Diffraction Microscopy of biological specimens: imaging of a freeze-dried yeast cell

Enju Lima[1]
Veit Elser[2], Malcolm Howells[3], Xiaojing Huang[1], Chris Jacobsen[1], Janos Kirz[1, 3], Huijie Miao[1], David Sayre[1], David Shapiro[1, 4], Pierre Thibault[2]
[1] Department of Physics and Astronomy, Stony Brook University, Stony Brook, NY 11794-3800 USA
[2] Department of Physics, Cornell University, Ithaca, New York 14853 USA
[3] Advanced Light Source, Lawrence Berkeley National Laboratory, Berkeley, California 94720 USA
[4] Center for Biophotonics Science and Technology, University of California at Davis, Sacramento, CA 95817 USA

Diffraction microscopy provides an alternative to lens-based methods of imaging non-crystalline objects. Thus, one can potentially reach resolutions beyond the limit imposed by optics. Image reconstruction in this case is a simple inverse Fourier transform of the correctly phased diffraction pattern. Phasing diffraction data of non-crystalline objects is achieved by iterative algorithms: the two most widely used are Fienup's HIO algorithm and Elser's Difference map. [1, 2] Both of these algorithms utilize available information about a sample as constraints. The important constraint in the real image space is called the finite support, which is guaranteed by oversampling diffraction pattern. [3] The Fourier space constraint is the measured diffraction pattern. Several groups have reported successful reconstructions of biological or material science samples by this technique. [4, 5, 6, 7, 8]

In our experiment, the X-ray diffraction pattern of a freeze-dried yeast cell was collected at 750 eV and phasing was performed using the Difference map. The freeze-dried yeast cell was 3 microns in diameter and its exit wave became complex-valued at 750 eV. The reconstruction of complex valued objects has been found to be particularly challenging [9,10], and the success of the reconstruction illustrates a step forward in this technique. The reconstructed image shows the nucleus and cell membrane clearly in 30 nm resolution. The reconstruction of a freeze-dried yeast cells gives us confidence that the phasing algorithm would work when one has diffraction data from frozen hydrated biological samples, which most resemble the living biological state.

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