Bayesian Inference of Cell-Dependent RNA Velocity Using Variational Mixtures from Multi-Omic Data

Abstract

Traditional molecular biology techniques for measuring gene expression require fixing cells at specific states, known as 'cell capture time'. RNA velocity is an innovative concept that predicts future gene expression, offering insights into the future states of cells. This method models RNA transcript dynamics using ordinary differential equations (ODEs), incorporating transcription, splicing, and degradation rates. Previous approaches estimated ODE parameters for individual genes, assuming uniformity across all cells and independently predicting latent cell time. However, these methods are limited in scope. Here, we present a novel methodology that concurrently estimates the latent time of cells and gene-specific ODE parameters. Our approach allows for cell-dependent ODE parameter estimation and integrates both single-cell RNA sequencing and multiomics data, providing a more comprehensive and accurate analysis of cellular gene dynamics.