PURDUE UNIVERSITY | Purdue Quantum Science and Engineering Institute
DISCOVERY PARK

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"Biological 3D Structures by Cryo-EM: Challenges in Computations and Instruments"

Tuesday, September 17, 2019
3:30 – 4:30 p.m.; MRGN 129

Single particle cryo-EM is revolutionizing structural biology. Many structures of viruses and protein complexes have been determined to 2-4 Å resolutions. While stable structures that can be expressed/purified in large quantities can be solved routinely, the dynamic compositions and conformations of many protein complexes pose serious challenges to current image processing/3D reconstruction algorithms and computing resources. Novel algorithms or computational methods will be needed to overcome these challenges.

While single particle cryo-EM solve the in vitro structures using isolated protein complexes, high resolution in situ structures in the context of cells using electron tomography are the ultimate goal of structural biology. Due to the limited penetration power of current TEMs at 300 kV, the cells are too thick and must be sectioned into thin slices before being imaged with a TEM. Direct imaging of whole cells will require MeV TEM instruments which are too expensive and inaccessible. Novel design of compact TEMs might make it possible to directly image whole cells.