

SHSB1102	GENERAL ENGLISH- I	L	T	P	EL	Credits	Total Marks
		3	0	0	0	3	100

COURSE OBJECTIVES

- To provide opportunities for students to read and respond to representations of current issues.
- To prepare the students to effectively communicate by applying reflective thinking practices.
- To provide an opportunity to the students to improve their vocabulary.
- To create and apply lateral and critical thinking.
- To learn academic writing strategies.

UNIT 1**9 Hrs.**

Listening to identify vocabularies- Self Introduction - Developing dialogue between characters -Talking about neighbors, family members, likes and dislikes, Reading Comprehension strategies- Parts of Speech- Kinds of Sentences Connectives and Discourse markers - Rearranging the Jumbled sentences, E-Mail Writing.

UNIT 2**9 Hrs.**

Listening for Inference- Just a Minute speech- Types of words- Compound words, abbreviations and acronyms, Word Association- Tenses and its Types- Voice- Impersonal Passive- Rules of Passive voice formation - Transcoding - Encoding and Decoding- Bar chart, Pie Chart.

UNIT 3**9 Hrs.**

Listening to telephonic talk to fill blanks- Giving information- travel, hotel booking, making enquiries about availability of seats for admission, asking about courses - Question Tags – Open ended and Close ended questions, Concord, Single - Line Definition - Note Making - Preparing checklists.

UNIT 4**9 Hrs.**

Listening to summarize the information- Reading and identifying the topic sentence, - Editing - Punctuation- Error Corrections, 'If 'Conditionals, Idioms & Phrases, Instructions & Recommendations – Drafting a brochure/Advertisement.

UNIT 5**9 Hrs.**

Listening to Movie reviews and book reviews, Listening and summarizing- Giving impromptu talks - Reading and Summarizing -Types of words- Homonyms, Homophones, eponyms, acronyms- Writing a Paragraph, Descriptive Essay, Dialogue Writing.

Max.45 Hrs.**COURSE OUTCOMES:**

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

- CO1** - Remember knowledge of linking words related to both spoken and written discourse.
- CO2** - Understand collocations, words to express one's point of view in both writing and speaking.
- CO3** - Apply the rules for writing compare and contrast paragraphs by using cohesive devices based on prompts given.
- CO4** - Analyze critical thinking skills by framing questions related to elements of reasoning.
- CO5** - Evaluate written pieces to self-correct in the topic areas of verbs, reported speech, and punctuation.
- CO6** - Equip the students with the required Professional Skills.

TEXT / REFERENCE BOOKS

1. Sen S, Mahendra et al. (2015) Communication and Language Skills. Foundation books. Chennai
2. Strunk, William Jr., and E.B. White. The Elements of Style. Allyn and Bacon, 2000.
3. Murphy, Raymond. English Grammar in Use. Cambridge University Press, 2012.
4. Thomson, A.J., and A.V. Martinet. A Practical English Grammar. Oxford University Press, 1986.
5. Straus, Jane. The Blue Book of Grammar and Punctuation. John Wiley & Sons, 2014.
6. O'Conner, Patricia T. Woe is I: The Grammarphobe's Guide to Better English in Plain English. Riverhead Books, 2019.

END SEMESTER EXAM QUESTION PAPER PATTERN**Max. Marks: 100****Exam Duration: 3 Hrs.****PART A:** 10 Questions of 2 marks each uniformly distributed – No choice**20 Marks****PART B:** 2 Questions from each unit of internal choice, each carrying 16 marks**80 Marks**

SMTB1107	BASIC STATISTICS	L	T	P	EL	Credits	Total Marks
		3	0	0	0	3	100

COURSE OBJECTIVE

- To Be Familiar With Basic Concepts Sample Space.
- To Be Familiar With Discrete And Continuous Random Variables.
- To Be Familiar With Correlation And Regression Analyses.
- To Understand The Standard Distribution And Time Series.

UNIT 1 DESCRIPTIVE STATISTICS**9 Hrs.**

Collection, Classification and Tabulation of data, Bar diagrams and Pie diagrams, Histogram, Frequency curve and frequency polygon, Ogives. Mean, median, mode, Standard deviation.

UNIT 2 CURVE FITTING, CORRELATION AND REGRESSION**9 Hrs.**

Fitting A Straight Line and Second-Degree Parabola by Least Squares. Correlation – Scatter Diagram – Limits Of Correlation Coefficient – Spearman's Rank Correlation Coefficient – Simple Problems – Regression – Properties Of Regression Coefficients And Regression Lines.

UNIT 3 PROBABILITY THEORY & RANDOM VARIABLES**9 Hrs.**

Probability theory, Random experiments, Sample Space, Conditional Probability, Baye's theorem, Random variable, (discrete and continuous), Probability density function (discrete and continuous), Distribution function (discrete and continuous random variable).

UNIT 4 STANDARD DISTRIBUTION**9 Hrs.**

Binomial distribution, Poisson distribution, Geometric Distribution, Uniform distribution, Exponential distribution, Normal distributions.

UNIT 5 TIME SERIES**9 Hrs.**

Component of time series – Measurement of trend – Graphical Method – Semi average method - Moving average method –Measurement of seasonal variation – Method of simple average method – Ratio Moving average method.

