

RUTGERS UNIVERSITY
DEPARTMENT OF STATISTICS AND BIostatISTICS
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Seminar

Speaker: **Professor Ying Wei**
Columbia University

Title: **Quantile Secondary Analysis for Case-Control Studies with Application to GWAS Data**

Time: **3:20 – 4:20pm, Wednesday, December 4, 2013**

Place: **552 Hill Center**

Abstract

Genome-wide association (GWA) studies often employ the case-control design to compare a large number of genetic variants between patients with disease and healthy controls, and generate rich data for studying genetic component of complex diseases. It is cost-effective to perform secondary analyses that utilize existing GWA data to examine the association between genetic variants with other phenotypes. For quantitative phenotype, research focus has been on identifying genetic variants that influence the mean of quantitative trait. However, it is common that the high-risk group to a certain disease consists of subjects with abnormal values for their quantitative traits. The underlying genetic variants may influence the entire distribution of quantitative traits, and their impact may differ at various quantiles. In this paper, we propose a quantile-based approach to secondary analyses of quantitative traits in GWA studies. We construct a new family of estimating equations to make consistent and efficient estimation for genetic effects on conditional quantiles, and also develop related statistical tools for inference. Simulations are conducted to evaluate the practical performance of the proposed approach, and a case-control study on genetic association with asthma is used to demonstrate the method.

**** Refreshments will be served @2:50pm in Room 502 Hill Center ****