



THE UNIVERSITY OF
CHICAGO

Department of Statistics

MASTER'S THESIS PRESENTATION

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Department of Statistics
The University of Chicago

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

MONDAY, February 22, 2021, at 9:00 AM
ZOOM Meeting

ABSTRACT

Transcriptomic profiling of cells from single-cell RNA sequencing provides new opportunities to study the dynamic biological processes such as tumor growth, immune response, and brain development. Trajectory inference, a computational technique for analyzing single-cell RNA sequencing data, aims to infer the developmental lineages and order cells based on their pseudotimes within these lineages. However, in many existing trajectory inference methods, the concepts of “trajectory” and “pseudotime” are vaguely defined. In addition, there is a growing interest in inferring shared trajectories from multiple datasets. In this paper, we propose a novel statistical framework for modeling the trajectory structure and a computationally efficient method Vitae to perform trajectory inference with uncertainty quantification. Vitae combines a latent hierarchical mixture model with variational autoencoders, outperforming other state-of-the-art trajectory inference methods on both real and synthetic datasets. In a case study on the mouse neocortex, we show that Vitae can successfully uncover a shared developmental trajectory of the projection neurons by jointly analyzing two datasets and reliably identify marker genes that are actively expressed through different stages of neuron development.