

PubH 5470-2 Special Topics
Spring 2003, 3 credits, A/F or S/N

Title: Statistics for Human Genetics and Molecular Biology

Course Description: With the exciting developments in genetics and genomics, the challenge now is how to extract useful information from the resulting large amounts of data. It has been recognized that statistics is going to play an increasingly important role. This course will introduce statistical applications in genetic mapping, DNA or protein sequence alignment, and analyses of gene expression data from microarray experiments.

Course Instructors:

- Dr Cavan Reilly (covering genetic mapping and sequence alignment), email: cavanr@biostat.umn.edu, phone: (612)624-9644, office: Mayo A440, office hours: TTh 11:30-12:30pm.
- Dr Wei Pan (covering microarray data), email: weip@biostat.umn.edu, phone: (612)626-2705, office: Mayo A428, office hours: TBA

For whom intended: This course is designed for second-year biostatistics/statistics graduate students who want to learn genetics/genomics, and biology graduate students who have a statistical background and want to learn statistical applications.

Prerequisites: Statistics at the level of PubH 5450–5452 or equivalent or permission of instructor. Some background with molecular biology is desirable.

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.

Textbooks: There is no required textbook. There will be some readings drawn from recommended references and journal articles. Some course notes may be distributed in class. The following are recommended references:

1. Durbin, R., Eddy, S., Kroug, A. and Mitchison, G. (1998), *Biological Sequence Analysis*, Cambridge University Press. (Sequence alignment: reserved in Biomed library)
2. Falconer, D. and Mackay, T. (1996), *Introduction to Quantitative Genetics*, Prentice Hall. (Population genetics: reserved in Biostat Reading Room, Mayo A460)

3. 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)
4. Lodish et al. (2000), *Molecular Cell Biology*, Freeman. (General molecular biology: reserved in Biomed library)
5. Lynch, M. and Walsh, B. (1998), *Genetics and Analysis of Quantitative Traits*, Sinauer. (Population genetics: reserved in Biomed library)
6. Ott, Jurg (1999), *Analysis of Human Genetic Linkage*, John Hopkins University Press. (Genetic mapping; reserved in Biostat Reading Room, Mayo A460)
7. Thompson, M., McInnes, R. and Willard, H. (1991), *Genetics in Medicine*, W.B. Saunders Co. (General genetics; reserved in Biomed library)
8. Vernables, W.N. and Ripley, B.D. (1999), *Modern Applied Statistics with S-plus*. Springer-Verlag, New York. (Multivariate analysis for microarray data; reserved in Biostat Reading Room)
9. Waterman, M. (1995) *Introduction to Computational Biology*, Chapman Hall. (Physical mapping and sequence alignment: reserved in Biomed library)

Weekly Schedules:

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