SBIB5101	BIOLOGICAL FOUNDATIONS FOR BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To familiarize students with the basics of biology including cell structure and function.
- To teach the mechanism of central dogma.
- To impart knowledge on the structure and function of biomolecules.
- To provide understanding on genomics aspects.
- To make students learn about the different aspects of proteome studies.

UNIT 1 CELL BIOLOGY **9 Hrs.**

Basic properties of cells; Cell theory; Prokaryotic and eukaryotic cells - Structure and functions. Cytoskeleton; Cell- Cell and cell-matrix interactions. Cell division, Cell cycle regulation and Checkpoints.

UNIT 2 MOLECULAR BIOLOGY **9 Hrs.**

Central Dogma; DNA replication. Prokaryotic and eukaryotic transcription; transcriptional regulation (Operon concept) Genetic code and Translation.

UNIT 3 GENOMICS **9 Hrs.**

Structure and organization of Prokaryotic and eukaryotic genome. Genome sequencing Genome mapping: Markers, Genetic mapping – RFLP, SSLP, SNPs. Physical Mapping –FISH, Restriction mapping, STS mapping. Gene expression studies: DNA microarrays.

UNIT 4 PROTEOMICS **9 Hrs.**

Introduction to Proteomics-characterization of proteome. Protein sequencing - Edman degradation. Protein interaction techniques: Yeast Two Hybrid System. Protein nucleic acid interactions. Protein expression profiling – protein microarrays.

UNIT 5 OMICS **9 Hrs.** Genome editing. Transcriptome analysis. Pharmacogenomics and Comparative genomics, Metabolomics studies in health and disease, Proteomics Applications in Health: Biomarker and Drug Discovery and Food Industry. Integrative omics for health and medicine.

Max.45 Hrs.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Decipher the basic structure and functionality of cells.
CO2 - Analyze the process of central dogma.
CO3 - Create an approach to decode a genome via theoretical knowledge.
CO4 - Comprehend the proteome and its functional significance.
CO5 - Familiar with different biomolecular omics studies in medical research.

CO6 - Identify problem areas at the molecular level for understanding the disease mechanism.

TEXT/ REFERENCE BOOKS

1. Karp's Cell and Molecular Biology 9th Edition by Gerald Karp, Janet Iwasa, Wallace Marshall Wiley; 9th edition (February 19, 2020).
2. Genomes 5 5th Edition by Terry A. Brown CRC Press; 5th edition (April 28, 2023).
3. Molecular Cell Biology (842581) Ninth Edition by Harvey Lodish (Author), Arnold Berk (Author), Genomics and Proteomics: Functional and Computational Aspects by Miguel Rudolph Syrawood Publishing House (June 10, 2019).
4. Bioinformatics: methods and applications: (Genomics, Proteomics and Drug Discovery) 4th Edition PHI Learning; 4th edition (May 22, 2013).

5. Genomics and Proteomics Principles, Technologies, and Applications Devarajan Thangadurai, Jeyabalan Sangeetha Apple Academic Press 2015.

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A:	6 Questions of 5marks each – No choice	**30 Marks**
PART B:	5 Questions from each unit of internal choice; each carrying 14 Marks	**70 Marks**

SBIB5102	PYTHON PROGRAMMING FOR BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		3	0	0	0	3	100

COURSE OBJECTIVES

- Develop proficiency in Python for bioinformatics applications, including data manipulation, analysis, and Visualization.
- Apply key Python libraries and tools in bioinformatics, such as Bio python, NumPy, Pandas, and Matplotlib.
- Gain practical experience in handling and parsing diverse bioinformatics file formats.
- Implement fundamental bioinformatics algorithms and data structures using Python.
- Explore advanced topics like high-throughput sequencing data analysis, machine learning, workflow automation, and tool integration.

UNIT 1 INTRODUCTION TO PYTHON PROGRAMMING 9 Hrs.

Introduction to Python as a programming language for bioinformatics - Basic syntax, variables, data types, and control structures in Python - Working with strings, lists, and dictionaries in Python - Reading and writing files in Python.

UNIT 2 PYTHON LIBRARIES FOR BIOINFORMATICS 9 Hrs.

Introduction to popular Python libraries for bioinformatics, such as Bio python, NumPy, and Pandas - Working with biological sequences and sequence alignment using Bio python - Performing data manipulation and analysis using NumPy and Pandas - Visualizing biological data with Matplotlib and Seaborn.

UNIT 3 FILE HANDLING AND DATA PARSING IN BIOINFORMATICS 9 Hrs.

Reading and parsing different file formats commonly used in bioinformatics, such as FASTA, FASTQ, and GFF/GTF files - Extracting relevant information from large datasets using Python - Parsing and analyzing data from databases, such as NCBI databases or UniProt.

UNIT 4 BIOINFORMATICS ALGORITHMS AND DATA STRUCTURES 9 Hrs.

Implementing common bioinformatics algorithms in Python, such as sequence alignment algorithms (e.g., Needleman-Wunsch, Smith-Waterman) - Understanding and using data structures relevant to bioinformatics, such as trees and graphs - Exploring algorithms for sequence searching, motif finding, and sequence similarity analysis.

UNIT 5 ADVANCED TOPICS IN PYTHON FOR BIOINFORMATICS 9 Hrs.

Handling high-throughput sequencing data using Python tools and libraries - Machine learning and data mining techniques applied to bioinformatics using Python - Workflow automation and pipeline development for bioinformatics analysis - Integrating Python with other bioinformatics tools and resources.

Max.45 Hrs.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Proficiency in using Python for bioinformatics tasks, including data manipulation, analysis, and visualization.
CO2 - Application of Python libraries and tools commonly used in bioinformatics to solve problems.
CO3 - Skills in handling and parsing diverse bioinformatics file formats.
CO4 - Implementation of bioinformatics algorithms and utilization of appropriate data structures using Python.

CO5 - Application of Python for high-throughput sequencing data analysis, machine learning, automation, and integration with other tools.
CO6 - Effective communication and presentation of bioinformatics results and analyses using Python.

TEXT / REFERENCE BOOKS

1. Python for Bioinformatics by Sebastian Bassi (2010).
2. Bioinformatics Programming Using Python: Practical Programming for Biological Data by Mitchell L. Model (2010).
3. Bioinformatics with Python Cookbook by Tiago Antao (2015).
4. Python for Biologists: A complete programming course for beginners by Dr. Martin Jones (2013).
5. Python for Data Analysis: Data Wrangling with Pandas, NumPy, and I Python by Wes McKinney (2017).

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A:	6 Questions of 5marks each – No choice	**30 Marks**
PART B:	5 Questions from each unit of internal choice; each carrying 14 Marks	**70 Marks**

SMTB5109	STATISTICS AND RANDOM PROCESS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To acquire skills in handling situations involving more than one random variable and functions of random variables.
- This gives exposure to statistical methods designed to contribute to the process of making scientific judgments in the face of uncertainty and variation.

UNIT 1 POINT ESTIMATION 9 Hrs.

Properties of estimators, Unbiasedness, Efficiency, Consistency, Sufficiency - Rao - Blackwell theorem, C.R. Rao Inequality - Methods of estimation: Method of Likelihood Estimation, Method of Minimum χ2Modified χ2 - Method of moments.

UNIT 2 THEORY OF SAMPLING AND TEST OF HYPOTHESIS 9 Hrs.

Test of Hypothesis - large sample - test of significance - Single mean, difference of means, single proportion, difference of proportions -small sample - students 't' test - single mean - difference of means - Fisher's test or difference of variance - Chi square test - goodness of fit - independence of attributes.

UNIT 3 NON - PARAMETRIC TESTS 9 Hrs.

Sign test, Wilcoxon Signed Rank Test, Median test, Mann-Whitney U test, Kruskal - Wallis H test.

UNIT 4 INTRODUCTION TO STOCHASTIC PROCESSES 9 Hrs.

Definition, Classification of Stochastic processes, Random walk, Markov chains, Transition Probability Matrix, Graphical representation of Markov chains, Classification of states and chains- Simple Problems-Chapman Kolmogorov Theorem.

UNIT 5 MARKOV PROCESS 9 Hrs.

Introduction to Markov Process- Poisson Process-Postulates and properties-Birth and Death Process-Hidden Markov Model - Introduction - Viterbi Algorithm, Forward and Backward Algorithm, Estimation algorithms.

Max.45 Hrs.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Define characteristics of good estimators, List the methods of estimators, and Evaluate the MLE of estimators.

CO2 - Understand the basis and applications of sampling; Choose the appropriate tests of significance, Formulate the hypothesis for testing the significance of difference, Identify the size of the sample, level of significance, degrees of freedom of the samples.

CO3 - Evaluate the various methods of non-Parametric tests.

CO4 - List the classification of stochastic process, evaluate problems in tpm, Identify the classification of states and chains.

CO5 - Enable students to understand the tools used in bioinformatics and their corresponding algorithms used for evaluating the bio models.

CO6 - Explore the statistical methods designed to contribute to making scientific judgments in the face of uncertainty and to design suitable models.

TEXT / REFERENCE BOOKS

1. Veerarajan T, Probability, Statistics and Random Process, 4th edition, Tata McGraw Hill, 2008.
2. Medhi J, Stochastic Processes, Second Edition, New Age International Publishers. 2002.
3. Stephen Bernstein Schaum's Outline of Elements of Statistics I: Descriptive Statistics and Probability,McGraw- Hill,1998.
4. Jerrold H zar, Bio statistical Analysis, 5th edition, Prentice Hall, 2010.
5. Irvin Miller John E Freund, Probability and Statistics for Engineers, Prentice Hall, 1977.

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A: 6 Questions of 5marks each – No choice **30 Marks**

PART B: 5 Questions from each unit of internal choice; each carrying 14 Marks **70 Marks**

S739BLH11	SCIENTIFIC COMPUTING FOR BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		2	0	2	2	4	100

COURSE OBJECTIVES

- Develop proficiency in utilizing Unix/Linux command line interface for efficient file system navigation, manipulation, and automation.
- Gain practical skills in writing and executing shell scripts to automate repetitive tasks and enhance process management.
- Learn the fundamentals of Sed and Awk for text manipulation, pattern matching, and data processing in bioinformatics.
- Acquire proficiency in using Mathematica for symbolic computation, data visualization, and mathematical modeling in scientific research.
- Develop practical skills in using MATLAB for numerical analysis, data visualization, and programming for bioinformatics applications.

