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Computational methods for analyzing spatially-resolved single-cell transcriptomics data

Abstract: The expression profiles and spatial distributions of RNAs regulate many cellular functions. Image-based transcriptomic approaches provide powerful means to measure both expression and spatial information of RNAs in individual cells within their native environment. Among these approaches, multiplexed error-robust fluorescence in situ hybridization (MERFISH) has achieved spatially resolved RNA quantification at transcriptome scale by massively multiplexing single-molecule FISH measurements. Recently, we increased the gene throughput of MERFISH and demonstrated simultaneous measurements of RNA transcripts from ~10,000 genes in individual cells with ~80% detection efficiency and ~4% misidentification rate.

However, scalable computational methods for statistical analysis capable of taking advantage of this spatial information are still lacking. Here, I will describe a few recent computational approaches for analyzing spatially-resolved single-cell transcriptomics data in order to identify mRNA species enriched in different subcellular compartments, characterize the spatial organization of transcriptionally distinct cell states, and predict the future transcriptional state of cells.

We anticipate that such spatially resolved transcriptome profiling coupled with spatial computational analyses could help address a wide array of questions ranging from the regulation of gene expression in cells to the development of cell fate and organization in tissues.

Keck Seminar

Friday, October 2, 4pm **LINK to join:**

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For questions, please contact Vanessa Herrera (herrera@rice.edu)