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## **Reconstruction of the complex trajectories of cell developments based on single-cell RNAseq data**

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The unprecedented accumulation of high-throughput single-cell RNAseq data provides an essential opportunity for researchers to study the dynamics of biological systems. At the same time, it raises new questions and grand challenges in view of the key characteristics of these data that include high-dimensionality and heterogeneity. In response, we develop a data-driven computational framework to map and reconstruct of dynamical trajectories of cell based on the high-dimensional molecular profiles from snapshot single-cell data. By integrating tools from topological data analysis (level-set method) and the nonparametric statistics, we first perform nonlinear dimension reduction on the data to construct the cell developmental landscape, and then reconstruct the complex trajectories by finding the cell state transition path on the landscape. We apply this method in the analysis of cell developmental processes and provide novel insights into the field of mathematical and computational biology.

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