

2-D Membrane Protein Crystallography at Future XFELs

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Basics of Coherent Diffractive Imaging

XFEL
pulse

Coherent radiation

Sample must have
compact support

Signal-to-Noise ratio should be
high, because the detected
intensities constrain the phasing

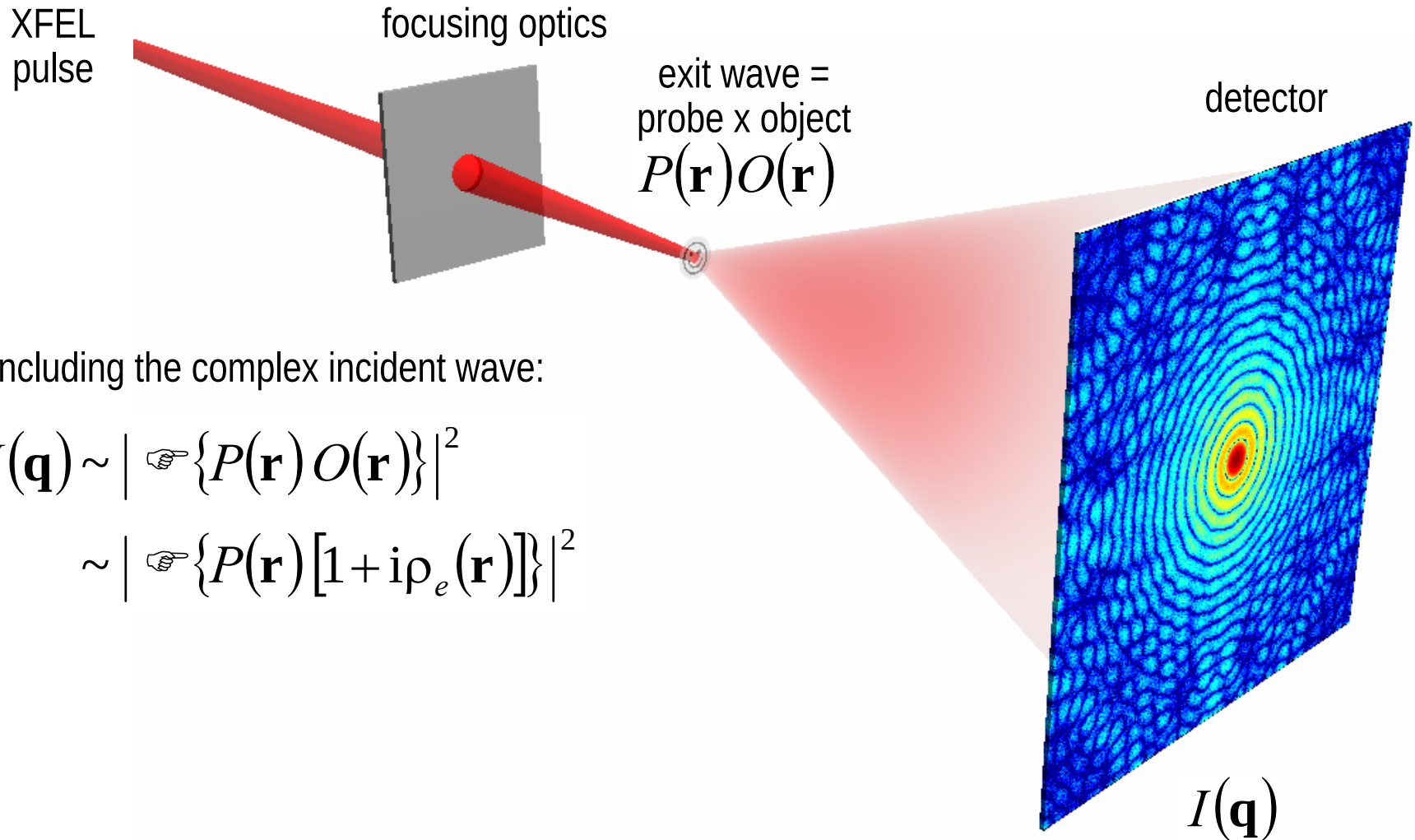
Resolution is limited by detector
solid angle and photon counting statistics...

object
 $O(\mathbf{r})$

detector

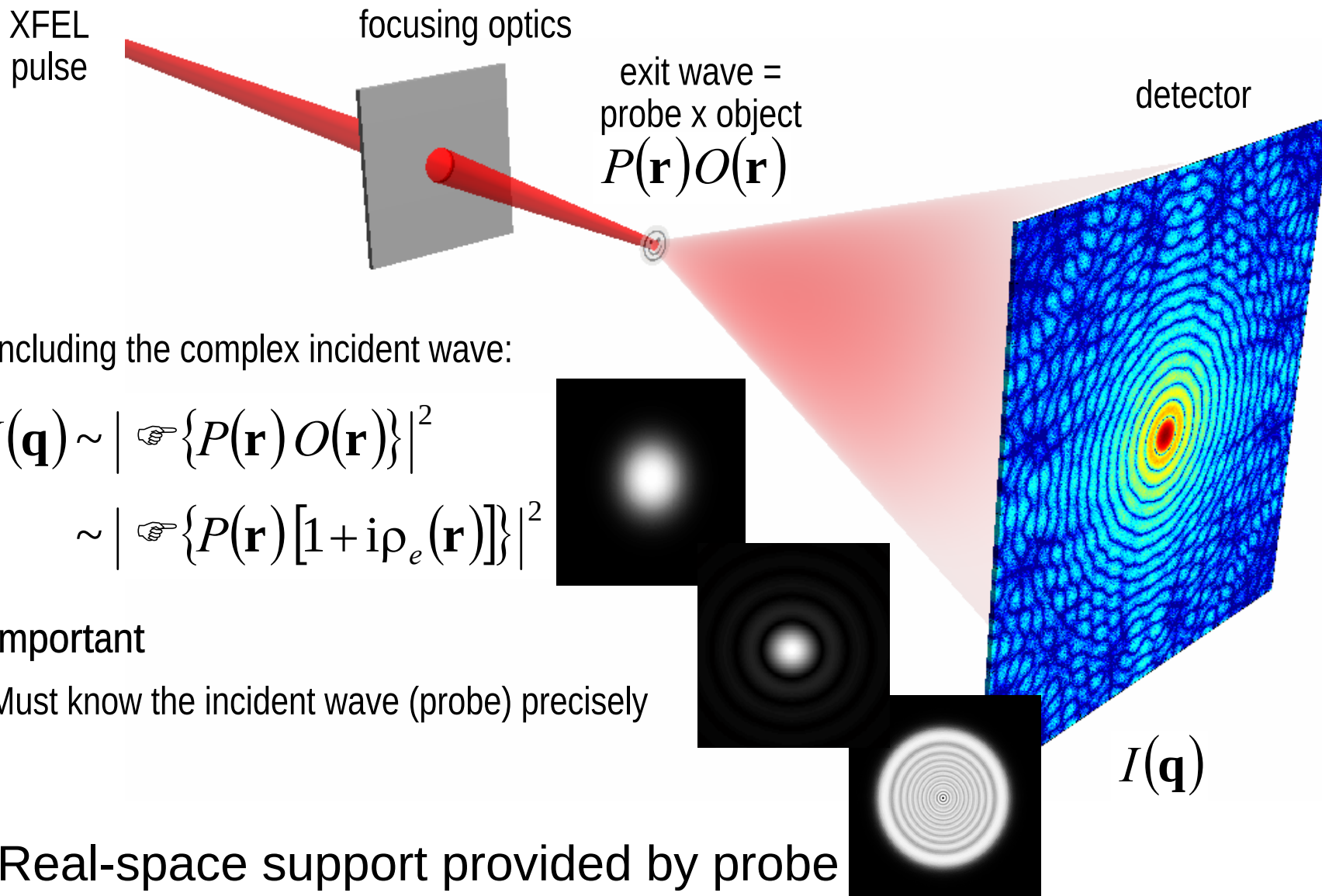
$I(\mathbf{q})$

From parallel to focused beam geometry

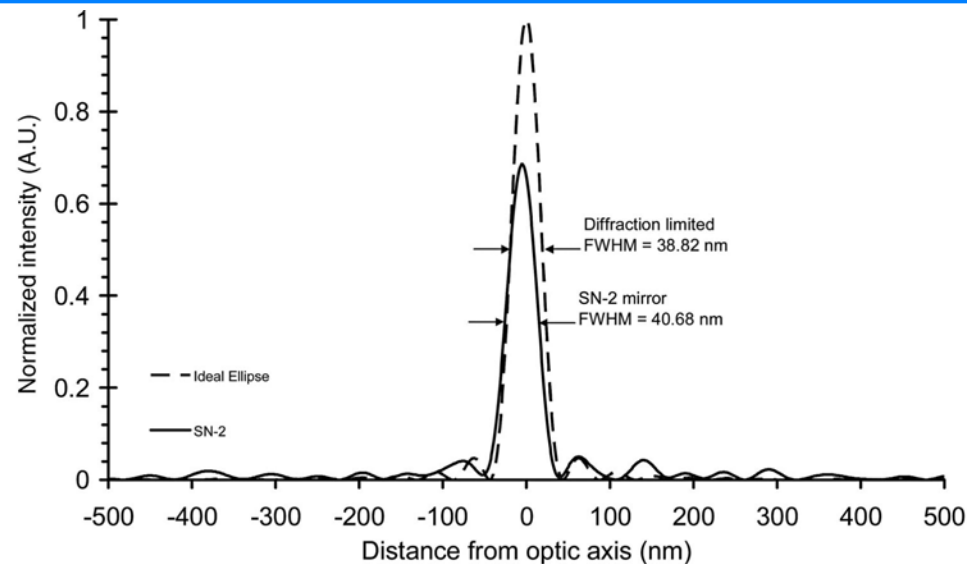
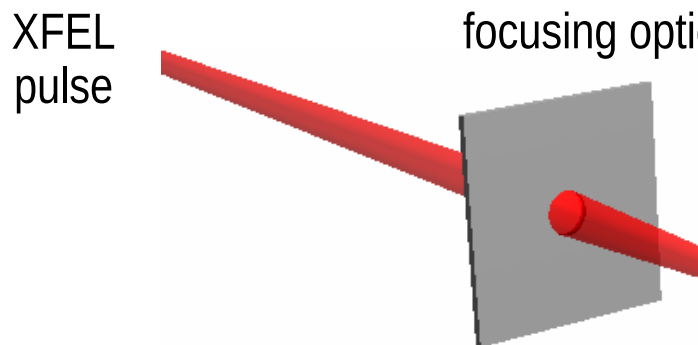


Real-space support provided by probe

From parallel to focused beam geometry



From parallel to focused beam geometry



(a)

Including the complex incident wave:

