

Ying Ma

*PhD Candidate
University of Michigan*

**Monday,
January 30, 2023**

**In Person
Olmsted Hall Rm 1431
@11:15am-12:15pm**

*Light Refreshments will be provided
in Olmsted Hall Rm 1331 @ 10:45am*

Hybrid Option Available via [Zoom](#)

*Meeting ID: 985 3870 6427
Passcode: 216936*

Department of Statistics
Special Colloquium



**“STATISTICAL AND
COMPUTATIONAL METHODS FOR
HIGH-DIMENSIONAL GENOMICS
DATA”**

Abstract

Recent explosion of various transcriptomic technologies such as single-cell RNA sequencing (scRNA-seq) and spatially resolved transcriptomic (SRT) has provided invaluable tools for building comprehensive cell atlas and characterizing the transcriptomic landscape of complex tissues. These new transcriptomic technologies often generate large-scale and complex data that require the development of new computational and statistical methods. In this talk, I will present several methods that I have developed for analyzing scRNA-seq and SRT datasets and that have enabled new types of analysis and produce novel biological insights. Specifically, I will talk about methods for integrative differential expression and gene set enrichment analysis in scRNA-seq studies, for spatially informed cell type deconvolution in SRT studies, and for integrative reference-informed tissue segmentation analysis in SRT studies. I will illustrate how my methods help improve biological understanding of various systems by applications that range from stem cells, cancer, to the nervous system.

Biography

Ying Ma is a Ph.D. candidate in the Department of Biostatistics at the University of Michigan, Ann Arbor. Her research interests focus on developing efficient statistical learning methods to address a variety of biological problems and computational challenges in genomics and genetics, particularly single-cell RNA sequencing, and spatially resolved transcriptomics. In addition to her methodological research, she also works on genetic risk prediction analysis for common health exposure traits in large biobanks such as UK Biobank, and the Michigan Genomics Initiative (MGI)