

A fluctuation x-ray scattering approach for biological imaging

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■ Introduction: x-ray scattering approaches for biological structure determination

- Serial femtosecond crystallography (SFX)
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 - 3D structure of viruses from single-particle imaging experiments
- Summary

X-Ray Free-Electron Lasers (XFELs)

FERMI 2011

European

PAL XFEL 2016



LCLS 2009



FLASH 2005





11.49

 10^{2}

ALS U5.0

 10^{3}

Energy [eV]

10⁴

PETRA

10⁶

10⁵

BESSY U-125

10¹

10²¹

10¹⁹



- **Unprecedented peak** \checkmark brilliance
- **Ultra-short pulse** \checkmark duration
- High repetition rate \checkmark
- **High coherence** \checkmark

T. Tschentscher et al., Appl. Sci. 7(6), 592 (2017)





European XFEL (2017)

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Serial Femtosecond Crystallography (SFX)







SFX is an excellent tool for high-resolution structure studies of macromolecules and their complexes.
 Requires crystalline samples.

H. N. Chapman *et al.*, Nature 470, 73 (2011) K. Ayyer *et al.*, Nature 530, 202 (2016)

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European XFEL

Single Particle Coherent Diffractive Imaging (SPI)





Requires extremely high photon flux (XFELs)

K. J. Gaffney, H. N. Chapman, Science 316, 5830 (2007)
M. M. Seibert *et al.*, Nature 470, 78 (2011)
F. M. Hantke *et al.*, Nat. Phot. 8, 943 (2014)
T. Eckeberg *et al.*, PRL 114, 098102 (2015)

Mimivirus





Coarboxysome (cell organelle)











Incident

x-ray beam

Small-Angle X-ray Scattering









fH12-13



Particles in native environmentLow-resolution particle structure

H. D. T. Merens and D. I. Svergun, J. Struct. Biol. 172, 128-141 (2010)



Small-angle x-ray scattering (SAXS):

Dilute system of particles





Scattered intensity from *N* particles:

$$I(q, \varphi) = \sum_{i=1}^{N} I_i(q, \varphi)$$
(1)

where $I_i(q, \varphi)$ is an individual contribution from the *i*-th particle.

SAXS intensity:

$$I(q) \equiv \left\langle I(q,\varphi) \right\rangle_{\varphi} = \frac{1}{2\pi} \int_{0}^{2\pi} I(q,\varphi) d\varphi,$$

or

$$I(q) = \left\langle \sum_{i=1}^{N} I_i(q, \varphi) \right\rangle_{\varphi}$$
(2)



Scattering of coherent ultrashort pulses from a system of N particles







Avoids intensity smearing due to rotational diffusion by applying ultrashort x-ray pulses (XFELs)
 Advantageous for weakly-scattering particles, since multiple-particle hits can be used along with the single hits

Z. Kam, Macromolecules 10, 927 (1977) R.P. Kurta, M. Altarelli, I.A. Vartanyants, Adv. Chem. Phys. 161, Ch.1 (2016)



X-ray cross-correlation analysis:

two-point cross-correlation function





Two-point cross-correlation function (CCF):

$$C(q,\Delta) = \left\langle I(q,\varphi)I(q,\varphi+\Delta)\right\rangle_{\varphi} \tag{1}$$

Fourier components:

$$C^{n}(q) = \frac{1}{2\pi} \int_{0}^{2\pi} C(q, \Delta) \exp(-in\Delta) d\Delta$$
(2)

$$I^{n}(q) = \frac{1}{2\pi} \int_{0}^{2\pi} I(q,\varphi) \exp(-in\varphi) d\varphi$$
(3)

$$\left\langle \left\langle I(q, \boldsymbol{\varphi}) \right\rangle_{\boldsymbol{\varphi}} \right\rangle_{M} = \left\langle I^{0}(q) \right\rangle_{M}^{-} \text{ conventional SAXS (4)}$$
$$\left\langle C^{n}(q) \right\rangle_{M} = \left\langle \left| I^{n}(q) \right|^{2} \right\rangle_{M}^{-} \text{ ``higher-order SAXS'' (5)}$$

 $\langle \rangle_{M}$ - averaging over diffraction patterns.

