An Introduction to Small Angle X-ray Scattering (SAXS)



Adam Leontowich CLS XRD school, Thursday, June 20, 2024



The small angle X-ray scattering (SAXS) region

Instrumentation, sample prep, data collection and reduction

Basic data processing with examples from BXDS



Brockhouse X-ray Diffraction and Scattering (BXDS) sector





WLE beamline

High-resolution powder diffraction



IBM (rapid thermal annealing to 1100 °C)

Thin film studies: XRD, resistivity, \succ roughness, under ultra-high purity gas



- Peak shape analysis
- Complex mixtures
- **Complex structures**



WAXS (XRD with area detector)

Biopolymers for bandages Youchao Teng, Yimin Wu, U. Waterloo

Measure WAXS, voltage and current while stretching (0 - 100 N)



- Texture on surfaces \geq
- Degree of orientation \geq
- % crystallinity >
- Speed/in-situ \geq

SAXS/WAXS

SAXS has been running since February 2021

No dedicated SAXS beamline at CLS

X-ray scattering

synchrotron

Source

Atomic form factors (or atomic scattering factors)



From scattering to diffraction



X-ray scattering and diffraction reveals structural order within materials on the atomic to 100s of nanometer length scale



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What is SAXS all about?

 $\lambda = 2 d \sin \theta$



SAXS is generally $2\theta = 0.05 - 5^{\circ}$

Probe relatively big things (1 - 150 nm) by measuring elastic X-ray scattering at small angles





Atomic distances, spacing between planes of atoms, bond lengths

How is SAXS related to other X-ray diffraction techniques?



Nano-scale

Atomic-scale

Inter-molecular distances and packing arrangements, particle size and shape

Inter-atomic distances, bond lengths, nearest neighbor atoms Crystal structures with atomic resolution



Applications



SAXS is highly complementary to microscopy



- Observe a small fraction of the complete sample at a time
- Challenging sample prep at smaller size

SAXS provides nanoscale information averaged over the beam volume (~mm³)

Complementary info: shape, folding/unfolding, assembled state in solution



Instrumentation, sample prep, data collection and reduction



How to measure small angle X-ray scattering?

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1) Special instrumentation required for SAXS 2) SAXS instruments are long!





- More flux (better SNR), weakly scattering objects (organics/biology)
- Better q resolution
- Time resolved, SAXS mapping
- Choice of many wavelengths

- Highly collimated hard X-ray beam (multiple slits)
- Large area detector with beamstop
- Space for >2 m sample to detector distance
- Some ability to change detector distance (SAXS/WAXS)
- All or most components in vacuum



State of the art instrumentation

CATERETÊ beamline @ SIRIUS Campinas, Brazil

Dedicated SAXS beamline, new for 2022

- 4th gen synchrotron, 88 m source to sample
- Modern large area detector with beamstop
- 0 28 m sample to detector distance
- All components in vacuum, no windows from source to detector











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CLS SAXS instrument

New for next cycle (Jan-June 2025)

New table

- Easily go between SAXS and WAXS
- q_{min} from 0.005 Å⁻¹ to 0.003 Å⁻¹

Optional Eiger 2 detector

- Strongly scattering samples
- Dynamic processes (sub-second)

HPLC system

- Size exclusion chromatography-coupled SAXS





Sample preparation and mounting

Transmission



Grazing incidence

Thin *flat* films on Si wafers, or glass slides Min θ step = 0.01°





Calculate the transmission of your sample... 1/e is ideal Bring blanks, Bring a range of concentrations Bring a sample where you know what to expect MUST buy your own capillaries

Sample preparation and mounting

Operando solar cells (sunlight, humidity, temperature)



Multi-sample transmission

We are flexible!



Automated multi-sample grazing



Helium box with Linkam heating and cooling (-193 - +350°C)



Automated multisample Helium box for GIWAXS, also with mild heating



Liquid flow cell and syringe pump



Oxford cryostream (-193 - +226°C)



1000°C furnace with gas flow



In-situ spin coater (soon with heating)



Electric field/Electrochem SAXS



Stretching



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During your beamtime, note the wavelength, the approximate detector distance, and detector details



0.5380

1.168

GSAS-II demo, "Calibration of an area detector"

🐝 GSAS-II project: <unnamed project>



Data correction, and reduction to 1D plot

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Source



5 tips for a great data collection experience

- 1) Know what q range you want, and include it in your proposal. We can tune the endstation to your problem.
- 2) Know what your data should look like. Find published examples, and bring a known good sample.
- 3) Get in contact ~2 weeks in advance.
- 4) Choose quality over quantity: Work up data as you go along, check for radiation damage at the start, many blank measurements.
- 5) It's your experiment.





