

(<https://norbis.w.uib.no>)



Genetic epidemiology and genome-wide association analyses

The course will be given online

Dates: 30th November – December 4th, 2020

Location: The course will be given digitally. Link will be provided to participants.

Lecturers: Håkon K. Gjessing, Rolv Terje Lie, Anil Jugessur and others

Course code: GENESTAT

Credits: 4 ECTS

Registration: [Here \(https://forms.gle/pfrJ38bybQhEuhkm8\)](https://forms.gle/pfrJ38bybQhEuhkm8) Students who like to gain ECTS will have to register at UiB in addition. Visiting PhD students have to register as [visiting students HERE asap \(https://skjemaker.app.uib.no/view.php?id=6690414\)](#). Registration deadline for the course is 22nd November.

Main course page: Will be updated and made available closer to course start.

Detailed course program: Will be updated and made available closer to course start.

Preparations for the course: please read **these instructions**

(https://folk.uib.no/gjessing/genetics/software/haplin/other/NORBIS_2018/preparations/)

carefully NOW, to make sure you are up to speed. There is software to be installed BEFORE going to the course, and a suggested R tutorial that will be useful to those with less than excellent R skills.

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, linkage disequilibrium, complex diseases and “missing heritability”, as well as topics from epigenetics, with focus on methylation data.

The second part will cover genetic association analyses in detail: Designs, including case-family trios, case-control, time-to-event etc. Data handling and basic quality control for candidate genes, genome-wide association analyses, and standard methylation platforms (GWAS and EWAS), data imputation, and selection of tagging SNPs. Study planning and power calculations/sample size calculations for complex models. 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). Postprocessing of results, regional association plots, assessing haplotype blocks. Control for multiple testing: False Discovery Rate (FDR), q-values, and some general principles from empirical Bayes testing. The course will use freely available software/resources, including numerous R-packages, PLINK, 1000genomes, HaploView, Haplin (in R), and others.

Course program (will be subject to minor changes):

Day I: Monday

1000-1700 Lectures and exercises/practicals

Day II: Tuesday

0900-1700 Lectures and exercises/practicals

Day III: Wednesday

7 hours colloquium, group work/exercises

Day IV: Thursday

0900-1100 Follow-up of group work

1100-1700 Lectures and exercises/practicals

Day V: Friday

0900-1300 Lecture and exercises/practicals

1300-1700 Wrap-up/summary, prepare take-home project

Following (one full) week:

Work on take-home project, return within two weeks

Learning outcome:

To obtain a general overview and understanding of the field of genetic epidemiology. 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.

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.

NEWS FROM NORBIS

[Dissertation for Xiaokang Zhang! \(https://norbis.w.uib.no/dissertation-for-xiaokang-zhang/\)](https://norbis.w.uib.no/dissertation-for-xiaokang-zhang/) 28. October 2020

[6th NORBIS Annual Conference \(https://norbis.w.uib.no/6th-norbis-annual-conference/\)](https://norbis.w.uib.no/6th-norbis-annual-conference/) 28. October 2020

[Boston University research stay by Snorre Sulheim \(https://norbis.w.uib.no/boston-university-research-stay-by-snorre-sulheim/\)](https://norbis.w.uib.no/boston-university-research-stay-by-snorre-sulheim/) 22. October 2020

[New director of NORBIS \(https://norbis.w.uib.no/new-director-of-norbis/\)](https://norbis.w.uib.no/new-director-of-norbis/) 16. October 2020

[NORBIS Covid_19 webinar mini-series \(https://norbis.w.uib.no/norbis-covid_19-webinar-miniseries/\)](https://norbis.w.uib.no/norbis-covid_19-webinar-miniseries/) 22. May 2020

UPCOMING EVENTS

Genetic epidemiology and genome-wide association analyses
(<https://norbis.w.uib.no/event/genetic-epidemiology-and-genome-wide-association-analyses-2/>)

November 30 @ 9:00 am - December 4 @ 4:00 pm

Genome assembly and annotation course (<https://norbis.w.uib.no/event/genome-assembly-and-annotation-course/>)

3. May 2021 @ 9:00 am - 7. May 2021 @ 4:00 pm

[View All Events \(https://norbis.w.uib.no/events/\)](https://norbis.w.uib.no/events/)



Visiting adress: Høyteknologisenteret i Bergen, Thormøhlensgate 55, N-5008 Bergen, Norway

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(<http://www.uib.no/form/organisering/profil-og-designseksjonen>) - UiB

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