Department of Statistics and Data Science
THE CHINESE UNIVERSITY OF HONG KONG

SEMINAR

DEPARTMENT OF STATISTICS AND DATA SCIENCE
THE CHINESE UNIVERSITY OF HONG KONG

From Sparse Tissue Sampling to Whole-Tissue Molecular Reconstruction

INVITED SPEAKER

Jean Yang
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School of Mathematics and Statistics
The University of Sydney

TIME

June 25th, 2026 (Thursday) · 2:30pm – 3:30pm

VENUE

LSB LT2 · CUHK

ABSTRACT

Spatial transcriptomics provides molecular measurements within intact tissues, but current technologies remain difficult to scale to whole tissue sections and large patient cohorts. As a result, many studies rely on tissue microarrays or sparse spatial profiling designs, where only a small fraction of the tissue can be measured. This raises a fundamental question: given a limited measurement budget, how should we sample a tissue, and what can we infer about the unobserved molecular landscape? In this talk, I will discuss methods for addressing these challenges through the integration of experimental design and spatial modelling. The central idea is to use routine HE histology as a source of tissue-wide structural information, enabling sparse molecular measurements to guide the reconstruction of unmeasured regions while accounting for tissue heterogeneity and partially overlapping molecular panels. I will also discuss how multi-objective optimisation can be used to identify representative tissue regions for spatial profiling, balancing tissue coverage, molecular diversity and downstream translational objectives. Applications across cancer cohorts and normal tissues demonstrate that these approaches can recover biologically meaningful tissue-wide molecular organisation from sparse measurements while preserving spatial architecture, cell-type composition and tissue state. More broadly, this work highlights the potential of combining experimental design with spatial modelling to extend sparse spatial profiling experiments to larger tissue sections and patient cohorts.