Z. Kam, Macromolecules 10, 927 (1977)R.P. Kurta, M. Altarelli, I.A. Vartanyants, Adv. Chem. Phys. 161, Ch.1 (2016)



Single-particle structure recovery from solution x-ray scattering

$$\left\langle I(q, \varphi) \right\rangle_{\varphi, M} = \left\langle I^{0}(q) \right\rangle_{M}$$

$$\left\langle C^{n}(q)\right\rangle_{M} \Longrightarrow \left\langle \left|I^{n}(q)\right|^{2}\right\rangle_{M}, n = 1, 2, 3...$$





where
$$\langle f(q,\varphi) \rangle_{\varphi} = \frac{1}{2\pi} \int_{0}^{2\pi} f(q,\varphi) d\varphi$$
 - angular average,
 $\langle \rangle_{M}$ - statistical average (over diffraction patterns).

R.P. Kurta, R. Dronyak, M. Altarelli, E. Weckert and I.A. Vartaniants, New J. Phys. 15, 013059 (2013)



- (a) A large number M of realizations of a disordered system composed of N reproducible particles;
- (b) Measured set of diffraction patterns;
- (c) Diffraction pattern corresponding to a single particle;
- (d) Structure of the single particle.

R.P. Kurta, R. Dronyak, M. Altarelli, E. Weckert and I.A. Vartaniants, New J. Phys. 15, 013059 (2013) R.P. Kurta, M. Altarelli, I.A. Vartaniants, Adv. Cond. Matt. Phys. 2013, 959835 (2013)

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Recovery of the scattered intensity from a single particle by means of XCCA





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Real space constraints:

- Finite support
- Positivity

R.W.Gerchberg ,W.O. Saxton, Optik 35, 237 (1972)J.R. Fienup, Appl. Opt. 21, 2758 (1982)V. Elser, J. Opt. Soc. Am. A 20, 40 (2003)

Reciprocal space constraints:

• Intensity constraint (taking into account missing data due to a beamstop, detector gaps, etc)

$$|F_i(\mathbf{q})| \rightarrow \sqrt{I_{\exp}(\mathbf{q})}$$

Structure recovery of a single pentagonal cluster





European



Coherent scattering, N=10 clusters, Fluence: $4 \cdot 10^{10}$ ph/µm², Poisson noise, $M=10^5$ diffraction patterns.



Diffraction pattern of a single cluster, recovered from $M=10^5$ patterns of the form (2)



Projected electron density of the cluster, reconstructed using iterative phase retrieval algorithms.



R.P. Kurta et al., New J. Phys. 15, 013059 (2013)

Single-particle structure from disordered 2D ensembles





European



R.P. Kurta et al., New J. Phys. 15, 013059 (2013)R.P. Kurta et al., Adv. Chem. Phys. 161, Ch. 1 (2016)



R.P. Kurta, J. Phys. B: At. Mol. Opt. Phys. 49, 165001 (2016)



B. Pedrini et al., Nat. Comm. 4, 1647 (2013)



B. Pedrini et al., Sci. Rep. 7, 45618 (2017)





Z. Kam, Macromolecules 10, 927 (1977)

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Analysis of 3D systems: indirect approaches



✓ Spherical harmonics



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SPI experiments on aerosolized virus particles at the AMO instrument, LCLS





RDV



The Rice Dwarf Virus was the first studied plant pathogenic virus; an icosahedral double shelled virus, ranging from 70-75 nm in diameter.



The Parenteral Drug Association virus filter task force has chosen PR772 as a model bacteriophage to standardize nomenclature for largepore-size virus-retentive filters (filters designed to retain viruses larger than 50-60 nm in size).

H. K. N. Reddy *et al.*, Scientific Data 4, 170079 (2017) M. Bogan *et al.*, Nano Lett. 8, 310 (2008) Photon energy: E=1.6keV Sample-detector distance: 581 mm Detector: pnCCD Sample injection: aerodynamic lens stack system with a GDNV



PR772



Size distribution histograms for RDV and PR772











R.P. Kurta et al., PRL 119, 158102 (2017)



Advanced correlation analysis







CCF defined on the same pattern *i*:

$$\left\langle C_{ii}(q_1,q_2,\Delta) \right\rangle_M = \left\langle \left\langle I_i(q_1,\varphi) I_i(q_2,\varphi+\Delta) \right\rangle_{\varphi} \right\rangle_M$$
(1)

