

Complex trait genetics (aka Quantitative Genetics) 2018

Taught by:

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Course objective

Provide the theoretical background into human population and biometrical genetics, as they are applicable to the genetic analysis of complex traits

Course content

Quantitative genetics is concerned with the inheritance of those differences between individuals that are of degree rather than of kind (quantitative rather than qualitative). Such differences are seen for most human complex traits (e.g. BMI, depression, cognition, attention problems). This course aims to provide the theoretical understanding of the inheritance of such quantitative differences in behavior, behavioral disorders, endophenotypes (e.g. blood pressure or brain volumes) underlying disease traits (e.g. hypertension or schizophrenia). Quantitative differences, as far as they are inherited, depend on genes with on average small effects and are usually influenced by gene differences at many loci. Consequently these genes cannot be identified by Mendelian segregation ratios (though they are subject to the laws of Mendelian transmission). The methods of quantitative genetics are characterized by studies of large populations and families / twins and by the fact that the nature of quantitative differences requires the measurement (and not just the classification) of individuals. The extension of Mendelian genetics into quantitative genetics will be made in two stages: the genetic properties of populations (population genetics) and the inheritance of measurements (biometrical genetics). Quantitative genetics is now merging with molecular genetics and the last part of this course will be devoted to methods for the localization and characterization of genes causing quantitative variation. One lecture will be devoted to the new field of epigenetics.

Form of tuition

Lectures, homework assignments, and participation in class

Type of assessment

Home work, essays and oral presentation (20%, 50%, 30%); see below

Course Literature

-Falconer DS & Mackay TFC, Introduction to Quantitative Genetics (4 ed), Longman, London, 1996

-Recent papers (please see reading list)

Entry requirements

Behavior genetics; sufficient knowledge of statistics; quantitative methods and molecular genetics. When entrance requirements are met, the course is open to MA students, PhD students and post-docs. Attendance of class meetings is obligatory.

When in doubt, please contact di.boomsma@vu.nl or j.van.dongen@vu.nl

Course program

<u>Lecture</u>	<u>Time</u>	<u>Date</u>	<u>Where</u>	<u>Falconer chapter*</u>	<u>Topic</u>
1	13.30	4/09	<u>HG-1G05</u>	chapter 1 & 2	Genetic Constitution of a population Changes of gene frequency (Boomsma)
2	13.30	11/09	<u>HG-1G05</u>	chapter 6 & 7	Continuous variation Values and means (Boomsma)
<i>18/09 Deadline first assay (email to: di.boomsma@vu.nl and j.van.dongen@vu.nl)</i>					
3	13.30	18/09	<u>HG-1G05</u>	chapter 8	Variance and variance decomposition (Boomsma)
4	13.30	25/09	<u>HG-1G05</u>	chapter 9	Resemblance between relatives (Boomsma)
5	13.30	2/10	<u>HG-1G05</u>	chapter 9 / 10	Heritability based on data from relatives Heritability based on SNP data (Boomsma) Application to IL-6R data (Van Dongen)
6	13.30	9/10	<u>HG-1G05</u>	Epigenetics	van Dongen
7	13.30	16/10	<u>HG-1G05</u>	chapters 17, 18, 19	Scaling, dichotomous traits, causality and correlated characters (Boomsma)

Symposium 17/10 NTR-AVERA “**Personalized Medicine**” at VU

8 13.30 23/10 HG-1G11 *Assignments (presentations by students)*

30/10 Deadline for second assay (email to: di.boomsma@vu.nl and j.van.dongen@vu.nl)

*for additional reading assignments see literature list

Classrooms are in the VU main building (Hoofdgebouw Filosofenhof)

Assessment

1. Homework: will be assigned each week (selected problems from Falconer & Mackay).
2. Essay 1: an essay about you: your background, interests in genetics, why this course is important to you and what your expectations are for this class.
3. Presentation: a choice from the topics on the reading list
4. Essay 2: connected to your presentation choice: discuss how the method / approach / topic of your choice might be of relevance to your interests (as introduced in essay 1) and how they might fit into your own PhD or RM thesis project.