Max.45 Hrs.**COURSE OUTCOMES:**

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

- CO1** - Identify, classify and tabulate the data. Construct various frequency charts. Evaluate the various measures of central tendency and measures of variation.
- CO2** - Evaluate the Karl Pearson's correlation coefficient, Spearman's correlation coefficient and Regression Equations and fitting of straight line by least squares.
- CO3** - Understand the basic concepts of probability and apply Baye's theorem for solving conditional probability.
- CO4** - Use standard distributions to solve real time problems.
- CO5** - Solve problems based on components of time series.
- CO6** Acquaint knowledge to estimate the least square methods of trend analysis.

TEXT / REFERENCE BOOKS

- David S. Moore, George P. McCabe, Bruce A. Craig. Introduction To The Practice Of Statistics, 7th Edition, W.H. Freeman And Company, New York 2011.
- Pss Sunder Rao And J. Richard, An Introduction To Biostatistics And Research Methods, 5th Edition Phi Learning Private Ltd, New Delhi, 2012.
- P. R. Vittal, Mathematical Statistics, Margham Publications, Chennai, 2002.

4. J. N. Kapur And H. C. Saxena, Treatment And Content As In Mathematical Statistics, 20th Edition, S. Chand & Co. Ltd., New Delhi, 2010.
5. Hogg, R.V. & Craig. A. T. (1998): Introduction To Mathematical Statistics, Macmillan.

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100

Exam Duration: 3 Hrs.

PART A: 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B: 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB1101	CELL AND MOLECULAR BIOLOGY	L	T	P	EL	Credits	Total Marks
		3	0	0	0	3	100

COURSE OBJECTIVES

- To introduce the students to the basics of cell and its components.
- To provide comprehensive background of Salient features of Nucleic Acids and DNA model to the course learners.
- To impart detailed understanding of key events of molecular biology comprising of mechanism of DNA Replication, Transcription and Translation in Prokaryotes and Eukaryotes.
- To provide adequate knowledge about Post Transcriptional Modifications and Processing of Eukaryotic RNA to the course learners.
- To give detailed explanation of Transcriptional Regulation.

UNIT 1 CELL AND CELL ORGANELLES**9 Hrs.**

Discovery of cells; Basic properties of cells; Cell theory; Different classes of cells: Prokaryotic and eukaryotic cells. Cell Structure: Animal cell and Plant cell; Cell Organelles: Nucleus, Plasma membrane, Mitochondria, Endoplasmic reticulum, Golgi apparatus, Ribosomes, Chloroplast; Plastids; Vacuoles.

UNIT 2 TRANSPORT MECHANISM OF ETMECELL**9 Hrs.**

Cytoskeleton; Cell-Cell and cell-matrix interactions: Extracellular matrix and cell-matrix interactions. Cell-Cell interactions. Membrane transport: Pumps, channels, transporters: Ions channels, Active transport driven by ATP hydrolysis, Active transport driven by Ion gradients, Passive transport, Facilitated transport, Endocytosis.

UNIT 3 CELL DIVISION**9 Hrs.**

Cell division – Mitosis and meiosis; Cell cycle regulation and Checkpoints; Cell death and cell renewal: Programmed cell death, stem cells and maintenance of adult tissues.

UNIT 4 CENTRAL DOGMA**9 Hrs.**

Central Dogma; Mechanism of prokaryotic and eukaryotic DNA replication. Prokaryotic and Eukaryotic transcription mechanisms. Post-Transcriptional Control of Gene Expression.

UNIT 5 RNA BIOLOGY**9 Hrs.**

RNA-processing, mRNA export. Post transcriptional modifications- RNA splicing: Spliceosome, RNA editing. Genetic code. Translation: Protein synthesis, post-translational modifications; Prokaryotic transcriptional regulation (Operon concept).

Max.45 Hrs.**COURSE OUTCOMES:**

On completion of the course the student will be able to

- CO1** - Comprehend the structures and purposes of basic components of prokaryotic and eukaryotic cells, especially macromolecules, membranes, and organelles.
- CO2** - Familiar with cellular interactions and transport mechanisms.
- CO3** - Understand the cellular components underlying cell division, growth and death.
- CO4** - Emphasize the molecular mechanism of DNA replication and transcription.
- CO5** - Appreciate the mechanisms of RNA splicing and protein synthesis.
- CO6** - Realize the mechanisms of gene regulation in prokaryotes.

TEXT BOOKS/REFERENCE BOOKS

1. Karp's Cell Biology, Gerald Karp, Janet Iwasa, Wallace Marshall, Wiley; 8th Edition, Global.
2. Karp's Cell and Molecular Biology 9th Edition by Gerald Karp, Janet Iwasa, Wallace Marshall Wiley; 9th edition (February 19, 2020).
3. Genomes 5 5th Edition by Terry A. Brown CRC Press; 5th edition (April 28, 2023).
4. Molecular Cell Biology (842581) Ninth Edition by Harvey Lodish (Author), Arnold Berk (Author), Chris A. Kaiser (Author), Monty Krieger (Author), Anthony Bretscher et al W. H. Freeman; Ninth edition (January 27, 2021).
5. Cell Biology by Verma and Agarwal S CHAND & Company limited 2022.

