

STAT 580: Design and Data Analysis for Bioinformatics
Spring 2010
9:30-10:45 T/R Statistics 006

Instructor:

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Topics:

- Design and analysis for gene expression/microarray experiments
- Design and analysis for proteomics experiments
- Pathways analysis
- Introduction to other bioinformatics topics including metabolomics, sequence analysis and genetic association analysis.

Objectives: The goal of this course is to introduce students to various statistical methods used for bioinformatics data analysis. There will be a strong emphasis on application and appropriateness of methods, rather than theory and derivation. Students will also learn to program in R, but no prior knowledge of R is assumed. Introductions to biological topics and corresponding technologies will be incorporated throughout the semester. By the end of the semester students should understand design and analysis issues for bioinformatics and feel comfortable programming and running their own analyses.

Prerequisite: STAT511, STAT540, or permission of the instructor

Textbook: There is no required textbook, but the following texts might be helpful:

- Bioinformatics and Computational Biology Solutions Using R and Bioconductor by Gentleman et al.
- Introductory Statistics with R by Dalgaard

Course Webpage at RamCT: Much of the course material and information will be available on RamCT. This will include lecture notes, examples, assignments and important dates. Students are expected to print a copy of the notes and bring them to class. Students will need an eID and password to log onto RamCT.

Software: R, ArrayTrack and other programs will be used throughout the semester. R and ArrayTrack are both free and publically available. Since different R libraries will be used throughout the semester, it is **strongly recommended that you have access to a computer with internet access and administrator privileges.**

Grading:

40% Homework

30% Project 1

30% Project 2

Homework: There will be at least 5 assignments during the semester. Students are encouraged to work together, but the **work turned in should be the work of the individual student**. By that I mean that all computer output should be generated by the student and the answers should be written by the student. Students will be given at least a week to complete each assignment. **No late homework will be accepted (without prior approval).**

Projects and Presentations: There will be 2 required projects for the course. The first will focus on gene expression data, the second will be in an area chosen by the student. Both projects will include both a written component and a class presentation.