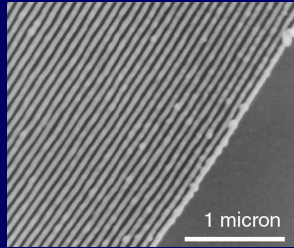
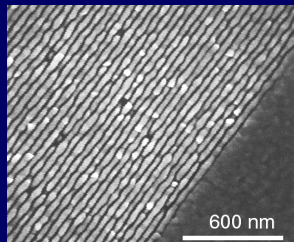


Zone plate microscopy

- SUNY Stony Brook: A. Stein, C. Jacobsen (past: S. Spector)
- Bell Labs: D. Tennant
- Image resolution essentially equal to outermost zone width
- JEOL JBX-9300FS: 1 nA into 4 nm spot at 100 keV, 500 μm field



40 nm zones in 120 nm Ni
(have also done 45 nm in 180 nm Ni)



20 nm zones in 60 nm Ni

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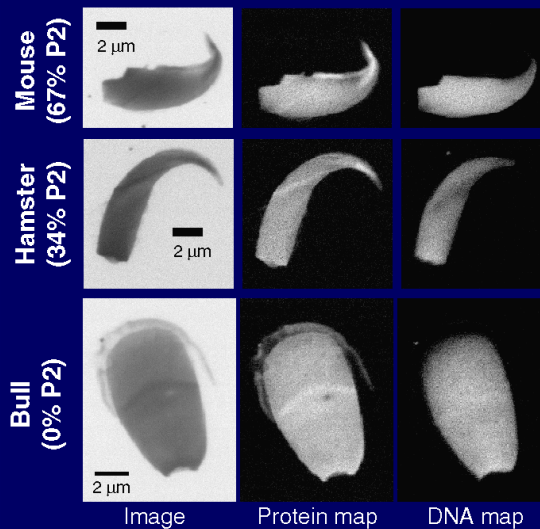


S. Spector, C. Jacobsen, D. Tennant, *J. Vac. Sci. Tech. B* **15**, 2872 (1997)

1

Spectromicroscopy of DNA packing in sperm

- X. Zhang, R. Balhorn, J. Mazrimas, and J. Kirz, *J. Structural Biology* **116**, 335 (1996)
- Use XANES/NEXAFS resonances for chemical state mapping
- Each sample imaged at $N=6$ energies; images aligned by hand
- Conclusion: protamine II replaces protamine I, rather than binding to protamine I complex (implications for infertility)



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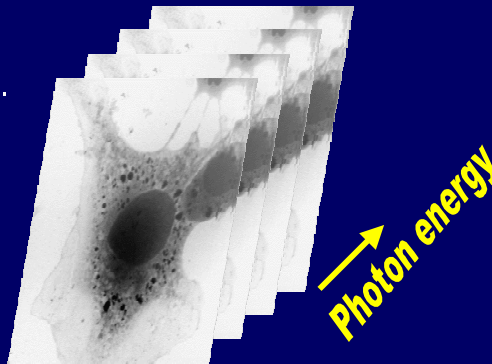
2

Spectromicroscopy by image stacks

- Acquire sequence of images over XANES spectral region; automatically align using Fourier cross-correlations; extract spectra.
- Full data set to exploit with multivariate statistics (e.g., principal component analysis)
- C. Jacobsen *et al.*, *J. Microscopy* **197**, 173 (2000).

Images at $N=150$ energies are common.

Total acquisition time at NSLS X-1A (10^{18} brightness): 3-10 hours for a $10\ \mu\text{m}$ field at 50 nm resolution



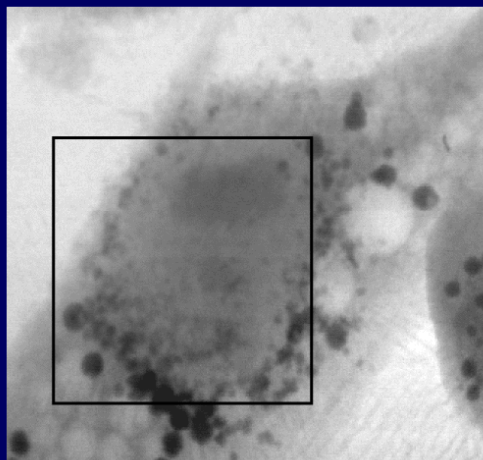
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3

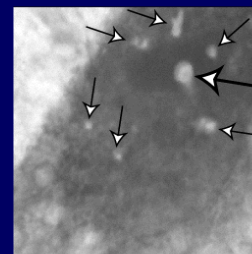
Cryo specimens can withstand multiple images

Left: frozen hydrated image *after* exposing several regions to $\sim 10^{10}$ Gray (about 10^4 times single image dose)

Right: after warmup in microscope (eventually freeze-dried): holes indicate irradiated regions!