END SEMESTER EXAM QUESTION PAPER PATTERN**Max. Marks: 100****Exam Duration: 3 Hrs.****PART A:** 10 Questions of 2 marks each uniformly distributed – No choice**20 Marks****PART B:** 2 Questions from each unit of internal choice, each carrying 16 marks**80 Marks**

S738BLH11	DATABASES AND TOOLS IN BIOLOGY	L	T	P	EL	Credits	Total Marks
		2	0	2	2	4	100

COURSE OBJECTIVES

- Understand the scope and applications of bioinformatics, including its role in biological research.
- Familiarize with different biological databases and learn to retrieve and analyze biological information.
- Develop skills in sequence comparison and alignment using popular tools.
- Gain proficiency in DNA and protein analysis techniques.
- Explore various bioinformatics applications, including feature identification, gene finding, and structure prediction.

UNIT 1 INTRODUCTION

12 Hrs.

Definition of Bioinformatics - History of Bioinformatics - Scope and Applications of Bioinformatics - Fields related to Bioinformatics - Emerging areas of Bioinformatics - Introduction to Biological Databases - Classification of Databases - Nucleotide sequence databases - Protein sequence databases - Protein structure databases - Introduction to Bibliographic Databases - OMIM (Online Mendelian Inheritance in Man) – PubMed Lab Exercise: Perform a literature search on a specific genetic disorder using PubMed. Identify relevant research articles, analyze the information, and summarize the key findings. Retrieval of sequence and structure information from databases.

UNIT 2 FORMATS AND VISUALIZATION

12 Hrs.

Sequence file formats - Sequence submission: Bankit and Sequin macrosend - Visualization of biomolecules – RASMOL - SWISS PDB viewer PyMOL Lab Exercise: Download a protein structure file from the Protein Data Bank (PDB) and visualize it using PyMOL. Explore different visualization options and analyze the protein's structure.

UNIT 3 SEQUENCE COMPARISON

12 Hrs.

Sequence comparison and alignment - Global and local alignments - Pairwise and multiple sequence alignment - Tools for sequence alignment – Needle – Water - Scoring matrices - Basics of database similarity search - Homology search: BLAST algorithm and modules - FASTA algorithm and modules
Lab Exercise: Perform a pairwise sequence alignment using the Needle program. Analyze the alignment results and identify conserved regions and gaps.

UNIT 4 MULTIPLE SEQUENCE ALIGNMENT AND PHYLOGENETIC ANALYSIS

12 Hrs.

Steps and algorithms for multiple sequence alignment - Phylogenetic analysis: terms and concepts - Relationship between multiple sequence alignment and phylogenetic analysis - Phylogenetic trees - Steps in phylogenetic tree construction.

Lab Exercise: Construct a phylogenetic tree using a multiple sequence alignment dataset. Use a tool such as MEGA or ClustalW, analyze the tree topology, and interpret the evolutionary relationships among the sequences.

UNIT 5 DNA AND PROTEIN ANALYSIS

12 Hrs.

Feature identification of DNA - Gene finding - Restriction site analysis - ORF prediction - SNP identification - Primer designing - Introduction to protein structure - Secondary structure prediction - Tertiary structure prediction - Domain identification using PROSITE.

Lab Exercise: Design primers for a specific DNA sequence using online primer design tools. Check for potential secondary structures and optimize the primer parameters to ensure efficient PCR amplification.

Max.60 Hrs.

COURSE OUTCOMES:

On completion of the course the student will be able to

- C01** - Understand bioinformatics fundamentals, including its definition, scope, and emerging areas.
- C02** - Apply bioinformatics tools and techniques for analyzing biological data and performing sequence alignments.
- C03** - Effectively use biological and bibliographic databases for retrieving and analyzing information.
- C04** - Proficiently visualize biomolecules using relevant software and tools.
- C05** - Develop critical thinking skills to interpret bioinformatics results and solve practical problems in biology and medicine.
- C06** - Apply bioinformatics techniques for DNA and protein analysis, including feature identification, gene finding, restriction site analysis, ORF prediction, SNP identification, primer designing, and domain identification using PROSITE.

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. Baxeavanis and B. F. Francis Ouellette (Wiley-Blackwell, 2004).
5. Essential Bioinformatics by Jin Xiong (Cambridge University Press, 2006).

SBIA2101	CELL AND MOLECULAR BIOLOGY LAB	L	T	P	EL	Credits	Total Marks
		0	0	4	0	2	100

LIST OF EXPERIMENTS

1. Light Microscopy
2. Simple staining
3. Studying plant cell (Onion cells)
4. Isolation of Plant Genomic DNA / bacterial genomic DNA
5. Estimation of DNA/RNA content in the given sample by spectrophotometer
6. Determination of T_m of DNA.
7. Agarose gel electrophoresis
8. Poly acrylamide gel electrophoresis
9. Staining of DNA with ethidium bromide
10. Staining of proteins with Coomassie brilliant blue/ silver

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

SHSB1201	GENERAL ENGLISH- II	L	T	P	EL	Credits	Total Marks
		3	0	0	0	3	100

COURSE OBJECTIVES

- To provide opportunities for the students to read and respond to representations of current issues through texts that present themes and topics that are familiar, insightful and informative.
- To provide an opportunity to the students to improve their vocabulary.
- To develop skills relating to creative writing.
- To provide an opportunity to the students to improve their Spoken Language.
- To comprehend the overall idea of a written and oral context.

