

Modelling cell type differentiation via phylogenetic inference of scRNA-seq data

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Developmental biology aims to understand why and how a cell type differentiates into another. A common approach to achieving this goal is to evaluate changes in gene expression of cells during differentiation via single-cell RNA sequencing (scRNA-seq). However, scRNA-seq captures only a static snapshot of each cell's transcriptomic state, making it challenging to understand past or ongoing dynamic processes. Therefore, we propose to explicitly model the absence of ancestral information using a phylogenetic framework: We introduce cellREST, a bioinformatics method that infers maximum likelihood trees linking cells assumed to share a common ancestral gene expression profile. The stochastic variability of the maximum likelihood tree search allows cellREST to recover multiple equally likely topologies that approximate different details of a differentiation process underlying a scRNA-seq dataset. By combining these trees into a single-cell network, we can visualize and analyze complex, even non-tree like differentiation scenarios as cyclic or parallel processes.

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