

SEMINAR

DEPARTMENT OF STATISTICS THE CHINESE UNIVERSITY OF HONG KONG

Statistical modelling of single-cell dynamics and spatial interaction

INVITED SPEAKER

Yuanhua Huang Assistant Professor the School of Biomedical Sciences & the Department of Statistics and Actuarial Science the University of Hong Kong (HKU)

TIME

November 19, 2024 (Tue) · 2:30 pm - 3:30 pm

VENUE

LSB C2 (G/F) · Lady Shaw Building C2 · CUHK

ABSTRACT

Single-cell sequencing technologies have become a new routine in dissecting cellular heterogeneity and disease progress. However, grand statistical challenges remain in detecting cellular differentiation trajectories and identifying their regulations from snapshots of cell populations. Here, we will first introduce how cellular transition inference can be enhanced via modeling RNA kinetics in an RNA velocity framework or predicting cell staging from a time-series cell atlas. Then, we will also present our latest work in spatial transcriptomic (ST) analysis, concentrating on cellular interaction via modeling spatial correlation and data imputation by fusing multiple modalities from ST, histology image, and scRNA-seq.