UNIT 1 INTRODUCTION TO UNIX/LINUX OPERATING SYSTEM 12 Hrs.

Overview of Unix/Linux OS, command line interface, and file system manipulation - Shell scripting basics for automation and process management.

PERFORM ANY ONE EXERCISE:

Laboratory Exercise 1: File System Navigation and Manipulation

Task: Write a shell script that navigates through a given directory structure, identifies files with a specific extension (e.g., fasta), and moves them to a different directory.

Bioinformatics Application: Sorting and organizing genomic sequence files based on file extensions.

Laboratory Exercise 2: Process Management and Automation

Task: Write a shell script that automates the process of downloading a large dataset from a remote server, unzips the files, and performs initial data processing.

Bioinformatics Application: Efficient retrieval and preprocessing of gene expression data from public repositories.

Laboratory Exercise 3: Creating a Custom Command-line Tool

Task: Develop a shell script that takes a user-provided DNA sequence as input, performs a specific bioinformatics analysis (e.g., sequence alignment or motif search), and returns the results in a readable format.

Bioinformatics Application: Enabling researchers to perform custom analyses on DNA sequences using a command- line interface.

UNIT 2 SHELL SCRIPTING, SED, AND AWK FUNDAMENTALS 12 Hrs.

Shell scripting essentials, including variables, conditionals, loops, and user input - Introduction to Sed for text manipulation using patterns and regular expressions - Awk for data processing and manipulation of fields and records.

PERFORM ANY ONE EXERCISE:

Laboratory Exercise1: Text Manipulation using Sed

Task: Write a shell script that uses Sed to extract specific information (e.g., gene names or sequence motifs) from a text file containing genomic annotations.

Bioinformatics Application: Extracting relevant gene information from large annotation files for downstream analysis. Laboratory Exercise 2: Data Processing with Awk

Task: Write an Awk script that processes a tab-separated data file containing gene expression levels, calculates the average expression for each gene across multiple samples, and outputs the results.

Bioinformatics Application: Analyzing gene expression data and identifying differentially expressed genes.
Laboratory Exercise 3: Advanced Shell Scripting Techniques
Task: Develop a shell script that automates the process of downloading multiple sequence alignment files from a database, performs sequence clustering using external tools, and generates a visualization of the clusters. Bioinformatics Application: Analyzing and visualizing sequence similarity and clustering patterns in genomic data.

UNIT 3 MATHEMATICA FOR SCIENTIFIC COMPUTING 12 Hrs.
Introduction to Mathematica for symbolic computation, data visualization, and mathematical modelling - Syntax and expressions for variables, functions, and mathematical operations.

PERFORM ANY ONE EXERCISE
Laboratory Exercise 1: Symbolic Computation in Mathematica
Task: Use Mathematica to solve a system of differential equations modeling a biological process, visualize the results, and interpret the biological implications.
Bioinformatics Application: Modeling gene regulatory networks and studying dynamical behavior.
Laboratory Exercise 2: Data Visualization in Mathematica.
Task: Import a genomic dataset into Mathematica, explore the data using various visualization techniques (e.g., heatmaps, scatter plots), and identify patterns or correlations.
Bioinformatics Application: Visualizing gene expression patterns or DNA sequence features.
Laboratory Exercise 3: Mathematical Modeling in Mathematica.
Task: Develop a mathematical model of a biochemical reaction network involved in a specific metabolic pathway, simulate the model, and analyze the system behavior under different parameter values.
Bioinformatics Application: Modeling metabolic pathways and studying their dynamics.

UNIT 4 MATLAB FOR SCIENTIFIC COMPUTING 12 Hrs.
Introduction to MATLAB for numerical analysis, data visualization, and programming - MATLAB syntax, variables, and mathematical operations.

PERFORM ANY ONE EXERCISE:
Laboratory Exercise1: Numerical Analysis in MATLAB
Task: Implement an algorithm to calculate the eigenvalues and eigenvectors of a given matrix, apply the algorithm to a gene expression matrix, and interpret the results in the context of principal component analysis.
Bioinformatics Application: Dimensionality reduction and clustering analysis of gene expression data.
Laboratory Exercise 2: Data Visualization in MATLAB
Task: Load and visualize a DNA sequence using MATLAB, highlight specific sequence motifs or patterns, and create a publication-quality figure for presentation.
Bioinformatics Application: Visualizing genomic sequences and identifying biologically relevant features.
Laboratory Exercise 3: Programming in MATLAB for Bioinformatics
Task: Write a MATLAB script that reads a DNA sequence file, performs a sequence alignment against a reference genome, and identifies sequence variations (e.g., single nucleotide polymorphisms) in the aligned regions. Bioinformatics Application: Analyzing genetic variations and their potential impact on gene function.

UNIT 5 ADVANCED TOPICS IN SCIENTIFIC COMPUTING 12 Hrs.
Advanced techniques for numerical methods, optimization, and parallel computing - Data analysis, machine learning, and integration of scientific computing tools - Emerging trends and future directions in scientific computing for bioinformati

PERFORM ANY ONE EXERCISE:

Laboratory Exercise 1: Parallel Computing in Bioinformatics

Task: Implement a parallelized version of a bioinformatics algorithm (e.g., sequence alignment or sequence assembly) using a parallel computing framework, and measure the performance improvement compared to the sequential version.

Bioinformatics Application: Accelerating computationally intensive bioinformatics analyses using parallel processing.

Laboratory Exercise 2: Machine Learning in Bioinformatics

Task: Use a machine learning library (e.g., scikit-learn in Python or MATLAB's machine learning toolbox) to train a classification model on a genomic dataset and evaluate its performance using appropriate metrics.

Bioinformatics Application: Predicting functional elements in genomes or classifying disease subtypes based on genomic data.

Laboratory Exercise 3: Integration of Scientific Computing Tools

Task: Develop a workflow that combines multiple scientific computing tools (e.g., MATLAB, R, and Python) to perform a comprehensive analysis of a complex bioinformatics dataset, such as whole-genome sequencing data. Bioinformatics Application: Integrating diverse computational tools for a holistic analysis of genomic data.

Max.60 Hrs.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Understand the fundamental principles of bioinformatics and its applications in biological research, including genomics, proteomics, transcriptomics, and systems biology.

CO2 - Develop proficiency in using MATLAB and R programming languages for bioinformatics and systems biology analysis, including data manipulation, statistical analysis, and visualization.

CO3 - Apply data structures, algorithms, and computational methods to analyze and interpret biological data, such as sequence alignment, motif finding, gene expression analysis, and protein structure prediction.

CO4 - Gain knowledge of statistical methods and machine learning techniques relevant to bioinformatics and systems biology, including classification, clustering, feature selection, and dimensionality reduction.

CO5 - Integrate and analyze multi-omics data, such as genomics, transcriptomics, and proteomics, to understand complex biological systems and identify biomarkers or regulatory elements.

CO6 - Construct and simulate mathematical models of biological processes in systems biology, and interpret the results to gain insights into system behavior, stability, and dynamics.

TEXT / REFERENCE BOOKS

1. Bioinformatics Toolbox User's Guide by MathWorks (Publisher: MathWorks, Year of Publication: Varies based on edition)
2. MATLAB for Biologists: A Beginner's Guide by Lars Gustafsson (Publisher: Springer, Year of Publication: 2019)
3. Bioinformatics Data Analysis Using R by Gautier Koscielny (Publisher: CRC Press, Year of Publication: 2018)
4. R Programming for Bioinformatics by Robert Gentleman (Publisher: CRC Press, Year of Publication: 2008)
5. Applied Bioinformatics: An Introduction using R by Paul M. Selzer (Publisher: Springer, Year of Publication:

S739BLH12	BIOLOGICAL DATABASES AND DATA ANALYSIS	L	T	P	EL	Credits	Total Marks
		2	0	2	0	4	100

COURSE OBJECTIVES:

- Develop a comprehensive understanding of biological databases and tools used in bioinformatics research.
- Gain proficiency in retrieving, analysing, and interpreting biological data from various databases.
- Acquire expertise in using specialized software tools for data analysis and visualization.
- Learn to integrate multiple data sources for generating biological insights.
- Develop effective communication skills for presenting and interpreting bioinformatics results.

UNIT 1: INTRODUCTION TO BIOLOGICAL DATABASES 12Hrs.

Types and classification of biological databases - Data formats and standards in bioinformatics - Data curation, integration, and quality assessment - Overview of database search and retrieval strategies - Data privacy and ethical considerations in data sharing

Lab Exercise: Search and retrieve gene sequence information from nucleotide databases. Analyze the retrieved data for relevant features and annotations.

UNIT 2: SEQUENCE DATABASES AND TOOLS 12Hrs.

Nucleotide sequence databases (GenBank, DDBJ, EMBL) - Protein sequence databases (UniProtKB, RefSeq) - Sequence alignment tools (BLAST, FASTA) - Functional annotation tools (InterProScan, GO) - Comparative genomics databases (Ensembl, NCBI)

Lab Exercise: Perform a sequence similarity search using BLAST and analyze the results. Use InterProScan to predict protein functional domains.

UNIT 3: STRUCTURE DATABASES AND TOOLS 12Hrs.

Protein structure databases (PDB, CATH, SCOP) - Molecular visualization tools (PyMOL, Chimera, VMD) - Structure prediction methods (I-TASSER, Phyre2) - Ligand binding and docking tools (AutoDock, Vina) - Structural analysis and validation tools (MolProbity, PROCHECK)

Lab Exercise: Download a protein structure from the PDB and visualize it using PyMOL. Perform molecular docking simulations to predict ligand binding interactions.

UNIT 4: OMICS DATABASES AND ANALYSIS TOOLS 12Hrs.

Genomic databases (Ensembl, NCBI Genomes) - Transcriptomic databases (GEO, ArrayExpress) - Proteomic databases (PRIDE, PeptideAtlas) - Metabolomic databases (HMDB, METLIN) - Data analysis pipelines (R/Bioconductor, Galaxy)

Lab Exercise: Retrieve and analyze gene expression data from a public repository. Perform differential gene expression analysis using R/Bioconductor.

UNIT 5: NETWORK DATABASES AND INTEGRATION TOOLS 12Hrs.

