

Course Overview

Bioinformatics II is primarily oriented toward computer science students who wish to gain an in depth understanding of the techniques and algorithms used in bioinformatic analyses. It involves detailed study of the major bioinformatics algorithms such as those for sequence alignment and for searching sequences databases (BLAST). Bioinformatics II is a programming course. Some experience in programming is required. Students will implement bioinformatic algorithms and submit detailed, formal documentation of their programs. This documentation will include documents describing the inputs, outputs and processing for each sub-component as well as hierarchical structure charts to illustrate the organization of the programs. Successful completion of the course will give the student an awareness and understanding of current bioinformatic algorithms that can serve as a starting point for research in the field. The current text book is, Genomic Perl by Rex A. Dwyer.

The following topics will be covered in the course.

1. Brief Review of Biology. Survey of Bioinformtics Databases
2. Pairwise Sequence Alignment
3. Protein Substitution Matrices
4. Protein Motifs
5. Multiple Sequence Alignments
6. k-tuple Methods
7. Phylogenetics
8. RNA Secondary Structure
9. Gene Finding Algorithms
10. Species Prediction
11. Restriction Mapping
12. Satellite Identification