Data analysis with examples



Origins of the SAXS signal

 $I(Q) = S(Q) \times P(Q)$

S(Q) is the structure factor

- *Inter*-particle interferences
- High concentrations (>5% vol.)
- Ordering/packing of particles

P(Q) is the form factor

- Intra-particle interferences

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- Low concentration (dilute limit)
- Size/polydispersity/shape of particles



Phospholipid Self-Assembly in Cocoa Butter Provides a Crystallizing Surface for Seeding the Form V Polymorph in Chocolate

J.A. Stobbs, Alejandro G. Marangoni et al., Cryst. Growth Des. 24, 7, 2685–2699 (2024)

Marangoni group Dept. Food Science University of Guelph

The nanostructure of chocolate is manipulated using time and energy-intensive "tempering"

Guides crystallization of cocoa butter to "polymorph V"





Tempering of cocoa butter and chocolate using minor lipidic components

Jay Chen⊚¹, Saeed M. Ghazani⊚¹, Jarvis A. Stobbs^{1,2} & Alejandro G. Marangoni⊙^{1⊠}

NATURE COMMUNICATIONS | (2021)12:5018





4sinθ



Environmental science: Waste water treatment

Scientific Reports 12, 15832 (2022) J. Molecular Liquids 367, 120551 (2022) Physics of Fluids 34, 097119 (2022)

 a_2

 c_1 C_2

Separating solvents (THF, DMSO, DMF and acetonitrile) and metals from waste water using amphiphiles, emulsifiers and surfactants



Pensini group School of Engineering University of Guelph

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Pharmacy: Liposomes for RNA delivery

Pure mRNA degraded by enzymes in tissues Hide it inside a liposome NP to get it into cells



ACS Appl. Nano Mater. 2020, 3, 11, 10634–10645

Pfizer, Moderna COVID-19 mRNA vaccines

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In situ L_a to H_{II} transition Nature Comm. 15, 1303 (2024)



Lipid phase affects transfection efficiency



Y. Huang, S. Gui, RSC Adv., 2018, 8, 6978–6987



Lamellar phase	1:2:3:4
Im3m	$\sqrt{2}:\sqrt{4}:\sqrt{6}:\sqrt{8}$
Pn3m	$\sqrt{2}:\sqrt{3}:\sqrt{4}:\sqrt{6}:\sqrt{8}:\sqrt{9}$
Ia3d	$\sqrt{6}:\sqrt{8}:\sqrt{14}:\sqrt{16}:\sqrt{20}:\sqrt{22}$
Fd3m	$\sqrt{3}:\sqrt{8}:\sqrt{11}:\sqrt{16}:\sqrt{19}$
Reverse hexagonal	$1:\sqrt{3}:2:\sqrt{7}$

Cryo-TEM

Energy materials: Quantum dot solar cells

Sargent group Elec. & Computer Engineering U. Toronto/Northwestern U.



Efficient exciton generation Size-based, tune-able band gap

QD films deposited layer-by-layer using spin coating Top electrodes deposited using thermal evaporation

18.1% record efficiency in 2022

- Performance improved by tuning:
- Particle size distribution or polydispersity
- How particles pack and the interparticle distance

Control the size and packing by:

- Ligand exchanges cycles, centrifuge to remove largest QDs
- Rinsing steps during buildup
- Spin speeds, solvents, additives



M. Yuan et al., Adv. Mater. 2014, 26, 3513-3519

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GISAXS - Lab X-ray source vs. Synchrotron

Turak group Concordia, Physics



- Horizontal stripes indicate stacked layers of NPs, layer spacing.
- Vertical stripes indicate lateral ordering of the NPs, lateral distance.
- Peak width indicates size distribution and disorder in the system.



10000

8000

- 6000

4000

- 2000

$I(Q) = S(Q) \times P(Q)$

S(Q) is the structure factor

- *Inter*-particle interferences
- High concentrations (>5% vol.)
- Ordering/packing of particles -

~An extension of PXRD Looking for and analyzing Bragg peaks

Amy2_10s.5016.N051.16352014.N051.139211.74223_1s.5091.N050.6639108_B81.tif



Sea cucumber dermis M. Harrington, McGill



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Origins of the SAXS signal

 $I(Q) = S(Q) \times P(Q)$

P(Q) is the form factor

- Intra-particle interferences
- Low concentration (dilute limit)
- Size, shape, polydispersity of particles



Sample prep is critical !!!

 Dilute (~1 – 10 mg/mL) no interparticle interactions

2. Pure

3. Monodisperse



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But there are limits!

