Image processing for Cellular tomography using soft X-rays

C.O.S. Sorzano[1*], J. Otón[1], J. Cuenca[1], A. Zaldivar-Pérez[1], G. Caffarena[2], J. Sánchez-Jiménez[2], C. Messaoudi[3], S. Marco[3], R. Marabini[4], J.M. Carazo[1]

[1]National Center of Biotechnology (CSIC)
[2]Univ. San Pablo - CEU
[3]Institute Curie
[4]Univ. Autónoma de Madrid

Abstract

Cellular tomography using X-rays is a novel technique that allows acquisition of structural information of complete cells, in their native environment without the need of sectioning or staining. To acquire three-dimensional information, samples must be tilted inside the microscope. This acquisition technique is shared with Electron Tomography (ET), and the acquired images share with ET the limitations on the maximum tilt and the alignment problems. However, the soft X-ray microscope differs from ET in the way it produces the image. First, image is formed mostly by amplitude contrast (attenuation of the incident beam); second, since the sample is much thicker, the microscope depth of focus is clearly visible along the tilt series. The image formation model for X-rays has recently been published by our group. In this paper, we present the main image processing steps needed from the tilt series acquisition to the final interpretation of the volume. In brief these steps are normalization, alignment, 3D reconstruction explicitly considering the depth of focus differences, denoising, and segmentation. We will also present Xmipp-TomoJ, a publicly available software tool allowing the execution of all these steps.