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Title: Multi-scale computational analysis of spatially resolved transcriptomic imaging data

Abstract: Spatially resolved transcriptomic imaging technologies provide powerful means to measure both the quantitative expression level and spatial organization of mRNAs in individual cells within their native tissue environment. Such spatially resolved transcriptomic data demand new computational methods to take advantage of this new spatial dimension of information to derive relevant biological insights. In this talk, I will describe a few recent computational approaches developed in my lab for analyzing such spatially resolved transcriptomic imaging data at both the cellular and subcellular scale. At the cellular scale, we developed MERINGUE, a computational framework based on spatial auto-correlation and cross-correlation analysis to characterize cellular spatial gene expression heterogeneity in both 2D and 3D in a manner that is robust to the nonuniform cellular densities inherent within tissues. At the subcellular scale, we leverage the continuum of transcriptional states for cells along dynamic processes and the subcellular organization of mRNAs to infer RNA velocity, the time derivative of the gene expression state, in situ by distinguishing between nuclear and cytoplasmic mRNAs. We further developed VeloViz to take into consideration each cell's predicted future transcriptional states inferred from RNA velocity analysis to more robustly visualize cellular trajectories. 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.