

**PubH 7445/8445**

*Fall 2009, 3 credits, A/F or S/N*

**Title:** Statistics for Human Genetics and Molecular Biology

**Course Description:** This course will introduce statistical applications in genetic mapping, DNA or protein sequence alignment, and analyses of gene expression data from microarray experiments.

**Course Instructor:** Dr Cavan Reilly, email: [cavanr@biostat.umn.edu](mailto:cavanr@biostat.umn.edu), phone: (612)624-9644, office: Mayo A440, office hours: M and W 2:30-3:30.

**For whom intended:** This course is designed for second-year biostatistics/statistics graduate students who want to learn about statistical issues in genetics/genomics, and biology graduate students with a statistical background who want to learn about statistical methods specific to a number of important problems in genetics/genomics.

**Dual applicability:** This course can be taken either for MS or PhD credit. The difference in terms of workload will be more homework problems per assignment, and higher expectations for the final project for PhD credit. **It is assumed that all students will work at the MS level, it is up to the student to notify the instructor within 3 weeks of the semester if PhD credit is sought. This decision is irreversible after that point.**

**Prerequisites:** Statistics at the level of PubH 6450–6451 or equivalent or permission of instructor. Some background with molecular biology is desirable and knowledge of calculus and linear algebra is necessary (at the level required to be in the Biostatistics MS program).

**Objective:** After taking the course, the student should have a working biological and statistical knowledge in the three areas covered.

**Evaluations:** Course evaluation will be based on homework assignments and projects. No exam.

**Course web site:** <http://www.biostat.umn.edu/~cavanr/pubh7445.html>.

**Disability statement:** If you have a disability that affects participation in class activities and requirements, please contact the Office of Disability Services (612-626-1333, Suite 180 in the University Gateway Building, 200 Oak Street) and we will work together to accommodate you.

**Textbooks:** Reilly, C. (2009) *Statistics in Human Genetics and Molecular Biology*, Chapman & Hall/CRR Press.

The following are recommended references:

1. Falconer, D. and Mackay, T. (1996), *Introduction to Quantitative Genetics*, Prentice Hall. (Population genetics: reserved in Biostat Reading Room, Mayo A460)
2. Gelman, A., Carlin, J.B., Stern, H.S. and Rubin, D.B. (1995), *Bayesian Data Analysis*, Chapman and Hall. (General statistics: reserved in Biostat Reading Room, Mayo A460)
3. Lodish et al. (2000), *Molecular Cell Biology*, Freeman. (General molecular biology: reserved in Biomed library)
4. Lynch, M. and Walsh, B. (1998), *Genetics and Analysis of Quantitative Traits*, Sinauer. (Population genetics: reserved in Biomed library)
5. Ott, J. (1999), *Analysis of Human Genetic Linkage*, John Hopkins University Press. (Genetic mapping; reserved in Biostat Reading Room, Mayo A460)
6. Thompson, M., McInnes, R. and Willard, H. (1991), *Genetics in Medicine*, W.B. Saunders Co. (General genetics; reserved in Biomed library)
7. Waterman, M. (1995) *Introduction to Computational Biology*, Chapman Hall. (Physical mapping and sequence alignment: reserved in Biomed library)

### Weekly Schedules:

Week	Topics
1	Course introduction; Preliminary biology and statistics
2	Physical mapping and radiation hybrid maps
3	Two point parametric linkage
4	Extensions of the basic par. linkage model, multipoint linkage
5	Nonparametric linkage analysis
6	Violations of assumptions in par. linkage, complex traits, and linkage in practice
7	Introduction to sequence alignment
8	Alignment of Pairs of Sequence
9	Sequence Alignment and Hidden Markov Models
10	Sequence motif recognition
11	Introduction to microarray data
12	Detecting differential expression
13	Cluster analysis
14	Discriminant analysis
15	Other applications