TULANE UNIVERSITY
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Tulane University Center for Biomedical Informatics & Genomics

TIIDHS Research Seminar

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Computational Methods for Spatial Transcriptomics

April 24, 2023 | 3:00PM – 4:00PM
Hutchinson Bldg. 6th Floor - RM. 6065

Zoom Link

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 method that allows for rigorous statistical analysis of spatial expression patterns in spatial transcriptomics. 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. 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.

Biography

Dr. Xiang Zhou an Associate Professor in the Department of Biostatistics in the School of Public at the University of Michigan. He is also an Assistant Director at the University of Michigan Precision Health. He has been an Associate Professor since 09/2019. Dr. Zhou joined the department as an Assistant Professor in 2014 and became the John G. Searle Assistant Professor in the department in 2018-2019. Before joining UM, he was a Williams H. Kruskal Instructor in the Department of Statistics at the University of Chicago in 2013-2014. He received an MS degree in statistics in 2009 (adviser: Prof. Scott Schmidler) and a PhD degree in neurobiology in 2010 (adviser: Prof. Fan Wang), both from Duke University. He was a postdoctoral scholar working with Prof. Matthew Stephens at the University of Chicago during 2010-2013.