عنوان مقاله:

RNA tracking: predicting cell types in nervous system

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خلاصه مقاله:

Cellular differentiation is a process in which a cell changes from one cell type to another. Understanding this dynamic process is of particular importance, especially for cells in nervous system. RNA abundance in a cell is a strong signal of the state of that cell. Single-cell RNA sequencing (scRNA-seq) provides the expression profiles of individual cells and is considered the gold standard for defining cell states. The main challenge is that scRNA-seq provides only a static snapshot at a point in time, but cellular differentiation is a time-resolved phenomenon. Recent work, called RNA velocity, suggests a method to predict the future state of cells by distinguishing between unspliced and spliced mRNAs in a common cell. RNA velocity calculates the time derivative of the gene expression state which can be used to predict the future state of cells on a timescale of hours. We proposed a method (called RNA tracking) to estimate the second time derivative of the gene expression state which can be exploited to predict cell states more accurately. We used two different dataset to test our method: 1) the mouse hippocampus cells dataset 2) the mouse chromaffin cells dataset. Both hippocampus and chromaffin cells play crucial roles in nervous system, so understanding how they are made from embryonic stem cells are essential. Our results show that not only RNA tracking achieves up to 30% increase in accuracy compared with RNA velocity but also RNA tracking achieves up to 75% increase in the duration of prediction compared with RNA velocity.

کلمات کلیدی:

Cellular differentiation, single-cell RNA sequencing, machine learning in bioinformatics

لینک ثابت مقاله در پایگاه سیویلیکا:

https://civilica.com/doc/1172022