Shri Vile Parle Kelavani Mandal's

Dwarkadas J. Sanghvi College of Engineering

(Autonomous College Affiliated to the University of Mumbai)

Scheme and detailed Syllabus (DJS22)
of
Honors Degree Program
in
Computational Biology

Shri Vile Parle Kelavani Mandal's
DWARKADAS J. SANGHVI COLLEGE OF ENGINEERING
(Autonomous College Affiliated to the University of Mumbai)
NAAC Accredited with "A" Grade (CGPA : 3.18)

Proposed Scheme for B.Tech.in Artificial Intelligence (AI) and Data Science with Honors Degree Program in Computational Biology:
Semester VI(Autonomous) Academic year (2024-25)

Sr. No.	Course Code	Course	Teaching Scheme (hrs.)				Continuous Assessment (A) (marks)			Semester End Assessment (B) (marks)				Aggregate (A+B)		Total Credits
			Th.	P	T	Credits	Th.	T/W	Total CA (A)	Th.	O	P	O &P	Total SEA (B)		
	SEM V															
1	DJS22ADHN1C1	Introduction to Biological Science	4	--	--	4	35	--	35	65	--	--	--	65	100	4
	SEM VI															
2	DJS22ADHN1C2	Algorithms for Computational Biology	4	--	--	4	35	--	35	65	--	--	--	65	100	4
3	DJS22ADHN1L1	Algorithms for Computational Biology Laboratory	--	2	--	1	--	25	25	--	--	--	--	--	25	1
	SEM VII															
4	DJS22ADHN1C3	Bigdata in Bioinformatics	4	--	--	4	35	--	35	65	--	--	--	65	100	4
5	DJS22ADHN1L2	Bigdata in Bioinformatics Laboratory	--	2	--	1	--	25	25	--	--	--	--	--	25	1
	SEM VIII															
7	DJS22ADHN1C4	Genomic Data Science	4	--	--	4	35	--	35	65	--	--	--	65	100	4
	Total		**16**	**4**	**-**	**18**	**140**	**50**	**190**	**260**	**0**	**0**	**0**	**260**	**450**	**18**

Prepared by | Checked by | Head Of Department | Vice Principal | Principal

Program: B.Tech. in Artificial Intelligence (AI) and Data Science with Honors in Computational Biology				Semester : VI				
Course : Algorithms for Computational Biology				Course Code: DJS22ADHN1C2				
Course : Algorithms for Computational Biology Laboratory				Course Code: DJS22ADHN1L1				
Teaching Scheme (Hours / week)				Evaluation Scheme				
				Semester End Examination Marks (A)			Continuous Assessment Marks (B)			Total marks (A+ B)
Lectures	Practical	Tutorial	Total Credits	Theory			Term Test 1	Term Test 2	Total	
				65			20	15	35	100
				Laboratory Examination			Term work			
4	2	--	5	Oral	Practical	Oral & Practical	Laboratory Work	Tutorial / Mini project / presentation/ Journal	Total Term work	25
				--	--	--	15	10	25	

Prerequisite:

1. Basic knowledge of biological sciences

Objectives: The Objective of course is

1. Apply Algorithmic Techniques.
2. Design and Analyze Algorithms for Sequence Analysis and Genome Assembly.
3. Analyze Biological Networks.

Outcomes: On completion of the course, the learner will be able to:

1. Understand Computational Biology and Algorithms
2. Apply Sequence Alignment and Evolutionary Analysis Techniques
3. Analyze Protein Structures and Molecular Interactions
4. Interpret Gene Expression Data Using Advanced Algorithms
5. Model and Analyze Biological Networks
6. Leverage Machine Learning for Biological Data Analysis

