Genetic Association and Beyond:
Statistical Methods to Elucidate Complex Trait Etiology

Course, September 14-18, 2026
Max Delbrück Center for Molecular Medicine (MDC)
Berlin, Germany

Emphasis: This course will cover a wide variety of statistical and bioinformatic methods (e.g., association analysis/GWAS, Mendelian randomization, polygenic scores, PWAS) to gain insights into complex trait etiology. It will include both theory and applied exercises.

Topics: Processing genotype data from arrays, exome and whole-genome sequencing; association analysis of qualitative & quantitative traits using rare & common variants (GWAS); data quality control; linear mixed models (LMM & GLMM); genotype imputation; controlling for population admixture/substructure and other confounders; detecting interactions; pleiotropy analysis; mediation analysis; Mendelian randomization (MR); heritability estimation; genetic correlations; polygenic scores (PGS); power and sample size estimation; multiple testing (FWER & FDR); meta-analysis; fine mapping; PWAS (protein expression level prediction using cis- & *trans*-variants, association analysis of measured and predicted levels).

Computer exercises: will be carried out using a variety of programs (bcftools, Annovar, GCTA, LDSC, PLINK, R, REGENIE, TwoSampleMR, etc).

Instructors: Suzanne Leal (Columbia University) & Michael Nothnagel (University of Cologne)

For additional information, course schedule and application visit:
https://statgen.us/GABeyond2026