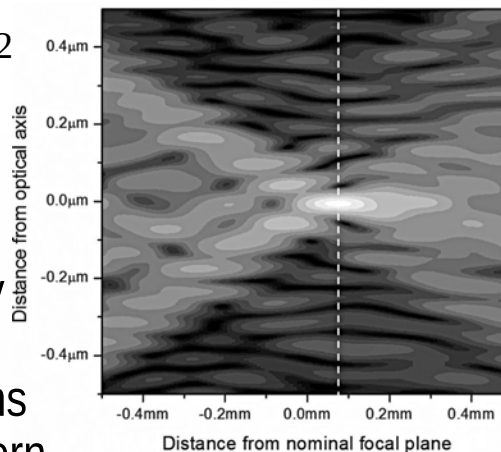
$$I(\mathbf{q}) \sim \left| \{P(\mathbf{r}) O(\mathbf{r})\} \right|^2$$

$$\sim \left| \{P(\mathbf{r}) [1 + i\rho_e(\mathbf{r})]\} \right|^2$$

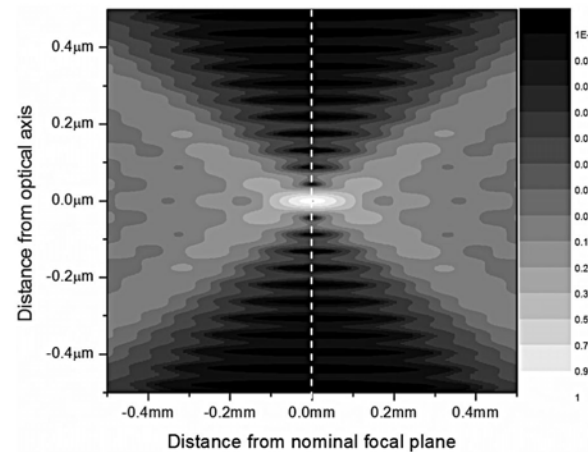
Important

Must know the incident wave precisely

Separate contributions from aberrations of focus and specimen diffraction pattern



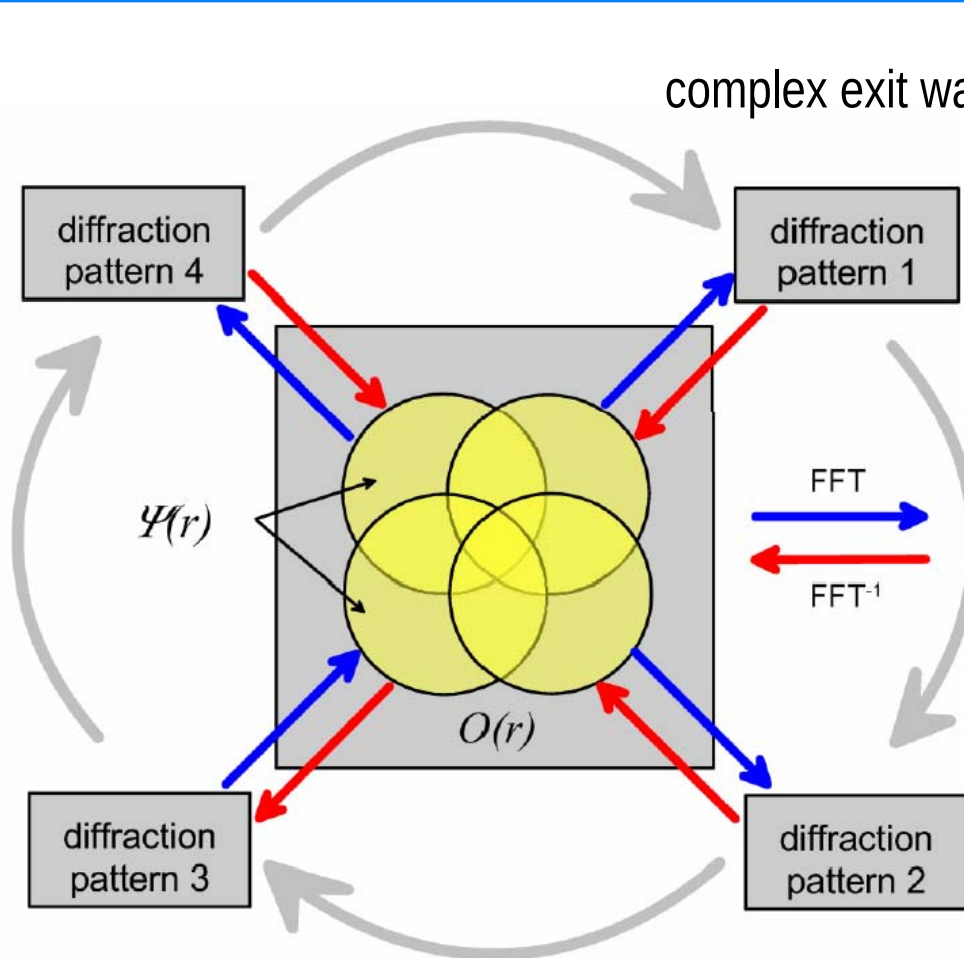
(b)



(c)

C.M. Kewish et al., *Appl. Opt.* **46**, 2010 (2007)

Ptychographic CDI



current estimate of object probe

$$\psi(\mathbf{r}, \mathbf{R}) = O_n(\mathbf{r})P(\mathbf{r} - \mathbf{R})$$

apply Fourier space constraints

$$O_{n+1}(\mathbf{r}) = O_n(\mathbf{r}) + U(\mathbf{r} - \mathbf{R})(\psi_{c,n}(\mathbf{r}, \mathbf{R}) - \psi_n(\mathbf{r}, \mathbf{R}))$$

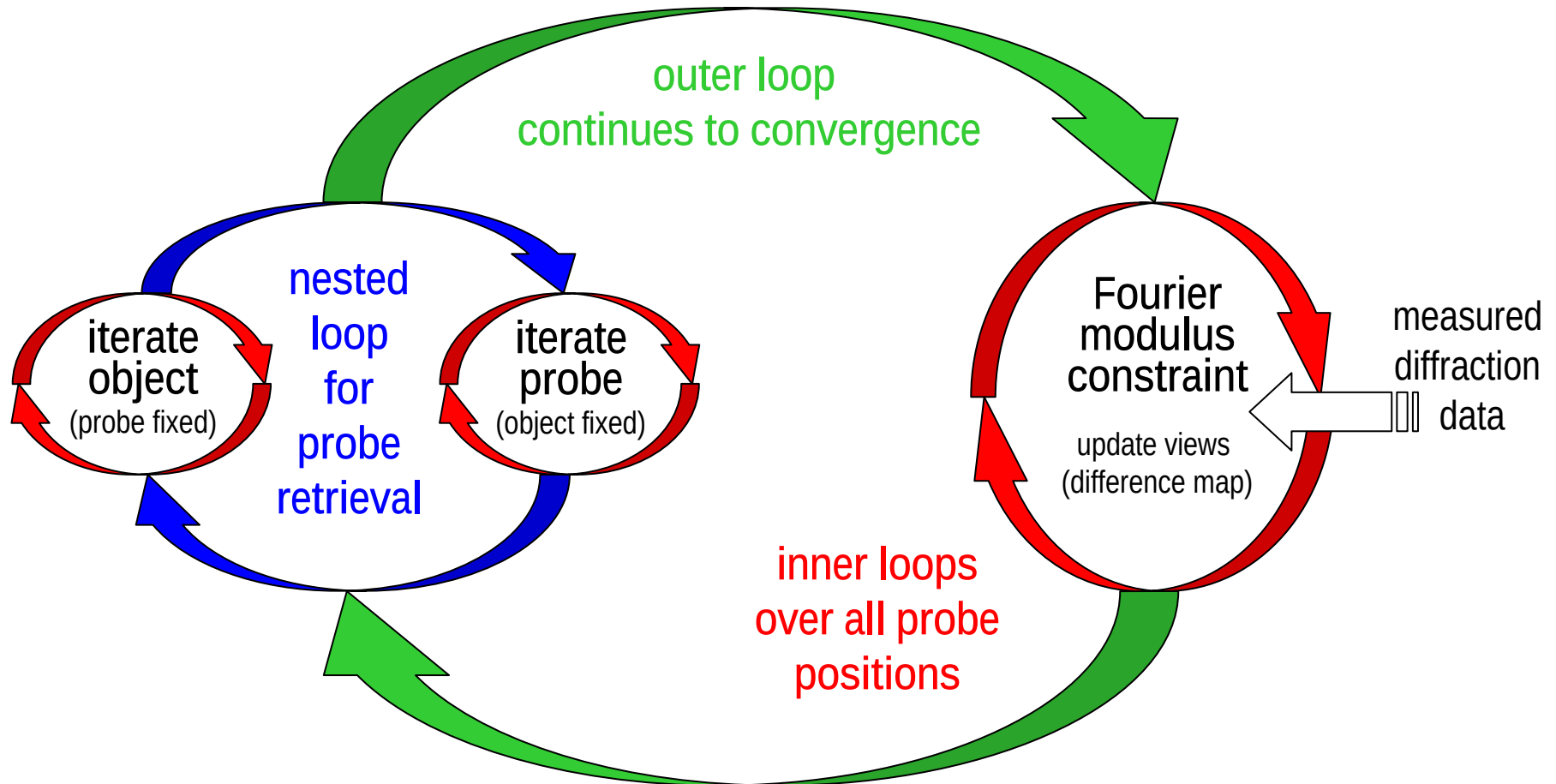
update function

$$\frac{|P(\mathbf{r} - \mathbf{R})|}{|P_{\max}(\mathbf{r} - \mathbf{R})|} \frac{P^*(\mathbf{r} - \mathbf{R})}{(|P(\mathbf{r} - \mathbf{R})|^2 + \alpha)}$$

move to next aperture position

J.M. Rodenburg & H.M.L. Faulkner, PRL **98**, 034801 (2007)

Ptychography with difference map



Overlap constraint

Applies known probe positions and uses coupled equations for the probe and object to refine the illumination function

Fourier constraint

Applies measured diffraction amplitudes and keeps the calculated phases

P. Thibault et al. *Ultramicroscopy* **109**, 338 (2009)

“Why?”

1. Why XFEL? Source must be bright enough to get information before damage
2. Why 2D crystals? Many relevant proteins do not form 3D crystals, and are active in 2D crystal form
3. XFEL pulses destroy the sample, but we have many copies of the sample
4. Having multiple copies of the unit cell in the beam improves the signal-to-noise
5. They restrict orientation to in-plane rotation and translation
6. If diffraction patterns can be registered in 2D, we can take ‘mostly’ overlapping exposures – within a unit cell translation in each axis → Ptychography
7. Reconstructing a projection from multiple exposures exploits the redundant info
8. Combining Ptychography and Tomography allows a 3D electron density map to be reconstructed.

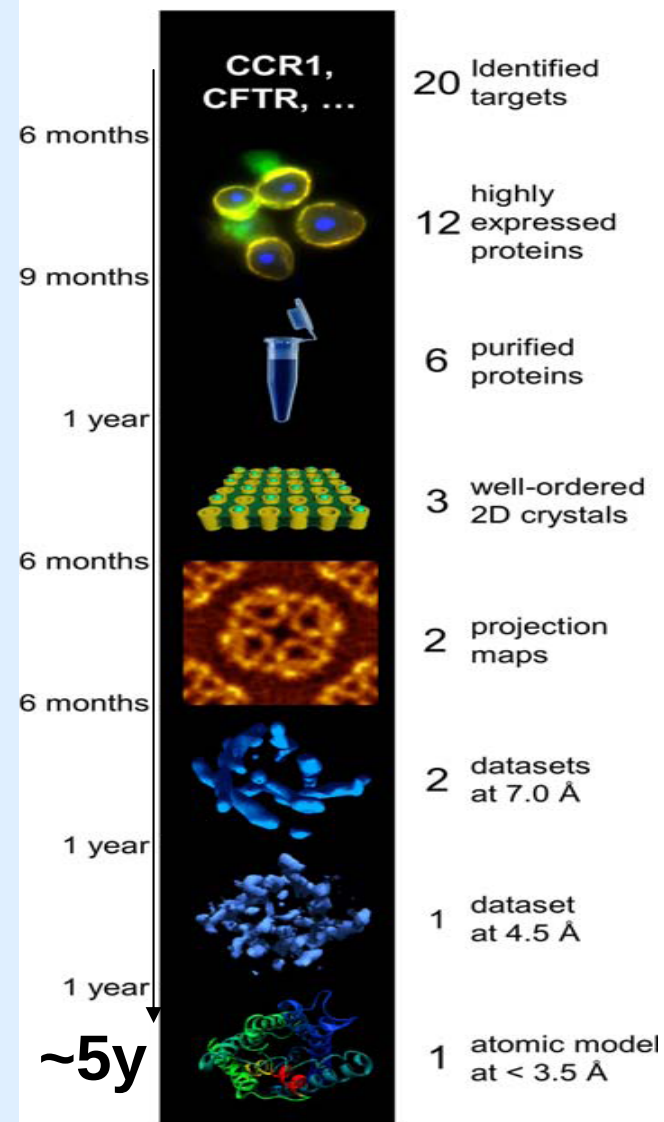
Obtaining membrane protein structures...

