



THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY

Department of Mathematics

PHD STUDENT SEMINAR

A reference-guided probabilistic framework for integrating spatial multi-omics to reconstruct fine-grained cell-type distributions

By

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Abstract

Spatial omics technologies provide complementary molecular measurements at the transcript and protein levels, yet jointly analyzing these modalities remains challenging because of mismatched feature spaces, disparate spatial resolutions, and imperfect cross-section alignment. To address these challenges, we introduce BRIDGE, a reference-guided probabilistic framework that integrates paired low-resolution spatial transcriptomics with high-resolution multiplexed protein imaging. By leveraging cell-type profiles learned from single-cell RNA-seq, BRIDGE reconstructs a single-cell-resolution cell-type map across the tissue section. Our experiments demonstrate BRIDGE's effectiveness in cell-type deconvolution and in accurately identifying fine-grained cell subpopulations across diverse datasets, further facilitating downstream analyses such as spatial microenvironment characterization.

Date : 30 April 2026, Thursday

Time : 10:00am

Venue : Room 4472 (Lifts 25/26)

All are Welcome!