



THE UNIVERSITY OF GEORGIA  
DEPARTMENT OF STATISTICS

# Colloquium Series

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**3:45 PM, Thursday, October 29, 2020**

**Zoom link: <https://zoom.us/j/7979236528>**

### **Kernel-based genome-wide gene-set association test**

With the radical breakthrough in biotechnology, high throughput genomic data are routinely generated. These data present unprecedented opportunities in disentangling the genetic secret of complex diseases, while also present daunting challenges in statistical modeling and inference. In the last few years, we have witnessed significant advancement in statistical methodology development for genetic/genomic data analysis, among which kernel-based methods have becoming increasingly popular, owing to the advantage in handling nonlinear relationship. In this talk, I will introduce some background and present a kernel-based association test focusing on a univariate disease trait to assess gene set association. Then I will extend the method to a multi-trait analysis framework to understand potential pleiotropic genetic effect (i.e., one gene affects multiple traits) from a gene-set analysis perspective. Examples of synthetic and real data analyses will be shown to demonstrate the utility of the methods.

For more information, please contact us at:

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