## 3-D Reconstruction of Molecules using Cryo-Electron Microscopy

## Amit Singer Princeton University amits@math.princeton.edu

Single-particle cryo-electron microscopy (cryo-EM) has recently joined X-ray crystallography and NMR spectroscopy as a high-resolution structural method for biological macromolecules. Cryo-EM was selected by Nature Methods as Method of the Year 2015, large scale investments in cryo-EM facilities are being made all over the world, and the Nobel Prize in Chemistry 2017 was awarded to Jacques Dubochet, Joachim Frank and Richard Henderson for "developing cryo-electron microscopy for the high-resolution structure determination of biomolecules in solution".

In single particle cryo-EM the three-dimensional molecular structure needs to be estimated from many twodimensional noisy tomographic projection images taken at unknown viewing angles. In addition, for flexible (non-rigid) molecules, it is desired to estimate the entire conformational space of the molecule, rather than just a single structure. This talk will focus on the mathematical, statistical, and computational principles underlying existing algorithms for structure determination using single particle cryo-EM.