

Division of Biostatistics Seminar Series

**GEM: Scalable and Flexible
Gene-Environment Interaction
Analysis in Millions of Samples**

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When: Friday, March 5, 2021
12:30pm - 1:30 pm

**Registration Link
via Zoom:**

<https://wustl.zoom.us/meeting/register/tJEpdumtrTluGNLF-fNziY4jTgPculPBxaug>



GEM: Scalable and Flexible Gene-Environment Interaction Analysis in Millions of Samples

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Gene-environment interaction (GEI) studies are a general framework that can be used to identify genetic variants that modify the effects of environmental, physiological, lifestyle, or treatment effects on complex traits. Moreover, GEIs can enhance our understanding of the genetic architecture of complex diseases by accounting for heterogeneous genetic effects across age, sex, race/ethnicity groups. However, statistical power of GEI tests is limited in typical cohort studies, and a much larger sample size than traditional genome-wide association studies (GWAS) is needed for testing GEIs. Commonly-used existing statistical software programs for GEI studies are either not applicable to testing certain types of GEI hypotheses or have not been optimized for use in large samples. Here, we develop a new software program, GEM (Gene-Environment interaction analysis in Millions of samples), which supports the inclusion of multiple GEI terms, adjustment for GEI covariates, and robust inference, while allowing multi-threading to reduce computation time. GEM can conduct GEI tests as well as joint tests of genetic effects for both continuous and binary phenotypes. Through simulations, we demonstrate that GEM scales to millions of samples while addressing limitations of existing software programs. We additionally conduct a gene-sex interaction analysis on waist-hip ratio in 352,768 unrelated individuals from the UK Biobank, identifying novel loci in the joint test that have not previously been reported in combined or sex-specific analyses. Our results demonstrate that GEM can facilitate the next generation of large-scale GEI studies and help advance our understanding of genomic contributions to complex traits.