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Dynamo: flexible software tools for subtomogram averaging of cryo electron tomography data

While Cryo Electron Tomography offers an unique potential for direct visualization of the three dimensional structure of macromolecular compounds in their cellular environment, the severely noisy nature of the low dose images delivered by the microscope makes this imaging technique heavily dependent on a suitable computational treatment of the raw data. In particular, structure determination through Subtomogram Averaging requires the localization of large number of noisy copies of the compound of interest and extraction of the common signal through classification and alignment.

This presentation focuses on several data processing challenges appearing in different stages of this technique, discussed in the context of the unified processing framework provided by the *Dynamo* software package. In particular, the new modules for full automation of the basic logistics of tomographic data management will be presented, a recent development of the package that provides non-expert groups with a fast entry gate into the technique.

Further modules address the analysis of the identified subtomograms, guiding the users through the use of standardized analysis steps or rather supporting the design of new, case specific approaches. The software can harness High Performance Computing environments like CPU or GPU clusters, in order to cope with the numerically demanding nature of the technique, an aspect that will be showcased by different case studies.

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