Bindley Bioscience Center & Birck Nanotechnology Center Joint Virtual Seminar

“Technology Challenges in seeing how molecules work at atomic resolution in a cell-structural biology today, tomorrow and later.”

Dr. Wen Jiang

Thursday, July 29, 2021
11:00 am – 12:00 pm
Zoom: https://purdueedu.zoom.us/j/99221627543?pwd=YUkvdy9aR1R5OTAxUVpFNzVVNTlRdz09

Bio: Dr. Jiang’s primary appointment is as professor in the Department of Biological Sciences. He is also the scientific director of the Purdue Cryo-EM Facility. In addition, he has a courtesy appointment in the Department of Chemistry, Purdue University and is a member of the Purdue Center for Cancer Research, Purdue Institute for Drug Discovery, Purdue Institute of Inflammation, Immunology and Infectious Disease (PI4D). Dr. Jiang has a B.S. in Physics from Peking University, M.S. in Biophysics from the Institute of Biophysics, Chinese Academy and Sciences, and Ph.D./Postdoc in Cryo-EM with Prof. Wah Chiu from Baylor College of Medicine.

Abstract:

Single particle cryo-EM imaging and 3D reconstruction methods are revolutionizing structural biology and drug developments. While stable structures that can be expressed/purified in large quantities can be solved routinely to 2-4 Angstrom resolutions, the dynamic compositions and conformations of many protein complexes (“machines”) that are essential for their functions pose serious challenges to current sample preparation/characterization methods and image processing/3D reconstruction. To fully understand how these macromolecular “machines” function in situ in the cells, thin sections of cells or tissues need to be imaged and 3D reconstructed using cryo-correlative light microscopy and electron tomography. However, accurate targeting of the protein complexes in the large volume of cells and the limited power of electrons penetrating the thick cells pose serious challenges in sample preparation, data collection, computational analysis, and computing resources.

In the Jiang Lab we utilize cryo-electron microscopy (cryo-EM) and cryo-electron tomography (cryo-ET) to study structures of protein filaments implicated in neurodegenerative disease, human viruses, phages, macromolecular complexes involved in cancer, nanobiology technologies, and drug discovery. We also aim to broaden the applicability of high resolution (2-4 Å) cryo-EM to targets of low abundance or high level of dynamics by experimental and computational methods.

In this presentation, Dr. Jiang will first briefly review the past and current state of cryo-EM, its impact in structural biology, and the essential contributions from physics, materials, data science, and other fields. Dr. Jiang will then focus on the discussion on the future developments of cryo-EM to address the challenges in single particle cryoEM and cryo-ET and advocate for close collaborations with experts in microfluidics, light/mass spectroscopy (sample preparation and characterization), polymer chemistry/materials (sample preparation), particle accelerators and instruments (affordable MeV TEM and desktop TEM), deep learning and data science (image analysis and 3D reconstruction).

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