

Image processing in cryo Electron Microscopy (cryo EM): Analyzing reliability and quality

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Modern electron microscopes equipped with direct electron detectors are nowadays providing 2D images (“micrographs”) with quasi atomic resolution. However, the way from 2D image collection to the calculation of accurate structural maps showing the electrostatic potential of biological macromolecules demands complex image processing operations, involving many local optimizers. Naturally, the possibility always exists of getting trapped into local minima, representing wrong structural maps. In this context, I will present several approaches to analyze reliability and quality in cryo EM, including ways to analyze precision and accuracy in estimating the relative geometrical orientation among images (a key step in the 3D reconstruction process) and a novel approach to resolution estimation, totally automatic, allowing for local (pixel-based) analysis. All these new approaches are freely available as part of both XMIPP and Scipion image processing suites.

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