Shri Vile Parle Kelavani Mandal's

Dwarkadas J. Sanghvi College of Engineering

(Autonomous College Affiliated to the University of Mumbai)

Scheme and Detailed Syllabus (DJS23)

Third Year B.Tech

in

Artificial Intelligence (AI) and Data Science

Honors Degree Program

in

Computational Biology

(Semester VI)

Prepared by: - Board of Studies in Artificial Intelligence (AI) and Data Science

To be Recommended by: - Academic Council of Dwarkadas J. Sanghvi College of Engineering

To be Approved by: - Governing Body of Dwarkadas J. Sanghvi College of Engineering

With effect from the Academic Year: 2025-2026

Scheme for Honors in Computational Biology
Department of Artificial Intelligence and Data Science
Academic Year(2025-26)

Sr. no.	Course Code	Course	Teaching Scheme				Semester End Examination (SEE) - A						Continuous Assessment (CA) - B						Aggregate (A+B)	Credits Earned	
			Theory (Hrs)	Practical (Hrs)	Tutorial (Hrs)	Credits	Duration (Hrs)	Theory	Oral	Pract	Oral & Pract	SEE Total (A)	Term Test 1 (TT1)	Term Test 2 (TT2)	Term Test 3 (TT3)	Term Test Total (TT1 + TT2 + TT3)	Term Work	CA Total (B)			
SEM III																					
1	DJS23SCH1301	Computational Cellular Biology	3	--	--	4	2	60	--	--	--	60	15	15	10	40	--	40	100	3	3
SEM IV																					
2	DJS23SCH1401	Computational Molecular Biology	3	--	--	3	2	60	--	--	--	60	15	15	10	40	--	40	100	3	3
SEM V						1															
3	DJS23SCH1501	Algorithms for Computational Biology	3	--	--		2	60	--	--	--	60	15	15	10	40	--	40	100	3	4
	DJS23SLH1501	Algorithms for Computational Biology Laboratory	--	2	--	3	--	--	--	--	--	--	--	--	--	--	25	25	25	1	
SEM VI						1															
4	DJS23SCH1601	Computational Models for Biology	3	--	--		2	60	--	--	--	60	15	15	10	40	--	40	100	3	4
	DJS23SLH1601	Computational Models for Biology Laboratory	--	2	--	4	--	--	--	--	--	--	--	--	--	--	25	25	25	1	
SEM VIII																					
5	DJS23SCH1801	Bigdata in Bioinformatics	4	--	--	2	2	60	--	--	--	60	15	15	10	40	--	40	100	4	4
Total			**16**	**4**	**0**	**18**	**10**	**300**	**0**	**0**	**0**	**300**	**75**	**75**	**50**	**200**	**50**	**250**	**550**	**18**	**18**

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

Program: B. Tech in Artificial Intelligence (AI) and Data Science **T.Y. B. Tech** **Semester: VI**

Course: Computational Models for Biology (DJS23SCH1601)

Course: Computational Models for Biology Laboratory (DJS23SLH1601)

Prerequisite: Basic knowledge of biological sciences

Course Objectives: The Objectives of the course are

1. Understand and explain the fundamental principles of computational biology
2. Develop and Analyse deterministic and stochastic computational models for biological systems
3. Apply computational, statistical, and machine learning techniques to genomic, population, and biomedical data

Course Outcomes: Students will be able to

1. Explain the interdisciplinary foundations of computational biology
2. Develop and analyse deterministic and stochastic computational models to represent biological systems.
3. Apply computational models to genomic data
4. Apply machine learning techniques and computational modelling approaches to analyse biological data

Computational Model for Biology (DJS23SCH1601)		
Unit No	**Description**	**Duration**
1	**Introduction to Computational Biology:** Interdisciplinary nature: biology, mathematics, statistics, computer science, Role of computation in modern biological research, Overview of biological data types (genomic, transcriptomic, proteomic) **Biological Data and Databases:** Types of biological data, Data formats (FASTA, FASTQ, GFF) **Introduction to Modelling Concepts:** What is a model? Model abstraction and assumptions, Static vs dynamic models, Deterministic vs stochastic models	**10**
2	**Deterministic Models in Biology:** Concept of deterministic modelling, Ordinary Differential Equation (ODE) based models, Population growth models: exponential and logistic growth, Enzyme kinetics: Michaelis–Menten model, Advantages and limitations of deterministic models **Stochastic Models in Biological Systems:** Biological variability and noise, Probability-based modelling, Markov processes in biology, Applications of stochastic models in gene expression **Insulin–Glucose Feedback System (minimal Model):** Biological overview of glucose–insulin regulation, Negative feedback control mechanism, Mathematical formulation using ODEs, Steady-state analysis and stability, Simulation of normal and diabetic conditions, Applications in diabetes modelling and drug response analysis **Infectious Disease Models:** SIS, SIR, SEIR models, R_0 and equilibrium analysis, Epidemic prediction **Immune Response Models:** Overview of innate and adaptive immunity, Modelling pathogen–immune cell interactions, Virus–immune response models, Cytotoxic T-cell and antibody response, Feedback and regulation in immune response	**10**

