

Subtomogram averaging is a powerful technique used in cryo-electron tomography to obtain a three-dimensional structure of macromolecular complexes in their native context. In recent years, high-resolution subtomogram averaging has emerged and allows for advances in structure determination and biophysical analysis of the biological complex of interest. A pipeline is currently under development utilizing HIV tomograms from Dr. John Briggs' laboratory. The method aims to process raw tomograms collected from SerialEM, perform reconstruction, and apply subtomogram averaging techniques to obtain a high-resolution structure of the virus capsid. In this method, tomograms were reconstructed using IMOD, Etomo, CTFFIND4, and NovaCTF and subtomogram averaging was done using Dynamo. In the future, this pipeline will be adapted and extended for reconstruction of surface proteins in flaviviruses.