THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY
Department of Mathematics

SEMINAR ON STATISTICS AND DATA SCIENCE

Statistical Modeling for Spatial Transcriptomics: Methods for Deconvolution and Spatial Gene Discovery

By

Prof. Yuehua CUI
Department of Statistics and Probability
Michigan State University

Abstract

Spatial transcriptomics has transformed our ability to study gene expression within intact tissues, revealing how cellular organization shapes biological function. However, fully realizing its potential requires rigorous statistical and computational modeling. In this talk, I will present some of our recent method developments in modeling spatial transcriptomics data, focusing on three topics. First, I will introduce new developments in reference-free spatial deconvolution, which infers cellular composition from multicellular-resolution data under a latent Dirichlet allocation (LDA) modeling framework. Second, I will describe methods for identifying cell type-specific spatially variable genes (ctSVGs) and temporally-informed SVGs (TSVGs) using kernel mixed-effects models, enabling the discovery of context-dependent transcriptional patterns. Third, I will present a robust nonparametric batch correction-free approach for SVG detection with multi-sample integration. Together, these advances demonstrate how principled statistical modeling can translate experimental complexity into meaningful biological insight.

Short bio: Yuehua Cui is a Professor in the Department of Statistics and Probability at Michigan State University (MSU). He joined MSU after earning his PhD in Statistics from the University of Florida in 2005, and has since been promoted to full professor. His research focuses on statistical genetics and genomics, with an emphasis on gene-gene and gene-environment interactions, multi-omics data integration, causal inference, and spatial transcriptomics. He has published in leading journals such as *Nature Communications*, *Nucleic Acids Research*, *JRSSB* and *Biometrics*. He is an elected Fellow of the American Statistical Association (ASA) and an elected member of the International Statistical Institute (ISI). He currently serves as an Academic Editor for *PLOS Genetics* and *PLOS Computational Biology*, and an Associate Editor for several journals in statistics and computational genomics including *Statistics and Probability Letters* and *Statistical Applications in Genetics and Molecular Biology*.

Date	:	**19 March 2026 (Thursday)**
Time	:	**10:30a.m.-11:30a.m.**
Venue	:	**Room 1410 (near Lift 25/26)**

All are welcome