UNIT 1**9 Hrs.**

Listening for details, Speaking - making a presentation, reading for details and Global Comprehension. Vocabulary Binomials, Types of Words- Synonyms, Antonyms that describe people, things and their actions - Paired Expressions -Letter Writing - Informal Letters- Letter to a Friend / Family Members - Creating blogs to post written materials.

UNIT 2**9 Hrs.**

Listening for details - Speaking: Giving Interview, Public Speech based on specific topics given. Reading for Comprehension and for overall idea - Vocabulary: phrases - Sentence Pattern – Contextual guessing of words– Singular, Plural– Letter writing- Formal letters- Inviting dignitary for a function, Application for job with resume.

UNIT 3**9 Hrs.**

Listening for details - Telephonic conversation – Speaking: Narrating a Story - Vocabulary: positive and negative connotations - Language Focus: Adjective- Degrees of Comparison, Direct and Indirect Speech - Types of Sentences (simple, compound, complex) - Collocations -Letter to the Editor (Social Issues) – Hints Development.

UNIT 4**9 Hrs.**

Listening for Overall information - Making requests and suggestions - Speaking: Group Discussion - Vocabulary: Homonyms and Homophones - Language Focus: Transitive and Intransitive verbs - Writing: Precis writing, Story Writing - Process description (Flow chart).

UNIT 5**9 Hrs.**

Listening for specific details - Speaking using imagination. Reading to identify facts - Language focus: Modal Auxiliary Verbs Writing: Imaginative writing by predicting, Argumentative Essay, Writing a Book or Film review. Vocabulary: Countable and Uncountable Nouns, foreign nouns and framing of plurals.

Max.45 Hrs.**COURSE OUTCOMES:**

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

- CO1** - Remember knowledge of linking words related to both spoken and written discourse.
- CO2** - Understand collocations, words to express one's point of view in both writing and speaking.
- CO3** - Apply the rules for writing compare and contrast paragraphs by using cohesive devices based on prompts given.
- CO4** - Analyze critical thinking skills by framing questions related to elements of reasoning.
- CO5** - Evaluate written pieces to self-correct in the topic areas of verbs, reported speech, and punctuation.
- CO6** - Equip the students with the required Professional Skills.

TEXT / REFERENCE BOOKS:

1. Sen S, Mahendra et al. (2015) Communication and Language Skills. Foundation books. Chennai.

REFERENCES

1. Strunk Jr., William, and E.B. White. The Elements of Style. Allyn and Bacon, 2000.
2. Murphy, Raymond. English Grammar in Use. Cambridge University Press, 2019.
3. Thomson, A.J., and A.V. Martinet. A Practical English Grammar. Oxford University Press, 2013.
4. Straus, Jane. The Blue Book of Grammar and Punctuation. John Wiley & Sons, 2014.
5. Swan, Michael. Practical English Usage. Oxford University Press, 2016.

END SEMESTER EXAM QUESTION PAPER PATTERN**Max. Marks: 100****Exam Duration: 3 Hrs.****PART A:** 10 Questions of 2 marks each uniformly distributed – No choice**20 Marks****PART B:** 2 Questions from each unit of internal choice, each carrying 16 marks**80 Marks**

SMTB1207	MATHEMATICAL FOUNDATIONS FOR BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		3	0	0	0	3	100

COURSE OBJECTIVES

- The Objective of this Course is to identify, reflect upon, evaluate and achieve conceptual understanding and knowledge of traditional Calculus to form independent judgements.
- The purpose of this course is for modelling the biological problems and obtaining its solutions mathematically.
- This helps in understanding and solving Problems in Biological Science, Engineering analytically and logical thinking is attained.

UNIT 1 MATRICES**9 Hrs.**

Matrix Algebra- Row reduces echelon form of a matrix-System of linear equations-Consistency and inconsistency of linear system of equations-eigen values and eigen vectors of a matrix.

UNIT 2 NUMERICAL LINEAR ALGEBRA**9 Hrs.**

Solution of transcendental equations- Newton Raphson method- Solution of linear system of equations-Gauss. Elimination method- Iterative methods-Gauss Jordan and Gauss Seidal method.

UNIT 3 SETS RELATIONS AND FUNCTIONS**9 Hrs.**

Introduction to set theory, set relations, set operators, cardinality of sets, Cartesian product of sets Fundamentals of functions – range, domain, injection, surjection, bijection of functions Fundamentals of relations, reflexive, symmetric and transitive properties in relations, representing relations, applications of relations, equivalence relations, partial order relations.

UNIT 4 BOOLEAN ALGEBRA**9 Hrs.**

Lattices - Boolean Identities – Atomic Boolean Algebra – Boolean Functions – Simplification of Boolean Functions.

UNIT 5 GRAPH THEORY**9 Hrs.**

Introduction to Graphs – directed and undirected graphs, handshaking theorem-Graph Terminology – Cycles – Paths – Complete and Bipartite Graphs – Matrix Representation of Graphs – Graph Isomorphism – Connectivity. – Trees – Euler and Hamiltonian Graphs.

