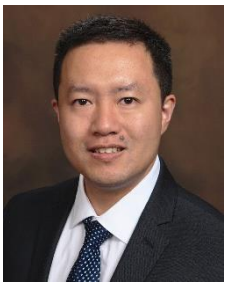

Biomedical Informatics Grand Rounds

Wednesday, May 4th, 2022 3:00 pm – 4:00 pm

Automatic analysis of cryo-electron tomography using computer vision and machine learning

Min Xu, PHD
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Remote Access
Join Zoom Meeting https://stonybrook.zoom.us/j/95617197636?pwd=KytzZ2pVRG9SZGpKZUtpNXJISjNjZz09
Meeting ID: 956 1719 7636 Passcode: 924293

Bio: Dr. Min Xu is an Assistant Professor at the Computational Biology Department (with a Courtesy Appointment at the Robotics Institute) within the School of Computer Science at Carnegie Mellon University. He serves as training faculty at the Joint CMU-Pitt Ph.D. Program in Computational Biology. He also serves as training faculty at the Master of Science in Computer Vision (MSCV) program at CMU. He is an investigator at the National Center for Multiscale Modeling of Biological Systems. He is also affiliated with the Computer Vision Department at the Mohamed bin Zayed University of Artificial Intelligence, UAE. Dr. Xu has a career centered around the development of computer vision and machine learning methods for the analysis of cellular systems using imaging and omics data. Working in the domain of Computational Biology and Bioinformatics since 2000, Dr. Xu has established himself as a pioneer in this field. While his early work focused on developing machine learning methods for the analysis of functional genomics data, he later on (2008) moved onto developing computer vision methods for the analysis of Cellular Cryo-Electron Tomography (Cryo-ET) 3D image data. Dr. Xu has designed novel structural pattern mining methods and has been the first to demonstrate the feasibility of De Novo extraction of structures and spatial organizations of macromolecular complexes in single cells using Cryo-ET data. His current research focuses on Cryo-ET derived modelling of cellular organization at molecular resolution. Dr. Xu has published papers in peer-reviewed top journals and conferences, such as PNAS, Bioinformatics, PLOS Computational Biology, ISMB, CVPR, ICCV, and MICCAI. He serves as PI of US NIH R01 and NSF awards.

Abstract: The cell is the basic structural and functional unit of all living organisms. Understanding how cells function is fundamental to life science. Macromolecules are nano-machines inside cells that govern the cellular processes. To fully understand such processes, it is necessary to know the native structures and spatial organizations of macromolecules inside single cells, and their interactions with other subcellular components. Such information has been extremely difficult to obtain due to a lack of suitable data acquisition techniques. The recent revolution of Cryo-electron tomography (cryo-ET) 3D imaging technology has made collecting such information possible. Cryo-ET captures a 3D image of a single cell's subcellular structures at sub-molecular resolution and in a near-native state. It provides unprecedented opportunities for systematically studying the native spatial organization of subcellular structures, especially macromolecules. However, cryo-ET has a high degree of structural complexity and imaging limits, such as high structural diversity and crowding, low signal-to-noise ratio, and missing values. These have made the automated systematic analysis of such images extremely difficult. Since 2008, we have been developing image analysis methods to address this challenge. In particular, we focus on systematic recognition and recovery of the structures of large numbers (millions) of macromolecules captured by cryo-ET, without relying on external structural knowledge. To do so, we have developed different cryo-ET image registration, classification, segmentation restoration techniques. Our effort is a key step for systematic analysis of macromolecules' structures and spatial organizations inside single cells captured by cryo-ET.

Educational Objects: Upon completion, participants should be able to:

- Integrate cryo-ET image analysis research with undergraduate research training.
- Integrate cryo-ET image analysis research results into bioimage analysis course materials.
- Integrate cryo-ET image analysis research results with recruitment of underrepresented minorities.

Disclosure Statement: The faculty and planners have no relevant financial relationship with ineligible companies whose primary business is producing, marketing, selling, re-selling, or distributing health care products used by or on patients.

Continuing Medical Education Credits: The School of Medicine, State University of New York at Stony Brook, is accredited by the Accreditation Council for Continuing Medical Education to provide continuing medical education for physicians. The School of Medicine, State University of New York at Stony Brook designates this live activity for a maximum of **1** ***AMA PRA Category 1 Credits™.*** Physicians should only claim credit commensurate with the extent of their participation in the activity.