

ESAM SEMINAR SPEAKER

Exploring the Molecular State Space of Cells in the Brain

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The brain contains a diverse array of cells with dramatically different shapes, activity patterns, and molecular composition. The advent of single-cell RNA-sequencing, which quantifies the gene expression-based molecular makeup of individual cells, has resulted in brain-specific data sets with measurements for thousands of features in each cell. Two fundamental mathematical questions arise from this type of large-scale data: 1) a clustering problem, with the goal of grouping cells together in the molecular state space to identify stable cell type profiles, and 2) a combinatorial optimization problem, with the goal of identifying putative locations in state space that are likely to be stable, but have not been observed yet. The clustering problem is well-formulated and studied, and can be solved with a number of matrix decomposition methods under reasonable assumptions. The second question – that of predicting the existence of stable profiles that have not been observed directly – is degenerate from a strictly dynamical systems point of view, but can be formulated as a combinatorial optimization problem, yielding experimentally testable predictions. Ultimately, applying these methods to these data sets leads to new insight into diverse array of components that make up the brain.

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