



Yan (Dora) Zhang, PhD

Postdoc Fellow, Dept. of Biostatistics
Bloomberg School of Public Health
Johns Hopkins University

Friday, February 8, 2019

12n–1:00p, Biotech Center Auditorium

Estimation of Complex Effect-Size Distributions Using Summary-level Statistics from GWAS

Abstract: Nowadays, sample sizes for genome-wide association studies (GWAS) of many complex traits have been rising rapidly due to the successes of large consortia. The yields of future GWAS critically depend on the underlying effect-size distributions. Summary-level statistics from GWAS have been widely used to estimate heritability and co-heritability of traits using the popular linkage-disequilibrium (LD) score regression method. In this talk, I will present a novel likelihood-based approach for analyzing summary-level statistics and external LD information to estimate effect-size distributions of common variants. The effect-size distribution is characterized by the proportion of underlying susceptibility SNPs and a flexible normal-mixture model for their effects. We applied the proposed method to analyze the summary-level data across 32 GWAS, and identified a wide diversity in genetic architecture of the traits, with consequences for the yields of future GWAS in terms of discovery and risk prediction.



**School of Medicine
and Public Health**

UNIVERSITY OF WISCONSIN-MADISON