... with X-rays demands big crystals:
microns in size.

Some of the most scientifically relevant
proteins are impossible to crystallize

There is no guarantee that the crystal
form of the protein is representative of
the form in vivo.

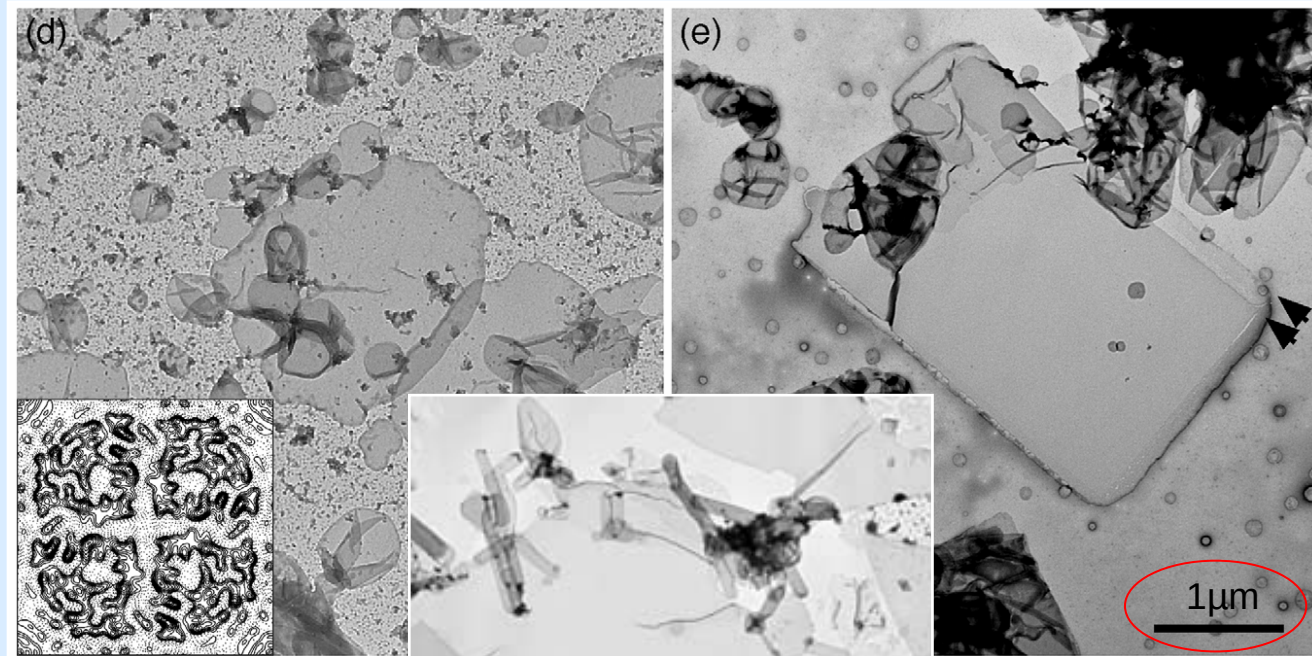
*Can one determine the structure of a
protein without large 3D crystals?*



Renault et al. *J Comput Aided Mol Des* **20**, 519 (2006)

2D membrane protein crystals

Engel et al., *Curr. Opin. Struct. Biol.* **18** (2007)

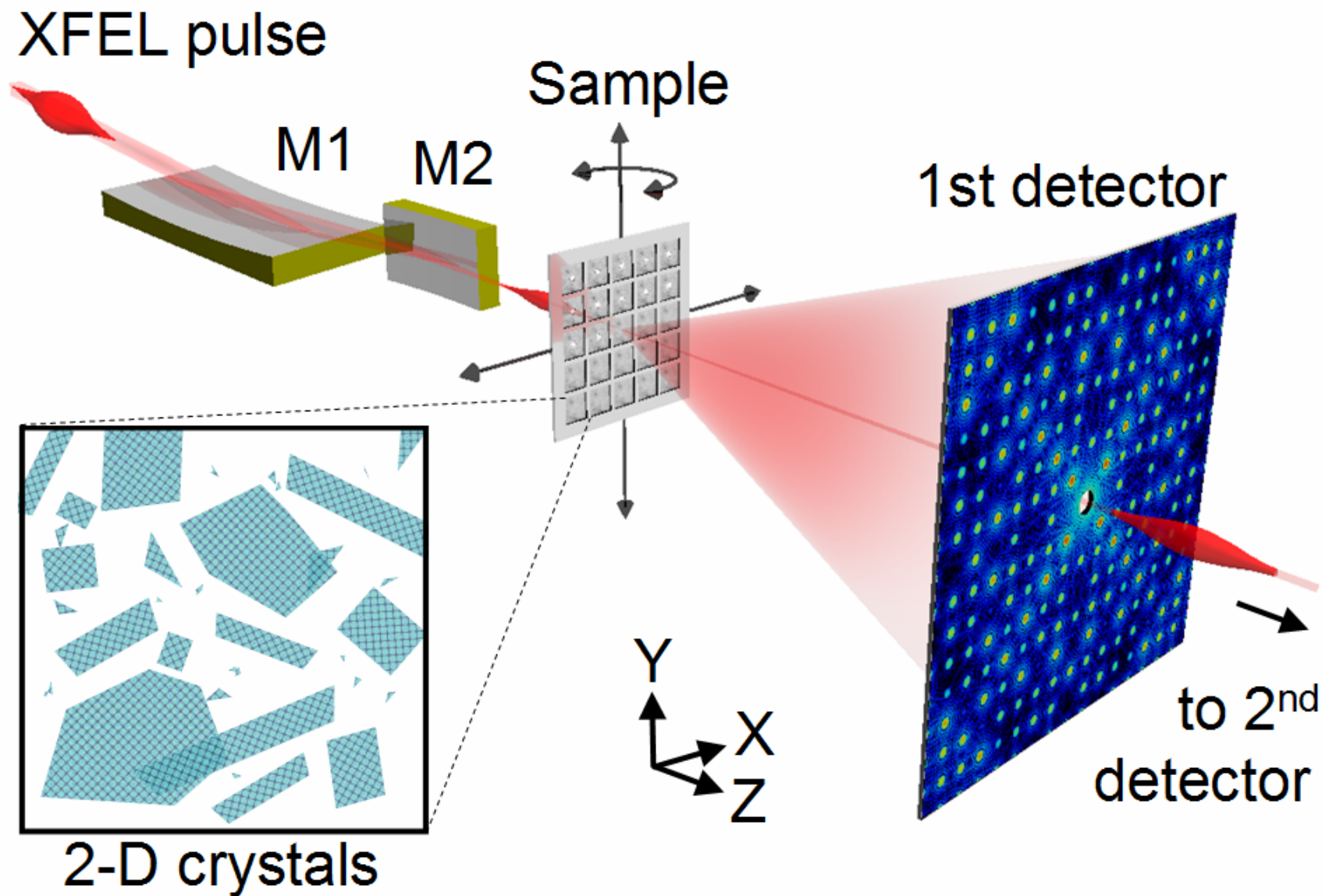


2D crystals can
be grown

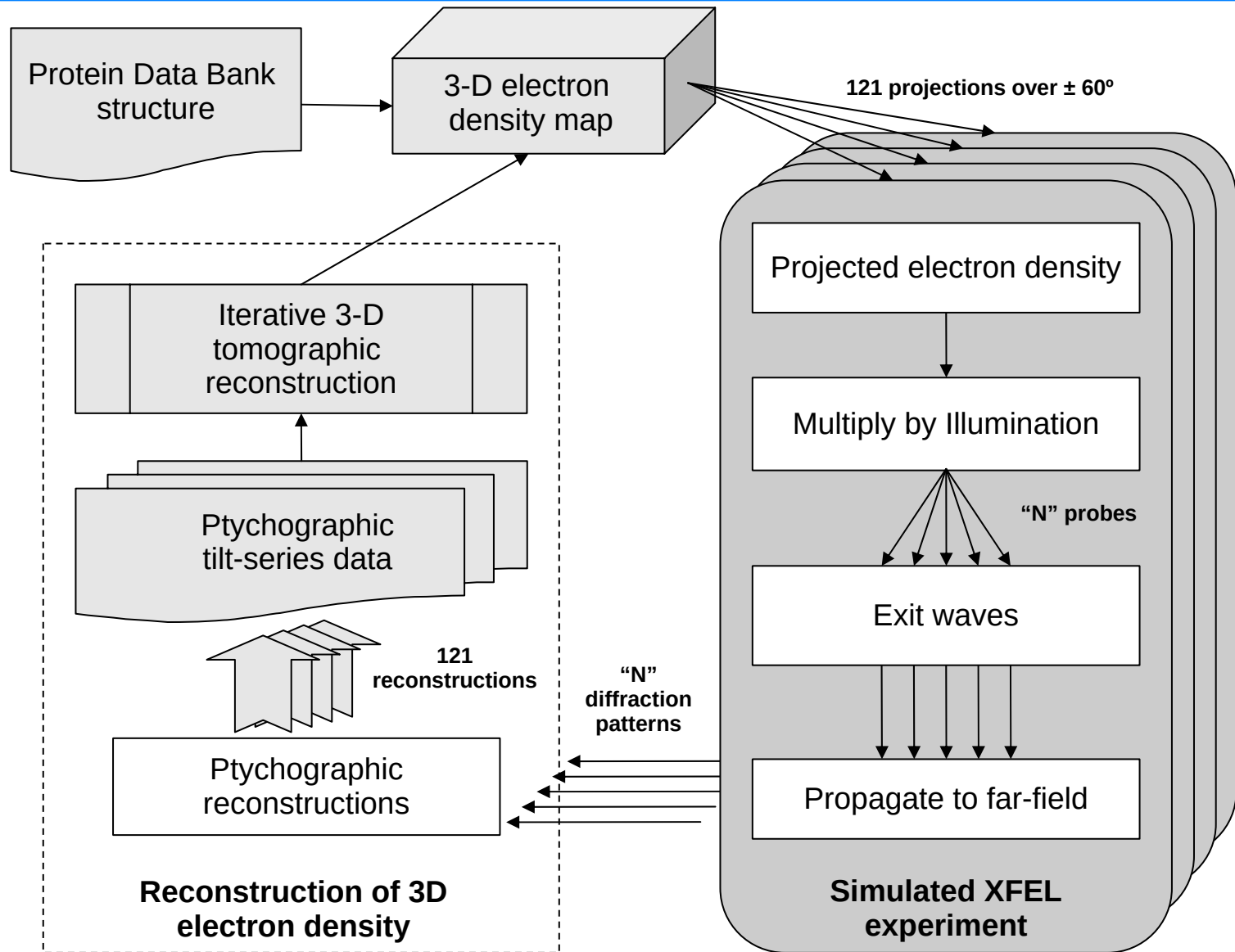
Gonen et al., *Nature* **438** (2005)

