

Towards a Common Coordinate Framework: Comparative Analysis of Spatially Resolved Transcriptomics Data



Jean Fan, PhD
John Hopkins University

In this talk, we will provide an overview of the latest spatially resolved transcriptomics technologies and associated computational analysis methods developed by her lab. Specifically, we have developed MERINGUE to identify genes with spatially heterogeneous expression patterns and infer putative cell-cell communication in 2D and 3D in a density-agnostic manner in spatially resolved transcriptomics data using spatial auto-correlation and spatial cross-correlation testing. We have developed STdeconvolve to recover cell-type specific gene expression and spatial organizational patterns from multi-cellular pixel resolution spatially resolved transcriptomics datasets without reliance on external single cell transcriptomics references. We are actively developing STalign to align 2D spatially resolved transcriptomics datasets within and across technologies and to 3D common coordinate framework and enable cross sample comparisons regarding cell-type and molecular composition at matched spatial locations.

We anticipate that such statistical approaches and computational methods for analyzing spatially resolved transcriptomic data will offer the potential to identify and characterize the heterogeneity of cells within their spatial contexts and contribute to important fundamental biological insights regarding how tissues are organized in both the healthy and diseased settings.

Thursday August 18, 2022, 3:30-4:30 PM Eastern

133 Rosenau Hall

Virtual using link and info below.

Link: <https://unc.zoom.us/j/92602267820?pwd=YW1wN1pjdUNVd1A4TTI2OStmVHBjQT09>

Meeting ID: 926 0226 7820 Passcode: 533114