Indiana University-Purdue University Indianapolis
Department of Mathematical Sciences

Statistics Seminar

12:15pm—1:15pm, Tuesday, January 31, 2023
Zoom Meeting: Meeting ID: 845 0989 4694

Speaker: **Jialin Qu**
Biostatistician at Moderna

Title: **Gene set analysis with graph-embedded kernel association test**

Abstract:

Kernel-based association test (KAT) has been a popular approach to evaluate the association of expressions of a gene set (e.g., pathway) with a phenotypic trait. KATs rely on kernel functions to capture potential linear or nonlinear relationship among features in a gene set. A kernel function captures the sample similarity across multiple features. When calculating the kernel functions, features in a gene set are treated as independent in all the KAT-based methods. While genes in a functional group (e.g., a pathway) are not independent in general due to regulatory interactions, incorporating such regulatory network (or graph) information can potentially increase the power of KAT. In this work, we propose a graph-embedded kernel association test, coined as gKAT. gKAT incorporates prior pathway knowledge when constructing the kernel function into hypothesis testing. We apply a diffusion kernel to capture feature similarities in a pathway, then incorporate such information to calculate sample similarities for further association test. We illustrate the geometric meaning of the approach. Through extensive simulation studies, we show that the proposed gKAT algorithm can improve testing power compared to the one without considering feature similarities. Application to a real data set further demonstrate the utility of the method.

Bio:

Dr. Jialin Qu received her doctoral degree in statistics from Michigan State University in 2022. She has research experience in kernel association test, causal mediation analysis and Mendelian Randomization. She is working as a biostatistician at Moderna after her graduation. She works on early and late phase clinical trials in infectious disease.