Max.45 Hrs.**COURSE OUTCOME**

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

- CO1** - Evaluate consistency and inconsistency of system of linear equations.
- CO2** - Formulate numerical solution of transcendental and simultaneous linear equations.
- CO3** - Explain the concept of set theory.
- CO4** - Understand Boolean operations to equivalent truth tables and logic networks. **CO5** Develop Euler, Hamiltonian paths. Identify graph isomorphism.
- CO5** - Analyze the generality of tree, binary tree and tree expression.

TEXT / REFERENCE BOOKS:

1. Tremblay. S. Manohar. R. Discrete mathematics structure with application to computer science, McGraw-Hill, 2017.
2. Kenneth H. Rosen, Discrete mathematics and its applications, 6th Edition, McGraw-Hill, 2016.
3. Venkataraman, Dr. M. K., Dr. N. Sridharan and N. Chandrasekaran, Discrete Mathematics. Chennai: The National Publishing Company, 2004.
4. Kandaswamy P & Co., Numerical Methods, S.Chand Publications, Chennai. 2009.

5. E.Balagurusamy, Numerical Methods, McGraw-Hill Education, 2017
6. Veerarajan. T, Engineering Mathematics for First Year, Tata McGraw Hill Publishers, II Edition, 2008.

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100

Exam Duration: 3 Hrs.

PART A: 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B: 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB1201	BIOMOLECULAR STRUCTURES AND INTERACTIONS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To train students to appreciate the salient features of biomolecules in the organization of life.
- To provide explanation related to the classification, functions and application aspects of biomolecules.
- To make students recognize the structure and importance of various biomolecules.
- To understand chemical properties, structure and function of Lipids, Proteins, carbohydrates.
- To realize the interactions in biomolecules and their significance in functionality.

UNIT 1 PROTEINS**9 Hrs.**

Amino acids: Structure and classification- essential and non-essential amino acids, protein and non-protein amino acids, Zwitter ions. Proteins: Classification, Structure: primary, secondary, tertiary and quaternary, biological significance. Concept of isoelectric point and its significance.

UNIT 2 NUCLEIC ACIDS**9 Hrs.**

Nucleic Acids: Nitrogenous bases - Purines and Pyrimidines - Nucleoside, Nucleotides. - Structure of nucleic acids - DNA, RNA: m-RNA, t-RNA, r-RNA - Biological importance of nucleic acids.

UNIT 3 CARBOHYDRATES AND LIPIDS**9 Hrs.**

Carbohydrates – Definition, classification. Structure, properties and biological functions of monosaccharides, disaccharides, oligosaccharides and polysaccharides. Lipids – definition, nomenclature of fatty acids. Biological significance and classification of lipids. Simple lipids: triglycerides, waxes, steroids, prostaglandins, Compound lipids: Phospholipids, sphingolipids, glycolipids and lipoproteins.

UNIT 4 BIOMOLECULAR INTERACTIONS**9 Hrs.**

Interaction: Types- Columbic forces, dipole interactions, hydrogen bonds and hydrophobic interactions. Interactions stabilizing DNA and protein structures.

UNIT 5 MACROMOLECULAR STRUCTURE DETERMINATION**9 Hrs.**

Principle, Techniques and applications of X-ray Diffraction, Nuclear Magnetic Resonance, Mass Spectrometry, Electron microscopy - Cryo electron microscopy.

Max.45 Hrs.**COURSE OUTCOMES:**

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

- CO1** - Understand the structural complexity of proteins.
- CO2** - Comprehend the detailed structure of nucleic acids.
- CO3** - Familiar with carbohydrates and lipids including their structure and classification.
- CO4** - Appreciate the interactions between molecules at the atomic level.
- CO5** - Summarize on the experimental techniques involved in structure determination.
- CO6** - Understand the principles and working of instruments for structure determination.

TEXT BOOKS/REFERENCE BOOKS

1. Biochemistry 9th Edition by Lubert Stryer W.H. Freeman; 9th edition (January 1, 2019).
2. Lehninger Principles of Biochemistry 8th Edition by David L. Nelson W.H. Freeman; 8th edition (January 1, 2021).
3. Harper's Illustrated Biochemistry McGraw Hill / Medical; 32nd edition (11 August 2022).

4. Biochemistry, 6e Satyanarayana Elsevier; 6th edition (1 January 2021).
5. Biomolecular Interactions Part A Part 1 Arun K. Shukla Elsevier Science 2021.

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100

Exam Duration: 3 Hrs.

PART A: 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B: 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

S738BLH22	PROBLEM SOLVING TECHNIQUES USING C	L	T	P	EL	Credits	Total Marks
		2	0	2	2	4	100

COURSE OBJECTIVES

- To introduce students to the fundamental concepts of computer architecture, focusing on bits and bytes.
- To develop students' understanding of the C programming language and its mathematical operations.
- To enhance students' programming skills with C for instant output and problem-solving.
- To educate students on managing homogenous data using C arrays.
- To train students in handling heterogenous data in C using structures and unions.