3	**Computational Models for Sequence Alignment:** Genomic data as input to computational models, Sequence alignment as an optimisation and inference problem, Pairwise and multiple sequence alignment models, Global and local alignment formulations, Dynamic programming concepts (conceptual view), **Scalable Alignment Algorithms and Scoring Models:** Heuristic and scalable alignment models: BLAST, BWA, Bowtie, Alignment scoring models, gap penalties, and statistical significance. **Read mapping models**: Applications of alignment models in variant detection and comparative genomics	08
4	**Computational and Statistical Models of Genetic Variation:** Genetic variation as a probabilistic and statistical modelling problem, Types of genetic variants: Single Nucleotide Polymorphisms (SNPs), Insertions and Deletions (INDELs), Variant calling as a computational pipeline model, Statistical models for variant detection and confidence estimation **Gene Prediction, Annotation, and Functional Genomics:** Gene prediction and annotation models, Coding vs non-coding regions **Population-level models:** Allele frequency, Hardy–Weinberg equilibrium, Population structure, Introduction to Genome-Wide Association Studies (GWAS) as association models, Comparative genomics – epigenomics – metagenomics – pharmacogenomics – gene regulatory network analysis.	08
5	**Machine Learning Models:** Supervised and unsupervised learning, Classification and clustering of biological data, Applications in disease prediction **Case Studies:** Cancer genomics, Drug discovery, Personalised medicine, Ethical issues and future directions	06
	Total	42

List of Experiments (Any eight):

1. Study of biological data types and Genomic file formats
2. Simulation of exponential and logistic population growth models
3. Modelling and analysis of enzyme kinetics using the Michaelis–Menten model
4. Simulation and analysis of infectious disease spread using SIR models
5. Computational modelling of the insulin–glucose feedback control system
6. Stochastic modelling of gene expression dynamics
7. Computational modelling of global and local sequence alignment
8. Analysis of read mapping and alignment quality in genomic data
9. Population genetics modelling using the Hardy–Weinberg equilibrium
10. Machine learning–based analysis of biological data for disease prediction

Any other experiment based on the syllabus will be included, which would help the learner to apply the concept learnt

Textbooks:

1. Alex Peh and Catherine Nez, An Introduction to Systems Biology: Design Principles of Biological Circuits, Kruger Brentt Publisher Uk. Ltd., 2024
2. Klipp, E., Liebermeister, W., Wierling, C., & Kowald, A. Systems biology: A textbook (2nd ed.). Wiley-VCH, 2026

3. Richard C. Deonier, Simon Tavare, Michael S. Waterman,"Computational Genome Analysis: An Introduction", Springer India.

Reference Books:

1. Pinto, C. M. A., & Ionescu, C. M. (Eds.). Computational and mathematical models in biology. Springer. 2023.
2. Ingalls, B. P., Mathematical modeling in systems biology: An introduction. MIT Press,2013
3. V. Makinen, D. Belazzougui, F. Cunial and A. Tomescu, "Genome-Scale Algorithm Design", Cambridge, University Press, 2015

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/
5. Centre for Disease Control and Prevention: https://www.cdc.gov/cfa-behind-the-model/php/data-research/rt-estimates/index.html

Online Resources:

1. Biology Meets Programming: Bioinformatics for Beginners, https://www.coursera.org/learn/bioinformatics.
2. Bioinformatics Specialization, https://www.coursera.org/specializations/bioinformatics
3. Systems Biology and Biotechnology Specialization, https://www.coursera.org/specializations/systems-biology
4. Computational Systems Biology, https://nptel.ac.in/courses
5. Genomic Data Analysis Online Graduate Certificate & Courses: https://online.uconn.edu/graduate-programs/genomics-data-analysis/

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