Virginia Western Community College
Bio 255
Bioinformatics and Computer Applications in Biotechnology

Course Description

Covers basic computer concepts and Internet skills and uses a software suite, which includes word processing, spreadsheet, database, and presentation software to demonstrate skills as they are applied to biotechnology. Introduces students to basic online tools and resources to retrieve and analyze biological data, such as DNA, RNA, and protein sequences, structures, functions, pathways, and interactions. Includes hands-on sessions to allow students to become familiar with these resources and their navigation and applications.
(2 Cr.) Lecture 2 hours. Total 2 hours per week.
2 credits

General Course Purpose

This course is designed to prepare students to be successful entry level laboratory technicians by teaching and reinforcing their computer skills, including the navigation and adept use of biological information databases. Computer skills are requisite in most of the upcoming careers in the knowledge based economy, and this course is designed to equip students with the skills necessary to use office management programs, send netiquette appropriate emails, and use the online bioinformatics databases and tools to mine for information relevant to biotechnology.

Course Prerequisites/Corequisites

Biology 101

Course Objectives

- Effectively use word-processing, spreadsheet, presentation, and email software tools as applied to biotechnology
- Recognize DNA and protein sequences in various formats (FASTA, RAW, etc.)
- Identify and navigate important biological databases
- Use appropriate tools for searching and analyzing biological data (BLAST, CLUSTALW, etc.)
- Prepare a phylogenetic analysis using a computer program
- Use a basic protein folding program

Major Topics to be Included

- Productivity Tools as Used by Biotechnologists
  - Word Processing
    - Perform basic editing and text formatting in bioinformatics files and documents (cut, copy, paste, etc.)
    - Save, backup and print FASTA formatted files and other biological sequence data.
- Manipulate bioinformatics data stored in word files to be properly formatted (font size, margins, alignment, etc.)
  - Spreadsheets
    - Perform basic editing and data entry of raw bioinformatics data into a spreadsheet (move, copy, and cut and paste).
    - Manipulate data using built-in spreadsheet functions and formulas to analyze biological trends in the data.
    - Print out results of bioinformatics analysis of data and represent as a graph and/or chart.
  - Presentation Graphics
    - Create and manipulate slide show on a relevant bioinformatics topic.
    - Include text, graphics, animation, and transitions to synthesis biological data into a focused story.
    - Use design layouts or custom templates in presentation of biologically relevant material to class.
- Bioinformatics Tools (the following sections have been enhanced to specify and explain the topics to be covered; the final official course content summary could just include the underlined topics)
  - Overview of Bioinformatics
    - Review of DNA and Protein Structure; Review of the Genetic Code and How it Works; How are Proteins and DNA represented in an electronic format; reading DNA and ORFs; Reading RNA/Distinctions between DNA and RNA; Overview of the Field of Bioinformatics including Sequence Analysis and Genomics
    - Gaining knowledge through PubMed; Searches and Parameters of PubMed; Using ExPASy server/SwissProt to search for protein information and sequences; FASTA and RAW file formats; Cross-referencing DNA sequences from protein sequences using ExPASy.
    - Using BLAST to compare protein sequences; Parameters and filters within BLAST; Multiple protein sequence alignments with ClustalW.
    - Review of prokaryotes vs. eukaryote transcription/translation (introns/exons, genomic content, etc). Using Nucleotide sequence databases such as NCBI, EMBL, DDBJ and GenBank to decipher gene content of prokaryotes and eukaryotes. Understanding cross-referencing from within a GenBank entry and how the accession system works.
  - Protein Sequences
    - Using a Gene-centric database (NCBI Entrez) and comparing to GenBanks protocol. Working with whole genome databases, bacterial

    (TIGR database) and viral genomes. Exploring the human genome. Using the Ensembl collaboration project.
    - Protein and Specialized Sequence Databases. Review of Maturation process in proteins post-translation. ORFs vs. Mature protein sequences. Bioinformatic methods of deducing mature protein structures. Reading Swiss-Prot entries to understand complex folding and diversity in proteins. How structure relates to function in proteins. Using Swiss-Prot entries to explore biochemical pathways of a specific protein. Exploring protein families.
  - Single and Multiple DNA Sequences and ORFs
    - Single DNA Sequences; removing vector sequences and correcting other errors in the sequence; verifying a restriction map; What is PCR? How PCR primers are designed; Analyzing the composition of the DNA sequence including word count, G/C content, finding internal repeats, finding protein-coding regions and isolating ORFs using GeneMark.
    - Produce a dot plot to identify internal repeats in a DNA sequence.
    - Locating ORFs within a given DNA sequence (GeneMark).
  - Whole Genome Analysis
    - Finding internal exons in vertebrate genomic sequences. Complete gene parsing of a eukaryotic genome. Assembling Sequence Fragments. Commercial software for genome-sequencing (Sequencher, Lasergene,etc).
    - Analyze a DNA sequence with GenomeScan.
    - Construct a sequence using CAP3.
  - RNA Folding and Phylogenetic Tree Construction
    - RNA Folding.
    - Construct RNA sequence map from Adenovirus sequence.
    - Construct energy graph from Adenovirus sequence
    - Phylogenetic Tree Construction

ADA Statement (PDF)
Title IX Statement (PDF)