

Introduction to Bioinformatics and Computational Biology

Credit Hours: 2-1

Contact Hours: 2-3

Pre-requisites: None

Code BI-4XX

Course Description

This course will help undergraduate students to understand the need, development, fundamentals and techniques in Bioinformatics. Several techniques such as pairwise sequence alignment and multiple sequence alignment, protein structure prediction, and online tools will be discussed. Students will also understand basic central dogma of cell, different algorithms and biological data bases. Construction of bi-molecular networks will be discussed and analysis will be performed using Boolean **state representations**.

Course Learning Outcomes:

At the end of this course students will have a better understandings of following terms:

1. Sequence Alignment techniques
2. Molecular Evolution and Phylogeny Information
3. Homology Modelling techniques
4. Understandings of Biological data bases and algorithms
5. Protein structure and sequence prediction techniques
6. Understanding of constructing bi-molecular networks and Boolean state representations

Assessment System

Quizzes	10-15%
Assignments	5-10%
Midterms	30-40%
ESE	40-50%

Topics Covered

Week No	Description	Quizzes	Assignment
1	Background & Need of bioinformatics		
2	Storage of Biological Sequence Information		01
3	Comparing Sequences	01	
4 - 5	Pairwise Sequence Alignments, Dot Plots		

6	Dynamic Programming - Essentials Backtracking Alignments, Overlap Matches	02	
7	Introduction to Scoring Alignments, Deriving scoring matrices		
8	Introduction to Multiple Sequences Alignment, Progressive Alignment for MSA		
9	MIDTERMS		
10	BLAST Algorithm	03	
11	FASTA Algorithm		
12	Molecular evolution and phylogeny Introduction to UPGMA		02
13	Strategies for RNA Structure Prediction Dot Plots for RNA 2' Structure Prediction		03
14	From DNA/RNA Sequences to Proteins Sequencing Proteins Online Proteomics Tools		
15	Introduction to Protein Folding Computing Protein Folding Possibilities	04	
16	Introduction to Homology modelling		
17	Workflow for Structural Modelling		04
18	END SEMESTER EXAMINATION		

Lab Practical

Lab No	Description
1 - 2	Gene finder
3 - 4	ORF finder
5 - 6	EST database
7 - 8	SNP data
MIDTERMS	
10 -11	Protein structure prediction using online server
11 - 12	Protein structure visualizing
13 - 14	Secondary structure prediction
15 - 16	pfam database

Reference Material

1. Arthur Lesk (2019) An Introduction to Bioinformatics ISBN 978-0198794141
2. Jonathan Pevsner (2015) Bioinformatics and Functional Genomics 3rd Edition ISBN 978-1118581780
3. Richard E. Neapolitan (2009) Probabilistic Methods for Bioinformatics: With an Introduction to Bayesian Networks ISBN 978-0323165464
4. Dr. Robert I Colautti (2022) R Crash Course for Biologists: An introduction to R for bioinformatics and biostatistics (Coding and Quantitative Biology) ISBN 979-8849115917

Mitchell L. Model. (2010) Bioinformatics Programming Using Python: Practical Programming for Biological Data ISBN 978-0596154509

