

# Indiana University-Purdue University Indianapolis

## Department of Mathematical Sciences

### STATISTICS SEMINAR

12:15pm—1:15pm, Tuesday, March 22, 2022

Zoom Meeting: Meeting ID: 845 0989 4694

**Speaker:** Travis S Johnson

*Department of Biostatistics and Health Data Science,  
Indiana University School of Medicine*

**Title:** Identifying high risk components of disease from single cell, spatial, and imaging data

#### **Abstract:**

In many incurable diseases, such as multiple myeloma and Alzheimer's disease, new data types such as single cell and spatial gene expression, as well as histology images become available. However, there lacks a method to associate single cells, spatial regions, and image features with clinical outcomes from patient-level data. We propose the use of deep transfer learning algorithms to transfer outcome information learned from patient cohorts, onto single cells, spatial regions, and histology image features to better understand the high-risk components of disease and guide development of novel targeted therapies.

In this talk, I will describe our most recent work in this area as it relates to cancer, Alzheimer's disease, and other diseases. These recent works include our new deep transfer learning framework, Diagnostic Evidence Gauge of Single cells (DEGAS), and our new spatial transcriptomics smoothing method, Spatial and Pattern Combined Smoothing (SPCS). In addition to our latest methods, I will describe our future directions as it relates to identifying the most high-risk components of disease using statistical and machine learning techniques.

#### **Bio:**

Dr. Travis S Johnson is an Assistant Research Professor in the Department of Biostatistics and Health Data Science at Indiana University School of Medicine. He received his PhD in Biomedical Sciences from Ohio State University in 2020. Dr. Johnson's research interests focus on the methods development for omics data analysis, including novel machine learning techniques for single cell RNA sequencing, bulk RNA sequencing, and multi-omic data.