THE UNIVERSITY OF CHICAGO | **DEPARTMENT OF STATISTICS**

MASTER'S THESIS PRESENTATION

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Model-Based Trajectory Inference for Single-Cell RNA Sequencing Using Deep Learning with a Mixture Prior

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ABSTRACT

In this paper, we present VITAE, a statistical method for trajectory inference in single-cell sequencing data. Trajectory inference methods analyze the developmental trajectories of thousands of cells using computational approaches. Despite numerous trajectory inference tools available, most lack a coherent statistical model and reliable uncertainty quantification. To overcome these limitations, VITAE combines a latent hierarchical mixture model with condition variational autoencoders. This allows for the inference of trajectories from posterior approximations, enabling reliable uncertainty quantification. Additionally, VITAE is computationally scalable and can adjust for confounding covariates to integrate multiple source and omics datasets. VITAE is unique in that it learns trajectory and aligns datasets simultaneously, unlike existing trajectory analysis methods that first align data from different sources and omics, then learn the trajectory on the joint embedding. Empirical results show that trajectory-oriented information induces better effects in merging datasets. Our method has demonstrated state-of-the-art performance in identifying biologically meaningful trajectories across datasets from various sources and omics. VITAE represents a significant advancement in trajectory inference for single-cell sequencing data and has the potential to enhance our understanding of cellular development and differentiation.