Protein-protein interaction databases (STRING, BioGRID) - Pathway databases (KEGG, Reactome) - Gene ontology databases (GO, QuickGO) - Data integration platforms (BioMart, Cytoscape) - Network analysis tools (CytoNCA, Gephi)

Lab Exercise: Construct a protein-protein interaction network using STRING. Analyze network properties and identify key hub proteins.

Max.60 Hrs.

COURSE OUTCOMES:

By the end of this course, students should be able to-

CO1 - Navigate and utilize diverse biological databases for retrieving relevant biological data.
CO2 - Apply specialized tools for sequence analysis, structure visualization, and functional annotation.
CO3 - Analyse omics data and perform basic data analysis using bioinformatics pipelines.
CO4 - Interpret biological networks, pathways, and functional annotations from integrated data sources.
CO5 - Demonstrate proficiency in using software tools for bioinformatics research and data interpretation.
CO6 - Present and communicate bioinformatics results effectively, both orally and in writing.

TEXT / REFERENCE BOOKS:

1. Bioinformatics: Sequence and Genome Analysis by David W. Mount (Cold Spring Harbor Laboratory Press, 2018).
2. Introduction to Bioinformatics by Arthur M. Lesk (Oxford University Press, 2013).
3. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids by Richard Durbin, Sean R. Eddy, Anders Krogh, and Graeme Mitchison (Cambridge University Press, 1998).
4. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins by Andreas D. Baxevanis and B. F. Francis Ouellette (Wiley-Blackwell, 2004).
5. Essential Bioinformatics by Jin Xiong (Cambridge University Press, 2006.

SBIB6101	PYTHON PROGRAMMING FOR BIOINFORMATICS LAB	L	T	P	EL	Credits	Total Marks
		0	0	4	2	2	100

COURSE OBJECTIVES

- Develop proficiency in Python programming for bioinformatics applications, enabling students to effectively manipulate, analyze, and visualize biological data using Python libraries and tools.

1.READING AND PARSING SEQUENCE DATA:

Write a Python program to read and parse a FASTA file containing DNA sequences. Extract information such as sequence ID, length, and sequence data from the file.

2.SEQUENCE ALIGNMENT:

Implement the Needleman-Wunsch algorithm for global sequence alignment in Python. Align two DNA or protein sequences and calculate the alignment score.

3. BASIC DATA MANIPULATION:

Write a Python program to count the occurrence of nucleotides or amino acids in a given DNA or protein sequence. Calculate the GC content of a DNA sequence.

4. SEQUENCE SEARCHING:

Implement the Smith-Waterman algorithm for local sequence alignment in Python. Perform a local sequence alignment search against a database of sequences.

5. WORKING WITH BIOLOGICAL DATABASES:

Use Biopython to retrieve sequence data from the NCBI GenBank database.
Extract relevant information such as sequence features, annotations, and references.

6. GENOME ANNOTATION:

Write a Python program to parse a GFF file containing genomic annotations. Extract information such as gene names, locations, and functional annotations.

7. PROTEIN STRUCTURE ANALYSIS:

Use Biopython to retrieve protein structures from the Protein Data Bank (PDB). Analyze protein structures, calculate structural properties, and identify key features.

8. MOTIF FINDING:

Implement a motif finding algorithm, such as the Gibbs Sampling algorithm, in Python. Find and analyze sequence motifs in a set of DNA or protein sequences.

9. GENE EXPRESSION ANALYSIS:

Perform gene expression analysis using Python libraries like NumPy and Pandas. Analyze and visualize gene expression data from microarray or RNA-seq experiments.

10.MACHINE LEARNING IN BIOINFORMATICS:

Apply machine learning techniques, such as classification or regression, to solve bioinformatics problems. Train and evaluate a model to predict properties or outcomes using bioinformatics data

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

CAE	Evaluation of Regular Lab class	25 Marks	
	Model practical exam	25 Marks	**50 Marks**
ESE	University Practical exam		**50 Marks**

SMTB5205	MATHEMATICAL MODELLING FOR BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVE

- To learn the need and limitations of Mathematical modeling.
- To learn the population and epidemic models
- To acquire knowledge on biological modeling.

UNIT 1 INTRODUCTION 9 Hrs.

Basic Steps of Mathematical Modeling, its needs, types of models, limitations, Elementary ideas of dynamical systems, Equilibrium point, node, saddle point, focus, center and limit-cycle idea with simple illustrations and figures.

UNIT 2 POPULATION MODELS 9 Hrs.

Basic concepts, Exponential growth model, Population in Natural and Laboratory Environments. Logistic growth model, formulation, solution, interpretation and limitations.

UNIT 3 EPIDEMIC MODEL 9 Hrs.

Basic concepts, SI model, SIS model with constant coefficient, SIS model with coefficient as a function of time t, SIS model with constant number of carriers, SIS model when the carriers are a function of time t, SIR model, Epidemics with vaccination.

UNIT 4 NONLINEAR DYNAMICS 9 Hrs.

Solution of ODEs- Euler method and Runge-Kutta methods- Nonlinear Dynamics (ODEs) – fixed points of ODEs and stability- Matrix methods of linear systems.

UNIT 5 SOLUTIONS OF BIOLOGICAL MODELING 9 Hrs.

Curve Fitting and Biological Modeling; Fitting curves to Data, The Method of Least Squares, Polynomial curve Fitting. correlation and regression analysis.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - List the origin of Mathematical Modeling, needs and limitations.
CO2 - Discuss the components and facts of various Population models.
CO3 - Sketch the models used to explore the epidemics.
CO4 - Understand the non-linear systems.
CO5 - Analyze the solutions of biological models.
CO6 - Discuss the correlation and regression in biological models.

TEXTBOOKS/ REFERENCES

1. B.S. Bhargava and Poonam Bhargava," Mathematical Modelling in Systems Biology: An Introduction" , Springer publications, 2019.
2. Dipak Kumar Jana and Pranab Kumar Bhattacharya," Mathematical Modelling and Applications in Biology and Medicine", Springer publications, 2018.
3. Elizabeth S. Allman and John A. Rhodes, "Mathematical Models in Biology: An Introduction", Cambridge University Press, 2017.

4. Brian P. Ingalls," Mathematical Modeling in Systems Biology: An Introduction", The MIT Press, 2013. 5. J. N. Kapur, Mathematical Models in Biology and Medicine, East-West Press.

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100		**Exam Duration: 3 Hrs**
PART A:	6 Questions of 5marks each – No choice	**30 Marks**
PART B:	5 Questions from each unit of internal choice; each carrying 14 Marks	**70 Marks**

SBIB5201	NEXT GENERATION SEQUENCE DATA ANALYSIS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To familiarize students with Next Generation Sequencing (NGS) technologies starting from experimental planning to genome scale data assembly and data analysis.
- To teach the basics of typical NGS protocols currently used in genetics, ecology and evolution research.
- To make the students familiar with the nature of data produced by these technologies.
- To excavate biologically relevant information to address a wide range of scientific questions.
- To be able to articulate on DNA sequencing.

UNIT 1 SEQUENCING 9 Hrs.

DNA Sequencing, First generation DNA sequencing methods. Drawbacks of the first-generation sequencing method. Emergence of Next generation sequencing and biological applications

UNIT 2 NGS PLATFORMS 9 Hrs.

Second generation sequencing- Ion Torrent technology, Illumina/Solexa platform, and Solid (Sequencing by Oligonucleotide Ligation and Detection). Third Generation Sequencing: PacBio and Oxford Nanopore. Comparison of Next generation sequencing techniques, & applications. Drawbacks of NGS, NGS File formats.

UNIT 3 NGS DATABASES AND ANALYSIS OF NGS DATA 9 Hrs.

NGS databases. Data analysis work flow: Library preparation, Sequencing, Data analysis: reads, Alignment and assembly, variant calling.

UNIT 4 TRANSCRIPTOME ANALYSIS 9 Hrs.

Transcriptome (RNA) sequencing, Data acquisition- Read alignment – Transcriptome assembly - Differential expression analysis – Allele-specific expression - RNA editing.

UNIT 5 NGS APPLICATIONS 9 Hrs.

Exome sequencing, Targeted sequencing, Whole-genome sequencing, Pooled sequencing, methylome sequencing. Chip Sequencing Role of NGS in Agri-Biotech, health care, metagenomics, GWAS.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Understand the history of sequencing and proceed into the latest technology.
CO2 - Explain the different NGS platforms and data analysis.
CO3 - Explain key theoretical concepts in NGS data analysis and tools.
CO4 - Understand and analyze RNA sequencing strategies.
CO5 - Appreciate the applications of this technology.
CO6 - Independently create a basic NGS data analysis workflow.

REFERENCES/TEXTBOOKS

1. Next-Generation Sequencing Data Analysis by Xinkun Wang CRC Press; 1st edition (24 February 2016).

2. Next Generation Sequencing and Data Analysis Melanie Kappelmann-Fenzl Springer https://doi.org/10.1007/978-3- 030-62490-3 2021.
3. Next-generation Sequencing: Current Technologies and Applications Jianping Xu Caister Academic Press 2014.
4. Next Generation Sequencing - Advances, Applications and Challenges. Kulski, Jerzy K., ed. 2016. InTech. doi:10.5772/60489.

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100		**Exam Duration: 3 Hr**
PART A:	6 Questions of 5marks each – No choice	**30 Marks**
PART B:	5 Questions from each unit of internal choice; each carrying 14 Marks	**70 Marks**

SBIB5202	SYSTEMS BIOLOGY	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- Understand the principles and concepts of Systems Biology and its integration with bioinformatics and data science.
- Analyze and model biological networks to uncover emergent properties and understand system-level behaviors.
- Integrate and analyses diverse biological data types using computational tools and statistical techniques.
- Apply dynamic modelling and simulation techniques to study the behavior and regulation of biological systems.
- Apply Systems Biology approaches to real-world biological problems, such as disease modelling, drug discovery, and personalized medicine.

UNIT 1 INTRODUCTION TO SYSTEMS BIOLOGY 9 Hrs.

Overview of Systems Biology and its applications in bioinformatics and data science - Introduction to key concepts such as networks, dynamics, and emergent properties - Understanding the interdisciplinary nature of Systems Biology and its relationship with bioinformatics and data science

UNIT 2 NETWORK BIOLOGY AND MODELING 9 Hrs.

Introduction to biological networks and their representation (e.g., gene regulatory networks, protein-protein interaction networks) - Network analysis techniques, including topological analysis, network motifs, and clustering algorithms - Modeling approaches for biological systems, such as Boolean networks, ordinary differential equations (ODEs), and agent-based models.

