

Genetic Association Course

With Application to Sequence and Genotype Data

September 16-20, 2024

Max Delbrück Center for Molecular Medicine
Berlin, Germany

MDC
Berlin-Buch

Max Delbrück Center for Molecular Medicine, Berlin

Emphasis: Complex trait rare and common variant association analysis of population based data. This course will cover both theory and applied exercises. Computer exercises will be carried out using a variety of programs (R, PLINK, REGENIE, LDPhred2, etc).

Topics: Analysis of qualitative and quantitative traits with an emphasis on whole genome data, single marker, rare variant association analysis of exome and whole genome sequence data, data quality control (genotype & sequence data), linear mixed models (LMM) and generalized LMM, imputing rare and common variants, controlling for population admixture/substructure, detecting gene x gene & gene x environment interactions, power and sample size estimation for analysis of sequence and genotype data, polygenic risk score, permutation and FDR

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

For additional information, course schedule and application form visit the course websites:
<https://statgen.research.bcm.edu/index.php/Genassoc2024>

(Google: Berlin Genetic Association Course 2024)