

University of Arkansas - Fort Smith
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General Syllabus

BIOL 47084 Bioinformatics

Credit Hours: 4

Lecture Hours: 3

Laboratory Hours: 3

Prerequisite: BIOL 38093 Genetics

Effective Catalog: 2018~2019

I. Course Information

A. Catalog Description

A survey of basic and emerging techniques for computational analysis of biologically meaningful data (e.g., DNA sequence data, SNPs, haplotypes, pathogens, etc.).

B. Additional Information - None

II. Student Learning Outcomes

A. Subject Matter

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

1. Access, search, and acquire biological data from pertinent databases.
2. Align DNA and protein sequence data using established and emerging computational techniques.
3. Calculate genetic distances and use them to explore phylogenetic relationships and molecular sequence evolution.
4. Build phylogenetic trees and test hypotheses related to tree topology and sequence relationships.
5. Identify and annotate gene sequences in raw genomic data and determine likely gene function.
6. Reconstruct RNA and protein structure and use protein structures to explore protein interactions and adaptations.

B. University Learning Outcomes

This course enhances student abilities in the following areas:

Analytical Skills

Critical Thinking Skills: Students will utilize critical thinking skills to identify a problem, break it down into its component parts and use scientific method to answer biological questions.

Quantitative Reasoning: Students will analyze scientific data, create and use models, test hypotheses and draw statistical inferences, and support conclusions based on sound mathematical reasoning.

Communication Skills (written and oral)

Students will demonstrate proficiency in communication by composing coherent arguments presented both orally and in writing.

Ethical Decision Making

Students will model ethical decision-making processes by identifying ethical dilemmas and affected parties and applying ethical frameworks to resolve a variety of ethical dilemmas.

III. Major Course Topics

- A. Genomics and Genome Analysis
 - 1. Genomic elements
 - 2. Open reading frames
 - 3. Metagenomics
- B. DNA and Protein Sequence Alignment
 - 1. Needleman/Wunsch alignment
 - 2. BLAST
 - 3. Alignment software
- C. Phylogenetic Systematics
 - 1. Distance methods
 - 2. Parsimony methods
 - 3. Likelihood methods
 - 4. Bayesian methods
- D. Macromolecular Structure Prediction
 - 1. RNAs
 - 2. Proteins
 - 3. Fundamentals of rational drug design
- E. Gene expression analysis with emerging technologies
 - 1. Microarrays
 - 2. RT-PCR
 - 3. RNA-Seq analysis
- F. Genetics and evolution of human disease and pathogens