

Department of Statistics MASTER'S THESIS PRESENTATION

BOWEI KANG

Department of Statistics The University of Chicago

Topics on Single-Cell RNA Sequencing Data Analysis

MONDAY, October 26, 2020, at 3:00 PM ZOOM Meeting

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.

For information about building access for persons with disabilities, please contact Keisha Prowoznik at 773.702-0541 or send an email to kprowoznik@statistics.uchicago.edu. If you wish to subscribe to our email list, please visit the following web site: <u>https://lists.uchicago.edu/web/subscribe/statseminars</u>.