THE UNIVERSITY OF CHICAGO

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STATISTICS COLLOQUIUM

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Learning from Data in Single-Cell Transcriptomics

MONDAY, October 11, 2021 at 4:30 PM
Via Zoom

ABSTRACT

I will discuss statistical methods and software for the analysis of single-cell transcriptome sequencing (RNA-Seq) data to investigate the differentiation of olfactory stem cells. RNA-Seq studies provide a great example of the range of questions one encounters in a Data Science workflow. I will survey the methods and software my group has developed for exploratory data analysis (EDA), dimensionality reduction, normalization, expression quantitation, cluster analysis, and the inference of cellular lineages. Our methods are implemented in open-source R software packages released through the Bioconductor Project (https://www.bioconductor.org).