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THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY

Department of Mathematics

PHD STUDENT SEMINAR

A Unified Framework for Integrating Single-Cell and Spatial Transcriptomics to Uncover Spatiotemporal Tissue Architecture

By

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Abstract

Spatiotemporal transcriptomics offers new opportunities to characterize how cellular organization and tissue architecture evolve during development and aging. Currently, most computational approaches either analyze spatial transcriptomics snapshots independently without modeling temporal dynamics, or restrict temporal analysis to a single modality, limiting the ability to jointly identify cell-type-specific temporal programs and resolve spatial heterogeneity. Here, we present a unified framework that integrates single-cell RNA-sequencing (scRNA-seq) and spatial transcriptomics data across multiple time points through latent temporal effects to uncover spatiotemporal tissue architecture. By jointly modeling cell-type-specific temporal dynamics from scRNA-seq with spatially resolved transcriptomic profiles, our method simultaneously identifies temporally variable genes, deconvolves cell-type compositions across space and time, and characterizes dynamic changes in spatial cellular composition.

Date : 13 May 2026 (Wednesday)
Time : 4:30pm
Venue : Room 4472 (near Lifts 25/26)

All are Welcome!