X-RAY CELLULAR TOMOGRAPHY: HOW THE IMAGES ARE FORMED AND HOW THE VOLUMES SHOULD BE RECONSTRUCTED

R. Marabini[2], J.Oton[1], C. Sorzano-Sanchez[1] and J.M.Carazo[1]

1 Instruct Image Processing Center-Biocomputing Unit, Centro Nacional de Biotecnologia CNB-CSIC, Campus Universidad Autonoma, 28049 Madrid.

2 Escuela Politécnica Superior | Universidad Autónoma de Madrid | Francisco Tomás y Valiente, 11 | 28049 Madrid

roberto@cnb.csic.es

The use of cryo X-ray tomography as a new approach to gain quantitative 3D information from whole cells has been made possible recently thanks to the development of a series of “X-ray tomographic microscopes” in several synchrotrons world wide.

In these new microscopes, the absorption power of proteins is in the range of the so called “soft” X-rays (284 – 543 eV), which is ten times smaller than in electron microscopy and much smaller for water, give us the capability of obtaining projections from compounds in a watery buffer through tens of microns depth. However, these new capabilities come with new challenges in all fronts, including the image processing one. To start with, the relatively small depth of focus of these microscopes equipped with diffractive lenses makes that different planes of the observed object contribute to the projected image with different Point Spread Functions (PSF); i.e., the effective focus changes along the specimen in a much more noticeable manner than in electron microscopy.

In this contribution we develop a new image formation model that fully takes into account how an X-ray wavefront propagates through an absorbing media with a distance-varying PSF, also taking into account other factors which can introduce a lack in the alignment.

Once a proper image formation model has been developed, the next step is the derivation of new reconstruction algorithms that explicitly take it into account. At this moment we are addressing this issue, concentrating in the modification of a “conventional” tomographic algorithm, as the Algebraic Reconstruction Technique (ART), so it can lead us to a high performance computing algorithm optimized for the reconstruction from X-ray tomographic projections.

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