

**The College of Arts & Sciences**  
**Department of Mathematical Sciences**

Colloquium

# **Professor Dongjun Chung**

**The Ohio State University**

**Tuesday, November 28th 2023**

**Edwards Center 1, Room 6126**

**3:30-4:30pm**

## ***Statistical Methods for Design and Analysis of Spatial Transcriptomics Experiments***

High-throughput spatial transcriptomics (HST) is an emerging experimental technology that can capture high-dimensional gene expression profiles in tissue samples at or near single-cell level while retaining the spatial location of each sequencing unit. First, through analyzing HST data, we seek to identify cell sub-populations within a tissue sample that reflect biological cell types or states. Existing methods often either ignore the spatial heterogeneity in gene expression profiles, fail to account for important statistical features such as skewness and heavy-tails, or are heuristic-based methods that lack the inferential benefits of statistical modeling. In this talk, I will discuss our efforts to address this gap, namely SPRUCE, a Bayesian spatial multivariate finite mixture model based on multivariate skew normal distributions, which allows identification of distinct cellular sub-populations in HST data. Second, while various statistical methods for HST data analysis have been developed, a rigorous statistical framework for the design of HST experiments is still missing in the literature. However, researchers planning an HST experiment need to determine various experimental design parameters, such as the sequencing depth, and these choices need to be carefully made to achieve key goals of HST experiments, e.g., tissue architecture identification. In this talk, I will discuss our statistical power analysis framework for HST experiments, which aims to address this critical need.

**Refreshments will be served 2:45– 3:15 pm in the Faculty Lounge  
4118 French Hall West**