Maser *et al.*, *J. Microscopy* **197**, 68 (2000)



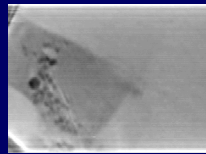
7 μm

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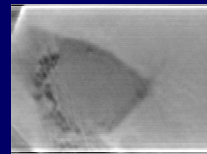
4

Tomography of a fibroblast

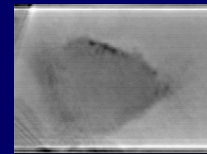
- Y. Wang *et al.* (Stony Brook), *J. Microscopy* **197**, 80 (2000)
- 3T3 fibroblast, extending over ~ 12 μm depth, $100 \times 100 \times 250$ nm minimum feature size
- Required ~ 30 hours to acquire data set at NLSL X-1A
- Future efforts aimed at higher resolution without a depth-of-field limit by using diffraction tomography



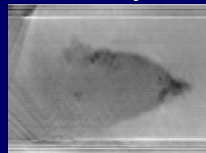
$z = 12.7 \mu\text{m}$



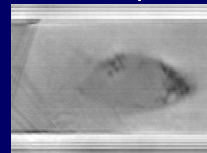
$z = 15.1 \mu\text{m}$



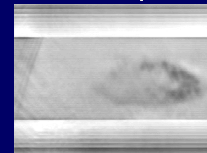
$z = 17.6 \mu\text{m}$



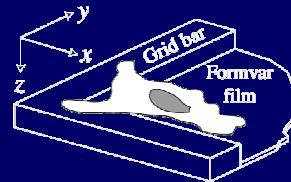
$z = 20.0 \mu\text{m}$



$z = 21.6 \mu\text{m}$



$z = 23.1 \mu\text{m}$



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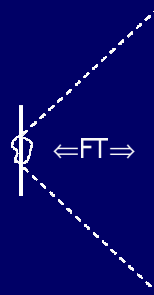
5

Imaging using x-ray diffraction from non-periodic specimens

- Diffraction pattern can be recorded with no optics-imposed resolution limits
- Proposed by Sayre (in Schlenker, ed., *Imaging and Coherence Properties in Physics*, Springer-Verlag, 1980)
- Previous experiments by Sayre, Yun, Chapman, Miao, Kirz
- Reconstruction: iterate between real and Fourier space

Real space:

- Finite support: object fills only part of the field
- Positivity?



Fourier space:

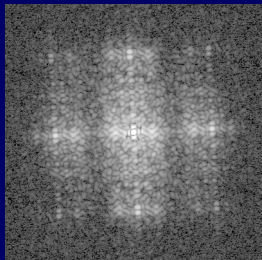
- Re-impose the measured intensities while letting the phases evolve

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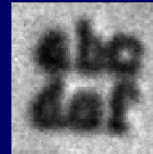
6

Imaging using soft x-ray diffraction from non-periodic specimens

- Reconstruction: $\lambda=1.8$ nm diffraction pattern, plus optical micrograph for low spatial frequencies
- Miao, Charalambous, Kirz, Sayre, *Nature* **400**, 342 (1999).



Soft x-ray diffraction pattern (left) with low-angle information from optical micrograph (below)



Scanning electron micrograph of object

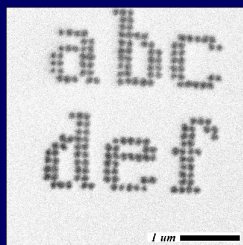


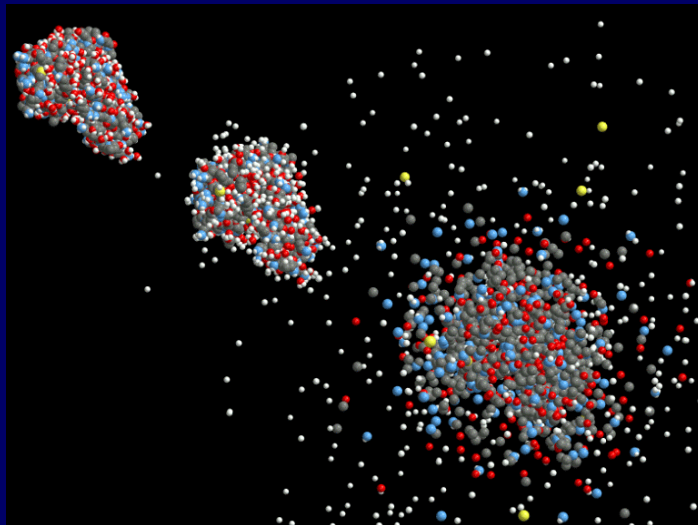
Image reconstructed from diffraction pattern (θ_{\max} corresponds to 80 nm)

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Single molecule imaging?

- R. Neutze *et al.*, *Nature* **406**, 752 (2000)
- For macromolecules that can't be crystallized, collect many single molecule diffraction patterns from fast x-ray pulses, and reconstruct
- Lysozyme explodes in ~ 50 fsec

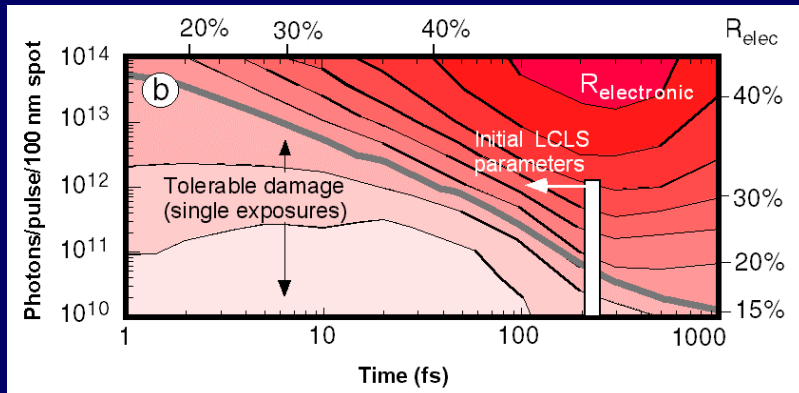


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Single molecule imaging: what's needed?

- Lots of coherent photons in a short pulse!
- R. Neutze *et al.*, *Nature* **406**, 752 (2000)
- LCLS (Stanford), TESLA (Hamburg) X-FEL experiment proposals led by J. Hajdu (Uppsala)



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