

Single-Cell Transcriptome and Regulome Data Integration

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Abstract: New single-cell genomic technologies such as single-cell RNA-seq (scRNA-seq) and single-cell ATAC-seq (scATAC-seq) provide the capability for assaying the transcriptome (i.e., gene expression) and regulome (i.e., cis-regulatory element activities) of individual cells. To understand gene regulation in a biological system, one needs the information from both transcriptome and regulome. However, in most experiments, the same cell is only examined by either one of these technologies. Computational tools for integrating different types of single-cell genomic data are needed. Here, we present a new method that learns the connection between different data types based on public database and utilize such connection to integrate single-cell transcriptome and regulome data. We show that our method outperforms existing methods in aligning known cell types between scRNA-seq and scATAC-seq data. We further demonstrated our method by integrating the scRNA-seq data from Human Cell Atlas with public scATAC-seq data to study gene regulation in hematopoietic cell development.