 28, 812-823.

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Relatively high-Z atom, e.g. Au



Experimental Strategy Using ASAXS

- 1. Incorporate high-Z atoms (Au) into biological molecule
- 2. Perform SAXS measurements at several energies near the Au absorption edge
- 3. Separate I(q) into resonant (R) and non-resonant (NR) terms
- 4. Solve for $I_R(q)$, $I_{NR}(q)$ and $I_{R,NR}(q)$





$$I(q) \sim f_R^2 I_R(q) + f_{NR}^2 I_{NR}(q) + 2f_R f_{NR} I_{R,NR}(q)$$





Probability Distance Distribution Function

• Related to I(q) by a Fourier Transform:

$$I(q) \sim \sum_{r=0}^{D_{max}} P(r) \frac{\sin(qr)}{qr}$$

Dmax: maximum distance in the molecule

$$P_R(r) \sim \sum_q I_R(q) q \sin(qr)$$

R: resonant term (Au)







The new code will extend the process to handle ensembles and experimental data.





Workflow





Validating Visualization



atoms)

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Progress

	Original Code	Independent Script	Prototype Code	Ensemble- ASAXS
Initialization		\checkmark	\checkmark	
Calculate Scattering	\checkmark		\checkmark	\checkmark
Construct T and Obtain G				
Obtain P(r)	\checkmark			





Future Work

- 1. Complete the remaining bits for the calculation process steps & enable CUDA/GPU.
- 2. Successfully use Ensemble-ASAXS for DNAprotein experimental data
- 3. Release Ensemble-ASAXS to the community in the Beta stage
- 4. Manuscript!

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ASAXS	
	run_0
reference pdb	Browse local files or Browse server
use simulation trajectory file	
Intensity Calculation Inputs	
magnitude of Gaussian noise (fraction of value of I(0))	0.001
number of q-values	31
maximum q-value	1
number of D-values	31
maximum D-value	1
model single atom in PDB files as a nanocluster	•
	Au
choose atom name to simulate nanocluster	



Thank you for listening!

Special thanks to Joseph Curtis and Susan Krueger!