UNIT 3 DATA INTEGRATION AND ANALYSIS IN SYSTEMS BIOLOGY 9 Hrs.

Integration and analysis of diverse biological data types, including genomics, transcriptomics, proteomics, and metabolomics - Methods for data preprocessing, normalization, and quality control - Statistical analysis techniques, such as differential expression analysis, pathway enrichment analysis, and network-based analysis.

UNIT 4 DYNAMICS AND SIMULATION OF BIOLOGICAL SYSTEMS 9 Hrs.

Understanding the dynamic behavior of biological systems and their mathematical representation - Simulation techniques for modeling and studying dynamic systems, including numerical integration and stochastic simulations. - Case studies of dynamic biological processes, such as cell cycle regulation, signal transduction, and gene regulatory networks.

UNIT 5 SYSTEMS BIOLOGY APPLICATIONS AND CASE STUDIES 9 Hrs.

Applications of Systems Biology in different areas of biology, including disease modeling, drug discovery, and personalized medicine - Case studies highlighting the use of Systems Biology approaches in studying specific biological systems or solving biological problems - Ethical considerations and challenges in Systems Biology research and applications.

Max.60 Hrs.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Apply systems thinking to understand and analyze complex biological systems.

CO2 - Interpret biological networks to uncover regulatory elements and emergent properties.

CO3 - Integrate and analyze diverse biological data types for system-level insights.
CO4 - Model and simulate dynamic biological systems to predict behavior.
CO5 - Apply Systems Biology techniques to real-world biological problems.
CO6 - Communicate research findings effectively to technical and non-technical audiences

TEXT / REFERENCE BOOKS

1. Systems Biology: Simulation of Dynamic Network States - Bernhard √ò. Palsson (2011)
2. Introduction to Systems Biology - Uri Alon (2019)
3. Systems Biology: Mathematical Modeling and Model Analysis - Vipul Periwal and Robert J. A. Lougee (2014)
4. Systems Biology: Properties of Reconstructed Networks - Bernhard √ò. Palsson (2006)
5. Biological Network Analysis: Trends, Approaches, Graph Theory, and Algorithms - Md. Altaf-Ul-Amin and Saad M. Khan (2019)

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A: 6 Questions of 5marks each – No choice **30 Marks**

PART B: 5 Questions from each unit of internal choice; each carrying 14 Marks **70 Marks**

S739BLH23	TRANSLATIONAL BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		2	0	2	2	4	100

COURSE OBJECTIVES

- The objective of this theory course on Translational Bioinformatics is to provide students with a comprehensive understanding of the principles, methodologies, and applications of bioinformatics in the context of translating genomic and biomedical data into clinically actionable insights.

UNIT 1 INTRODUCTION TO TRANSLATIONAL BIOINFORMATICS 12 Hrs.

Overview of translational research and its significance in healthcare - Introduction to bioinformatics and its role in translating genomic data into clinical applications - Key challenges and opportunities in translational bioinformatics - Ethical considerations and regulatory aspects in handling patient data for translational research.

UNIT 2 GENOMICS AND TRANSLATIONAL BIOINFORMATICS 12 Hrs.

Introduction to genomics and its impact on translational research - Techniques for genomic data generation and analysis, including next-generation sequencing and variant calling - Genome-wide association studies (GWAS) and identification of disease-associated variants - Genomic annotation, pathway analysis, and functional interpretation of genetic variants.

UNIT 3 TRANSCRIPTOMICS AND PROTEOMICS IN TRANSLATIONAL BIOINFORMATICS 12 Hrs.

Overview of transcriptomics and proteomics technologies in translational research - Analysis of gene expression data using bioinformatics tools and resources - Identification of biomarkers and drug targets through transcriptomics and proteomics analysis - Integration of genomic, transcriptomic, and proteomic data for comprehensive analysis.

UNIT 4 CLINICAL DATA INTEGRATION AND PERSONALIZED MEDICINE 12 Hrs.

Integration of clinical data, electronic health records (EHRs), and genomic information - Application of bioinformatics approaches for patient stratification and personalized medicine - Clinical decision support systems and predictive modeling in translational bioinformatics - Ethical considerations and privacy issues in managing and analyzing patient data.

UNIT 5 EMERGING TRENDS IN TRANSLATIONAL BIOINFORMATICS 12 Hrs.

Advancements in artificial intelligence (AI), machine learning (ML), and data mining for translational research - Data visualization and interpretation techniques for large-scale biomedical datasets - multi-omics integration and network- based approaches in translational bioinformatics - Future directions and emerging challenges in the field.

Max.60 Hrs.

LIST OF EXERCISES

1. Genome Alignment and Variant Calling: Analyzing DNA sequences to identify genetic variations and variations across genomes.
2. Differential Gene Expression Analysis: Comparing gene expression levels between different conditions or groups to identify genes that are differentially expressed.
3. Pathway Enrichment Analysis: Identifying biological pathways that are significantly enriched with differentially expressed genes or genes of interest.

4. Construction of Gene Co-expression Networks: Building networks that connect genes based on their co- expression patterns to understand functional relationships and regulatory mechanisms.
5. Disease Subtyping and Classification: Utilizing computational methods to categorize diseases into subtypes based on molecular characteristics or clinical data to aid in personalized medicine approaches.
6. Drug-Target Interaction Prediction: Predicting the interaction between drugs and target molecules to understand drug efficacy and potential side effects.
7. Functional Annotation of Genetic Variants: Assigning functional significance to genetic variants and understanding their potential impact on gene function or disease susceptibility.
8. Integration of Multi-omics Data: Integrating and analyzing diverse omics data types, such as genomics, transcriptomics, and proteomics, to gain a comprehensive understanding of complex biological systems.
9. Construction of Protein-Protein Interaction Networks: Building networks that represent protein-protein interactions to identify key players and understand cellular processes and disease mechanisms.
10. Clinical Data Analysis: Analyzing clinical data, such as patient demographics, medical records, and treatment outcomes, to identify patterns and associations that can aid in diagnosis, prognosis, and personalized treatment decisions.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Understand the principles and applications of bioinformatics in the context of translational research, bridging the gap between genomics and clinical applications.

CO2 - Develop proficiency in analyzing and interpreting genomic data to identify potential disease-associated biomarkers and drug targets.

CO3 - Gain knowledge of advanced bioinformatics techniques for integrating and analyzing multi-omics data, such as genomics, transcriptomics, and proteomics, to enhance translational research.

CO4 - Apply bioinformatics approaches to integrate clinical data, electronic health records, and genomic information for personalized medicine and improved patient care.

CO5 - Understand the ethical and regulatory considerations in translational bioinformatics, including privacy, consent, and responsible use of patient data.

CO6 - Explore emerging trends and future directions in translational bioinformatics, including the application of artificial intelligence, machine learning, and data mining techniques for clinical decision support and predictive modeling.

TEXT / REFERENCE BOOKS

1. Translational Bioinformatics: Applications in Healthcare and Drug Discovery by Dong-Qing Wei and Xiaobo Zhou (Wiley, Year: 2012).
2. Bioinformatics and Computational Biology Solutions Using R and Bioconductor by Robert Gentleman, Vincent J. Carey, Wolfgang Huber, Rafael A. Irizarry, and Sandrine Dudoit (Springer, Year: 2005).
3. Translational Medicine: Tools and Techniques by Zdenka Kuncic and Benjamin G. Davis (CRC Press, Year: 2015).
4. Bioinformatics for Translational Medicine: Principles and Applications by Xiaole Shirley Liu, Dong Xu, and Jason T. L. Wang (Cambridge University Press, Year: 2013).
5. Translational Bioinformatics and Systems Biology Methods for Personalized Medicine by Qing Yan (Academic Press, Year: 2017).

SBIB6201	NEXT GENERATION SEQUENCE DATA ANALYSIS LAB	L	T	P	EL	Credits	Total Marks
		0	0	4	2	2	100

LIST OF EXERCISES:

1. **Library Preparation**: Demonstrate the process of preparing a DNA/RNA library for sequencing. Discuss the importance of quality control checks (e.g., quantifying DNA/RNA, checking the size distribution of the library).

2. **Sequencing Run**: Perform a sequencing run using a small, benchtop sequencer, such as the Illumina MiSeq or the Ion Torrent PGM. Discuss the sequencing chemistry and the principles of operation.

3. **Raw Data Quality Check**: Teach students how to evaluate the quality of raw NGS data using software like FastQC.

4. **Data Trimming and Filtering**: Show how to improve data quality by trimming and filtering the raw data using software tools like Trimmomatic or Cutadapt.

5. **Genome Assembly or Mapping**: Teach the principles of de novo assembly or mapping to a reference genome using tools like SPAdes (for assembly) or Bowtie2 (for mapping).

6. **Variant Calling**: After mapping reads to a reference genome, demonstrate how to identify variants (SNPs, indels) using tools like GATK or SAMtools.

7. **RNA-seq Analysis**: Process an RNA-seq dataset to evaluate gene expression. Teach students how to align reads, quantify gene expression, and identify differentially expressed genes using tools like STAR (for alignment) and DESeq2 (for differential expression analysis).

8. **Metagenomics Analysis**: Guide students through the analysis of a metagenomic sample, starting from raw reads and moving through steps of quality control, assembly, binning, and taxonomic/functional annotation using tools like MEGAN or QIIME 2.

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

CAE	Evaluation of Regular Lab class	25 Marks	
	Model practical exam	25 Marks	**50 Marks**
ESE	University Practical exam		**50 Marks**

SBIB6202	SYSTEMS BIOLOGY LAB	L	T	P	EL	Credits	Total Marks
		0	0	4	2	2	100

COURSE OBJECTIVES

- Develop proficiency in applying computational and analytical techniques to analyze complex biological systems, integrating multiple data types and modeling approaches to gain insights into system-level behaviors and regulatory mechanisms.

