Biostatistics Seminar Series

Constructing local cell-specific-networks from single-cell reference

Date: 16 February 2023
(Thursday)

Time: 10:00am – 11:00am
(Hong Kong Time)

Seminar link:
https://cityu.zoom.us/j/99134610990

Dr. Xuran Wang
Assistant Professor
Icahn School of Medicine at Mount Sinai

About the speaker:

Dr. Xuran Wang is an Assistant Professor at Seaver Autism Center and Department of Psychiatry at Icahn School of Medicine at Mount Sinai. Dr. Wang has been working on developing new statistical models and methods to meet the challenges posed by data-driven biomedical research. In particular, her research has focused on the data generated with the latest technologies that have enabled the measurement of genome-wide features at the single-cell level, allowing for massive parallelization across cells. In a series of publications, Dr. Wang has developed methods to deconvolve bulk RNA sequencing data using single-cell data prior and to estimate cell-specific single-cell gene networks. Additionally, she has worked on causal inference and CRISPR data analysis. Dr. Wang's work has been successfully applied to studies related to but not limited to neuropsychiatric disorders and metabolism disorders.

Abstract:

Gene coexpression networks yield critical insights into biological processes, and single-cell RNA sequencing provides an opportunity to target inquiries at the cellular level. However, due to the sparsity and heterogeneity of transcript counts, it is challenging to construct accurate gene networks. We develop an approach, locCSN, that estimates cell-specific networks (CSNs) for each cell, preserving information about cellular heterogeneity that is lost with other approaches. LocCSN is based on a nonparametric investigation of the joint distribution of gene expression; hence it can readily detect nonlinear correlations, and it is more robust to distributional challenges. Although individual CSNs are estimated with considerable noise, average CSNs provide stable estimates of networks, which reveal gene communities better than traditional measures. Additionally, we propose downstream analysis methods using CSNs to utilize more fully the information contained within them. Repeated estimates of gene networks facilitate testing for differences in network structure between cell groups. Notably, with this approach, we can identify differential network genes, which typically do not differ in gene expression, but do differ in terms of the coexpression networks. These genes might help explain the etiology of disease. Finally, to further our understanding of autism spectrum disorder, we examine the evolution of gene networks in fetal brain cells and compare the CSNs of cells sampled from case and control subjects to reveal intriguing patterns in gene coexpression.

All are Welcome!

CityU Department of Biostatistics
香港城市大學
City University of Hong Kong

Enquiries: ✉ biosgo@cityu.edu.hk