THE UNIVERSITY OF CHICAGO

Department of Statistics

STATISTICS COLLOQUIUM

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Statistical Methods for Spatial Transcriptomics

MONDAY, November 15, 2021 at 4:30 PM

Jones 303, 5747 S. Ellis Avenue

Refreshments before the seminar at 4:00 PM in Jones 304

ABSTRACT

Spatial transcriptomics is a collection of groundbreaking new genomics technologies that enable the measurements of gene expression with spatial localization information on tissues or cell cultures. Here, I will discuss a few new statistical methods that our group has recently developed for analyzing spatial transcriptomics data. Specifically, I will first talk about SPARK, a new method that allows for rigorous statistical analysis of spatial expression patterns in spatial transcriptomics. SPARK directly models spatial count data through the generalized linear spatial models and relies on novel statistical formulas for hypothesis testing, providing effective type I error control and yielding high statistical power. SPARK is up to ten times more powerful than existing methods and leads to many biological discoveries that otherwise cannot be revealed by existing approaches. Next, I will talk about a non-parametric extension of SPARK, called SPARK-X, for rapid and effective detection of spatially expressed genes in large spatial transcriptomic studies. SPARK-X not only produces effective type I error control and high power but also brings orders of magnitude computational savings compared to SPARK, thus representing the only current spatial expression analysis method for large-scale spatial transcriptomics studies. If time allows, I will also talk about a spatially informed cell type deconvolution method, CARD, that leverages cell type specific expression information from single cell RNA sequencing for the deconvolution of spatial transcriptomics. A unique feature of CARD is its ability to model the spatial correlation in cell type composition across tissue locations using a conditional autoregressive modeling prior, thus enabling spatially informed cell type deconvolution. We demonstrate the benefits of CARD through extensive simulations and in-depth analysis of four spatial transcriptomics data sets with distinct technologies.

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