LIST OF EXERCISES:

1. Analysis of Biological Networks: Analyze and visualize protein-protein interaction networks or gene regulatory networks using publicly available databases and network analysis tools.
2. Gene Expression Data Analysis: Perform differential gene expression analysis using RNA-Seq or microarray data to identify differentially expressed genes between different conditions or tissues.
3. Network Motif Analysis: Identify and analyze network motifs in biological networks to understand common patterns and motifs associated with specific functions or biological processes.
4. Dynamic Modeling of Biological Systems: Use computational tools to model and simulate dynamic behavior of biological systems, such as gene regulatory networks or metabolic pathways.
5. Pathway Enrichment Analysis: Perform pathway enrichment analysis to identify significantly enriched biological pathways based on differentially expressed genes or proteins.
6. Drug-Target Interaction Prediction: Predict potential drug-target interactions using computational approaches and analyze the predicted interactions for drug discovery or repurposing.
7. Network-Based Disease Subtyping: Apply network-based approaches to classify or subtype diseases based on molecular signatures and clinical data, aiming to improve disease diagnosis and treatment strategies.
8. Multi-Omics Data Integration: Integrate and analyze multi-omics data (genomics, transcriptomics, proteomics) to gain a comprehensive understanding of complex biological systems or diseases.
9. Modeling and Simulation of Signaling Pathways: Model and simulate cellular signaling pathways using computational tools to understand how signaling cascades regulate cellular processes and responses.
10. Systems Biology Case Study: Choose a specific biological system or problem and apply systems biology approaches to gain insights into its underlying mechanisms, dynamics, or interactions.

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

CAE	Evaluation of Regular Lab class	25 Marks	
	Model practical exam	25 Marks	**50 Marks**
ESE	University Practical exam		**50 Marks**

SBIB5301	R FOR BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- Understand R programming and its application in bioinformatics for data manipulation, visualization, and analysis.
- Gain proficiency in importing, preprocessing, and exploring diverse bioinformatics data types using R.
- Learn statistical analysis techniques for hypothesis testing, differential expression analysis, and machine learning in bioinformatics.
- Develop skills in sequence analysis, including alignment, annotation, and functional analysis using R.
- Acquire knowledge of integrative omics data analysis, network analysis, and advanced R topics in bioinformatics.

UNIT 1 INTRODUCTION TO R AND BIOINFORMATICS 9 Hrs.

Overview of R and Bioinformatics - R Fundamentals - R Packages for Bioinformatics

UNIT 2 DATA MANIPULATION AND VISUALIZATION IN R 9 Hrs.

Data Import and Preprocessing - Exploratory Data Analysis - Working with Genomic Data

UNIT 3 STATISTICAL ANALYSIS IN R FOR BIOINFORMATICS 9 Hrs.

Statistical Testing and Hypothesis Generation - Differential Expression Analysis - Machine Learning in Bioinformatics.

UNIT 4 SEQUENCE ANALYSIS IN R 9 Hrs.

Sequence Alignment and Manipulation - Sequence Annotation and Functional Analysis - Next-Generation Sequencing Analysis.

UNIT 5 INTEGRATIVE ANALYSIS AND ADVANCED TOPICS 9 Hrs.

Integration of Omics Data - Network Analysis in Bioinformatics - Advanced Topics in R for Bioinformatics.

Max.45 Hrs.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Develop a strong understanding of R programming language and its application in the field of bioinformatics.

CO2 - Acquire skills in importing, preprocessing, and visualizing diverse bioinformatics data using R.

CO3 - Gain proficiency in statistical analysis techniques commonly used in bioinformatics, including hypothesis testing and differential expression analysis.

CO4 - Apply machine learning algorithms in bioinformatics to analyze and interpret complex biological data.

CO5 - Master sequence analysis techniques such as alignment, annotation, and functional analysis using R-based tools and packages.

CO6 - Demonstrate knowledge of integrative analysis approaches for omics data integration, network analysis techniques, and advanced topics in R for bioinformatics.

TEXT / REFERENCE BOOKS

1. Bioinformatics and Computational Biology: An Introduction by Jonathan Pevsner (2003, Wiley).
2. Bioinformatics Data Skills by Vince Buffalo (2015, O'Reilly Media).
3. R for Data Science by Hadley Wickham and Garrett Grolemund (2017, O'Reilly Media).
4. Bioinformatics with R Cookbook by Paurush Praveen Sinha and Shajia Adeeb (2014, Packt Publishing).
5. Bioinformatics: Sequence and Genome Analysis by David W. Mount (2004, Cold Spring Harbor Laboratory Press).

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A: 6 Questions of 5marks each – No choice **30 Marks**

PART B: 5 Questions from each unit of internal choice; each carrying 14 Marks **70 Marks**

SBIB5302	MACHINE LEARNING FOR BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- The objective of the Machine Learning for Bioinformatics theory course is to provide students with a comprehensive understanding of machine learning algorithms, techniques, and their applications in analyzing and interpreting biological data.

UNIT 1 INTRODUCTION TO MACHINE LEARNING AND BIOINFORMATICS 9 Hrs.

Overview of machine learning concepts and algorithms - Introduction to bioinformatics and its applications - Challenges and opportunities in applying machine learning to bioinformatics - Ethical considerations and biases in machine learning for bioinformatic.

UNIT 2 SUPERVISED LEARNING IN BIOINFORMATICS 9 Hrs.

Principles of supervised learning - Classification algorithms: decision trees, support vector machines (SVM), random forests - Evaluation metrics for classification performance - Case studies: classification of biological sequences, disease diagnosis, drug response prediction.

UNIT 3 UNSUPERVISED LEARNING IN BIOINFORMATICS 9 Hrs.

Principles of unsupervised learning - Clustering algorithms: k-means, hierarchical clustering - Dimensionality reduction techniques: principal component analysis (PCA), t-SNE - Case studies: gene expression clustering, protein function prediction, population structure analysis.

UNIT 4 DEEP LEARNING IN BIOINFORMATICS 9 Hrs.

Introduction to deep learning and neural networks - Convolutional neural networks (CNN) for image-based bioinformatics - Recurrent neural networks (RNN) for sequence-based bioinformatics - Transfer learning and pre- trained models in bioinformatics - Case studies: image classification, protein structure prediction, genomic sequence analysis

UNIT 5 ADVANCED TOPICS IN MACHINE LEARNING FOR BIOINFORMATICS 9 Hrs.

Ensemble methods: bagging, boosting, random forests - Feature selection and feature engineering in bioinformatics- Interpretability and visualization of machine learning models - Integrative analysis of multi-omics data - Emerging trends and future directions in machine learning for bioinformatics.

Max.45 Hrs.

COURSE OUTCOMES

On completion of the course the student will be able to

CO1 - Understand and apply fundamental concepts and principles of machine learning to bioinformatics problems.

CO2 - Analyze and interpret biological data using a variety of machine learning algorithms and techniques.

CO3 - Develop the skills to preprocess, clean, and transform biological data for effective application of machine learning methods.

CO4 - Evaluate and compare the performance of machine learning models using appropriate metrics and validation strategies.

CO5 - Apply machine learning techniques to address specific bioinformatics challenges, such as classification, clustering, and prediction.

CO6 - Demonstrate critical thinking and problem-solving abilities by designing and implementing machine learning solutions for real-world bioinformatics problems.

TEXT / REFERENCE BOOKS

1. Bioinformatics Data Skills: Reproducible and Robust Research with Open-Source Tools - Vince Buffalo (O'Reilly Media, 2015).
2. Machine Learning in Bioinformatics - Yanqing Zhang and Jagath C. Rajapakse (Wiley-IEEE Press, 2018).
3. Machine Learning Methods in Bioinformatics - Matthias Dehmer, Frank Emmert-Streib, and Armin Graber (Wiley, 2016).
4. Bioinformatics and Functional Genomics - Jonathan Pevsner (Wiley-Blackwell, 2019).
5. Practical Machine Learning for Computer Vision - Martin G√∂rner, Ryan Gillard, and Valliappa Lakshmanan (O'Reilly Media, 2020).

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs**

PART A: 6 Questions of 5marks each – No choice **30 Marks**

PART B: 5 Questions from each unit of internal choice; each carrying 14 Marks **70 Marks**

S739BLH34	STRUCTURAL BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		2	0	2	2	4	100

COURSE OBJECTIVES

- To acquire knowledge on biological macromolecules, structure, function, and their interaction in biological systems.
- To familiarize with the advanced High throughput techniques to study the biological macromolecules.

UNIT 1 INTRODUCTION 12 Hrs.

Structure & Organization of Prokaryotic & Eukaryotic Genome - Nucleotide and protein sequencing methods. Levels of Structures in Biological Macromolecules. Introduction to Functional Genomics - cytological maps - Hap Map – SNPs and variation- Genotyping, microarray- analysis, and applications. Quantitative Proteomics.

UNIT 2 BIOMOLECULES AND THEIR INTERACTIONS 12 Hrs.

Forces that determine protein and nucleic acid structure, basic problems, polypeptide chains geometrics, potential energy calculations, observed values for rotation angles, hydrogen bonding, hydrophobic interactions, and ionic interactions, disulfide bonds - Prediction of proteins structure - Nucleic acids, general characteristics of the nucleic acid structure, geometrics, glycosidic bond rotational isomers.

UNIT 3 STRUCTURAL ANALYSIS OF MACROMOLECULES 12 Hrs.

Size and shape of macromolecules - methods of direct visualization - X-ray crystallography–X-ray diffraction, determination of molecular structures, electron microscopy, NMR. Protein structure databases - Protein Data Bank - SCOP - CATH - structure superposition - RMSD - TM-score- structure alignment - Different structure alignment algorithms - DALI, CE, VAST, TM-align - protein folds in PD.

UNIT 4 IN-SILICO ANALYSIS OF MACROMOLECULES 12 Hrs.

Basics tools in bioinformatics, sequence retrieval from Database, BLAST analysis. Primer Designing, Insilico Cloning technique using Bioinformatics tools, Codon Optimization. Structure determination using Bioinformatics tools. Quantitative RT-PCR analysis.

UNIT 5 RECOMBINANT DNA TECHNOLOGY AND STRUCTURAL BIOLOGY 12 Hrs.

High-throughput cloning and expression strategies. Next Generation Sequencing Applications, Recombinant protein production. Purification and Characterization of recombinant protein for Structural Biology. Labeling of Protein for NMR studies. Preparing purified protein for X-Ray Crystallography.

Max.60 Hrs.

COURSE OUTCOMES:

On completion of the course, the student will be able to

CO1 - The student will acquire a basic knowledge of functional genomics.
CO2 - They will be able to analyze and predict the confirmations of the biological macromolecules.
CO3 - Will be able to construct a methodology for analyzing the Structural properties of the given protein.
CO4 - Able to evaluate the recombinant strains by molecular and structural biology techniques.
CO5 - Summarize the high throughput techniques in cloning, expression, purification, and Characterization.