CCF defined between different patterns *i* and *j*:

$$\left\langle C_{ij}(q_1, q_2, \Delta) \right\rangle_M = \left\langle \left\langle I_i(q_1, \varphi) I_j(q_2, \varphi + \Delta) \right\rangle_{\varphi} \right\rangle_M$$
(2)

Fourier components of the CCFs: $\left\langle C_{ij}^{n}(q_{1},q_{2})\right\rangle_{M} = \frac{1}{2\pi} \int_{0}^{2\pi} \left\langle C_{ij}(q_{1},q_{2},\Delta)\right\rangle_{M} \exp(-in\Delta) d\Delta \quad (3)$

Difference spectrum:

$$\left\langle \widetilde{C}^{n}(q_{1},q_{2})\right\rangle_{M} = \left\langle C^{n}_{ii}(q_{1},q_{2})\right\rangle_{M} - \left\langle C^{n}_{ij}(q_{1},q_{2})\right\rangle_{M}$$
(4)

Difference spectrum is used to reduce undesirable effect of various systematic issues and improve the FXS data quality.

 R.P. Kurta *et al.*, J. Phys.: Conf. Series 499, 012021 (2014)
 Various

 G. Chen *et al.*, J. Synch. Rad. 19, 695700 (2012)
 various

 R.P. Kurta, M. Altarelli, I.A. Vartanyants, Adv. Chem. Phys. 161, Ch.1 (2016)
 161, Ch.1 (2016)



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Experimental 2D correlation maps for RDV and PR772

Amplitudes:

$$\left|\left\langle \widetilde{\boldsymbol{C}}^{n}(\boldsymbol{q}_{1},\boldsymbol{q}_{2})
ight
angle _{M}
ight.$$

26

RDV



PR772



R.P. Kurta et al., PRL 119, 158102 (2017)

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Model-based structural analysis





Model structures



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Particle distortion







Multitiered iterative phasing (MTIP) for structure recovery





Fig. S7. Flowchart of the multitiered iterative phasing procedure. The mod superscript denotes values that have been modified to agree with the data. One uses circular harmonic transforms, I_m , and B_m for the 2D case and spherical harmonic transforms, I_{mn} and B_l for the 3D case.



J. J. Donatelli, P. H. Zwart, J. A. Sethian, PNAS 112 (33), 10286 (2015)



MTIP reconstructions for **RDV** and **PR772**





Reconstructed images of RDV and PR772.

Two different views (corresponding to a 72 degree rotation about the top axis) of the reconstructed RDV (a,b) and PR772 (f,g) particles, as well as density plots showing nonuniformities in the internal distribution of material inside RDV (c) and PR772 (h), 2D slices through the center of the reconstructed densities for RDV (d) and PR772 (i), and 2D projections of the reconstructed densities for RDV (e) and PR772 (j).

R.P. Kurta et al., PRL 119, 158102 (2017)

SPI experiments on PR772 virus particles at the AMO instrument, LCLS





AMO_86615 (August 2015):

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Photon energy: E=1.6 keV Sample-detector distance: 581 mm Detector: pnCCD Sample: PR772, RDV Sample delivery: GDVN

AMO 06516 (April 2016):

Photon energy: E=1.7 keV Sample-detector distance: 257 mm Detector: pnCCD Sample: PR772 Sample delivery: GDVN

AMO_11416 (August 2016):

Photon energy: E=1.7 keV Sample-detector distance: 205 mm Detector: pnCCD Sample: PR772 Sample delivery: GDVN



Experimental 2D correlation maps for PR772



AMO_86615 (PD=3nm, M=2705 patterns)



AMO_06516 (PD=3nm, M=621 patterns)



AMO_11416 (PD=3nm, M=115 patterns)





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Summary



- FXS approach offers an alternative way for structural analysis of biological particles with an XFEL;
- FXS is, in the simplest case, a generalization of SAXS;
 In more general case it may give several orders of magnitude increase of information content as compared to SAXS;
- Cross-correlation functions are valuable statistical means, which can be conveniently used for model-based and *ab-initio* structure recovery;
- First application of FXS to biological particles at an XFEL demonstrates substantial potential of the technique for the future studies of structure and dynamics of biomaterials.



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