

BIOF 518: Theoretical and Applied Bioinformatics I

The objective of this course is to give students an introduction into the theory and practice of a wide range of bioinformatic techniques and applications, enabling them to use these tools in their own research. This course will be divided into five modules: statistical approaches in sequence analysis; phylogenetic analysis of nucleotide and protein sequences; acquisition and analysis of sequence datasets, including EST and RNA-seq data; analysis of genomic datasets from an evolutionary perspective; and, prediction of protein secondary structure. Two or three of the five sessions in each module will be divided roughly 60 percent theoretical lecture and 40 percent learning to use relevant computational tools. The final session of each module will be split between a discussion of computational tools, a journal club, and a discussion of work on a project assigned for each module. By the end of the course, students should be able to acquire many types of sequence data, identify orthologous and paralogous genes, predict domains and motifs, identify alternative splicing, analyze genomic/protein alignments, and make a prediction of secondary protein structure from primary sequence.

Learning Objectives

- Introduce the theory and practice of a wide range of bioinformatic techniques and applications, enabling students to use these tools in their own research
- Search database searches using BLAST and hidden Markov models
- Predict gene structure and analyze domains and motifs
- Conduct phylogenetic analysis of nucleotide and protein sequences and identify orthologous and paralogous genes
- Analyze genomic and protein alignments, prediction of secondary protein structure from primary sequence

Credits: 2

Class Type: Graduate Course

Prerequisites:

Solid understanding of biology, computer science and mathematics.

Program: Bioinformatics and Data Science