BIOINF 184/BENG 184/BIMM 184/CHEM 184/CSE 184:
Computational Molecular Biology, UCSD Spring Quarter 2014

Instructor: Professor Wei Wang, wei-wang@ucsd.edu, 4254 Urey Hall
               Office Hour: 5:00 pm – 6:00 pm Th
Teaching Assistant: TBA
               Office Hour: TBA

Description:
       This course will introduce the challenging problems in the modern molecular biology, genomic and proteomic technologies as well as computational methods that have been developed to address these questions in the post-genome era. This course will survey cutting-edge research in the contemporary bioinformatics and systems biology at the introductory level and aims at exposing students to the up-to-date research topics. It emphasizes the combination of biological insights and statistical techniques to solve real research problems.

       The topics are inference of transcriptional regulatory network, which covers next generation sequencing, RNA-seq, ChIP-seq and DNA methylation analysis, prediction of regulatory elements in the human genome, identification of regulatory motifs, and network topology analysis, and protein interaction analysis, which covers protein folding, protein structure prediction, protein motif/domain identification, protein structure classification, and prediction of protein-protein interactions. The computational algorithms that will be introduced in the course include, for example, hierarchical clustering, k-means, support vector machine, expectation maximization and naïve Bayes net. The course consists of lectures, student presentation and project.

Prerequisites:
       BIOINF 181 and 182 or basic understanding of molecular biology and familiar with one of the following programming languages, Perl, Java, Python and C.

Readings:
       Optional readings will be suggested throughout the course (check the course website for updates).
       No required textbook.

Tentative Schedule
Introduction and overview of next generation sequencing technology (2 lectures)
Peak calling and visualization (2 lecture)
Histone modifications (2 lectures)
Enhancer predictions (3 lectures)
Motif analysis (2 lectures)
RNA-seq analysis (3 lectures)
Open chromatin and Hi-C analysis (2 lectures)
DNA methylation analysis (2 lectures)
Network analysis (2 lectures)