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THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY

Department of Mathematics

PHD STUDENT SEMINAR

MacSGP: a unified framework for mapping cell-type-specific spatial gene programs in spatial transcriptomics

By

Mr. Yeqin ZENG

Abstract

The complex organization of tissues is shaped by the spatial arrangement of diverse cell types executing specialized gene programs. Cell-type-specific spatial gene programs (SGPs) are transcriptional modules that capture expression variation and co-variation within a spatial context, encoding molecular signatures of tissue architecture and illuminating spatial heterogeneity. However, identifying these SGPs is challenging due to limitations in current spatial transcriptomics technologies, such as the low resolution of 10x Visium and limited transcript abundance per cell. In this study, we present MacSGP, a scalable framework that integrates deep graph neural networks with probabilistic modeling to identify cell-type-specific SGPs through low-rank structures while accounting for cell type mixtures and uncertainty in count data. Through comprehensive simulations and analyses of real spatial transcriptomic datasets spanning multiple tissues including mouse brain, kidney cancer and colorectal cancer and different platforms like Visium, Visium HD and Xenium, we demonstrate that MacSGP effectively uncovers biologically meaningful SGPs that reflect subregional cellular specializations, delineate disease-relevant trajectories, and define distinct cellular niches within tumor microenvironments.

Date : 4 May 2026 (Monday)
Time : 11:00am
Venue : Room 1104 (near Lift 19)

All are Welcome!