Department of Biostatistics and Medical Informatics Seminar

Qiongshi Lu, PhD

Assistant Professor
Department of Biostatistics and Medical Informatics
University of Wisconsin - Madison

Friday, February 25, 2022
12:00-1:00 pm
Biotech Center Auditorium and Zoom:
https://uwmadison.zoom.us/j/99878043944

Reimagining gene-environment interaction in the omnigenic era

Abstract: The environments are often ignored or treated as nuisance parameters in human complex trait genetics research. However, in epidemiology, social sciences, and clinical research, there is a great interest in quantifying the heterogeneity of the effect of an exposure (e.g., a treatment, a major policy change, a natural experiment), and more specifically, how it interacts with genetics. However, the typical statistical methodology used in gene-environment (GxE) interaction analysis (i.e., linear models with main effects of G and E and the interaction GxE) has a number of limitations, especially in the 'omnigenic' era (we have now realized that most human traits have a large number of non-zero but weak genetic effects). In this talk, I will introduce several recent statistical advances that reimagine the GxE analysis for 'omnigenic' human traits. First, I will introduce QUAIL, a novel, quantile-regression-based framework to identify genetic variants associated with the variability (rather than the mean) of human traits. I will demonstrate that robust findings of variance quantitative trait loci (vQTL) can effectively prioritize candidate genetic variants in GxE studies, and polygenic scores produced from vQTL effects (vPGS) can aggregate information across numerous genetic loci and improve both statistical power and biological interpretability of GxE studies. Next, I will discuss very recent work that links two seemingly unrelated topics: GxE interaction and genetic correlation estimation. I will illustrate that current tools used for genetic correlation estimation provide an ideal alternative strategy for quantifying GxE interactions and will have a number of advantages compared to a traditional linear model with interaction effects. I will show plenty of empirical examples that involve body mass index, education reform in the UK, and sex differences of the genetic basis of many complex traits to showcase the performance of these new statistical advances. Overall, these new tools address critical limitations in existing methodologies and may have broad applications in future GxE studies.

School of Medicine and Public Health
UNIVERSITY OF WISCONSIN–MADISON