Course Announcement
Complex Trait Analysis of Next Generation Sequence Data

MDC Berlin-Buch
Max-Delbrück-Centrum für Molekulare Medizin

September 8-12, 2025

Max Delbrück Center for Molecular Medicine
Berlin, Germany

Emphasis: both theory and application of methods to analyze next generation sequence (NGS) data will be taught. Attendees will learn how to design studies, call variants, analyze population and family-based sequence data and evaluate variant functionality. Analysis of NGS data will include performing complex trait rare variant association analysis for population and family data.

Topics: sequence alignment, variant calling, data quality control, association testing, rare variant association methods, GLMM, LMM, estimation of heritability, pleiotropy, polygenic risk scores, power estimation, imputation, and evaluating variant functionality.

Exercises: will be performed using a variety of computer programs including: ANNOVAR, BCFtools, GCTA, LDPRED2, LDSC regression, R, REGENIE, etc.

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

For additional information, course schedule and application form visit the course websites:
https://statgen.us/ComplexNGS2025