
Estimation of lineage trajectories from single cell mRNA data

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Abstract

Recently-developed methods for assaying individual cells afford researchers a highly detailed view of cellular transcription. One common target for these studies has been stem cells and their descendants, with analyses focused on charting the progression from multipotent cells to differentiated populations. We introduce a novel method, Slingshot, for inferring multiple developmental lineages from single-cell gene expression data. Slingshot is a robust and flexible tool for inferring developmental lineages and ordering cells to reflect continuous differentiation processes. It constructs a differentiation tree using clusters of cells as nodes, which provides stability and reduces the complexity of the inferred lineages. This tree is then used to assign individual cells to one or more developmental lineages, which are represented by smooth curves in a reduced-dimensionality space. These curves provide discerning power not found in methods based on piecewise linear trajectories, while also adding stability over a range of possible dimensionality reduction and clustering techniques.

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