

COURSE OUTLINE

BFMT-204 Intermediate Bioinformatics 3 Semester Hours

HOWARD COMMUNITY COLLEGE

Description

Course integrates biological concepts with computer and database methods to study biological systems. Concepts covered include modeling complex biological systems, mechanisms and integration of molecular and organism evolution, introduction to web-based biological databases, and computational tools for analysis of genomic and protein data. The Associate of Arts Bioinformatics Degree program prepares students for undergraduate schools or a career in the fast-paced pharmaceutical or biotechnology industries. (4 hours weekly) Prerequisites: BFMT-200.

Overall Course Objectives

Upon completion of this course the student will be able to:

1. Analyze DNA, RNA and protein sequences
2. Use comprehensive databases of the biomedical scientific literature, such as PubMed and Entrez PubMedsource.
3. Retrieve protein and DNA sequences from databases.
4. Apply bioinformatics to biological research
5. Use Perl to solve biological problems
6. Use BioPerl modules to manipulate and process sequences and nucleotides and proteins.
7. Use BioPerl moduales for searching biological databases
8. Create Perl programs for calculating DNA lengths

Major Topics

- I. Review of the fundamental dogma of biology: DNA->RNA->protein, bases, codons, amino acids
- II. Introduction to Hidden Markov models.
- III. Protein Structure Prediction and Analysis
- IV. Phylogenetic Analysis
- V. Using Perl to Facilitate Biological Analysis

Course Requirements

Grading and exams: Grading procedures will be determined by the individual faculty member, but will include the final grades calculated on the bases of exams, class projects, lab demonstrations, and written papers.

Other Course Information

This course serves as supplement in the Bioinformatics program and as a Computer Science elective.