THE UNIVERSITY OF CHICAGO

Department of Statistics
MASTER'S THESIS PRESENTATION

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Topics on Single-Cell RNA Sequencing Data Analysis

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ABSTRACT

The single-cell RNA sequencing (scRNA-seq) technique provides an unprecedented resolution for profiling the gene expression at the single-cell level, which makes it possible to identify functional heterogeneity across cell sub-populations at a genome-wide scope. However, analyzing scRNA-seq data is challenging due to the shallow sequencing depth and technical noise embedded. I discuss three topics on scRNA-seq data analysis in this thesis: First, investigating progenitor cells diversity and uncovering progenitor-neuron temporal link in the developing mouse cortex. Second, proposing a scientific gateway that efficiently denoises scRNA-seq data with transfer learning. Finally, modeling gene co-bursting using the deconvolution method.