

Cryo-electron tomography image analysis

March 5th | 12:00 p.m. EST | Via Zoom Meeting



SEMINAR

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.

SPEAKER

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SPEAKER BIO

Dr. Min Xu is an Assistant Professor at the Computational Biology Department in 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 a training faculty Master of Science in Computer Vision Program at Robotics Institute. He is an investigator at the National Center for Multiscale Modeling of Biological Systems. Dr. Xu's career has centered on developing computational methods to study cellular systems using imaging and omics data. He started his research career in the field of Computational Biology and Bioinformatics since 2000. He developed machine learning methods for gene selection for classifying cancer samples, for cancer gene network module discovery, and sample phenotype prediction by integrating hundreds of gene expression datasets. Since 2008, he started working in computational analysis of Cellular Cryo-Electron Tomography (Cryo-ET) data. He designed structural pattern mining methods and first demonstrated the feasibility of De Novo extraction of structures and spatial organizations of macromolecular complexes in single cells using Cryo-ET data. His current research focus on Cryo-ET-derived modeling of the cellular organization at molecular resolution. Dr. Xu has published over 60 research papers. Example publications include top image analysis conference papers such as CVPR and MICCAI, as well as prestigious journals and conference papers in computational biology, such as PNAS and ISMB. He is currently serving in the editorial board of Statistical Methods in Medical Research. Dr. Xu received a B.E. in Computer Science from the Beihang University, M.Sc from School of Computing at the National University of Singapore, M.A. in Applied Mathematics from the University of Southern California (USC), and Ph.D. in Computational Biology and Bioinformatics from USC. He was a postdoctoral researcher at USC.