



TITLE: Computational Innovations in Single-Cell and Spatial Transcriptomics for Translational Research

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ABSTRACT:

Recent advances in single-cell and spatial transcriptomics are enabling the characterization of tissues at unprecedented molecular and cellular resolution, fundamentally transforming our understanding of human disease. By generating rich, high-dimensional data from patient samples such as tumor biopsies, these technologies provide unique opportunities to uncover mechanisms of treatment response, identify novel therapeutic targets, and advance precision medicine. Realizing this potential, however, requires overcoming major statistical and computational challenges related to data integration, scalability, multimodal analysis, and biological interpretation. In this talk, I will present our work on developing and applying computational and statistical methods for the analysis and integration of single-cell and spatial omics data, with the goal of extracting robust and clinically meaningful insights from complex biological systems. I will also highlight how these methods are enabling large-scale translational initiatives, including the MOSAIC consortium and other collaborative efforts, which are generating multimodal datasets from hundreds to thousands of patient samples to bridge the gap between high-resolution molecular profiling and clinical impact.