
CSE 427 Computational Biology

Credits

3.0 (3 hrs. lecture)

Lead Instructor

Martin Tompa

Textbook

None

Course Description

Algorithmic and analytic techniques underlying analysis of large-scale biological data sets such as DNA, RNA, and protein sequences or structures, expression and proteomic profiling. Hands-on experience with databases, analysis tools, and genome markers. Applications such as sequence alignment, BLAST, phylogenetics, and Markov models.

Prerequisites

either CSE 326 or CSE 332

CE Major Status

Selected Elective

Course Objectives

The goal of this course is to give students enough exposure to Computational Biology that they can make informed choices about further exploration such as graduate programs. Another goal is to give the students hands-on experience with databases, analysis tools, and genome browsers.

ABET Outcomes

- (a) an ability to apply knowledge of mathematics, science, and engineering
- (b) an ability to design and conduct experiments, as well as to analyze and interpret data
- (c) an ability to design a system, component, or process to meet desired needs within realistic constraints such as economic, environmental, social, political, ethical, health and safety, manufacturability, and sustainability
- (j) knowledge of contemporary issues

Course Topics

1. Basics of Molecular Biology: proteins, DNA, RNA; DNA replication, transcription, translation, regulation of expression; gene structure; genome organization
2. Pairwise sequence alignment: optimal global and local alignment, affine gap penaltie

3. The algorithms and statistics of BLAST
4. Amino acid substitution matrix
5. Multiple sequence alignment: definition and NP-completeness, comparative sequence analysis and the UCSC Human Genome Browser, progressive alignment, methods for whole-genome multiple sequence alignment
6. Inference of phylogenetic trees
7. Markov chains and hidden Markov models
8. Challenges in Computational Molecular Biology