



The Hong Kong University of Science and Technology

Department of Mathematics

PhD THESIS EXAMINATION

A Unified Framework for Integrating Spatial and Single-cell Transcriptomics Data Using Deep Generative Models

By

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ABSTRACT

The rapid emergence of spatial transcriptomics (ST) technologies is revolutionizing our understanding of tissue spatial architecture and their biology. Current ST technologies based on either next generation sequencing (seq-based approaches) or fluorescence in situ hybridization (image-based approaches), while providing hugely informative insights, remain unable to provide spatial characterization at transcriptome-wide single-cell resolution, limiting their usage in resolving detailed tissue structure and detecting cellular communications. To overcome these limitations, we developed SpatialScope, a unified approach to integrating scRNA-seq reference data and ST data that leverages deep generative models. With innovation in model and algorithm designs, SpatialScope not only enhances seq-based ST data to achieve single-cell resolution, but also accurately infers transcriptome-wide expression levels for image-based ST data. We demonstrate the utility of SpatialScope through comprehensive simulation studies and then apply it to real data from both seq-based and image-based ST approaches. SpatialScope provides a spatial characterization of tissue structures at transcriptome-wide single-cell resolution, greatly facilitating the downstream analysis of ST data, such as detection of cellular communication by identifying ligand-receptor interactions from seq-based ST data, localization of cellular subtypes, and detection of spatially differently expressed genes.

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Zoom ID: 947 5594 3615 (passcode: hkust) ~ EE opted via online mode.

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The student's thesis is now being displayed on the reception counter in the General Administration Office (Room 3461).