Proteins in
native state

Schematic of the simulated experiments



Summary of the simulated experiments



Generating 3D electron density from PDB

Protein Data Bank
structure

3-D electron
density map

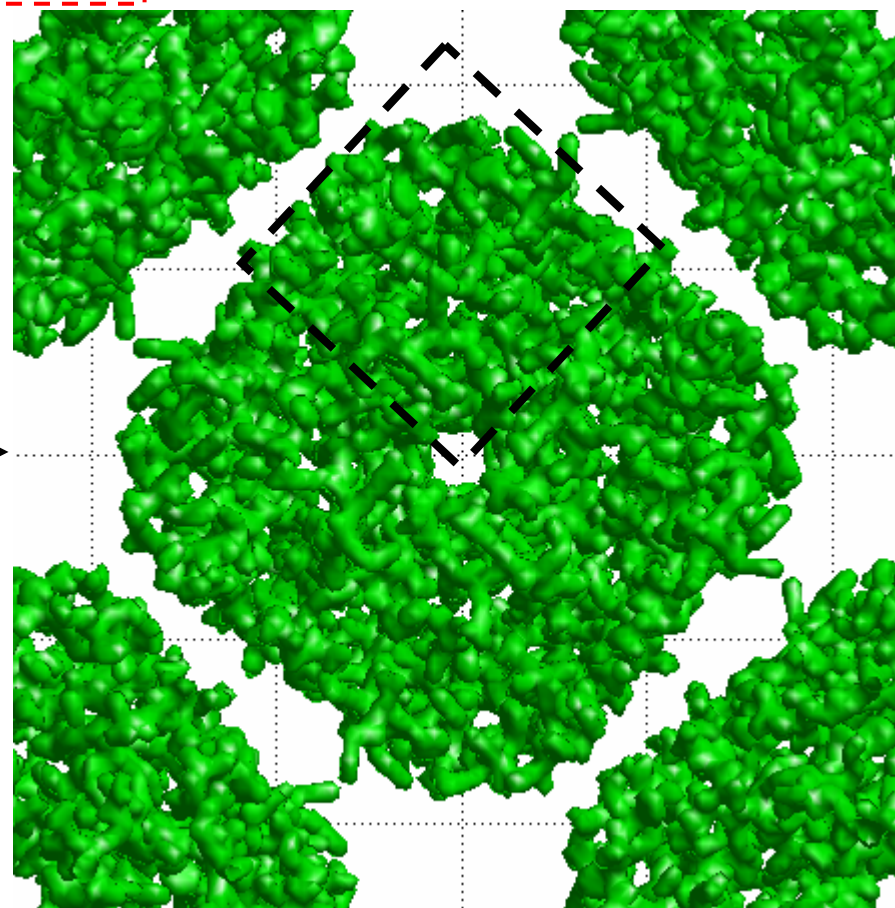
Unit Cell of Aquaporin-1

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HEADER    MEMBRANE PROTEIN                      07-SEP-00  1FQY
TITLE     STRUCTURE OF AQUAPORIN-1 AT 3.8 A RESOLUTION BY ELECTRON
TITLE     2 CRYSTALLOGRAPHY
AUTHOR    K.MURATA,K.MITSUOKA,T.HIRAI,T.WALZ,P.AGRE,J.B.HEYMANN,
AUTHOR    2 A.ENGEL,Y.FUJIYOSHI
REVDAT    1  18-OCT-00  1FQY  0
JRNL      AUTH  K.MURATA,K.MITSUOKA,T.HIRAI,T.WALZ,P.AGRE,
JRNL      AUTH  2 J.B.HEYMANN,A.ENGEL,Y.FUJIYOSHI
JRNL      TITL  STRUCTURAL DETERMINANTS OF WATER PERMEATION
JRNL      TITL  2 THROUGH AQUAPORIN-1.
JRNL      REF   NATURE                               V. 407   599 2000
JRNL      REFN  ASTM NATUAS  UK ISSN 0028-0836
REMARK    1
REMARK    2
REMARK    2 RESOLUTION. 3.80 ANGSTROMS.
  
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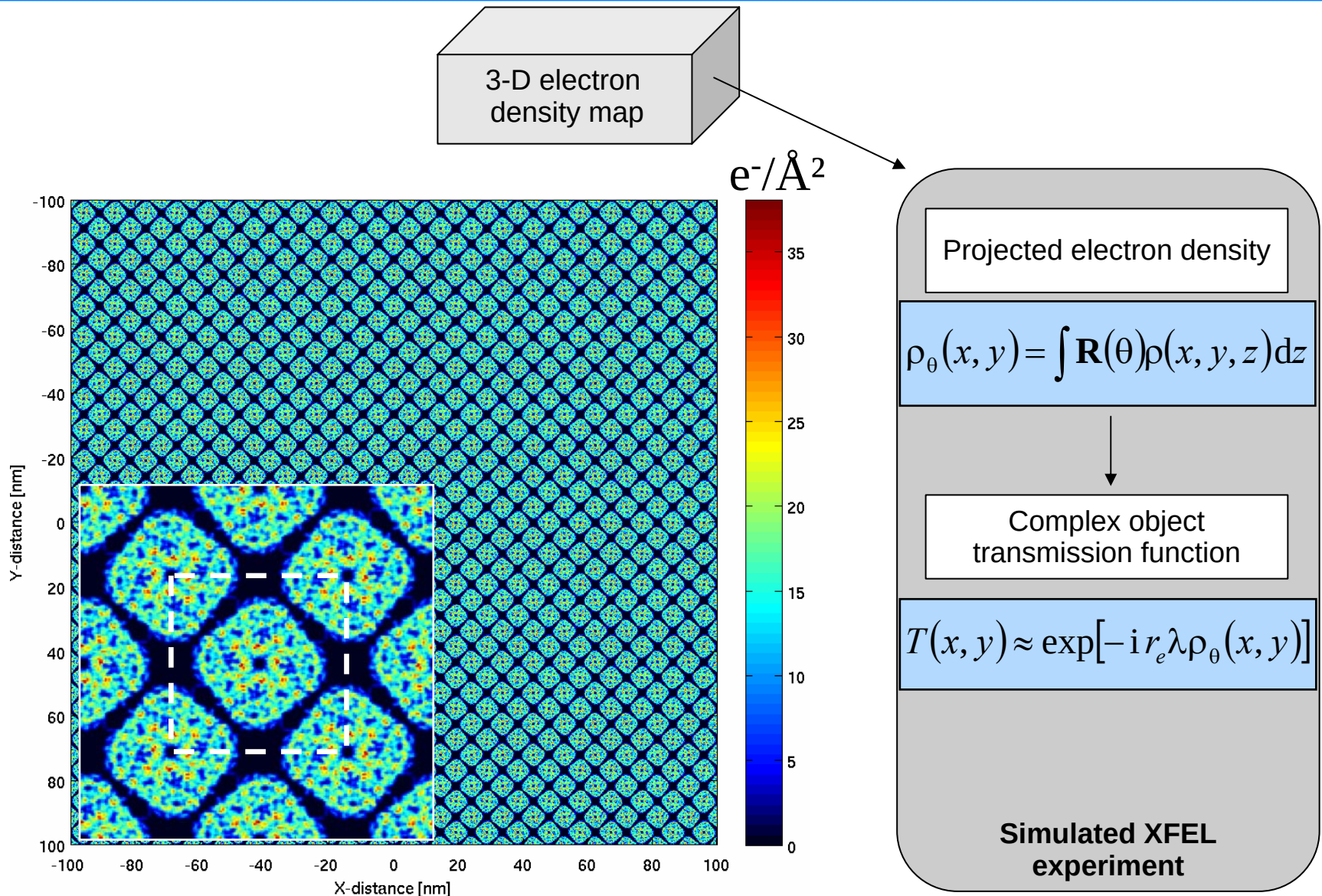
ATOM	1	N	LYS	A	8	56.812	30.226	17.376	1.00	10.00	N
ATOM	2	CA	LYS	A	8	57.972	30.061	16.444	1.00	10.00	C
ATOM	3	C	LYS	A	8	57.595	28.971	15.486	1.00	10.00	C
ATOM	4	O	LYS	A	8	57.990	28.922	14.332	1.00	46.93	O
ATOM	5	CB	LYS	A	8	59.210	29.616	17.216	1.00	46.93	C
ATOM	6	CG	LYS	A	8	59.575	30.484	18.403	1.00	46.93	C
ATOM	7	CD	LYS	A	8	59.667	31.974	17.988	1.00	46.93	C
ATOM	8	CE	LYS	A	8	59.865	32.934	19.166	1.00	46.93	C
ATOM	9	NZ	LYS	A	8	59.935	34.336	18.667	1.00	46.93	N
ATOM	10	N	LEU	A	9	56.864	28.048	16.039	1.00	10.00	N

