



Genetic epidemiology and genome-wide association analyses

Time and place:	6 th -10 th June 2016, University of Bergen, Norway
Lecturers:	Håkon K. Gjessing, Rolv Terje Lie, Anil Jugessur
ECTS:	3 credits

Course description

The first part of the course will provide a broad overview of genetic epidemiology and statistical genetics, including biometrical genetics such as twin studies, population genetics, Hardy-Weinberg equilibrium, population structure, complex diseases, "missing heritability," attributable fractions, and polygenic risk score. Family design versus case-control design, linkage versus linkage disequilibrium. Gene-environment interactions, case-only designs, Mendelian randomization. Phenotypes measured as continuous, dichotomous, or time-to-event data. Relative risk and penetrance models.

The second part will cover genetic association analyses in detail: Data handling and basic quality control for candidate genes and genome-wide association analyses (GWAS). Data imputation, selection of informative (tagging) SNPs. Power simulations. Analyses: Basic associations analyses, control for population structure, haplotype reconstruction, risk response models; estimation of maternal gene effects and parent-of-origin effects; X-chromosome models. Testing and measuring gene-environment interactions (GxE). Post-processing of results, regional association plots, assessing haplotype blocks, control for multiple testing, False Discovery Rate (FDR), q-values.

The course will use freely available software, including PLINK, GenABEL (in R), HapMap/HaploView, and Haplin (in R).

Course program

This is an intensive one-week course with lectures and hands-on exercises, Monday to Friday, 9-17, with 1 hour lunch break. About half the time with lectures and the other half with exercises. Take-home project will be prepared during the last afternoon.

Prerequisites

Basic understanding of genetic principles. Experience with regression models, including logistic regression and time-to-event models. Experience with the R software and some previous experience with genetic association analyses will be an advantage.

Learning outcome and competence

To acquire the tools and abilities to conduct genetic association analyses, including data quality control, analyses, interpretation of results, and post-processing/presentation of results

Evaluation

Take-home project following the course.

Note:

NORBIS will cover travel- and accommodation expenses for PhD students affiliated to our school.