SINGLE-CELL ANALYSIS USING HIERARCHICAL AUTOENCODER

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Abstract:

Motivation: Advances in microfluidics and sequencing technologies have allowed us to monitor biological systems at single-cell resolution. This comprehensive decomposition of complex tissues holds enormous potential in developmental biology and clinical research. However, the ever-increasing number of cells, technical noise, and high dropout rate pose significant computational challenges in the scRNA-seq analysis. These challenges affect both analysis accuracy and scalability and greatly hinder our capability to extract the wealth of information available in single-cell data.

Method: To detach noise from informative biological signals, we have developed a new analysis framework, called single-cell Decomposition using Hierarchical Autoencoder (scDHA). scDHA can transform the high dimensional to low dimensional data and use this data for downstream analysis. In one joint framework, the scDHA method conducts cell segregation through unsupervised learning, dimension reduction and visualization,

Results: We validated the method on 24 real single-cell datasets. Results show that scDHA can outperform current state-of-the-art methods in both clustering and visualization applications.

Future directions: We will continue to develop the method to work with different kinds of data as well as expanding the method to other research fields.