~1,660 atoms in monomer
MW ~ 28 kDa



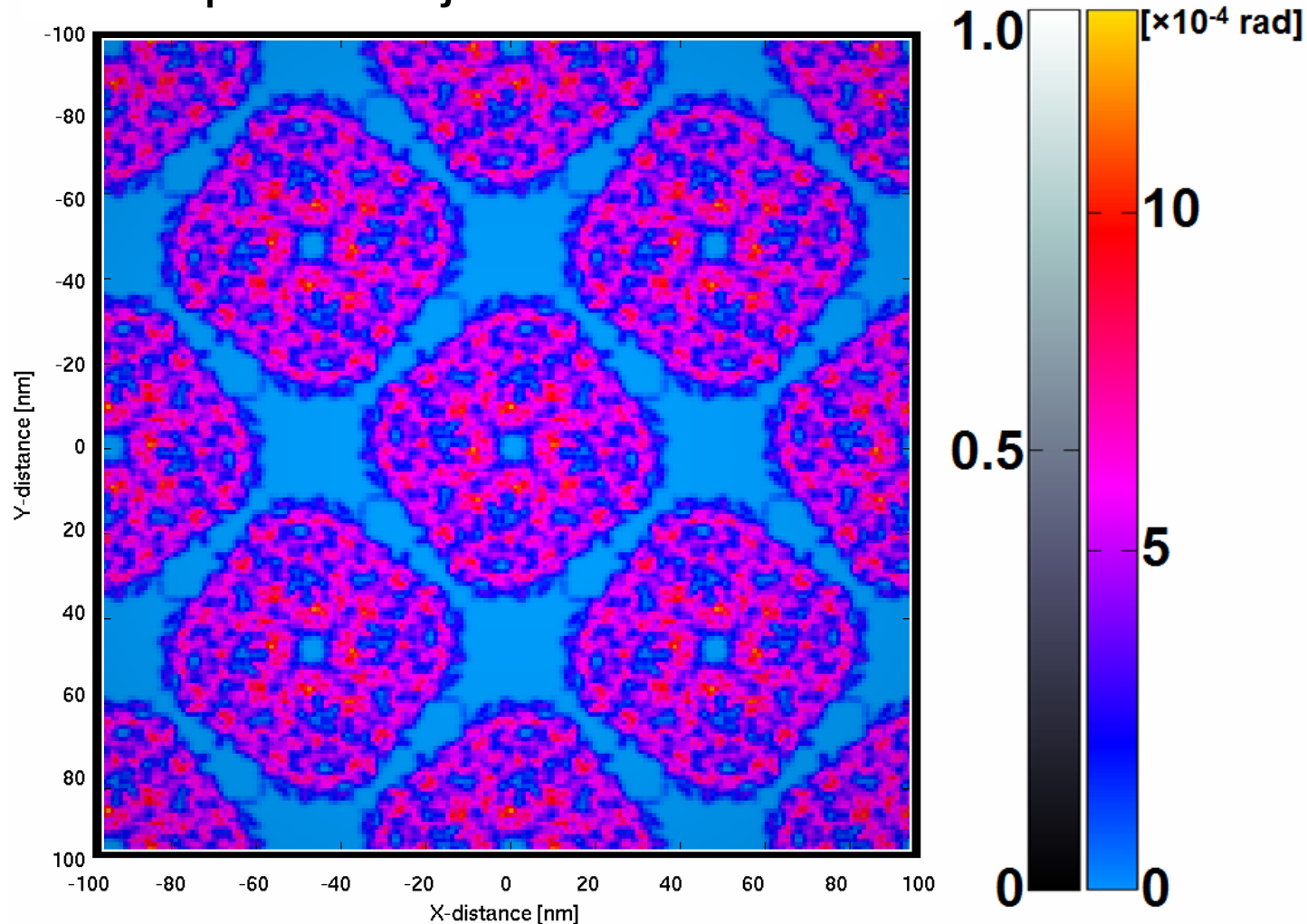
~13,300 atoms in unit cell

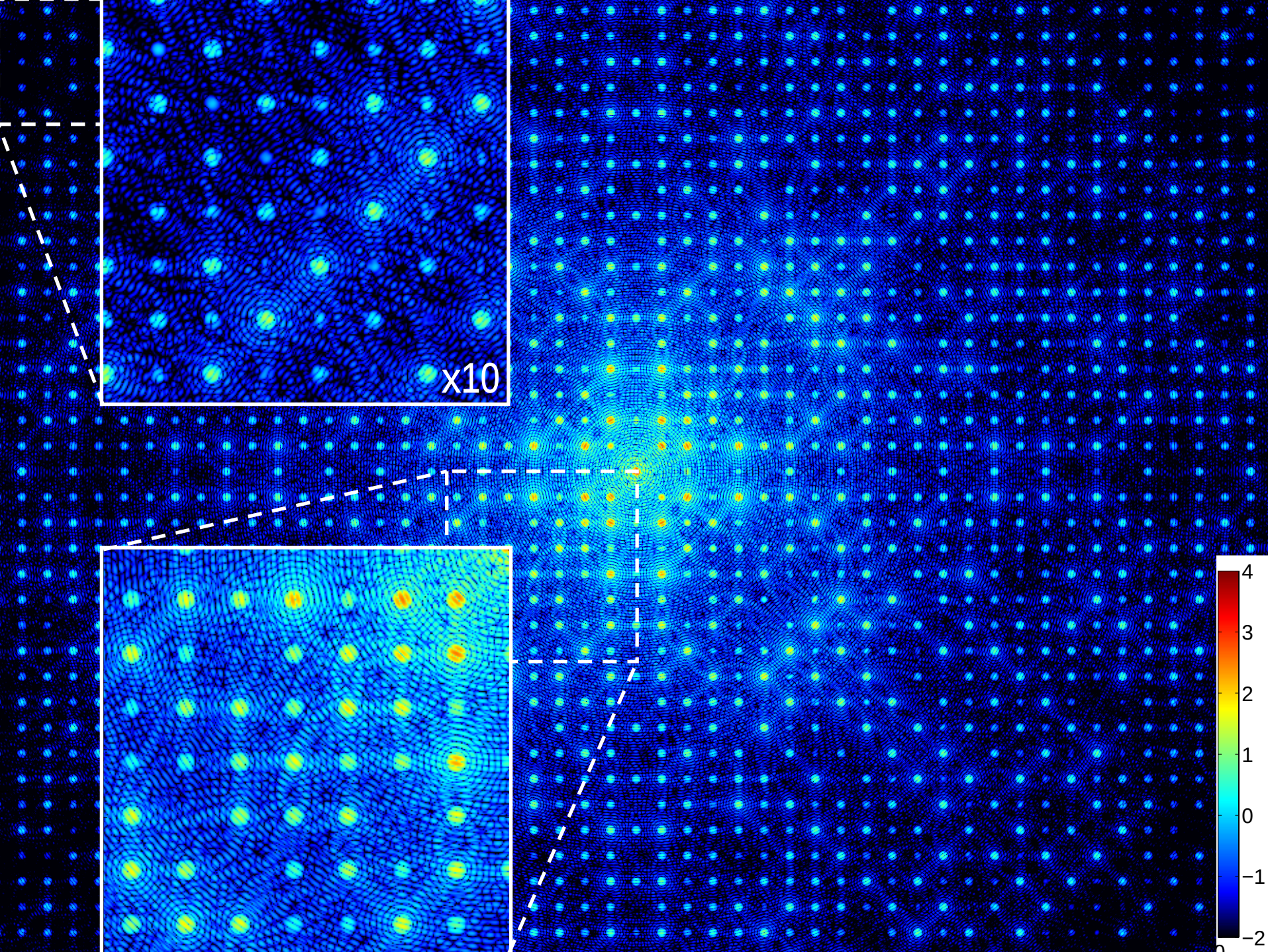
Electron density projected into 2D



Simulated XFEL Experiment

Weak phase object $\sim 10^{-4}$ - 10^{-3} radians

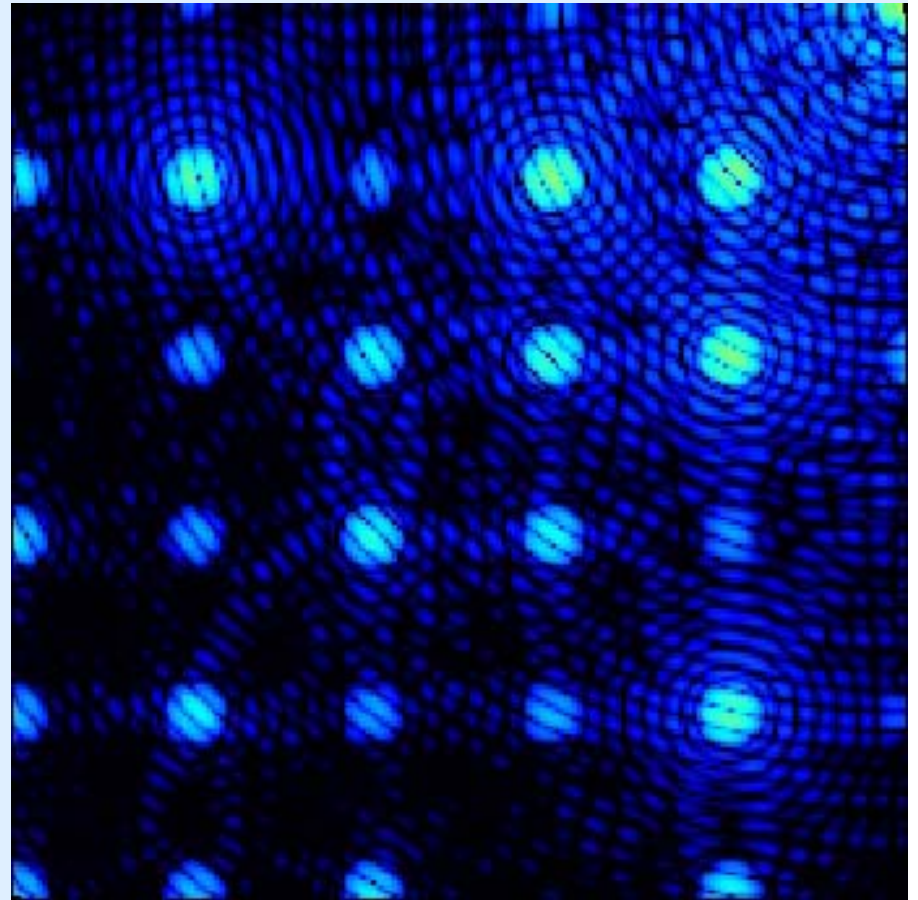




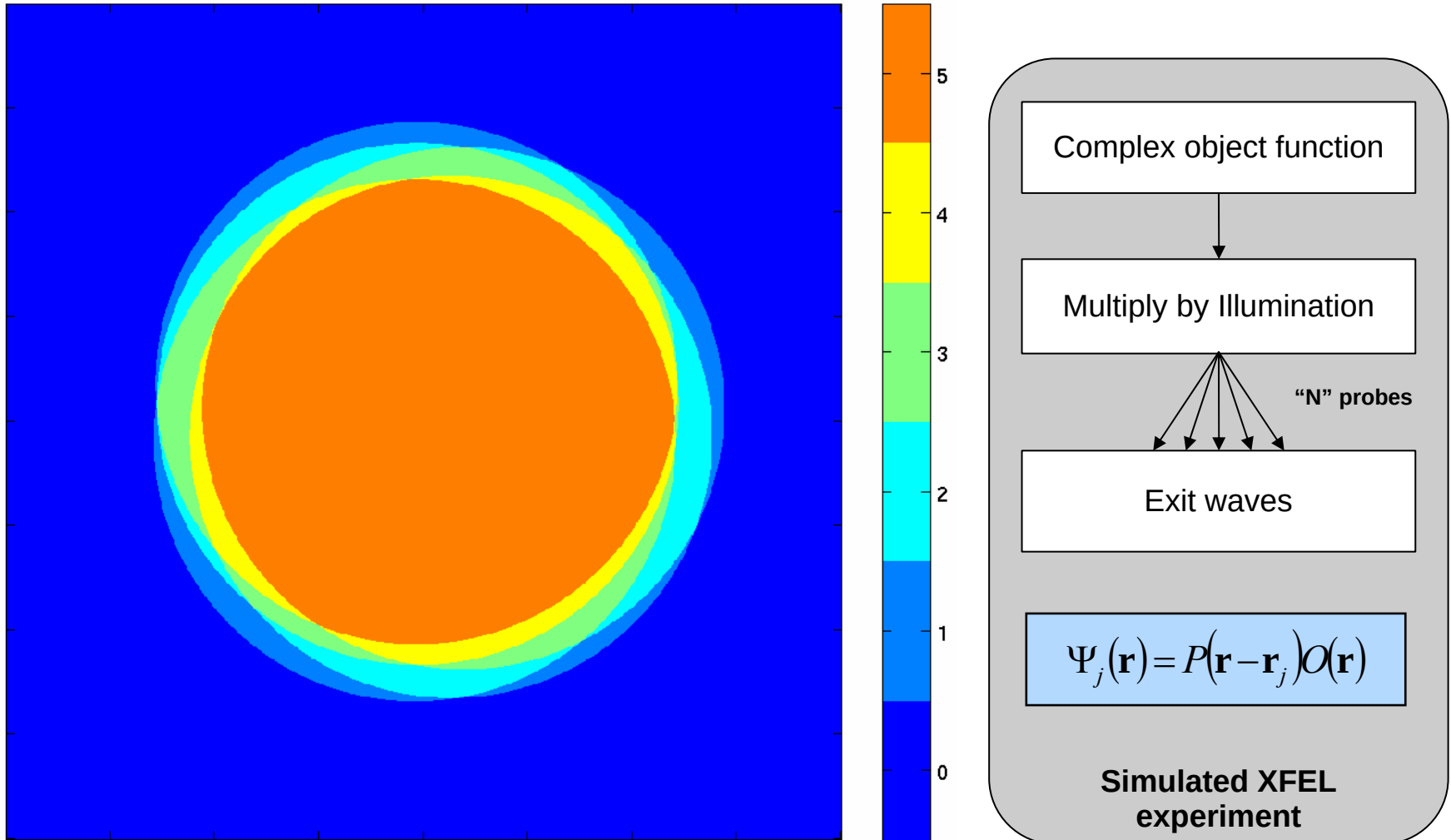
How does the coherence help?

Interference between diffraction from the aperture and the crystal in between the Bragg peaks changes with the position of the illuminating probe.

