

Genetic Association Course

With Application to Sequence and Genotype Data

September 13-17, 2021

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, FAST-GWA, REGENIE, Variant Association Tools, etc).

Topics: Analysis of qualitative and quantitative traits with an emphasis on whole genome data, single marker and haplotype analysis, rare variant association analysis of exome sequence and whole genome sequence data, data quality control (genotype & sequence data), imputing rare and common variants, controlling for population admixture/substructure, generalized linear mixed models and linear mixed models, detecting gene x gene & gene x environment interactions, polygenic risk scores analysis of rare variants, power and sample size estimation for analysis of sequence and genotype data, 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.us/Genassoc2021>

(Google: Berlin Genetic Association Course 2021)