

BIOSTAT/STAT551
Winter Quarter 2004
Statistical Genetics II: Quantitative Traits

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Meeting Times: TTh 8:30-9:50
Location: RR134 Health Sciences Building

Course Description

This course will provide a statistical basis for describing variation in quantitative traits. This will include decomposition of trait variation into components representing genes, environment and gene-environment interaction. Resemblance between relatives and heritability will be described. Important topics of discussion will include epistasis, oligogenic and polygenic traits, complex segregation analysis, methods of mapping and characterizing quantitative trait loci (QTL) and estimation procedures. Other topics that may be discussed include correlation between traits, maternal effects, sex linkage and threshold characters.

This course is the second in a three-quarter series in Statistical Genetics. The first course in the series, Statistical Genetics I: Discrete Mendelian Traits, is a prerequisite of this course. It is also assumed that students are comfortable with regression theory, covariance, correlation and likelihood theory. The interested student is urged to contact the instructor with concerns regarding assumed knowledge.

By the end of the course, the student should be able to

- statistically relate genetic and environmental effects to a quantitative trait
- identify procedures for estimation of genetic and environmental effects
- identify methods for localization of genes that influence variation in quantitative traits
- identify methods for quantifying the affects of genetic variants on quantitative traits
- read/understand the current applied and theoretical literature involving genetic influences on quantitative traits
- lead a discussion of a relevant paper from the literature or of material from the text (that has not been covered in class)

Grading Policy

Grades will be determined as follows:

- 55% Homework assignments
- 10% Participation in class
- 35% Final Project

There will be approximately 5 homework assignments. The “participation in class” grade will be determined by participation in discussions and by lecture summaries.

These summaries will be given by a pre-selected student and are to be informal five-minute reviews of the previous lecture. Each student will complete a final project.

Projects can pertain to methods in quantitative genetics that have not been covered in class, a data analysis or a proposal of study for a quantitative trait. The project is meant to build on the knowledge gained from class. More details are provided below.

Overview of Topics

The course will cover five topic areas. These are outlined below along with the relevant text chapters and a *tentative* schedule. Additional handouts will be given as needed.

1. Basics of quantitative genetics, Chapters 1, 4, 5, 6 and 7
2. Detections of major genes / segregation analysis, Chapter 13
3. Establishing regions of linkage, Chapter 16
4. Finding association between genes and traits (linkage disequilibrium methods), Chapter 14
5. Additional topics (time permitting): correlated traits, multivariate linkage

Week	Topic	Date	Reading
1	Properties of a single locus	Jan 6, 8	Chapters 1, 4
2	Sources of variation for multilocus traits; Components of environmental variation	Jan 13, 15	Chapters 5, 6
3	Project drafts; Resemblance between relatives	Jan 20, 22	Chapter 7
4-5	Detecting major genes	Jan 27, 29 Feb 3, 5	Chapter 13, handouts
6-7	Mapping and characterizing QTLs	Feb 10, 12, 17, 19	Chapter 16, handouts
8-9	Finding association between genes and traits	Feb 24, 26, Mar 2, 4	Chapter 14
10	Correlated traits; Multivariate linkage analysis	Mar 9, 11	Handouts

Other Items

The text for this course is Lynch M, Walsh B (1998) Genetics and Analysis of Quantitative Traits. Sinauer Associates, Inc. A web-site for the text is accessible at http://nitro.biosci.arizona.edu/zbook/volume_1/vol1.html

The text and the following three books have been placed on reserve in the library:

- Ott J (1999) Analysis of Human Genetic Linkage. John Hopkins University Press
- Khoury M, Beaty TH, Cohen BH (1993) Fundamentals of genetic epidemiology. Oxford University Press
- Weir BS (1996) Genetic data analysis II : methods for discrete population genetic data. Sinauer Associates: Sunderland, Mass

We also have a folder in the biostatistics suite where I'll place copies of notes, homework assignments, exams and, as needed, reference papers. The folder is in the file cabinets under the faculty mailboxes. Feel free to make copies of any of the materials but leave the original for your classmates.

A list of helpful books related to statistical genetics can be found at <http://depts.washington.edu/statgen/Statgen/steph.shtml>

Description of Project

Length:

15-20 pages of double-spaced typed text with 1 inch margins

Timeline:

- A one-page proposal is due **January 22**.
- Three copies of a detailed outline are due **February 5**.
- The project paper is due by 5:00pm on **March 17**. NO EXCEPTIONS!

Format:

The paper should include, but is not limited to, the following

- Statement of the importance of the topic as well as a statement of relevance to statistical methods in quantitative genetics
- Background and literature review
- Description of methods, results and discussion
- A description of how this particular topic/paper improves upon and is different from previous work
- If applicable, additional research suggested by the authors
- Additional research suggested by you
- Any programs, analyses or simulations that you use to support your points
- Any programs that you have completed for general use
- A Literature Cited section
- If applicable, a copy of the main paper on which the project is based should be attached to the project paper

Grading:

Grades will be determined as follows:

- Paper content:
 - Extent of coverage of the appropriate literature (30%)
 - Interpretation of previous research and methods (30%)
 - appropriateness and novelty of research suggested by you (20%)
- Relevance to Course (10%)
- Quality of Writing (10%)