# Complex Trait Analysis of Next Generation Sequence Data Course

**June 18-22, 2018**

**Max Delbrück Center for Molecular Medicine–Berlin, Germany**

Each session will begin with a theoretical introduction followed by practical exercises. The instructors for the course are Suzanne Leal (Baylor College of Medicine) and Michael Nothnagel (University of Cologne).

The course will be held daily from 9:00 a.m. to 5:00 p.m., except for Wednesday, June 20th when the course will end at 1:00 p.m. in order to have free time in for sightseeing. On Monday, June 18th, registration will be held from 8:30 to 9:00 a.m. A wine and cheese get together will be held for students and faculty directly after the course on June 18th.

**MONDAY** Morning *Lecture*

June 18th Aligning Sequence Data, Calling single nucleotide variants (SNVs), Variant quality score recalibration, VCF file format and Annotation, Visualization of next generation sequence (NGS) Data

*Computer Exercises*

Genome Analysis Toolkit (GATK)

Afternoon *Lecture*

Cloud computing

*Computer Exercises*

Integrative Genome Viewer (IGV)

17:00-18:30 Wine and Cheese Party

**TUESDAY** Morning *Lecture*

June 19thQuality control for NGS data

*Computer Exercises*

Variant Association Tools (VAT) – Part 1

Afternoon *Lecture*

Population history of rare and common variants;

Association analysis testing within a regression framework for qualitative and quantitative traits for fixed effects and controlling for confounders

*Pencil and Paper Exercises*

Hardy-Weinburg Equilibrium, FST

*Computer Exercises*

SFSCODE

**WEDNESDAY** Morning *Lecture*

June 20thControlling for population substructure and admixture

Regression Analysis – statistical interactions, random effects and mixed models.

*Computer Exercise*

R

Afternoon Free for sightseeing

**THURSDAY** Morning *Lecture*

June 21stRare variant association methods for population based and trio data, controlling for covariates and population substructure/admixture

*Computer Exercises*

PSEQ, VAT-Part 2

Afternoon *Lecture*

Association analysis of Trio and family Data

Replicating rare variant associations,

*Computer Exercises*

RV-TDT

**FRIDAY** Morning *Lecture*

June 22ndImputation of rare variants and their analysis, Power Analysis for rare variants

*Computer Exercises*

SEQPower

Afternoon *Lecture*

Predicting functionality of Variants using bioinformatics tools

*Computer Exercises*

CADD, FATHMM, GERP, LRT, Mutalyzer, Mutation Assessor, Mutation Taster, PhlyoP, Polyphen-2, PhastCons, PROVEAN, SIFT