Speaker:  Amit Singer, Princeton University

Title:  Mathematics, computation, and statistics for cryo-electron microscopy

Abstract:
Single particle cryo-electron microscopy (EM) recently joined X-ray crystallography and nuclear magnetic resonance (NMR) spectroscopy as a high-resolution structural method for biological macromolecules. Furthermore, cryo-EM has the potential to analyze compositionally and conformationally heterogeneous mixtures and, consequently, can be used to determine the structures of complexes in different functional states. I will give an overview of the computational and statistical challenges in cryo-EM analysis and how we and others are trying to face them, focusing on 3D ab initio modeling and the heterogeneity problem of determining structural variability.