UNIT 1 BITS AND BYTES IN COMPUTING**12 Hrs.**

Introduction to Computer Architecture, Binary System, Bitwise Operations, Data Types and Size, Memory Representation of Types in C, Application of Bitwise Operations in Genetic Sequence Analysis.

PRACTICE PROGRAMS:

1. Write a C program to demonstrate bitwise operations.
2. Create a C program to convert decimal numbers to binary and vice versa.
3. Implement a C program to encode nucleotide bases (A, T, C, G) using binary representation.

UNIT 2 C: MATH BEHIND CODING**12 Hrs.**

C Arithmetic Operators, Operator Precedence and Associativity, Mathematical Functions in C, Applications of Mathematics in Coding, Statistical Methods for Bioinformatics in C.

PRACTICE PROGRAMS:

1. Write a C program to solve quadratic equations.
2. Create a C program to calculate the area of various geometrical shapes based on user input.
3. Write a C program to calculate the mean and standard deviation of a set of gene expression values.

UNIT 3 C: MAGIC BEHIND INSTANT OUTPUTS**12 Hrs.**

Control Statements in C, Loops, Functions, Recursion, Time Complexity Analysis, Techniques for Efficient Coding, Efficient Algorithms in Bioinformatics.

PRACTICE PROGRAMS:

1. Write a C program to print the Fibonacci series up to n terms using recursion.
2. Create a C program to find the factorial of a number using a loop and by using recursion.
3. Compare their time efficiency.
4. Develop a C program to implement a simple sequence alignment algorithm.

UNIT 4 STORING GROUP OF HOMOGENOUS ELEMENTS: ARRAYS**12 Hrs.**

Arrays in C, Multidimensional Arrays, Dynamic Memory Allocation for Arrays, Array Operations (Insertion, Deletion, Searching, Sorting), Storage and Retrieval of Biological Sequences using Arrays.

PRACTICE PROGRAMS:

1. Write a C program to perform matrix operations (addition, subtraction, multiplication) using multidimensional arrays.
2. Create a C program to implement a simple dynamic array that allows insertions and deletions.
3. Write a C program to store a DNA sequence in an array and implement a function to search for a specific subsequence.
- 4.
- 5.

UNIT 5 STORING GROUP OF HETEROGENOUS ELEMENTS: STRUCTURES 12 Hrs.
AND UNIONS

Structures and Unions in C, Nested Structures, Dynamic Memory Allocation for Structures, Array of Structures, Applications of Structures and Unions, Managing Biological Data Using Structures.

Max.60 Hrs.

PRACTICE PROGRAMS:

1. Write a C program to store and display information (roll number, name, marks) of a student using structures.
2. Create a C program to demonstrate the use of union by creating a union containing 5 names and display them.
3. Implement a C program to store and display information of a gene (gene ID, gene name, sequence, etc.) using structures.

COURSE OUTCOMES:

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

- CO1** - Understand the concept of bits and bytes in computing and their manipulation in C programming.
- CO2** - Gain proficiency in mathematical operations and functions in C for problem-solving.
- CO3** - Master the use of control statements, loops, and functions in C for instant output and efficient coding.
- CO4** - Handle homogenous data effectively using arrays in C, with knowledge of various array operations.
- CO5** - Manage heterogenous data using structures and unions in C, with understanding their memory usage.
- CO6** - Develop problem-solving skills using C, with an emphasis on real-world bioinformatics and data science problems.

REFERENCE BOOKS:

1. Deitel, P. J., & Deitel, H. M. (2015). "C How to Program", 8th Edition, Pearson.
2. Kernighan, B. W., & Ritchie, D. M. (1988). "The C Programming Language", 2nd Edition, Prentice Hall.
3. King, K. N. (2008). "C Programming: A Modern Approach", 2nd Edition, W. W. Norton & Company.
4. Griffiths, D., & Griffiths, D. (2018). "Head First C: A Brain-Friendly Guide", 1st Edition, O'Reilly Media.
5. Prata, S. (2013). "C Primer Plus", 6th Edition, Addison-Wesley Professional.
6. Zambetta, F. (2022). "Problem Solving and Program Design in C", 9th Edition, Pearson.
7. Gustedt, J. (2019). "Modern C", 1st Edition, Manning Publications.
8. Reema Thareja (2021). "Data Structures Using C", 2nd Edition, Oxford University Press.

SBIB2201	BIOCHEMISTRY LAB	L	T	P	EL	Credits	Total Marks
		0	0	4	0	2	100

LIST OF EXPERIMENTS

1. Units, amounts and concentrations
2. Working principle of pH meter and its calibration
3. Working principle and standardization of colorimeter
4. Working principle of centrifuge
5. Preparation of buffer of given pH and molarity
6. Qualitative analysis of carbohydrates
7. Qualitative analysis of carbohydrates
8. Estimation of protein by Lowry's method

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

SBIB1301	SYSTEMS BIOLOGY	L	T	P	EL	Credits	Total Marks
		3	0	0	4	4	100

COURSE OBJECTIVES

- Develop a foundational understanding of systems biology and its interdisciplinary nature in studying complex biological systems.
- Acquire skills in mathematical modeling techniques and their applications in systems biology research.
- Gain proficiency in analyzing biological networks and understanding their properties in the context of complex systems.
- Learn techniques for generating and quality controlling high-throughput omics data, and integrate diverse omics data to reveal biological processes and disease mechanisms.
- Explore the applications of systems biology in drug discovery and personalized medicine, and understand its role in studying complex diseases and identifying therapeutic targets.