1:0

FFT Simulated SAXS Simulated 10 detector image sample 🛃 dots.bmp [FFT Modulus... — 🛛 🛛 dots.bmp [Value (max)] ... Intensity -50 μm⁻¹ μm⁻¹ μm⁻¹ 1.0 10-7 10^{-8} g polydisperse2.bmp [FFT... ydisperse2.bmp [Val... _ С ▶ ___50 ____0μm⁻¹ ___50 0,μm ομη 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1 1.0 1

Solutions must be monodisperse, and pure

Form factor oscillations smear out when size polydispersity is $\geq 15\%$



Solutions must be dilute: No interparticle effects

~1 – 10 mg/mL... Bring many concentrations





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Form factor data analysis: Catalytic nanoparticles R_g is the square root of the average squared distance of each scatterer from the particle center R_g: Radius of gyration $I(q)pprox I(0)e^{-q^2R_g^2/3}$ RMS distance of the objects parts from its center of mass Guinier's I(0): Intensity at q=0 approximation: \geq Particle radius 3 nm Pd NPs Thin disc $R_g^2 = \frac{L^2}{12}$ Guinier plot 105 $R_g^2 = \frac{3}{2}R^2$ $R_g^2 = \frac{R^2}{R}$ Fresh 11.5 R_g = 15.5 Å 3 days 11.4 11.3 104 If $q_{min} = 0.005 \text{ A}^{-1}$ q range required l(a) 11.1 Globular, disc: $q_{min} R_g < 1.0$ to ~1.3 $R_{a}max = 20 nm$ 11.0 Linear: $q_{min} R_{g} < 0.65$ to ~1.0 $R_{\sigma}max = 13 nm$ 10³ 10.9 0.002 0.003 0.004 0.005 0.006 0.000 0.001 0.007 https://bioxtas-raw.readthedocs.io/en/latest/saxs/saxs guinier.html 9.5 8. L. J. S. 0 q² (Å⁻²) D. Putnam et al. Quart. Rev. Biophys. 40, 191-285 (2007) 10² 10-2 10^{-1} Sample quality: non-linearity can indicate aggregation, q (Å-1) repulsion, radiation damage 11.1 R_g = 15.9 Å Repulsion No aggregation 11.0 Aggregation scale) Intensity (log scale) 10.9 n(l(a)) Intensity (log (log o 5 mg/ml 10.8 • 10 mg/ml 10.7 • 20 mg/ml $qR_{\rm G}$ limit = 1.3 40 mg/ml 10.6 0 **Infinite dilution** 10.5 0.002 0.004 0.000 0.002 0.004 0.000 0.05 0.10 0.000 0.001 0.002 0.003 0.004 0.005 0.006 0.007 0.008 $q(\text{Å}^{-1})$ q^2 (Å⁻²) $q^{2}(\text{\AA}^{-2})$ q² (Å⁻²) Canadian Centre canadien D. Putnam et al. Quart. Rev. Biophys. 40, 191-285 (2007) aht de ravonnement 25 Source synchrotron

Form factor data analysis: Catalytic nanoparticles



Reciprocal space intensity

Real space distance frequency

Histogram of atom-atom distances within a single particle, weighted by respective electron densities



D. Svergun, M.H.J. Koch, Rep. Prog. Phys. 66 1735 (2003)

D_{max} - Largest interatomic distance in the scattering particle

Shape of the P(r) function is related to the **shape** of the particle, with low spatial resolution

q range required

 $q_{min} \le \pi / D_{max}$ ($\pi/0$

(π/0.005 Å⁻¹ = 62 nm)

 $q_{max} \ge 2\pi / D_{max}$



D. Putnam et al. Quart. Rev. Biophys. 40, 191-285 (2007)

Optimized Chitosan-Based Nanoemulsion Improves Luteolin Release

C. Diedrich, I. Badea et al., Pharmaceutics 15, 1592 (2023)

Badea Group College of Pharmacy and Nutrition U. Saskatchewan



Figure 1. Luteolin structure.

Anti-oxidant, -inflammatory, -tumor, -viral Poor absorption after oral administration, limited water solubility

Nano-encapsulation might improve the solubility of luteolin?

Diameter: 20 – 200 nm Bilayer: ~5 nm



Oil phase: Aqueous: Luteolin, oleic acid, with ethylene glycol and Tween 20 as surfactants Chitosan solubilized in 0.25% acetic acid.

Canadian Centre canadien Light de rayonnement Source synchrotron Drop aqueous into oil while sonicating



The most reasonable fit was obtained modeling two spherical droplets

d = 27.0 ± 2.6 nm d = 1.4 ± 0.26 nm Liposomes Tween 20 micelles

Where is luteolin?