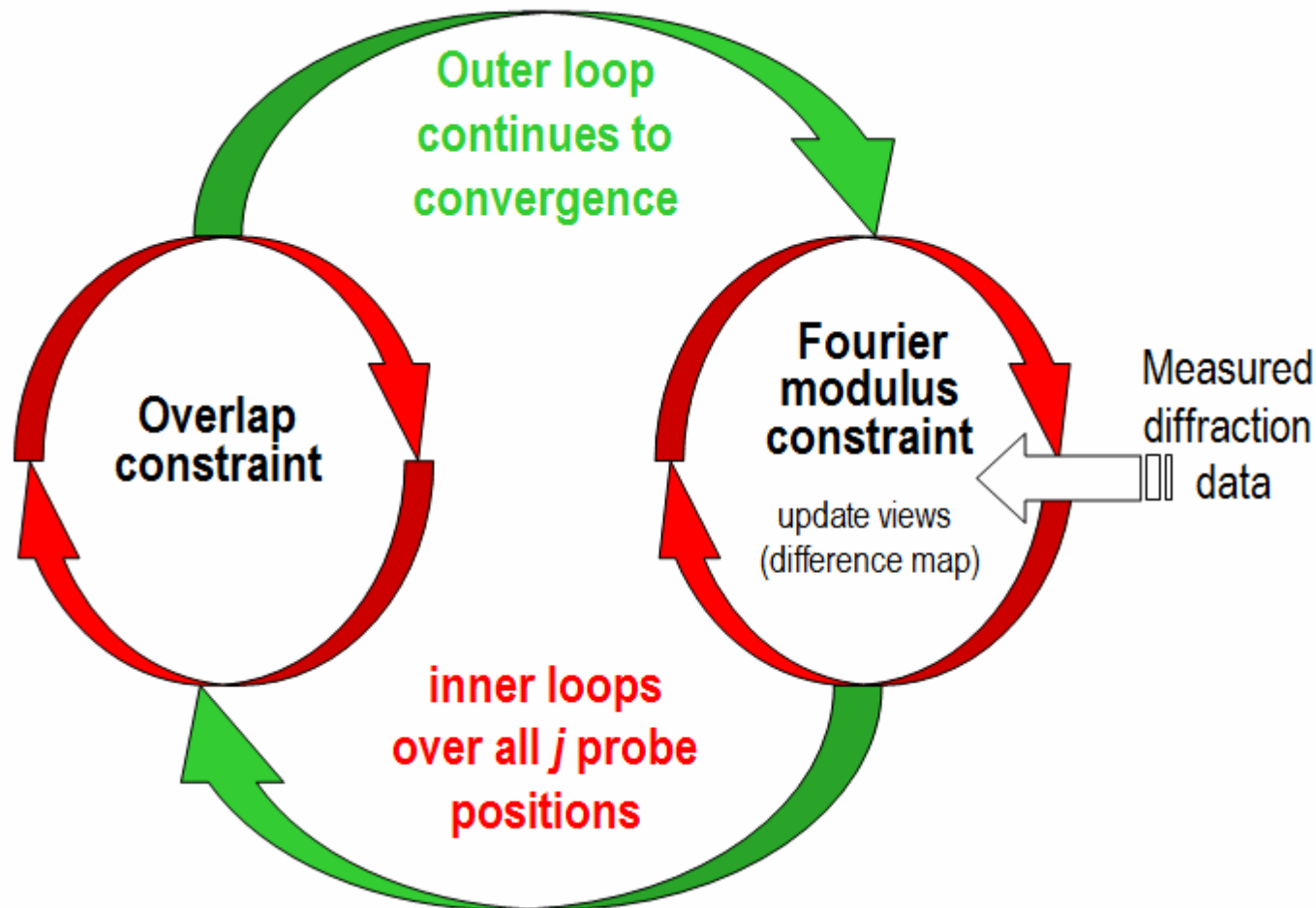
Using multiple “*overlapping*” exposure positions, the interference structure allows us to solve the phase problem with a ptychography algorithm.



Simulated XFEL experiment

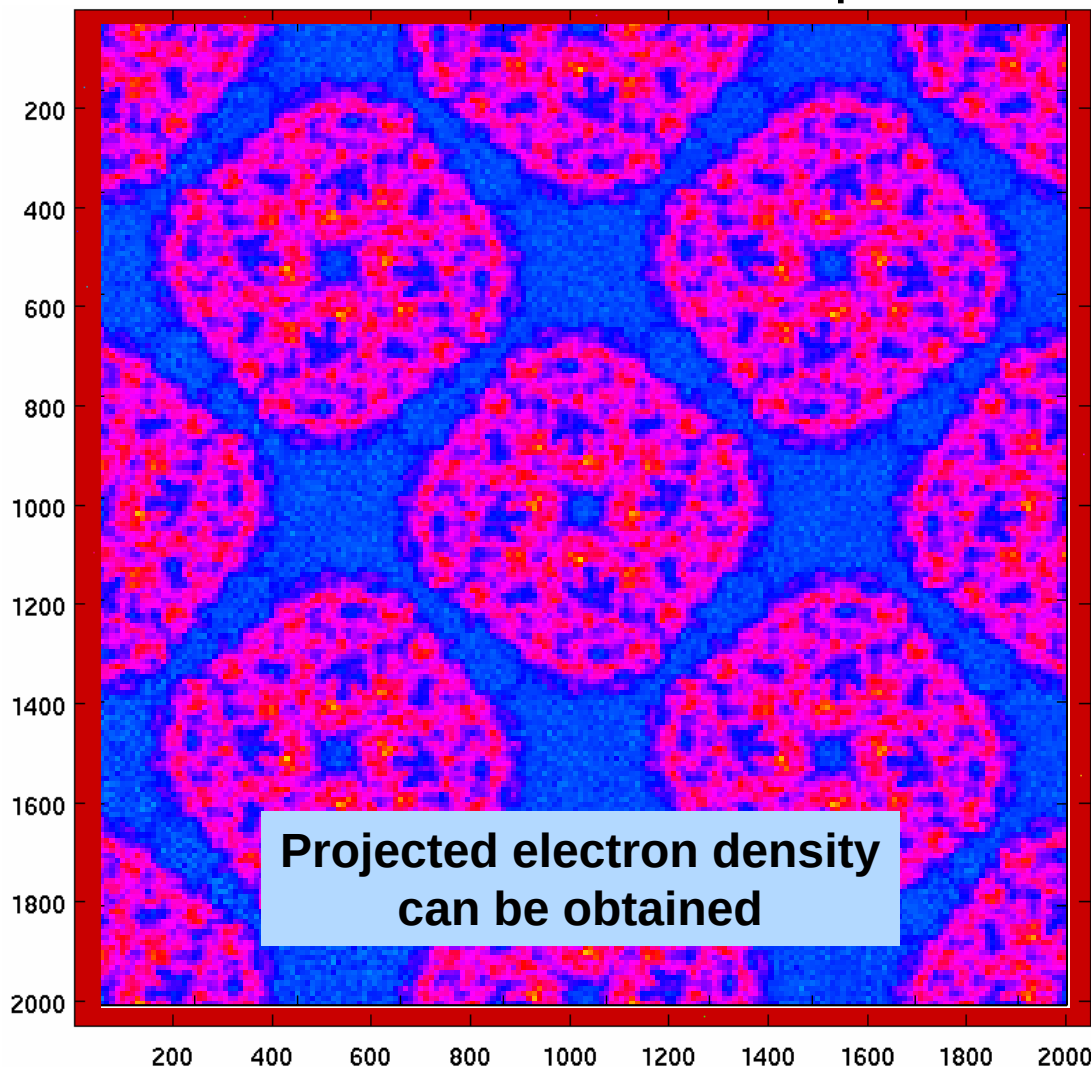
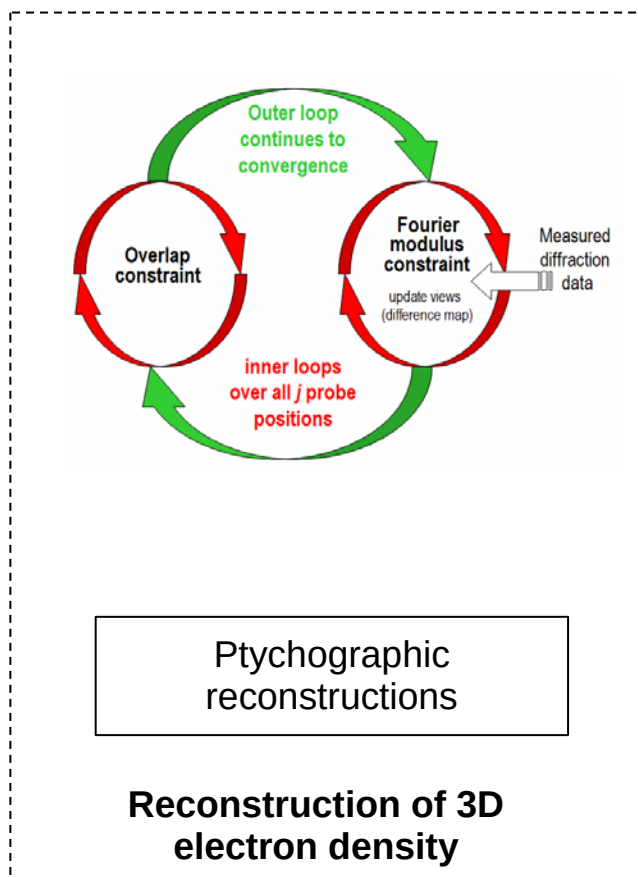


