



THE UNIVERSITY OF
CHICAGO

Department of Statistics

STATISTICS COLLOQUIUM

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Transfer Learning in Single Cell Transcriptomics

MONDAY, November 12, 2018 at 4:30 PM

Eckhart 133, 5734 S. University Avenue

Refreshments before the seminar at 4:00PM in Jones 111

ABSTRACT

Cells are the basic biological units of multicellular organisms. The development of single-cell RNA sequencing (scRNA-seq) technologies have enabled us to study the diversity of cell types in tissue and to elucidate the roles of individual cell types in disease. Yet, scRNA-seq data are noisy and sparse, with only a small proportion of the transcripts that are present in each cell represented in the final data matrix. We propose a transfer learning framework to borrow information across related single cell data sets for de-noising and expression recovery. Our goal is to leverage the expanding resources of publicly available scRNA-seq data, for example, the Human Cell Atlas which aims to be a comprehensive map of cell types in the human body. Our method is based on a Bayesian hierarchical model coupled to a deep autoencoder, the latter trained to extract transferable gene expression features across studies coming from different labs, generated by different technologies, and/or obtained from different species. Through this framework, we explore the limits of data sharing: How much can be learned across cell types, tissues, and species? How useful are data from other technologies and labs in improving the estimates from your own study? If time allows, I will also discuss the implications of technical batch artifacts in the joint analysis of multiple data sets, and propose strategies for alignment of data across batch.

For further information and inquiries about building access for persons with disabilities, please contact Jonathan Rodriguez at 773.702.8333 or send him an email at jgrodriquez@galton.uchicago.edu. If you wish to subscribe to our email list, please visit the following website:
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