

3D Structure Determination using Cryo-Electron Microscopy -- Computational Challenges

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Single particle cryo-electron microscopy (EM) recently joined X-ray crystallography and NMR spectroscopy as a high-resolution structural method for biological macromolecules. In single particle cryo-EM, the 3D structure needs to be determined from many noisy 2D projection images of individual, ideally identical frozen-hydrated macromolecules whose orientations and positions are random and unknown. In this talk we will discuss how old and new techniques from mathematics and computer science can be combined to tackle the main computational challenges in single particle cryo-EM, namely, estimation of the pose parameters and classification of heterogeneous particles.