Reconstruction from coherent diffraction

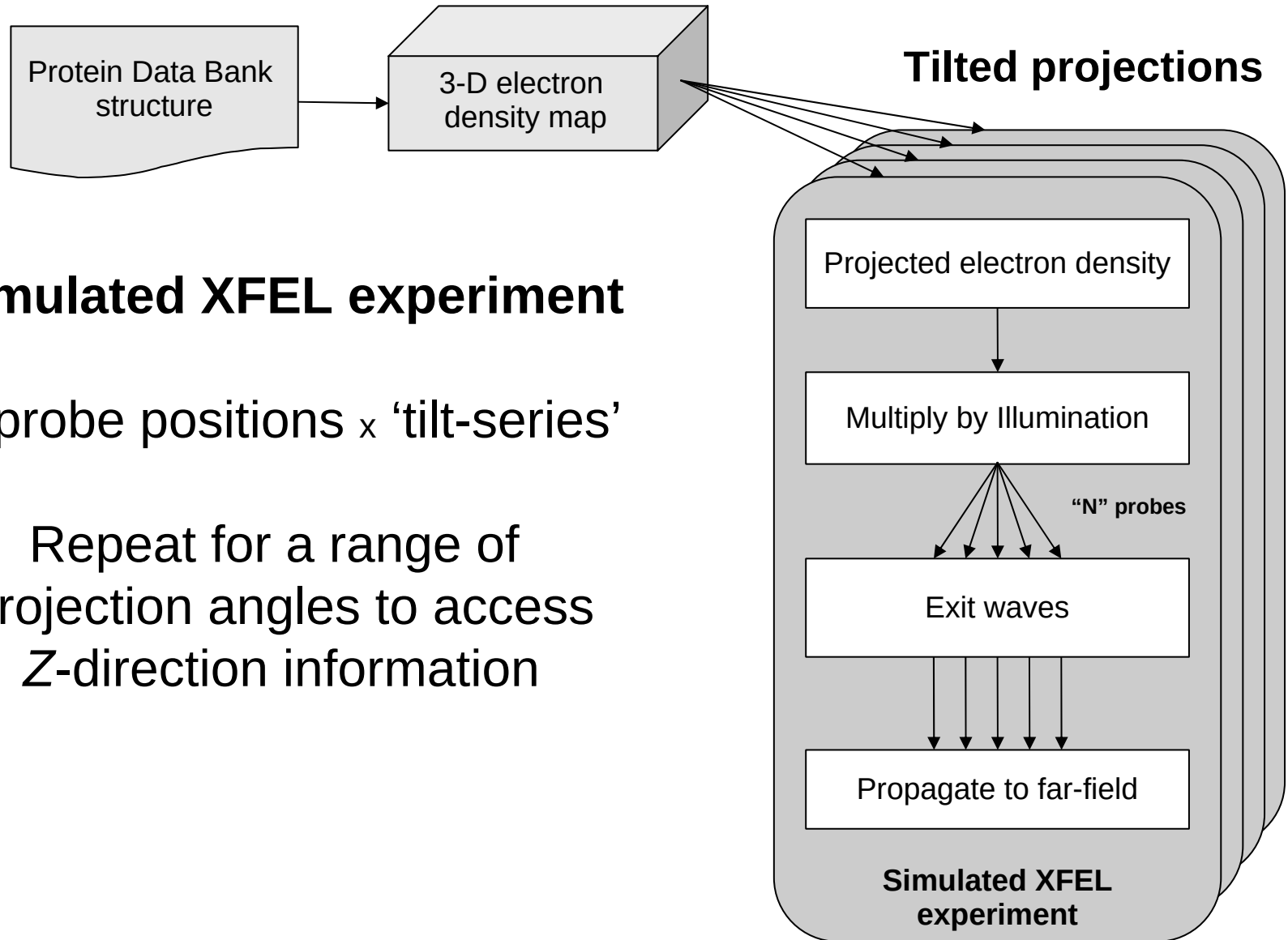


Reconstruction from coherent diffraction

Reconstructed exit wave phase



Summary of the simulated experiments

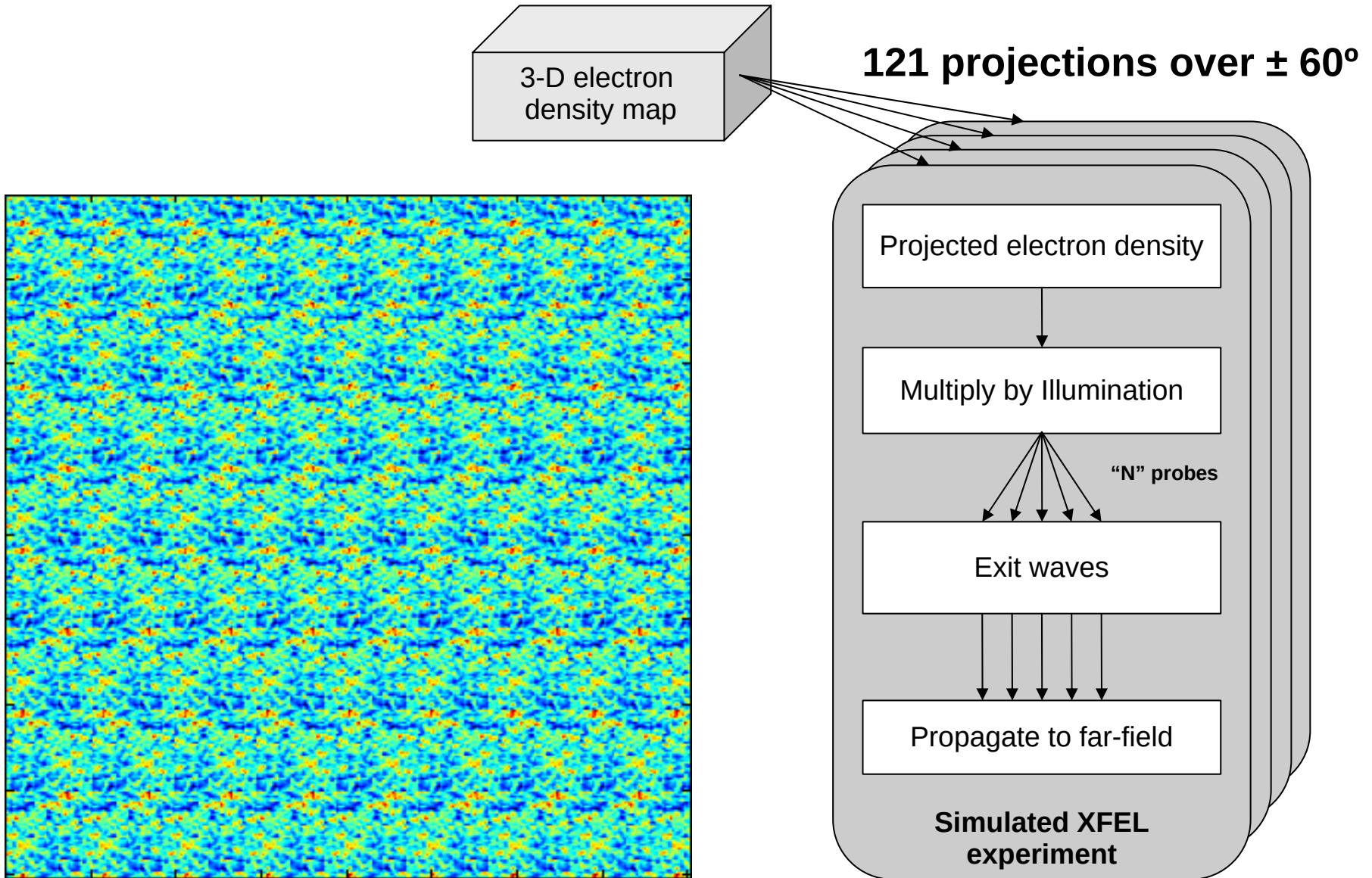


Simulated XFEL experiment

N probe positions x 'tilt-series'

Repeat for a range of
projection angles to access
Z-direction information

Simulated tilt-series

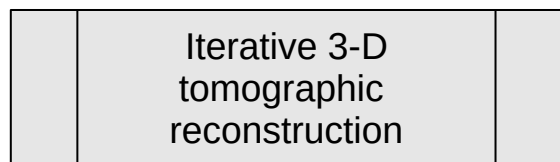


Tomographic reconstruction of protein

$$f_i^{new} = f_i^{old} + \gamma \frac{(p_j^{new} - p_j^{old})}{\sum_{k=1}^I w_{kj}^2} w_{ij}$$

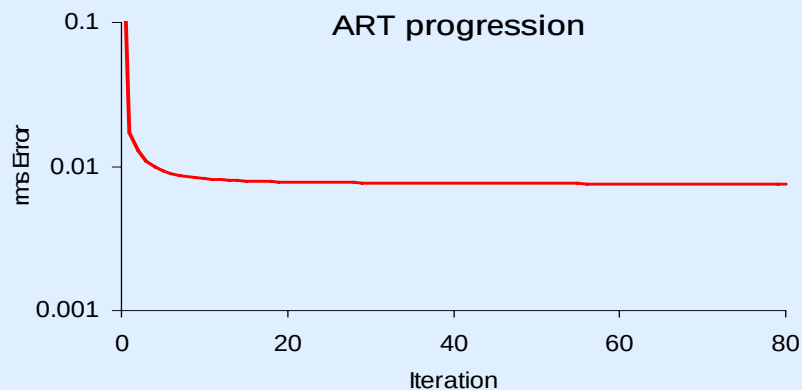
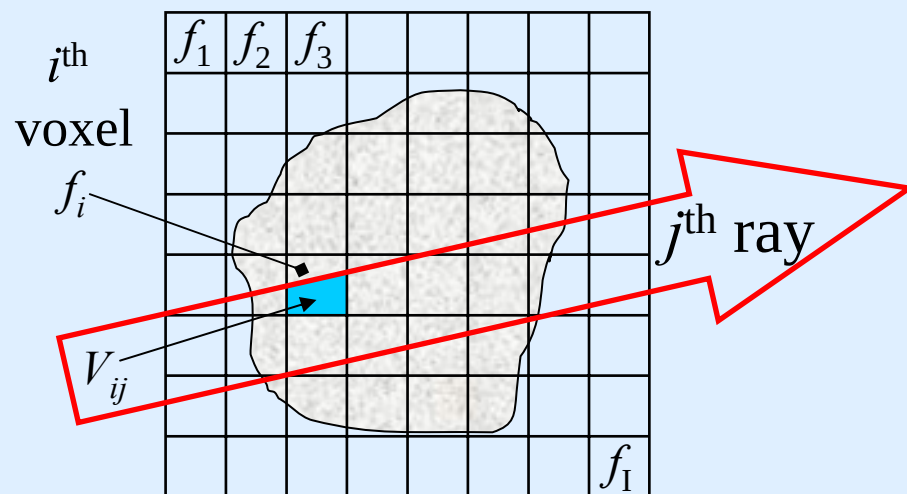
Handles missing Fourier coefficients using a weighting matrix, w_{ij}

Relaxation factor γ aids convergence

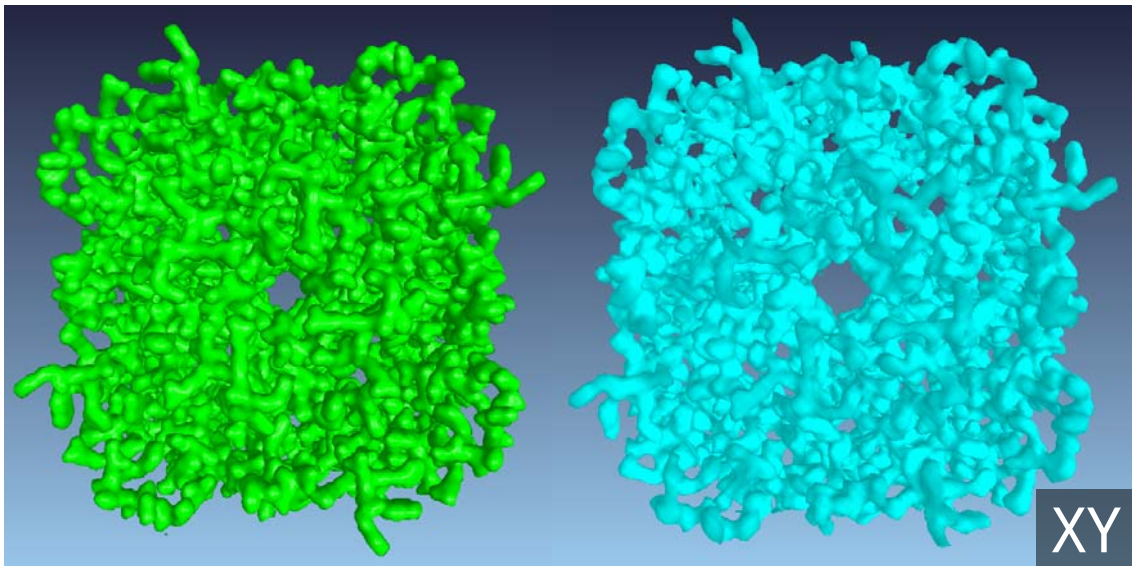


**Reconstruction of 3D
electron density**

Algebraic Reconstruction Technique (ART):