	Algorithms for Computational Biology (DJS22ADHN1C2)	
Unit	**Description**	**Duration**
1	**Module 1: Introduction to Algorithms and Biological Data** Introduction to computational biology and its applications.Overview of biological data types (sequences, structures, pathways).Basic algorithms and data structures commonly used in computational biology (e.g., sorting, searching, graphs),Programming fundamentals for scientific computing (Python, R)	9
2	**Module 2: Sequence Alignment and Analysis Techniques** **Align sequences**: Utilize basic and advanced alignment algorithms to compare DNA, RNA, and protein sequences. **Identify hidden patterns:** Discover recurring motifs and signatures in sequences that reveal functional elements. **Reconstruct evolutionary history:** Build phylogenetic trees using sequence data to visualize relationships between species.	10
3	**Module 3: Structural Analysis Algorithms** Protein structure prediction algorithms (Homology modeling, Ab initio modeling),Protein-protein interaction prediction algorithms. Molecular docking algorithms, Structural alignment and comparison techniques	8
4	**Module 4: Gene Expression Analysis Algorithms** Microarray analysis and differential expression, RNA-seq analysis and differential expression, Clustering algorithms for gene expression data (e.g., K-means, hierarchical clustering),Dimensionality reduction techniques (PCA, SVD)	8
5	**Module 5: Network Analysis Algorithms** Introduction to biological networks (protein-protein interaction, metabolic, signaling),Network topology analysis (centrality measures, community detection),Algorithms for network modeling and simulation, Applications of network analysis in systems biology	8
6	**Module 6: Machine Learning for Computational Biology** Supervised learning for classification and prediction (e.g., support vector machines, random forests), Unsupervised learning for clustering and dimensionality reduction, Deep learning for biological data analysis (e.g., convolutional neural networks for protein structure prediction)	9
	TOTAL	**52**

Algorithms for Computational Biology Laboratory (DJS22ADHN1L1)	
Exp.	**Suggested experiments**
1	Implementing the Needleman-Wunsch algorithm for global sequence alignment.
2	Using BLAST to perform sequence similarity searches.
3	Evaluating the quality of multiple sequence alignments using ClustalW or MAFFT Algorithms.
4	Implementing an overlap-layout-consensus (OLC) genome assembly algorithm.
5	Constructing phylogenetic trees using distance-based methods (Neighbor-Joining, UPGMA).

6	Analyzing gene family evolution using comparative genomics tools.
7	Analyzing protein-protein interaction networks and Identifying modules and hubs in biological networks.
8	Project-based Research • Undertaking a research project using computational biology algorithms. • Developing a bioinformatics tool or pipeline for specific biological analysis. • Presenting and demonstrating the project outcomes to the class.

Any other experiment based on syllabus may be included, which would help the learner to understand topic/concept.

Books Recommended:

Text books:

1. "Bioinformatics Algorithms: An Active Learning Approach" by Phillip Compeau and Pavel Pevzner,2015.
2. "Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids" by Richard Durbin, Sean R. Eddy, Anders Krogh, and Graeme Mitchison,1998.

Reference Books:

1. "Computational Biology: A Practical Introduction to BioData Processing and Analysis with Linux, MySQL, and R" by Röbbe Wünschiers,2004
2. "Bioinformatics: Sequence and Genome Analysis" by David W. Mount,2004

Web links:

1. National Center for Biotechnology Information (NCBI),https://www.ncbi.nlm.nih.gov/
2. bioinformatics research and education,https://www.bioinformatics.org/
3. community-driven platform,https://rosettacode.org/wiki/Rosetta_Code
4. European Bioinformatics Institute (EBI),https://www.ebi.ac.uk/

Online References:

- Biology Meets Programming: Bioinformatics for Beginners, https://www.coursera.org/learn/bioinformatics.
- Bioinformatics Specialization, https://www.coursera.org/specializations/bioinformatics
- Systems Biology and Biotechnology Specialization, https://www.coursera.org/specializations/systems-biology

Continuous Assessment (B):

Theory:

1. One term test of 20 marks and one term test of 15 marks will be conducted during the semester
2. Total duration allotted for writing each of the paper is 1 hr.
3. Total of the marks scored in both the two tests will be considered for final grading.

Laboratory: (Term work)

Laboratory work will be based on the experiments.
The distribution of marks for term work shall be as follows:

- Laboratory work (Performance of Experiments): 15 Marks
- Mini Project / Journal Documentation (Write-up and solution of selected problem statement): 10 marks

The final certification and acceptance of term work will be subject to satisfactory performance of laboratory work and upon fulfilling minimum passing criteria in the term work.

Prepared by | Checked by | Head of the Department | Vice Principal | Principal