

PySeg in Scipion: making easier template-free detection and classification of membrane-bound complexes in cryo-electron tomograms.

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The cellular environment is characterized by the presence of many different molecular complexes, stable or transient, which underlie critical cellular functions. Cryo-electron tomography is uniquely suited to high-resolution, direct three-dimensional imaging of unperturbed cellular environments. The opensource software package PySeg enables a comprehensive analysis of cryo-tomograms for template-free detection and unsupervised classification of heterogeneous membrane-bound molecular complexes. PySeg has proved fundamental for analyzing membranous organelles with heterogenous and/or sparse composition of complexes such as endoplasmic reticulum and synapse. However, PySeg is a package of python functions and scripts, consequently its adequate usage requires certain programming skills from users. Here, we present the integration of PySeg as plug-in for Scipion, a well-known image processing framework for electron microscopy, which facilitates input parametrization, results visualization, traceability, and communication with other software packages.