UNIT 1 INTRODUCTION TO SYSTEMS BIOLOGY**9 Hrs.**

Introduction to Systems Biology - Interdisciplinary nature - Biological networks (gene regulatory, protein-protein interaction, metabolic) - role in understanding complex systems - emergent properties, feedback loops, system dynamics.

UNIT 2 MATHEMATICAL MODELING IN SYSTEMS BIOLOGY**9 Hrs.**

Introduction - Mathematical equations to describe biological system behavior, Dynamic modeling approaches (differential equations, Boolean networks, agent- based models), Parameter estimation and model calibration, Simulation and analysis for insights and predictions.

UNIT 3 NETWORK ANALYSIS IN SYSTEMS BIOLOGY**9 Hrs.**

Analysis of Biological Networks, Gene regulatory, protein-protein interaction, and metabolic networks, Network topology and properties (degree distribution, centrality measures, clustering coefficients), Identification of network motifs and modules, Network-based pathway analysis and functional interpretation.

UNIT 4 INTEGRATION OF OMICS DATA IN SYSTEMS BIOLOGY**9 Hrs.**

High-throughput Omics Data Generation and Quality Control, Next-generation sequencing and mass spectrometry for genomics, transcriptomics, and proteomics, Pre - processing and quality control for reliable data. - Multi-Omics Data Integration and Analysis, Methods for integrating diverse omics data, Case studies.

UNIT 5 APPLICATIONS OF SYSTEMS BIOLOGY**9 Hrs.**

Systems Biology in Drug Discovery and Personalized Medicine, Computational models and network analysis for effective therapeutics, cellular processes and disease mechanisms. - Systems Biology in Complex Diseases, cancer and neurodegenerative disorders, molecular players and intervention points, Emerging trends and future directions in systems biology research.

Max.45 Hrs.**COURSE OUTCOMES:**

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

CO1 - Understand principles and interdisciplinary nature of systems biology in studying complex biological systems holistically.

CO2 - Apply mathematical modeling techniques to simulate biological processes using differential equations, Boolean networks, and agent-based models.

- C03** - Analyze biological networks (e.g., gene regulatory, protein-protein interaction, metabolic) using network analysis methods.
- C04** - Integrate and analyze multi-omics data to identify patterns, functional modules, and potential biomarkers
- C05** - Evaluate scientific literature, recognizing research methodologies and emerging trends in systems biology.
- C06** - Communicate effectively about complex biological systems and their analysis using systems biology approaches, both orally and in writing.

TEXT / REFERENCE BOOKS

1. Systems Biology: A Textbook - Edda Klipp, Wolfram Liebermeister, Christoph Wierling, and Axel Kowald (Wiley-VCH, 2009).
2. Introduction to Systems Biology - Uri Alon (Chapman and Hall/CRC, 2019)
3. Systems Biology: Simulation of Dynamic Network States - Bernhard Ø. Palsson (Cambridge University Press, 2015).
4. Systems Biology: Constraint-Based Reconstruction and Analysis - Bernhard Ø. Palsson (Cambridge University Press, 2015).
5. Computational Systems Biology - Andres Kriete and Roland Eils (Academic Press, 2019).

END SEMESTER EXAM QUESTION PAPER PATTERN**Max. Marks: 100****Exam Duration: 3 Hrs.****PART A:** 10 Questions of 2 marks each uniformly distributed – No choice**20 Marks****PART B:** 2 Questions from each unit of internal choice, each carrying 16 marks**80 Marks**

SBIB1302	ALGORITHMS IN BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		3	0	0	4	3	100

COURSE OBJECTIVES

- Understand the fundamental principles and applications of bioinformatics in molecular biology, including the role of algorithms in solving biological problems and analyzing biological data.
- Gain proficiency in algorithmic approaches for identifying regulatory patterns in DNA, analyzing genome assembly using graph algorithms, and understanding the process of DNA replication.
- Develop skills in sequence comparison and alignment techniques, including dynamic programming, pairwise sequence comparison, and alignment algorithms.
- Learn about evolutionary tree reconstruction, phylogenetic algorithms, and their application in understanding the evolutionary relationships between organisms.
- Explore combinatorial pattern matching algorithms for localization and identification of disease-causing mutations, and gain an understanding of Hidden.
- Markov Models and their application in HIV research and vaccine development challenges.

UNIT 1 INTRODUCTION TO BIOINFORMATICS AND BASIC MOLECULAR BIOLOGY

9 Hrs.

Introduction to Bioinformatics and its applications in molecular biology - Overview of DNA replication and identification of replication origins using algorithmic approaches.

UNIT 2 REGULATORY PATTERN FINDING AND GRAPH ALGORITHMS

9 Hrs.

Identification and analysis of regulatory patterns in DNA using greedy and randomized algorithms - Introduction to graph algorithms in genome assembly.

UNIT 3 SEQUENCE COMPARISON AND ALIGNMENT

9 Hrs.

Introduction to dynamic programming and its role in comparing biological sequences - Algorithmic techniques for sequence alignment and pairwise sequence comparison.

