BMI 826-001: Statistical methods for QTL mapping (Fall, 2012)

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Web	`http://www.biostat.wisc.edu/~kbroman`
Office hours	Tu 2:00-3:00pm, or by appointment
Lectures	TR 9:30–10:45am, 1209 Engr Hall
Textbooks	Broman and Sen, *A guide to QTL mapping with R/qtl* [required] Dalgaard, *Introductory statistics with R*, 2nd edition [recommended] Venables and Ripley, *Modern applied statistics with S*, 4th edition [recommended]
Course web	`http://www.biostat.wisc.edu/~kbroman/teaching/qtltopics`

Objectives

QTL are quantitative trait loci: genetic loci that contribute to variation in a quantitative trait (such as body weight or blood pressure). In this course, we will give an overview of statistical methods for mapping QTL in experimental crosses.

The course will focus largely on mouse genetics; however, it should also be valuable to students interested in human genetics or in animal and plant breeding. Mouse crosses are simple, and discussion of QTL mapping in this context can allow the basic principles to be elucidated with greater clarity.

The course will be aimed at PhD students in Biostatisitcs & Medical Informatics or Statistics, though we also welcome graduate students from the biological sciences. The statistical aspects should be accessible to any student with knowledge of analysis of variance and linear regression.

Prerequisites

Genetics 466 or equivalent; one of Statistics 310, 571, 610, or 710, or equivalent (that is, some basic statistics course); some knowledge of R.

Computing

We will use R (`http://www.R-project.org`) and R/qtl (`http://www.rqtl.org`) throughout the course.

Homework

There will be 4 homework assignments, which will mostly involve computational analyses to explore different aspects of QTL mapping.

Final project

There will be no exams in the course. Rather, each student will complete a final project: a 6–10 page paper describing the analysis of a specific QTL mapping dataset provided by Prof. Broman. This will be along the lines of a regular scientific paper: Introduction, Methods, Results, Discussion. Computer code is to be placed in an Appendix.

Academic honesty

You are *encouraged* to discuss homework assignments and your final project with other students. However, you must not present others' work as your own. If you work with other students in solving problems, make sure that you each write up your own solutions independently. It is not acceptable for one student to write a solution for another student to copy.

Grading

Your grade will be determined by four equally-weighted homework assignments. I will assign course grades according to the following scale, though this may be adjusted if it turns out that I've been grading too harshly.

Percentage	Grade
94 – 100%	A
87 – 94%	AB
80 – 87%	B
73 – 80%	BC

Percentage	Grade
60 – 73%	C
55 – 60%	D
0 – 55%	F

Approximate schedule (See the course web site for the definitive schedule.)

Date	Topic	Reading
Sep 4	Overview	Ch 1
Sep 6	Meiosis and recombination	
Sep 11	Hidden Markov models (HMMs) for QTL mapping	App D
Sep 13	Data diagnostics	Ch 3
Sep 18	Genetic map construction	tech report
Sep 20	Interval mapping	Sec 4.1-4.2
Sep 25	Significance thresholds and other topics	Sec 4.3, 4.5
Sep 27	Non-normal traits	Ch 5
Oct 2	Experimental design and power	Ch 6
Oct 4	**No lecture**	
Oct 9	Covariates	Ch 7
Oct 11	Two-dimensional, two-QTL genome scans	Ch 8
Oct 16	The X chromosome	Sec 4.4
Oct 18	Mapping multiple QTL I	Ch 9
Oct 23	Mapping multiple QTL II	
Oct 25	Multiple QTL mapping in R/qtl	
Oct 30	**No lecture**	
Nov 1	**No lecture**	
Nov 6	Bayesian methods I	
Nov 8	Bayesian methods II	
Nov 13	eQTL analysis I	
Nov 15	eQTL analysis II	