TEXT / REFERENCE BOOKS

1. Sambrook, Joseph, and David W. Russell, The Condensed Protocols: From Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, 2006.
2. T. A. Brown, Gene Cloning and DNA Analysis: An Introduction, 8th Edition.
3. Pennington SR, Dunn MJ, Proteomics from Protein Sequence to Function, Viva Books Ltd, 2002.
4. G. Gibson and M. V. Muse. A primer of Genome Science. Sinauer Associates Inc; 2 edition, December 2004.

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs**

PART A: 6 Questions of 5marks each – No choice **30 Marks**

PART B: 5 Questions from each unit of internal choice; each carrying 14 Marks **70 Marks**

S739BLH35	METAGENOMICS	L	T	P	EL	Credits	Total Marks
		2	0	2	2	4	100

COURSE OBJECTIVES

- To provide an overview of the history, definition, and composition of the microbiome, introducing students to the diverse range of microorganisms and the halobiont concept.
- To explore various sequencing technologies used in microbiome data generation and understand their evolution and applications.
- To equip students with the skills to analyze microbiome data, including pre-processing, assembly, and annotation, using various webservers and tools.
- To delve into the human microbiome and its impact on health and disease, including the role of antibiotics and potential for microbiome engineering.
- To investigate the practical applications of metagenomics in environmental control, pathogen identification, biodiscovery, and agriculture, alongside ethical and safety considerations.

UNIT 1 INTRODUCTION TO MICROBIOME 9 Hrs.

The journey from individual microorganisms to complex microbiomes - Defining and understanding the term "microbiome" - Components of the microbiota: Bacteria, Archaea, Fungi, Protists, Algae, and Viruses - The concept of the "Holobiont" and the "Hologenome Theory" - Exploring the functional roles of microbiomes in ecosystems.

UNIT 2 GENERATING MICROBIOME DATA 9 Hrs.

Evolution of sequencing technologies: First, second, and third generations - The process and purpose of Amplicon (gene marker) sequencing - Unpacking Shotgun metagenomics and whole genome sequencing.

UNIT 3 MICROBIOME DATA ANALYSIS 9 Hrs.

Pre-processing of data: Necessary steps before analysis - Assembly and annotation: Taxonomic and functional - Web servers and tools used for data analysis - Understanding metadata and key terms: Alpha and Beta Diversity, Dysbiosis, Rarefaction, Core Microbiome, Phylogenetics, and Phylogenomics.

UNIT 4 HUMAN MICROBIOME 9 Hrs.

Introduction to the Human Microbiome Project - Examination of the Oral and Gut microbiomes - Linking infectious diseases to host microbiome alterations - The impact of antibiotics on the human microbiome - The potential and ethics of microbiome engineering.

UNIT 5 APPLICATIONS OF METAGENOMICS 9 Hrs.

Using metagenomics in environmental pollution control - Identification and control of pathogenic microbes - Biodiscovery through metagenomics - The role of metagenomics in agriculture - An overview of key microbiome projects: The Earth Microbiome Project, Tara Oceans, and the Indian Soil Microbiome Project - Major stakeholders in metagenomics and the convention on biological diversity - Addressing Biosafety and IPR issues in metagenomics.

Max.45 Hrs.

COURSE OUTCOMES:

On completion of the course, the student will be able to

CO1 - Define and explain the concept and components of the microbiome, including the holobiont concept and hologenome theory.

CO2 - Understand and discuss the historical development and practical applications of various sequencing technologies.
CO3 - Apply a variety of tools and methods to analyze microbiome data, interpreting and explaining key terms such as alpha and beta diversity, dysbiosis, and core microbiome.
CO4 - Describe the role of the human microbiome in health and disease, including the impact of antibiotics and potential for microbiome engineering.
CO5 - Discuss and evaluate the application of metagenomics in various fields, acknowledging key projects, major stakeholders, and ethical considerations such as biosafety and IPR.
CO6 - Understand how the findings from metagenomic studies can be applied to real-world challenges in environmental control, public health, agriculture, and biodiscovery.

TEXT / REFERENCE BOOKS

1. Microbial Diversity in the Genomic Era: Advances in Metagenomics and Metagenome Analysis" edited by Varun Suresh and Ashish Verma (2019).
2. Microbiome Analysis: Methods and Protocols" edited by Chuanbin Mao (2019).
3. Metagenomics: Methods and Protocols" edited by Wolfgang R. Streit and Rolf Daniel (2020).
4. Metagenomics: Techniques, Applications, Challenges and Opportunities" edited by Mohammad Shafi Sabir and Jamal M. Arif (2022).

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A:	6 Questions of 5marks each – No choice	**30 Marks**
PART B:	5 Questions from each unit of internal choice; each carrying 14 Marks	**70 Marks**

SBIB6301	R FOR BIOINFORMATICS LAB	L	T	P	EL	Credits	Total Marks
		0	0	4	2	3	100

COURSE OBJECTIVE

- To equip post-bioinformatics graduates with the necessary knowledge and skills in R programming for bioinformatics, enabling them to proficiently analyze and interpret biological data, perform statistical analysis, and develop reproducible workflows for bioinformatics research.

1. Exercise: Importing and Manipulating Bioinformatics Data

Import a FASTA file containing DNA sequences into R and extract specific sequences based on their identifiers. Perform sequence manipulation tasks such as reverse complementing, sequence slicing, and extracting subsequences.

2. Exercise: Exploratory Data Analysis of Gene Expression Data

Load a gene expression dataset into R and explore the distribution of expression values using box plots and histograms. Identify and visualize patterns in gene expression data using scatter plots and heatmaps.

3. Exercise: Differential Expression Analysis

Perform differential expression analysis on RNA-seq data using popular R packages such as DESeq2 or edgeR. Identify significantly differentially expressed genes between two experimental conditions and visualize the results.

4. Exercise: Gene Ontology Enrichment Analysis

Perform gene ontology enrichment analysis using R packages such as cluster Profiler or top GO. Identify overrepresented biological processes, molecular functions, and cellular components in a gene list and visualize the results.

5. Exercise: Sequence Alignment and Annotation

Align a set of protein sequences using the pairwise Alignment function in the Bioconductor package Bio strings. Annotate the aligned sequences with functional information using tools like InterProScan and visualize the alignment results.

6. Exercise: Next-Generation Sequencing (NGS) Data Analysis

Perform quality control and filtering of NGS data (e.g., FASTQ files) using R packages such as FastQC and ShortRead. Align the filtered reads to a reference genome using a package like bwa or bowtie2 and visualize the alignment results.

7. Exercise: Network Analysis

Construct and visualize biological networks using R packages such as igraph or CytoscapeRPC. Perform network-based analysis, such as identifying highly connected nodes and identifying network modules or communities.

8. Exercise: Integrative Analysis of Omics Data

Integrate multiple types of omics data, such as gene expression, DNA methylation, and protein-protein interaction data, using appropriate R packages. Perform integrative analysis to uncover relationships and patterns across different omics layers.

9. Exercise: Machine Learning for Bioinformatics

Build a machine learning model (e.g., random forest, support vector machine) to classify biological samples based on genomic features. Evaluate the performance of the model using metrics such as accuracy, precision, recall, and ROC curves.

10. Exercise: Reproducible Research and Workflow Management

Create a reproducible workflow using R Markdown or Jupyter Notebooks, documenting the step-by-step analysis process.

Share the workflow with others, ensuring that it can be easily reproduced by following the provided code, explanations, and visualizations.

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

CAE	Evaluation of Regular Lab class	25 Marks	
	Model practical exam	25 Marks	**50 Marks**
ESE	University Practical exam		**50 Marks**

SBIB5401	MOLECULAR MODELLING AND DRUG DESIGN	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To gain some knowledge on modern approaches used in molecular modeling.
- To gather information on the basics of generating 3D models for molecules
- To have an insight into understanding the validation and stability of molecules
- To use powerful computer-based technology to identify and design molecules for new medications
- To greatly shortening the discovery phase of drug development by powerful computer-based technology.

UNIT 1 INTRODUCTION 9 Hrs.

Introduction to molecular modeling – co-ordinate systems, potential energy surfaces, molecular surfaces. Molecular geometry. molecular visualization and graphics. Introduction to Quantum mechanics.

UNIT 2 MOLECULAR MECHANICS 9 Hrs.

Introduction to Molecular Mechanics- bond stretching, angle bending, torsional terms, Vander waal's interaction, non- bonded and electrostatic interaction. Energy minimization - introduction - maxima, minima and saddle points - Applications of energy minimization. Introduction to Molecular dynamics- Molecular dynamics simulation of biomolecules, Conformational analysis.

UNIT 3 INTRODUCTION TO DRUGS 9 Hrs.

Drugs- classification, prodrugs, hard drugs and soft drugs. Mode of action – Drug Receptor interaction and kinetics. Routes of administration and Drug Targets. Pharmacokinetics and Pharmacodynamics of drugs. Drug Bioavailability. Drug toxicity.

UNIT 4 RATIONAL DRUG DESIGN 9 Hrs.

Drug development process. Introduction to computational drug discovery: methods in drug design. Pharmacophore analysis. Lead discovery and optimization. Molecular Docking, QSAR studies

UNIT 5 DATABASES AND TOOLS 9 Hrs.

Small molecule databases: Pubchem, Zinc, Drugbank. Representation of molecules. Drug likeness analysis – concept and SwissADME. Macromolecule structure databases: PDB. Protein modelling and Validation.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Understand the basics of modeling strategies.
CO2 - Analyze the role of simulation studies and perform them.
CO3 - Understand the fundamentals of drugs and their pharmacokinetic properties.
CO4 - Identify the drug development process and lead molecule discovery.
CO5 - Retrieve information related to small molecules from databases.
CO6 - Independently analyze the potential of ligands as drugs via insilico studies.

TEXT BOOKS/REFERENCE BOOKS

1. Computer Assisted Drug Designing Pushpendra Kumar Vishwakarma, Vikash Gupta, Leela Maharaj, LAP Lambert Academic Publishing (17 March 2012).

