NORBIS: Genetic epidemiology and genome-wide association analyses

COURSE PROGRAM 2020
Updated: 2020-11-27

Course Home Page
https://folk.uib.no/gjessing/genetics/software/haplin/other/NORBIS_2020/intro/

Lecturers:

Håkon K. Gjessing (HKG), Anil Jugessur (AJ), Rolv Terje Lie (RTL), Øystein Ariansen Haaland (ØAH), Øyvind Helgeland (ØH), Julia Romanowska (JR), Jon Bohlin (JB), Yunsung Lee (YL), Ellisif Nygaard (EN), Bjørn Olav Åsvold (BOÅ)

Day I: Monday, Nov. 30

09:30-10:30
        Welcome & Introduction. Course overview. (HKG)
            +   Introduction round!

10:30-11:00 + 15 min for questions and break
        General introduction to genetic epidemiology Lecture I, part I. (AJ)

11:15-11:45 + 15 min for questions and break
        General introduction to genetic epidemiology Lecture I, part II. (AJ)

12:00-13:00 LUNCH

13:00-16:00, with breaks and individual work
        Practicals and presentations (ØAH, JR, EN):
        R in genetics. More on R, PLINK (to produce ped-files)

Day II: Tuesday, Dec. 1

09:00-09:30 + 15 min for questions and break
09:45-10:15 + 15 min for questions and break
    General introduction to genetic epidemiology Lect II. (AJ)
10:30-11:00 + 15 min for questions and break
11:15-11:45 + 15 min for questions and break
    General introduction to genetic epidemiology Lect III. (AJ)

12:00-13:00 LUNCH

13:00-13:30 + 15 min for questions and break
13:45-14:15 + 15 min for questions and break
14:30-14:45 + 15 min for questions and break
15:00-15:30+ 15 min for questions and break
15:45-16:15 + 15 min for questions and break
    GWAS Quality control, Imputations etc., using PLINK and other software
    Presentations/practicals. (ØH)

Day III: Wednesday, Dec. 2

09:00-09:30
    Data preparation of GWAS family data with the Haplin package.
Lectures/practicals.(ØAH, JR, EN)

09:30-09:45 BREAK

09:45-10:15 + 15 min for questions and break
10:30-11:00 + 15 min for questions and break
11:15 - 12:00, with breaks and individual work
    Association analyses in Haplin. Lectures/practicals. (HKG, JR)
    Models behind Haplin, Analyses in Haplin, Interpretations of results

12:00-13:00 LUNCH

13:00-13:30 Sample size calculations for association analyses. (HKG)
13:30-13:45 15 min for questions and break (HKG)

13:45-14:15

Exercises/group work. Power + sample size.(HKG)

14:15-14:30 BREAK

14:30-15:00+ 15 min for questions and break
    Post-processing of results. (ØAH)
15:15-15:45+ 15 min for questions and break
    Polygenic risk scores (PRS). (YL)

Day IV: Thursday, Dec. 3

09:00-09:30 + 15 min for questions and break
09:45-10:15 + 15 min for questions and break
    Special inheritance models in Haplin. X-chromosome, Parent-of-origin
effects. Lecture. (HKG)

10:30-11:00+ 15 min for questions and break
11:15-11:45+ 15 min for questions and break
    EWAS/Methylation data analyses. Lectures (JB)

12:00-13:00 LUNCH

13:00-14:00
    Exercises EWAS/Methylation (JB)

14:00-14:10 BREAK

14:10-14:40+ 15 min for questions and break
    Case study: Methylation age clocks (YL)

15:00-16:00
    Exercises/group work EWAS. (YL).

Day V: Friday, Dec. 4

09:00-09:30+ 15 min for questions and break
09:45-10:15+ 15 min for questions and break

Multiple testing and GxE w/Haplin (HKG) + GxMe (JR)

10:30-11:15 + 15 min for questions and break
Registry studies, familial clustering, recurrence risk. Lecture. (RTL)

11:30-12:00
Orofacial clefts case study. Lecture (RTL)

12:00-13:00 LUNCH

13:00-13:30 + 15 min for questions and break
13:45-14:15 + 15 min for questions and break
Mendelian randomization (BOÅ)

14:30-15:00+ 15 min for questions and break
Bioinformatics services and DBs (JR)

15:15-15:35 Presentation from NORBIS (Ragna Breines)

15:35-16:00 Wrap-up/summary, prepare take-home project, course evaluation

Return take-home project. Deadline to be announced