Stats M254/Bioinfo M271/Biomath M271
Statistical Methods in Computational Biology

Course site: `http://www.stat.ucla.edu/~zhou/courses/Stats254`

Instructor: Qing Zhou (zhou@stat.ucla.edu), OH: Thursday 2:30-4pm, MS 8979.

Prerequisite: Stats 100A (Probability) or Stats 200A (Probability) or Bioinfo 260A (Bioinformatics).

Homework, project, and grading

1. Homework assignments (for practice only).

2. Description of a few candidate projects will be posted by the end of the 4th week, from which you may choose one to work on. You may form a group of no more than two students. Each group will write a paper on the project (total length ≤ 8 pages, font size ≥ 11 points, single space) and do a 20-min oral presentation during the last couple of weeks. Papers should be submitted in the last week. Your final grade will be determined by both the paper (80%) and the oral presentation (20%).

Topics

Introduction to statistical and computational methods in computational biology and bioinformatics. The topics include:

1. Introduction and Data: molecular biology of gene regulation, typical data.

2. Gene expression analysis: multiple tests, false discovery rate, clustering methods, liquid association, RNA-Seq data analysis.

3. Statistical Sequence Analysis: Bayesian inference, hidden Markov model, missing data, Monte Carlo, motif discovery, ChIP-Seq data analysis.

References

- Lecture notes (to be posted on the moodle site).
- Other papers posted on the course webpage.