2. Computer Aided Drug Design (CADD): From Ligand-Based Methods to Structure-Based Approaches, Mithun Rudrapal, Chukwuebuka Egbuna Elsevier 2022 eBook ISBN: 9780323914338.
3. Computer-Aided Drug Discovery and Design Alan Talevi Springer 2730-5465 2022
4. Textbook of Drug Design and Discovery Kristaina strom gaard Taylor & Francis Ltd CRC press.
5. A Textbook of Drug Design and Development M.R.Yadav VALLABH PRAKASHAN 2020.

SBIB6401	MOLECULAR MODELLING AND DRUG DESIGN LAB	L	T	P	EL	Credits	Total Marks
		0	0	4	2	2	100

LIST OF EXERCISES:

1. Determination of three-dimensional structure of protein
    i. Homology Modelling
    ii. Ab Initio/Threading
    iii. I-based protein structure prediction

2. Protein molecule energy calculation and Minimization
    I. Protein structure quality evaluation
    II. Molprobity-clash score calculation
    III. Ramachandran plot-based evaluation

3. Small molecule library construction and screening
    i. Druglikeness screening
    ii. Phamacophore feature mapping

4. Molecular docking
    i. Protein -small molecule docking
    ii. Protein -Peptide docking
    iii. Protein-Protein docking

5. Molecular dynamics and simulation

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

CAE	Evaluation of Regular Lab class	25 Marks	
	Model practical exam	25 Marks	**50 Marks**
ESE	University Practical exam		**50 Marks**

SBIB54001	BIOETHICS, BIOSAFETY AND INTELLECTUAL PROPERTY RIGHTS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- Understand and apply ethical principles in bioinformatics and data science research.
- Learn biosafety principles and effectively manage risks in handling biological data.
- Analyze ethical considerations in genomics, precision medicine, and data sharing.
- Comprehend intellectual property rights in bioinformatics and data science research.
- Develop critical thinking skills to address emerging ethical challenges in the field.

UNIT1 INTRODUCTION TO BIOETHICS AND RESPONSIBLE CONDUCT OF RESEARCH 9 Hrs.

Introduction to bioethics and its relevance in bioinformatics and data science - Ethical principles and guidelines for conducting research in the field - Responsible conduct of research, including issues related to data privacy, informed consent, and research integrity.

UNIT 2 BIOSAFETY AND BIOSECURITY IN BIOINFORMATICS AND DATA SCIENCE 9 Hrs.

Overview of biosafety and biosecurity principles and their importance in the field - Risk assessment and management in handling biological data and materials - Regulations and protocols for ensuring safe laboratory practices and data handling.

UNIT 3 ETHICAL ISSUES IN GENOMICS AND PRECISION MEDICINE 9 Hrs.

Ethical considerations in genomic research, including privacy, informed consent, and data sharing - Ethical implications of precision medicine, such as personalized treatment and genetic testing - Debates surrounding gene editing technologies, such as CRISPR-Cas9.

UNIT 4 INTELLECTUAL PROPERTY RIGHTS IN BIOINFORMATICS AND DATA SCIENCE 9 Hrs.

Introduction to intellectual property rights (IPR) and its relevance in the field - Patents, copyrights, and trademarks in bioinformatics and data science - Ethical aspects of IPR, including access to data and research tools, open-source software, and data sharing.

UNIT 5 EMERGING ETHICAL CHALLENGES IN BIOINFORMATICS AND DATA SCIENCE 9 Hrs.

Ethical implications of big data analytics, data mining, and machine learning in bioinformatics – Ethical considerations in the use of AI and algorithms in bioinformatics and data science - Addressing biases, fairness, and transparency in data-driven research.

Max.45 Hrs.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Understand and apply ethical principles in bioinformatics and data science research.
CO2 - Effectively manage biosafety risks associated with biological data and materials.
CO3 - Analyze and evaluate ethical considerations in genomics, precision medicine, and data sharing.
CO4 - Comprehend intellectual property rights in bioinformatics and data science.
CO5 - Address ethical challenges in big data analytics, AI, and algorithms.
CO6 - Develop critical thinking skills to propose responsible research guidelines.

TEXT / REFERENCE BOOKS

1. Principles of Biomedical Ethics by Tom L. Beauchamp and James F. Childress (2019, Oxford University Press).
2. Bioethics: Principles, Issues, and Cases by Lewis Vaughn (2019, Oxford University Press).
3. Introduction to Bioethics by John A. Bryant and Linda Baggott la Velle (2018, Cambridge University Press).
4. Biosafety in the Laboratory: Prudent Practices for the Handling and Disposal of Infectious Materials by the National Research Council (2009, National Academies Press).
5. Intellectual Property in Genomic and Personalized Medicine edited by Robert Cook-Deegan, Christopher Heaney, and Brian R. Lucey (2016, Oxford University Press).

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A: 6 Questions of 5marks each – No choice **30 Marks**

PART B: 5 Questions from each unit of internal choice; each carrying 14 Marks **70 Marks**

SBIB54002	RESEARCH METHODOLOGY	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To impart students the importance of research.
- To provide understanding on the approaching research problem.
- To enable students to design methodologies to deal with research problems.
- To perform research with ethics.
- To present the data generated in the work as article for publishing.

UNIT 1 INTRODUCTION 9 Hrs.

Meaning of Science and Scientific research, Scope and relevance of research for society, Steps in scientific research, Formulation of research problems, Multidisciplinary approaches in research.

UNIT 2 RESEARCH DESIGN CONCEPTS 9 Hrs.

Research design: features and types, Methodology and methods of research, Role of theory in research, Research questions and hypothesis building

UNIT 3 DATA AND SAMPLE COLLECTION 9 Hrs.

Types and sources of data, Tools and techniques of data collection, Variables and samples. Sample collection and steps in sampling designs and its characteristics.

UNIT 4 ETHICS 9 Hrs.

Ethical considerations in research. Moral, values, ethics and ethics in biology; Role and importance of ethics in research. Basic Approaches to Ethics; Post humanism and Anti-Post humanism. Applying for ethical approval/ clearance.

UNIT 5 SCIENTIFIC WRITING 9 Hrs.

Data analysis and Scientific writing, Essentials - Structure, Composition, Citation and Bibliography in scientific manuscripts. Impact factor, Citation index. Research abstracts, Research article, Format of scientific manuscripts and Thesis.

Max.45 Hrs.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Appreciate and contextualize the need of research.
CO2 - Develop a design for a research problem.
CO3 - Formulate data with respect to sample collection.
CO4 - Perform research on the basis of ethical guidelines.

CO5 - Use, apply and execute appropriate research methods to carry out multidisciplinary research.
CO6 - Apply the skills of data gathering, perform analysis and present data as research Publication.

TEXT / REFERENCE BOOKS

1. Research Methodology C.R. Kothari, Gaurav Garg New Age International Publishers; Fourth edition (1 September 2019).
2. RESEARCH METHODOLOGY AND APPLIED STATISTICS D N SANSANWAL SHIPRA PUBLICATIONS (1 January 2020).
3. Research Methodology for Health Professionals: Including Proposal, Thesis & Article Writing, Research Funding and Plagiarism RC Goyal JAYPEE BROTHERS MEDICAL PUBLISHERS PVT.LTD;2/E, 2023 edition (17 October 2022).

4. Research Methodology: Concepts and Cases Deepak Chawla, Neena Sondhi Vikas Publishing, House; Second edition (1 January 2016).

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A: 6 Questions of 5marks each – No choice **30 Marks**

PART B: 5 Questions from each unit of internal choice; each carrying 14 Marks **70 Marks**

SBIB54003	ANALYTICAL TECHNIQUES IN BIOSCIENCE	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVE

- To discusses the various separation techniques.
- To impart knowledge in viewing microscopic molecules.
- To provide an insight into separation of molecules and analyze.
- To be aware of radio and non-radioactive labeling techniques.
- To understand several instrumental techniques involved in biotechnological research.

UNIT 1 SEPARATION 9 Hrs.

Cell disruption methods and Cell fractionation - High pressure homogenization, Ultrasonication. Centrifugation: Principle, types and applications. Cell immobilization.

UNIT 2 MICROSCOPIC TECHNIQUES 9 Hrs.

Microscopy – Bright field, Dark field, Phase contrast, Fluorescence, Scanning and transmission electron microscopy - Flow cytometry.

UNIT 3 SPECTROSCOPY AND CHROMATOGRAPHY 9 Hrs.

Spectroscopy – Principle and applications - UV-Visible spectrophotometer - Infrared Red, Fluorescence Spectrophotometry Chromatography: Principle, and applications- TLC, Column Chromatography - Ion exchange, Gel Filtration and Affinity Chromatography, HPLC and GC.

UNIT 4 MOLECULAR TECHNIQUES 9 Hrs.

Electrophoresis of nucleic acid and proteins: Principles, methods and applications- Agarose gel electrophoresis, Pulse field gel electrophoresis, SDS – PAGE, 2D PAGE. Blotting techniques - principle, methods and applications - Southern, Northern, Western blotting. PCR and its types. Immunological techniques - Immunoelectrophoresis- ELISA, RIA.

UNIT 5 TRACER TECHNIQUES 9 Hrs.

The nature of radioactivity, Units of radioactivity; Detection and measurement of radioactivity -liquid scintillation counting – Basic principles of radioactive labeling. Non-Radioactive tracer Technology- fluorescence and nonradio isotopes, labeling and detection methods using fluorescent molecules.

Max.45 Hrs.

COURSE OUTCOMES:

On completion of the course, student will be able to

CO1 - Perform cell disruption.
CO2 - Able to demonstrate the different microscopic techniques.
CO3 - Illustrate and understand the basics in spectroscopy and chromatography.
CO4 - Understand the separation process and analysis of biomolecules.
CO5 - Explain the concept of labeling of molecules.
CO6 - Integrate various techniques to develop solutions for complex problems.

TEXT / REFERENCE BOOKS

1. Analytical Techniques in Biochemistry and Molecular Biology Rajan Katoch Springer; 2011th edition (23 July 2011); CBS PUBLISHERS AND DISTRIBUTORS PVT. LTD.,
2. Analytical Techniques in Biochemistry Mahin Basha Humana; 1st ed. 2020 edition (17 December 2020).

3. Biophysical Chemistry UPADHYAY A Himalaya Publishing House Pvt. Ltd.; Fourth Edition (1 January 2020).
4. Bioinstrumentation Techniques-Basics and applications Dr. Ankita Jain; Haresh Kalasariya; Ms. Varsha Tailor; Dr. Nikunj B. Patel Notion Press (10 April 2020).
5. Chemical Measurements in Biological Systems: 9 Kent K. Stewart (Author), Richard E. Ebel Wiley- Interscience; 1st edition (1 June 2000).

