

STT 855: Statistical Genetics Fall 2011 (3 credits)

Time: MW, 3:00 – 4:20 PM

Place: C316 Wells Hall

Instructor: Yuehua Cui

A432 Wells Hall

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Web: <http://www.stt.msu.edu/~cui>

Office Hours: MW, 4:20 - 5:00pm, or by appointment.

Text: Lecture notes will be made available.

Prerequisite: STT863 and STT442 or STT861 or equivalent.

Basic skills necessary for this course: Calculus; Basic probability distribution theory; t-test; Chi-square-test; (logistic) regression analysis; ANOVA; Maximum likelihood method; Computer software (e.g., S-plus/R, SAS, C/C++, or Matlab)

Course objectives

The course is designed for Master and PhD students in statistics, human, plant and animal biology, and other biological and life sciences. Students will learn advanced techniques of modern statistical methods for genetic data analysis, and are expected to do data analysis and basic research in the field after taking the class.

Course description

The course will introduce basic probabilistic and statistical methods in analyzing genetic data arising from plant, animal and human studies. It will cover fundamental concepts and theories as well as applications to real and simulated data. Topics include but are not limited to:

- Basic genetic concepts such as Mendel's law, Hardy-Weinberg equilibrium; Linkage and linkage disequilibrium (LD);
- Estimation and test of linkage and LD;
- Basic concept of QTL mapping, including single marker analysis, interval and composite interval mapping;
- Functional QTL mapping of dynamic/longitudinal traits;
- Statistical methods in linkage and association analysis of human genetic data with family-based and population-based designs, covering χ^2 test of independence, simple and multiple logistic regression, variance components analysis and TDT test;
- Single SNP and haplotype-based inference; Genome-wide association studies (GWAS);

- Issues of multiple testing in GWAS; Concept of false discovery rate (FDR);
- Design and analysis issues in eQTL mapping of transcriptional abundance.
- Next-generation sequencing data analysis (if have time)

References:

1. *Statistical Genetics of Quantitative Traits: Linkage, Map and QTL* by Rongling Wu, Chang-Xiang Ma and George Casella, Springer-Verlag, New York.
2. *Mathematical and Statistical Methods for Genetic Analysis* by Kenneth Lange, Springer-Verlag, New York.
3. *Genetics and Analysis of Quantitative Traits* by Michael Lynch, Bruce Walsh, Sinauer Assoc.

Grading

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| 40% | Homework |
| 60% | Research project |
| | <ul style="list-style-type: none"> • Analysis and written report (40%) • Class presentation (20%) |

Research Project

The instructor will conceive of multiple problems related to the topic of this course. Students can work singly or as a group. ***Each student/group will choose one of the problems as their final project.*** Students with different backgrounds are encouraged to work together. Different students/groups may choose the same problem, but they should accomplish their projects independently.

Alternatively, ***students are also encouraged to base their class projects on one of their own problems (with real data).*** But they should consult with the instructor first.

Format of written reports

Follow the format of a refereed journal, e.g., *Genetics* or *Biometrics*.

- Introduction
- Statistical Methods
- Results
- Discussion
- References

Page limit: ≤ 20 double-spaced pages (including tables, figures and references)

Tentative Schedule (will be announced later, check the course website for update)