

WORKSHOP

Advanced Quantitative Genetics Using Twin and Family Data

Date: June 7-9, 2022 | 09.00 am –15.00 pm

Place: Karolinska Institutet (details provided nearer the time)

Arranged within the Doctoral Programme in Epidemiology, support from the Strategic Research Programme in Epidemiology (SFO Epi)

Overview: Quantitative genetic modelling using twin- and/or family data often serves as an important part in investigations of etiology of diseases/traits/phenotypes. However, advanced implementations, such as estimation of genetic correlations, often requires in-depth knowledge of statistical models, as well as understanding of statistical software and programming. The most common statistical framework for twin and family based quantitative genetic modelling are structural equation models (SEMs).

Content: The framework of SEMs will be presented with a focus on how it is used in twin- and family based quantitative genetic modelling. Statistical theory and practical implementations in OpenMx will be covered for topics ranging from 'simple' univariate heritability analyses, through bivariate analyses estimating e.g. genetic correlations, to more complex models. Although the emphasis will be on the statistical models, we will discuss assumptions, strengths and weaknesses of using different type of relatives and designs.

Instructors: Ralf Kuja-Halkola, PhD, Ass. Professor, MEB, KI, Mark Taylor, Principal researcher, MEB, Cen Chen, PhD student, MEB.

Target group: Doctoral students, Postdocs, Master students, junior and senior researchers. It is recommended to have basic understanding of genetics, and at least some familiarity of programming in the statistical software R.

[Registration \(last day to register May 30\)](#)

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