Analysis of Next Generation Sequence Data Course For Complex and Mendelian Traits

June 23-27, 2014

Max Delbrück Center for Molecular Medicine
Berlin, Germany

MDC Berlin-Buch

Max-Delbrück-Centrum für Molekulare Medizin

Emphasis: both theory and application of methods to analyze next generation sequence (NGS) data for 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-based and trio data and also identifying variants for Mendelian traits .

Topics: sequence alignment, calling variants, population genetics, data quality control, association testing, rare variant association methods, power estimation, identifying Mendelian variants, imputation, and evaluating variant functionality.

Exercises: will be performed using a variety of computer programs including: GATK, Polyphen2, PSEQ, SEQPower, & VAT.

Instructors: Laurent Francioli; Suzanne Leal; Michael Nothnagel & Peter Robinson

For additional information, course schedule and application form visit the course websites:

http://www.bcm.edu/genetics/leal/ngscourse2014

(Google: Berlin NGS Course 2014)