CASE WESTERN RESERVE UNIVERSITY EST. 1826

Department of Epidemiology and Biostatistics
Biostatistics Seminar

Thursday, November 13, 2013
12:00pm - 1:00pm -- WG73

Novel meta-analysis of correlated traits using summary statistics from GWAS with an application in hypertension

Dr. Xiaofeng Zhu, Professor
Department of Epidemiology and Biostatistics,
Case Western Reserve University

Abstract: Genome wide association studies (GWAS) have identified many genetic variants underlying complex traits. Many detected genetic loci harbor variants that associate with multiple, even distinct traits. Most current analysis approaches focus on single traits, even though the final results from multiple traits are evaluated together. Such approaches miss the opportunity to systemically integrate the phenome-wide data available for genetic association analysis. In this study, we propose a general approach that can integrate association evidence from summary statistics of multiple traits, either correlated, independent, continuous or binary traits, which may come from the same or different studies. We allow for trait heterogeneity effects. Population structure and cryptic relatedness can also be controlled. Our simulations suggest that the proposed method has improved statistical power over single trait analysis in most of the cases we studied. We applied our method to the Continental Origins and Genetic Epidemiology Network (COGENT) African-Ancestry samples for blood pressure traits and identified four loci (/CHIC2, HOXA-EVX1, IGFBP1/IGFBP3/ and /CDH17, /P<5.0×10^-8) associated with hypertension related traits which were missed by a single trait analysis in the original report. Six additional loci with suggestive association evidence (P<5.0×10^-7) were also observed, including /CACNA1D/ and /WNT3/. Our study strongly suggests that analyzing multiple phenotypes can improve statistical power and such analysis can be executed using the summary statistics from GWAS. Our method also provides a way to study a cross phenotype (CP) association using summary statistics from GWAS of multiple phenotypes.**