ScipionTomo: a standard framework for cryoelectron tomography image processing

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Abstract

Cryo-Electron tomography (cryoET) is a well-established imaging technique that aims to reveal the structure of macromolecular complexes, organelles or cells. In the last years, cryoET has undergone a major revolution, exhibiting its potential for showing rich information about the biological processes inside the cells and obtaining reconstructions of complexes at resolutions as high as 3A. The advances in sample preparation, instrumentation, hardware, and software are responsible for this improvement. This communication is focused on the last one. The development of new image processing methods has allowed the extraction of more and more information from the data and has expanded the list of available software. Unfortunately, this broad variety of tools has also increased the complexity of the cryoET pipeline. The more methods, the more combinations between them are possible. This involves drawbacks for the users who want to use different software in the same workflow. Note that despite some efforts, the cryoET lacks standards for all software and each of them works with different data formats, metadata management and visualization tools. The users spend a lot of time dealing with these drawbacks, which push them away from the structure elucidation. ScipionTomo solves all these data management and traceability problems, by providing a common framework with graphical interface and visualization tools for cryoET image processing, where the different softwares are integrated as the so-called plugins. As a demonstration of ScipionTomo capabilities, different workflows are shown involving different plugins such as imod, dynamo, eman2, relion4, among the most highlighted.