

Computer Skills in Biotechnology - BIOL 358

Syllabus

Summary

This course is designed to introduce and explain the application of computational and analytical methods to address problems in biotechnology. Many popular software tools employed in biotechnology and bioinformatics research will be covered. The theoretical basis governing the use and importance of these tools will be explored.

Logistics

Semester: Spring 2005
Lecture Time: Mondays, 5:30 p.m. – 8:30 p.m.
Location: Science Hall 2, room 308

Instructor: Helge Weissig, Ph.D.
hweissig@csusm.edu
(858) 735 7476

Office Hours: Mondays, 4:30 p.m. – 5:30 p.m. (by appointment only)
Science Hall 2, room 141

Prerequisites: BIOL 210 & 211; CS 211 (concurrently)

Student Accounts: Student accounts for access to Unix, Perl and MySQL will be provided on login.bioinformaticscourses.com. Usernames are identical to CSUSM user names. Passwords will be distributed during class.

Grades

Grades will be assigned based on three projects, each of which is due at the end of each section below. There will be no mid-term and no final, however students are required to present their final projects during the last session of class.

Course Material

The course's website is at <http://www.bioinformaticscourses.com/BIOL358/>. All lecture notes and other course materials, including a list of recommended books will be made available at this location

Course Outline

Section I – Essential Basics

- Computers & the Internet
- HTML, CGI & Web Services
- Operating Systems & UNIX
- Relational Databases
- Perl & Other Programming Languages

Section II – Introduction to Bioinformatics

- NCBI Entrez
- The BLAST Algorithm
- Using BLAST online
- ORF Finder
- GENSCAN
- Principles and use of PSI-BLAST
- Multiple Sequence Alignments with ClustalW
- Protein analysis (Prosite, Pfam, PRINTS, Blocks)

Section III – Introduction to Structural Bioinformatics

- The Protein Data Bank
- Visualization w/ Rasmol & Chime
- Secondary Structure Calculation (Kabsch/Sander)
- Structure Classification (SCOP & CATH)
- Structure Determination
- Basic Geometry
- Structure/Function Assignment
- Structure Alignment
- Structure Prediction
- Protein Folding
- Protein/Ligand Docking
- Molecular Dynamics