A complete data processing workflow for in situ structure determination with cryo-electron tomography

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Electron cryotomography (CryoET) is currently the only method capable of visualizing cells in 3D at nanometer resolutions. While modern instruments produce massive amounts of tomography data containing extremely rich structural information, it takes tremendous effort to process those data and reach biological findings. Here we present an integrated workflow that covers the entire tomography data processing pipeline, from automated tilt series alignment and particle selection to subnanometer resolution subtomogram averaging. Resolution enhancement is made possible through the use of per-particle-per-tilt CTF correction and orientation refinement. This workflow greatly reduces human effort and increases the throughput of CryoET data processing, and is capable of determining protein structures at state-of-the-art resolutions for both purified macromolecules and cells.

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