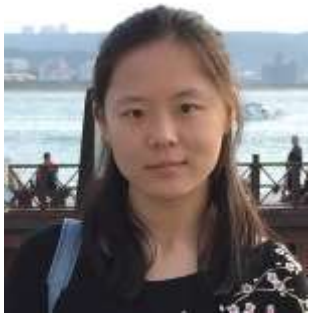
BIOSTATISTICS SEMINAR

A flexible model for correlated count data, with application to analysis of gene expression differences in multi-condition experiments



Yusha Liu, PhD
Post-Doctoral Researcher
University of Chicago
Department of Human Genetics

Detecting differences in gene expression is an important part of RNA sequencing (RNA-seq) experiments, and many statistical methods have been developed for this aim. Most differential expression analyses focus on comparing expression between two groups (e.g., treatment vs. control). But there is increasing interest in multi-condition differential expression analyses in which expression is measured in many conditions, and the aim is to accurately detect and estimate expression differences in all conditions.

We show that directly modeling the RNA-seq counts in all conditions simultaneously, while also inferring how expression differences are shared across conditions, leads to greatly improved performance for detecting and estimating expression differences than existing methods that can be used to perform multi-condition differential expression analysis, particularly when the power to detect expression differences in the individual conditions is low. We illustrate the potential of this new multi-condition differential expression analysis in analyzing data from a single-cell experiment for studying the effects of cytokine stimulation on gene expression.

Wednesday, February 8, 2023 5:00-6:00 PM Eastern

W. Fred Mayes Telecommunication Center (230 Rosenau Hall)

https://unc.zoom.us/j/97294580497?pwd=RlcwR2xRS0lVdmhpVFRWMHF2cGZ5Zz09

Meeting ID: 972 9458 0497

Passcode: 366790

UNC GILLINGS SCHOOL OF GLOBAL PUBLIC HEALTH Biostatistics