Course Announcement

Identifying Genes for Mendelian Traits using Next Generation Sequence Data

November 11-15, 2019

Max Delbrück Center for Molecular Medicine
Berlin, Germany

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

Emphasis: Mendelian trait variant/gene identification through application of linkage, homozygosity mapping and filtering methods. This course will cover both theory and applied exercises. Computer exercises will be carried out using a variety of programs (Gemini, Homozygosity Mapper, Merlin, Polyphen-2, SEQLinkage, Variant Mendelian Tools, etc).

Topics: Linkage analysis and homozygosity mapping using genotyping arrays and sequence data (exome and whole genome), filter approaches to identify Mendelian and de novo variants, study design and selection of individuals for sequencing, determining pedigree informativeness and power, variant annotation and accessing variant functionality

Instructors: Suzanne Leal (Baylor College of Medicine)
Michael Nothnagel (University of Cologne)

For additional information, course schedule and application form visit the course websites:
https://statgen.research.bcm.edu/index.php/NGSMendelian2019
(Google: Berlin NGS Mendelian 2019)