



香港中文大學統計學系

Department of Statistics
THE CHINESE UNIVERSITY OF HONG KONG

SEMINAR

DEPARTMENT OF STATISTICS

THE CHINESE UNIVERSITY OF HONG KONG

QuadST for Robust and Powerful Identification of Cell-Cell Interaction-Changed Genes in Spatially Resolved Transcriptomics Data.

INVITED SPEAKER

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TIME

March 11th, 2025 (Tue) · 2:30 pm - 3:30 pm

VENUE

LSB LT1 (1/F) · Lady Shaw Building LT1 · CUHK

ABSTRACT

Recent advances in spatially resolved transcriptomics (SRT) have provided valuable avenues for identifying cell-cell interactions and their critical roles in diseases. We introduce QuadST, a novel statistical method for the robust and powerful identification of cell-type-specific cell-cell interactions and their impacted genes in single-cell SRT. QuadST models interactions at different cell-cell distance quantile levels and innovatively contrasts signals to identify interaction-changed genes, which exhibit stronger signals at shorter distances. Unlike other methods, QuadST does not require the specification of interacting cell pairs. It is also robust against unmeasured confounding factors and measurement errors of the data. Simulation studies demonstrate that QuadST effectively controls the type I error, even in misspecified settings, and significantly improves power over existing methods. An application of QuadST to the Xenium profiled breast cancer data identified critical genes (CCL5 and LUM) involved in cancer and CD8+ T cell-cell interactions.