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A:	6 Questions of 5marks each – No choice	**30 Marks**
PART B:	5 Questions from each unit of internal choice; each carrying 14 Marks	**70 Marks**

SBIB54004	CANCER BIOLOGY AND THERAPEUTICS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To educate students on the nature of cancer.
- To provide information on molecular changes that normal cells undergo.
- To describe genetic factors that contribute to cancer development.
- To have an overview on diagnostic techniques to detect cancer.
- To presents an overview on currently available therapeutic treatments.

UNIT 1 INTRODUCTION **9 Hrs.**

Cancer, Salient Features of cancer- causes of cancer – Neoplasia, hypoplasia and metaplasia. Carcinogens- physical, chemical and Biological. Oncogenic viruses- Classification of cancer- Epidemiology of human cancer.

UNIT 2 MECHANISM **9 Hrs.**

Malignancy-Characteristics of malignant cells- Molecular mechanism - modification of extacellular matrix component cells – Extracellular matrix and cell – cell adhesion, cell cycle regulation, Apoptosis, Growth factor, signal transduction, mechanism of angiogenesis, biology of human metastasis.

UNIT 3 GENETICS OF CANCER **9 Hrs.**

Cancer and genetics- Chromatin structure and function, Split genes and RNA processing, genetic recombination, gene amplification, DNA methylation, Genomic imprinting, oncogenes, Tumor suppressor genes, mechanism of gene silencing, Gene therapy of cancer.

UNIT 4 DIAGNOSTIC METHODS **9 Hrs.**

Methods for the diagnosis - Tumor markers, Gene expression microarray, proteomic method, Molecular imaging, Nanotechnology, Pharmacogenomics.

UNIT 5 THERAPY **9 Hrs.**

Cancer therapy- Diet and cancer prevention, Chemotherapy - Molecular targets of chemoprevention, Immunotherapy, Radiation therapy: Advantages and limitation.

COURSE OUTCOMES:

On completion of the course, student will be able to

CO1 - Educate causes of cancer and its risks and databases.
CO2 - Acquire knowledge about types of carcinogenesis and their mechanism of actions.
CO3 - Study the role of ECM matrix, signal transduction mechanism to know the evolution of cancer.
CO4 - Molecular basis and modern methods are used for detecting the cancer.
CO5 - Know the techniques available Prevention of cancer.
CO6 - Wide knowledge about different therapies for cancer treatment.

TEXT BOOKS/REFERENCE BOOKS

1. Molecular Biology Of Cancer 5e: Mechanisms, Targets, and Therapeutics Lauren Pecorino OUP Oxford; 5th edition (23 June 2021).
2. PRINCIPLES OF CANCER BIOLOGY Kleinsmith Pearson Education India; First Edition (29 July 2016).
3. The Textbook of Cancer Biology Dr. Pradeep Kumar Prachi Digital Publication (1 January 2022).
4. Robert A. Weinberg The Biology of Cancer, Garland Science 2013.

5. Practical Guide to Cancer Systems Biology Hsueh-fen Juan, Hsuan-cheng Huang World Scientific Publishing Co Pte Ltd; 1st edition (17 January 2018).

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A: 6 Questions of 5marks each – No choice **30 Marks**

PART B: 5 Questions from each unit of internal choice; each carrying 14 Marks **70 Marks**

SBIB54005	EPIGENOMICS IN HEALTH AND DISEASE	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- Understand the fundamental principles of epigenetics and its role in human health and disease.
- Gain knowledge of the various epigenetic modifications and their impact on gene expression and cellular function.
- Learn the experimental techniques and technologies used for profiling epigenetic modifications in clinical samples.
- Explore the application of epigenomics in complex diseases, including cancer, cardiovascular diseases, neurological disorders, and metabolic disorders.
- Develop the skills to analyze and interpret epigenomic data, identify epigenetic biomarkers for disease diagnosis and prognosis, and explore the potential of epigenetic-based therapies.

UNIT 1 INTRODUCTION TO EPIGENETICS IN HEALTH AND DISEASE 9 Hrs. Overview of epigenetics and its role in human health and disease - Epigenetic mechanisms and their impact on gene expression and cellular function - Epigenetic modifications as biomarkers for disease diagnosis and prognosis.

UNIT 2 EPIGENOMIC PROFILING TECHNOLOGIES AND EXPERIMENTAL APPROACHES 9 Hrs.

Techniques for profiling epigenetic modifications in clinical samples - High-throughput technologies for genome-wide epigenomic analysis - Design and implementation of epigenetic experiments in a clinical setting.

UNIT 3 EPIGENOMICS IN COMPLEX DISEASES 9 Hrs.

Epigenetic alterations in cancer and their functional consequences – Epigenetic contributions to cardiovascular diseases, neurological disorders, and metabolic disorders - Epigenomics approaches for understanding disease etiology and progression.

UNIT 4 EPIGENETIC BIOMARKERS AND PERSONALIZED MEDICINE 9 Hrs.

Identification and validation of epigenetic biomarkers for disease diagnosis, prognosis, and treatment response - Epigenetic signatures for patient stratification and personalized medicine – Ethical considerations in the use of epigenetic biomarkers in clinical practice.

UNIT 5 EPIGENETIC THERAPEUTICS AND FUTURE PERSPECTIVES 9 Hrs.

Epigenetic-based therapies and interventions in clinical practice - Challenges and opportunities in developing epigenetic drugs -Emerging trends and future directions in epigenomic research.

Max.45 Hrs.

COURSE OUTCOMES:

On completion of the course the student will be able to

CO1 - Understand the principles and mechanisms of epigenetics in human health and disease.
CO2 - Apply epigenomic profiling technologies and experimental approaches in clinical settings.
CO3 - Analyze and interpret epigenomic data to identify disease-related epigenetic biomarkers.
CO4 - Evaluate epigenetic alterations in complex diseases like cancer, cardiovascular diseases, and neurological disorders.
CO5 - Assess ethical considerations related to the use of epigenetic biomarkers in personalized medicine.
CO6 - Explore the potential of epigenetic-based therapies and discuss future perspectives in epigenomics

TEXT / REFERENCE BOOKS

1. Epigenetics: Principles and Practice by Natalie Ahn and Andrew D. Hollenbach (Oxford University Press, 2019).
2. Epigenomics: From Chromatin Biology to Therapeutics by Anjana Rao and Chandanamali Punchaparambil (Springer, 2020).
3. Epigenetic Regulation in the Nervous System edited by J. David Sweatt and Michael J. Meaney (Academic Press, 2013).
4. Epigenetics in Human Disease edited by Trygve Tollefsbol (Academic Press, 2012).
5. Principles of Epigenetics by Tatiana G. Kutateladze (Elsevier, 2016).

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100 **Exam Duration: 3 Hrs.**

PART A: 6 Questions of 5marks each – No choice **30 Marks**

PART B: 5 Questions from each unit of internal choice; each carrying 14 Marks **70 Marks**

SBIB54006	CHEMINFORMATICS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To impart the students with the importance of cheminformatics.
- To provide resources to retrive chemical data.
- To create awareness to combinatorial approaches.
- To enable them to know the role of the pharmacophores.
- To design new molecules and apply them in drug discovery.

UNIT 1 INTRODUCTION 9 Hrs.

Introduction to Cheminformatics - History and evolution of Cheminformatics – Chemical representation - Sequence, 2D, 3D structures, Types of chemical representation – linear notation, tabular storage, graphical representation - Chemical data management – Chemical markup languages.

UNIT 2 CHEMICAL DATABASES 9 Hrs.

Chemical Databases - CHEMDB, KEGG LIGAND, CSD, CAS REGISTRY, BIOMETA DB, National Cancer Institute Database (NCI) - Chemical searching methods - exact searching, sub structure searching, similarity searching, reaction searching.

UNIT 3 COMBINATORIAL CHEMISTRY 9 Hrs.

Combinatorial chemistry: Introduction, Liquid Phase synthesis, Solid phase synthesis, Designing Combinatorial Synthesis, High through put screening

UNIT 4 COMBINATORIAL LIBRARY DESIGN 9 Hrs.

Combinatorial library design - Rational principles of compound selection for combinatorial library design and optimization approach, Descriptor Analysis, Modeling toxicity, Computer Assisted Synthesis design and structure- based library design.

UNIT 5 APPLICATION OF CHEMINFORMATICS 9 Hrs.

Application of cheminformatics - QSPR Drug design - Target identification and Validation, lead finding and optimization - Pharmacophore-Based Drug Design - Structure-Based Drug design - Application of Cheminformatics in Drug Design.

Max.45 Hrs.

COURSE OUTCOMES:

At the end of the course the students will be able to

CO1 - Learn the basics of cheminformatics.
CO2 - Understand the various databases needed cheminformatics.
CO3 - Appreciate the role of Combinatorial chemistry.
CO4 - Analyse the various descriptors used in cheminformatics.
CO5 - Work on pharmacophore-based drug design and SBDD.
CO6 - To develop novel approaches in designing molecules for drug development.

TEXT BOOKS/REFERENCE BOOKS

1. Computational Approaches in Cheminformatics and Bioinformatics Rajarshi Guha (Editor), Andreas Bender Wiley; 1st edition (4 January 2012);
2. Cheminformatics, QSAR and Machine Learning Applications for Novel Drug Development Kunal Roy Academic Press (23 May 2023).
3. Cheminformatics and its Applications Amalia Stefaniu (Editor), Azhar Rasul (Editor), Ghulam Hussain IntechOpen (15 July 2020).

4. Chemoinformatics in Drug Discovery Gerd Folkers, Hugo Kubinyi, Raimund Mannhold, Tudor Oprea Wiley 2006.
5. Chemoinformatics and Bioinformatics in the Pharmaceutical Sciences Himanshu Ojha, Navneet Sharma, Pawan Raghav, Ramesh K. Goyal Elsevier Science 2021

END SEMESTER EXAMINATION QUESTION PAPER PATTERN

Max. Marks: 100		**Exam Duration: 3 Hrs.**
PART A:	6 Questions of 5marks each – No choice	**30 Marks**
PART B:	5 Questions from each unit of internal choice; each carrying 14 Marks	**70 Marks**