BIOSTAT/STAT 552 Statistical Genetics III: Design and analysis

Winter Quarter 2016 (3 credits)

Time and place: Tuesdays & Thursdays, 9:00-10:20 AM, Rm. E212 Health Sciences
Course website: https://courses.washington.edu/b552/
Instructor: Ellen M. Wijsman, Professor, Dept. Biostatistics and Div. Medical Genetics

Prerequisites: BIOST/STAT 550 and 551; STAT 390, STAT 423, or BIOST 515 or equivalent; STAT 394, 395 or equivalent; Otherwise, permission of instructor.

Grading: Participation in class: 20% of grade for course; Problem sets: 20% of grade for course; Final project: 60% of grade for course, as outlined in description of the final project.

Course Description: This course is the third in a three-quarter series in Statistical Genetics. The first two courses in the series - Statistical Genetics I: Discrete Mendelian Traits, and Statistical Genetics II: Quantitative Genetics - are prerequisites for this course. Students should be comfortable with the material covered in these two prerequisite courses. They should also be comfortable with likelihood, conditional probability, and regression; should have some experience with a statistical package, such as SPlus, R, or Stata; and should know how to use a computer text editor.

This course will take the discrete and quantitative models from the previous two courses, and will use them to investigate problems of design and analysis for traits with a genetic basis. Important topics of discussion will include different approaches to pedigree- and population-based gene mapping, finescale mapping, interpretation, real-life constraints, choosing among alternative designs, sample size and power estimation, and ascertainment.

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

- Choose appropriate methods for analysis of genetic traits,
- Apply these methods of analysis correctly,
- Discuss strengths and weaknesses of methods for such analyses, using statistical principles to form the basis for discussion,
- Provide interpretation of results of such analyses with explanations for reasons for such interpretation,
- Describe the statistical advantages and disadvantages of commonly-used study designs,
- Compare and contrast the relative strengths and weaknesses of commonly-used statistical genetic methods and study designs,
- Design a study plan for a complex trait using statistical principles, with justification of analytic methods, required sample sizes, and expected interpretationis,
- Describe the effects of data ascertainment on analysis results and interpretation,

- Critically evaluate the current literature with regard to statistical procedures and methods used to investigate genetic traits.

Textbook: There is no official textbook for this course. Course material will be a combination of book readings from several books that are on reserve in the Health Sciences library, journal articles, and handouts/lecture notes. See reference list.

Software: We will use a few software packages. All are installed on the Biostatistics statgen website and computers. Instructions will be provided.