A CALCULATION OF THE PERFORMANCE OF A SCHEME FOR IMAGING MACROMOLECULAR ASSEMBLIES BY DIFFRACTION TOMOGRAPHY

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In this paper we discuss a holographic solution to the difficult problem of imaging the so-called molecular machines. These objects are large assemblies of proteins functioning as a group which in many cases cannot be crystallized. Determination their structure inside a cell of thickness several microns poses a microtomography problem at a resolution of 3-12 nm which we discuss in this paper.

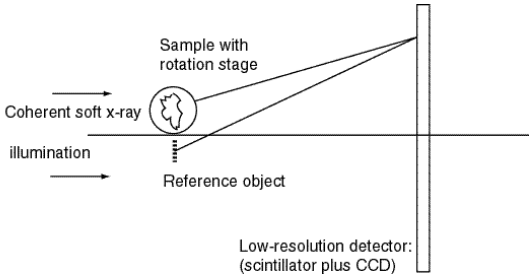

Figure 1: Fourier transform holography experiment.

There are fundamental limitations involved in applying more conventional techniques to this problem, e. g. the light microscope (wavelength), the electron microscope (multiple scattering) or the x-ray microscope (zone-plate manufacture). The solution we propose here is soft x-ray diffraction tomography. This method requires a recording of both the amplitude and phase of the diffracted wavefield at each view direction which we propose to do using holography.

A schematic of our proposed experiment is shown in Fig. 1. It is a standard Fourier transform holography scheme with a "generalized reference object". The latter is not point-like but must have structure out to the spatial frequencies that are to be resolved and a reasonably flat power spectrum. In other words it must be able to fill the detector with diffracted soft x-rays. In this paper we discuss the following issues using optical theory and computer modelling.

- How can the generalized reference object be realized in practice?
- How is a diffraction-limited image recovered when the reference object is not point-like?
- Is it necessary for the reference object to be accurately known?
- Could one use Fienup-type algorithms to recover the phases of the diffraction pattern without holography as demonstrated for model objects by Miao et al [1].?
- Are the exposure times using available synchrotron-radiation sources reasonable and are the radiation doses acceptable for frozen hydrated samples?

References

[1]. J. Miao, Charalambous, P., Kirz, J., and Sayre, D., Nature, **400** (1999) 342

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