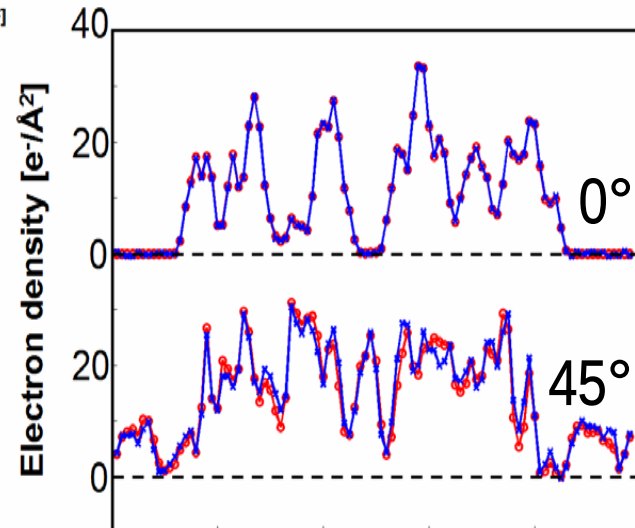
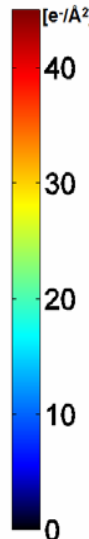
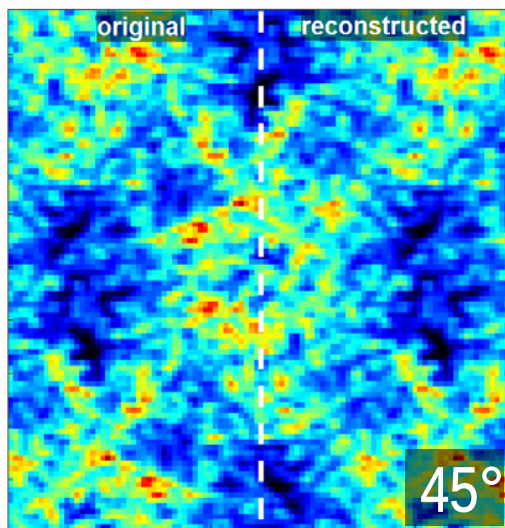
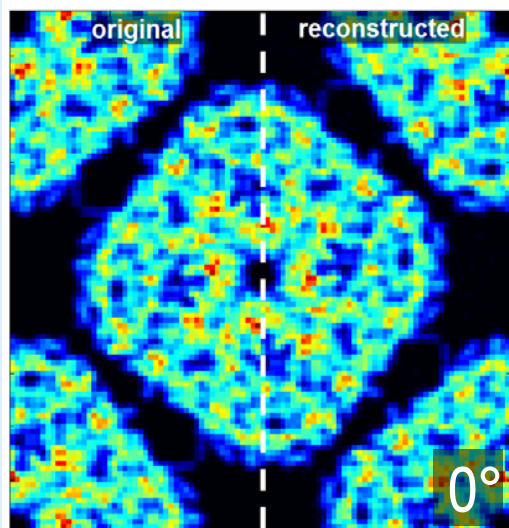


Reconstructed 3-D electron density map

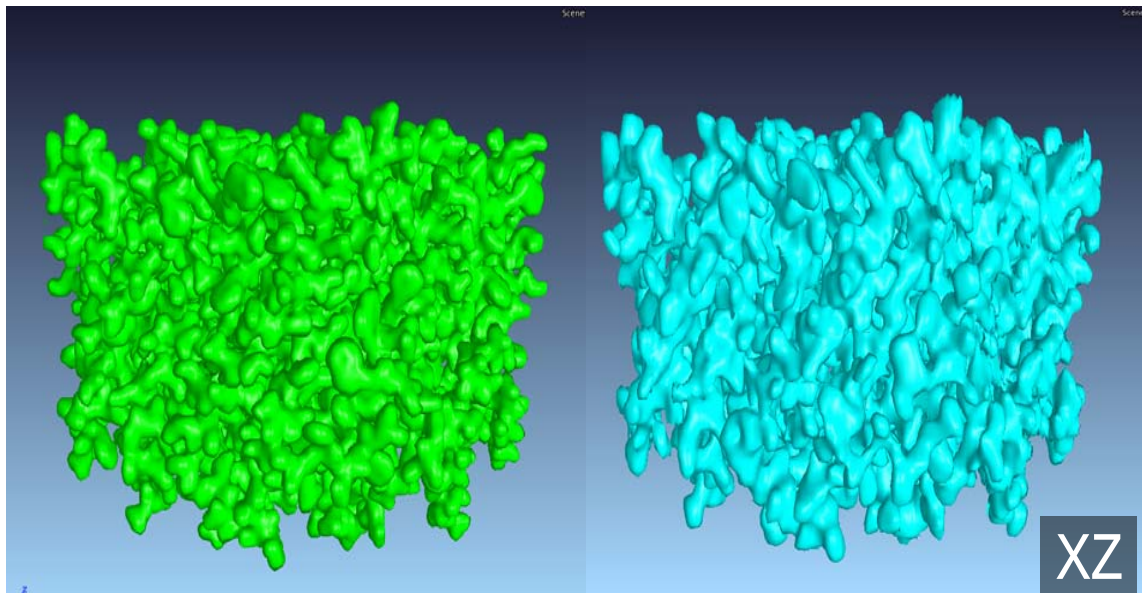


Isosurface rendered
at $0.5 \text{ e}/\text{\AA}^2$

Reconstructed
projections agree well
with original data

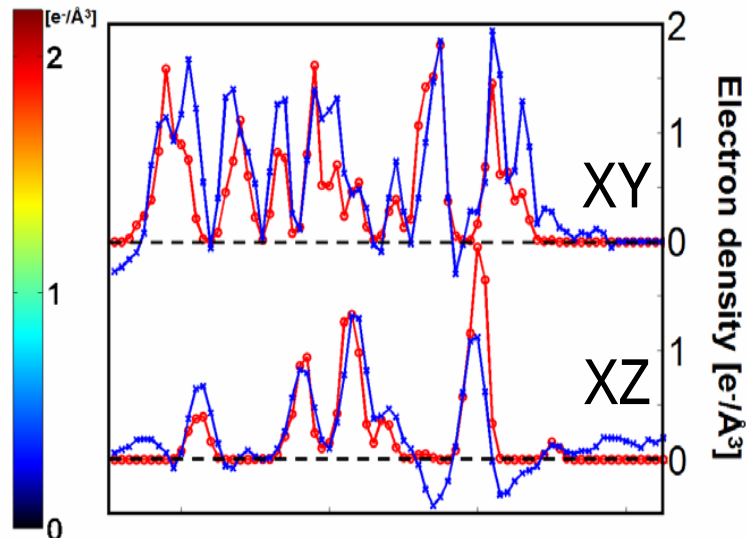
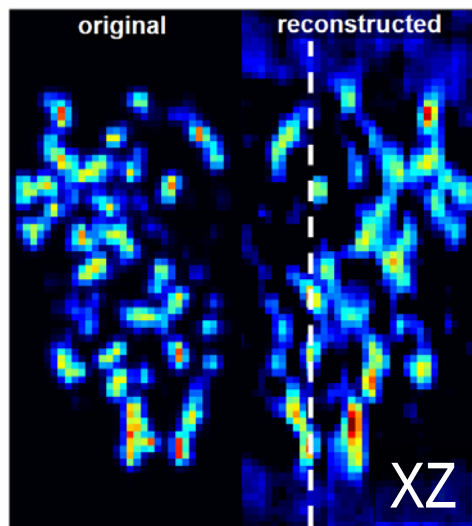
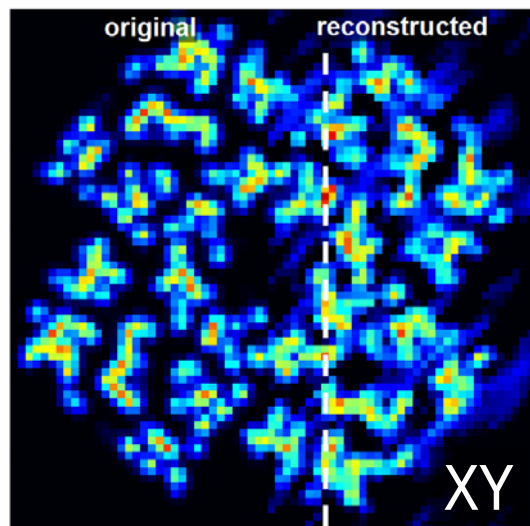


Reconstructed 3-D electron density map



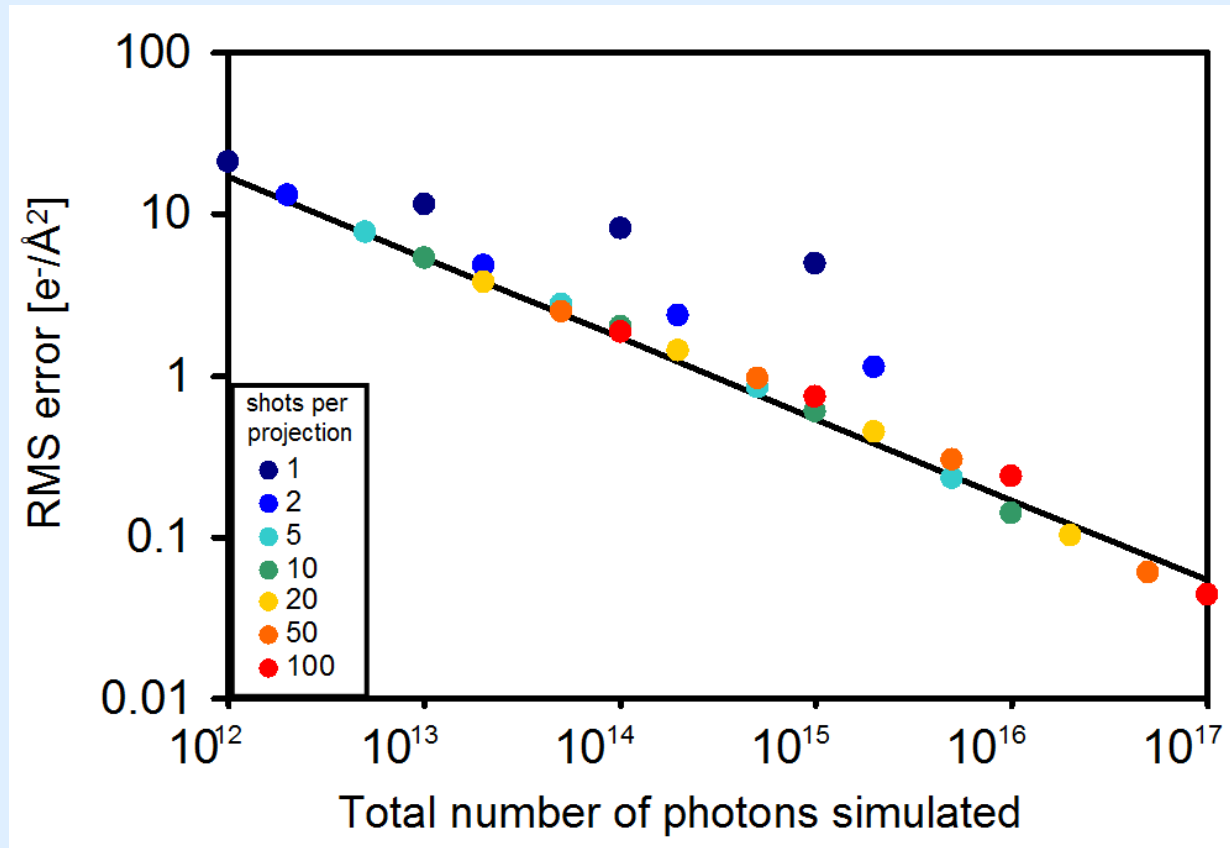
Isosurface rendered
at $0.5 \text{ e}/\text{\AA}^2$

Slices from 3-D density
map agree reasonably
well with original values



Reconstruction quality vs. Poisson noise

RMS error in reconstructed projections follows Poisson noise: As pulse intensity, or number of shots per projection is increased, the RMS error follows a log-log trend.



Conclusion

Thank you for your attention

Achieved:

- Finished the first 'full cycle' simulation: forward calculation & reconstruction
- Experiment & reconstruction seems feasible, even when including Poisson noise and expected XFEL flux values

Ongoing work:

- Assess effect of variation in the incoming XFEL wave fronts
- Influence of Coulomb explosion on reconstruction
- Ewald sphere lift-off
- Experimental background ...

