



THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY

Department of Mathematics

PHD STUDENT SEMINAR

M³: A statistical approach to cell-type-specific analysis of spatially variable genes in spatial transcriptomics data

By

Mr. Zhiwei WANG

Abstract

A central challenge in spatial transcriptomics analysis is the detection of spatially variable genes (SVGs) within the tissue context. However, existing methods often struggle with a high number of false positives when confronted with complex cell-type mixtures across space. While some methods attempt to address this issue, their statistical power is often insufficient as they primarily rely on simple linear models. Moreover, to achieve practical interpretability, such methods typically require a combination with predefined spatial covariates. In this work, we introduce our approach called Mixture of Mixed Models (M³), which effectively accounts for cell-type composition. We have developed a penalized quasi-likelihood based method to accurately and efficiently estimate the null model. By obtaining pseudo-data in the form of a classical linear mixed model, we enable the use of variance component significance tests with kernel matrices that can be flexibly designed to detect diverse spatial patterns.

Date : 10 May 2024 (Friday)

Time : 10:00am

Venue : Room 3598 (Lifts 27-28)

All are Welcome!