- 1. Dilute (~1 10 mg/mL), no interparticle interactions
- 2. Pure
- 3. Monodisperse

Sample prep is critical !!!

Proteins in solution

Several dedicated Bio-SAXS beamlines

Aid structure determination

- Size, molecular weight (>10%) to verify the oligomeric state
- Low resolution shape

Challenging !!

- Weakly scattering
- Radiation damage
- Limited amounts of material (~30 $\mu L)$





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Proteins in solution







R_g: 6.9 nm 📧 Guinier Fit - 🗆 × Filename Guinier Apoferritin_10mg_ml_30s_S095_N021_93441887620 Parameters 10: 349.1030 5.7 Rg: 69.2047 ∂ ^{5.6} r^2 (fit) : 0.9513 Ē 5.5 q_min*Rg q_max*Rg 0.6504 1.3003 5.4 Uncertainty Rg: 0.9203 10: 2.9107 0.00000 0.00005 0.00010 0.00015 0.00020 0.00025 0.00030 0.00035 q² Show Details More Info Normalized Residual Control n_min q_max n_max 171 - 0.01879 573 q_min 0.0094 Auto OK Cancel 0.00010 0.00015 0.00020 0.00025 0.00030 0.0003 q²





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Proteins in solution

https://www.sasbdb.org/

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LAR	GE1 Processive	ly Polymerizes M	atriglycan Using Act	tive Sites	on Alternate Protomers	Downlo

LARGE I Processively Polymerizes matrigiycan Using Active sites on Alternate Protomers Joseph S, Schnicker N, Xu Z, Yang T, Hopkins J, Watkins M, Chakravarthy S, Davulcu O, Anderson M, Venzke D, Campbell K, SSRN Electronic Journal () DOI

SASDNH8 – Xylosyl- and glucuronyltransferase LARGE2 (LARGE2dTM) dimer

Xylosyl- and glucuronyltransferase LARGE2



Synchrotron SAXS data from solutions of a secreted form that lacks the transmembrane domain of mouse LARGE xylosyl- and glucuronyltransferase 2 (LARGE2dTM) in buffer (20 mM HEPES pH 7.4, 150 mM NaCl) were collected on the BioCAT 18-ID-D beamline at the Advanced Photon Source (APS) (Chicago, IL, USA) using a Eiger2 XE 9M detector at a sample-detector distance of 3.67 m and at a wavelength of $\lambda = 0.1033$ nm (I(s) vs s, where s = $4\pi \sin\theta/\lambda$, and 2 θ is the scattering angle). In-line size-exclusion chromatography (SEC)-MALS-SAXS was employed. The SEC parameters were as follows: A 300 µl sample at 4 mg/ml was injected at a 0.6 ml/min flow rate onto a Superdex 200 increase 10/300 GL column (GE healthcare) at 23°C. 2500 successive 1 second frames were collected. The data were normalized to the intensity of the transmitted beam and radially averaged; the scattering of the solvent-blank was subtracted.



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boundary conditions for bead modelling programs



ATSAS package DAMMIF/DAMMIN GASBOR

Low resolution protein structure

Summary

The CLS has a SAXS endstation available and our user community is growing!

Probe nano-scale dimensions and ordering (1 - 150 nm) with X-rays by measuring elastic scattering at small angles

Can learn about 1) packing, 2) particle size, and 3) particle shape, but generally not all 3 at the same time

Limited structural information

Complementary information, that should be supported with supplementary techniques such as microscopy



Further reading

Basic SAXS concepts

H. Schnablegger, Y. Singh, "The SAXS Guide: Getting Acquainted With the Principles", Anton Parr, Austria. (2017)

Making a good measurement

B.R. Pauw, "Everything SAXS: small-angle scattering pattern collection and correction" J. Phys.: Condens. Matter 25 (2013) 383201

Basic data work up

J.B. Hopkins, R.E. Gillilan, S. Skou https://bioxtas-raw.readthedocs.io/en/latest/saxs_tutorial.html

BioSAXS, data workup, introduction to structure modelling

C.D. Putnam, M. Hammel, G.L. Hura, J.A. Tainer, "X-ray solution scattering (SAXS) combined with crystallography and computation: defining accurate macromolecular structures, conformations and assemblies in solution" Quarterly Reviews of Biophysics 40, 3 (2007), pp. 191–285.



Tutorials

Data processing

- Averaging
- Absolute intensity scale
- Data reduction

Data analysis

- Guinier plots
- Kratky plots
- PDDF
- Amphiphile phase identification

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