

Scipion 1.2: Cryo EM integration framework updates

P. Conesa, R. Melero et al

National Center for Biotechnology - CSIC, pconesa@cnb.csic.es

It's been 2 years since the first release of Scipion[1] and we are about to release our new version. We have added new methods, updated packages and designed new functionality, with special stress in features that CryoEM facilities might need.

Among the new methods you could find new validation methods, or a new local resolution estimation like Xmipp-local resolution [2] or updates of the most common programs used in Cryo EM.

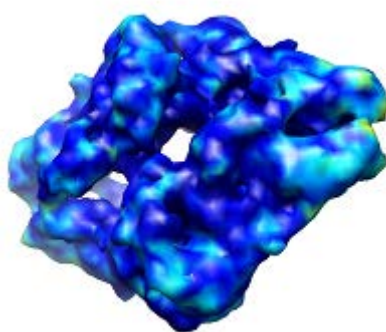


Figure 1: Colored output of Xmipp local resolution estimation.

As for facilities we have enabled Scipion to process data “on the fly” from movie alignment until particle picking and extraction. Additionally we have added monitoring functionality and HTML reporting to allow quick inspection and assessment of the acquisition process

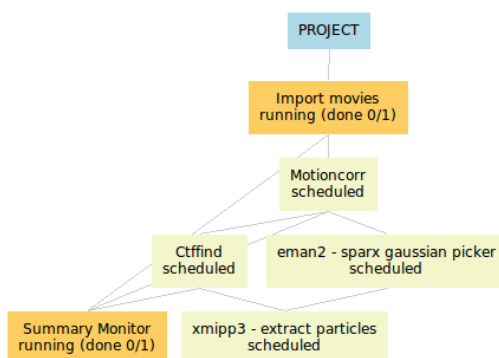


Figure 2:Scipion workflow running in streaming mode

References

[1] - Scipion: A software framework toward integration, reproducibility and validation in 3D electron microscopy.

[2] - MonoRes: Automatic and Accurate Estimation of Local Resolution for Electron Microscopy Maps.