UNIT 4 EVOLUTIONARY TREE RECONSTRUCTION AND CLUSTERING ALGORITHMS

9 Hrs.

Reconstruction of evolutionary trees and identification of the source animal for SARS using phylogenetic algorithms - Analysis of yeast evolution and the role of clustering algorithms in understanding yeast as a wine-maker.

UNIT 5 COMBINATORIAL PATTERN MATCHING AND HIDDEN MARKOV MODELS (HMM 'S)

9 Hrs.

Localization and identification of disease-causing mutations using combinatorial pattern matching algorithms - Introduction to Hidden Markov Models and their application in understanding HIV and vaccine development challenges.

Max.45 Hrs.

COURSE OUTCOMES:

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

- CO1** - Understand the fundamental concepts of algorithms and their relevance in bioinformatics.
- CO2** - Analyze the computational complexity of bioinformatics problems and design efficient algorithms to solve them.
- CO3** - Apply sequence alignment algorithms to compare and analyze biological sequences.
- CO4** - Design and implement algorithms for gene finding, genome annotation, and phylogenetic tree reconstruction.

CO5 - Utilize algorithms for protein structure prediction, analysis, and molecular interactions.

CO6 - Evaluate and interpret the results of bioinformatics algorithms and effectively communicate findings.

TEXT / REFERENCE BOOKS

1. Algorithms in Bioinformatics: A Practical Introduction - Wing-Kin Sung (CRC Press, 2019)
2. Bioinformatics Algorithms: An Active Learning Approach - Phillip Compeau, Pavel Pevzner (Active Learning Publishers, 2014)
3. Introduction to Computational Biology: An Evolutionary Approach - Bernhard Haubold, Thomas Wiehe (Springer, 2020)
4. Bioinformatics Algorithms: Techniques and Applications - Ion Mandoiu, Alexander Zelikovsky (Wiley, 2018)
5. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids - Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme Mitchison (Cambridge University Press, 1998)

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B : 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB1303	GENOMICS AND PROTEOMICS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To learn different aspects of genome and proteome and their applications in current times.
- To provide the knowledge and practical skills of functional genomics and proteomics.
- To teach students the techniques used such as sequencing and mapping.
- To enable students to understand the concepts in interaction proteomics.
- To familiarize students with omics concepts and their applications in medical research.

UNIT 1 GENOME STRUCTURE**9 Hrs.**

Overview- Structure and organization of Prokaryotic and eukaryotic genome - concept of central dogma. DNA sequencing – Generations of sequencing: First generation, Second generation, third generation and fourth generation sequencing.

UNIT 2 GENOME MAPPING**9 Hrs.**

Genome mapping: Markers, Genetic mapping – RFLP, SSLP, SNPs. Physical Mapping – FISH, Restriction mapping, STS mapping. Gene expression studies: DNA microarrays, Genome projects – objectives- Human genome project. Genome databases.

UNIT 3 PROTEOME STUDY**9 Hrs.**

Introduction to Proteomics - Proteomics Vs Genomics - Completed Proteome projects and their significance. Human proteome project. Proteomic Technologies - Protein separation technologies: 2D-PAGE for proteome analysis, affinity chromatography, Protein detection - Protein identification and characterization: Mass spectrometry. Proteome databases.

UNIT 4 INTERACTION PROTEOMICS**9 Hrs.**

Protein interactions, Protein - Protein interaction techniques: Yeast Two Hybrid System. Protein nucleic acid interactions. Protein expression profiling – protein microarrays. Applications of proteomics in medicine, drug discovery.

UNIT 5 APPLICATIONS OF OMICS CONCEPTS**9 Hrs.**

Pharmacogenomic studies and Comparative genomics, Transcriptome analysis, Genome editing. Metabolomics studies in health and disease, Proteomics Applications in Health: Biomarker and Drug Discovery and Food Industry. Integrative omics for health and disease.

Max.45 Hrs.**COURSE OUTCOMES:**

On completion of the course the student will be able to

- CO1** - Understand the genome structure and sequencing techniques.
- CO2** - Comprehend the mapping of genomes using markers.
- CO3** - Familiar with proteome characterization using experimental techniques.
- CO4** - Appreciate the interactions between proteins and the methods to study interactions.
- CO5** - Summarize various omics concepts in recent times.
- CO6** - Understand the applicability of these omics' concepts in health and medicine.

TEXT BOOKS/REFERENCE BOOKS

1. Genomics and Proteomics: Functional and Computational Aspects by Miguel Rudolph Syrawood Publishing House (June 10, 2019).

2. Bioinformatics: methods and applications: (Genomics, Proteomics and Drug Discovery) 4th Edition PHI Learning; 4th edition (May 22, 2013).
3. Genomics and Proteomics Principles, Technologies, and Applications Devarajan Thangadurai, Jeyabalan Sangeetha Apple Academic Press 2015.
4. Cytogenetics and Molecular Cytogenetics (Molecular Genomics and Proteomics) 1st Edition by Thomas Liehr CRC Press; 1st edition (December 7, 2022).
5. Principles of Genomics and Proteomics by Rakeeb Ahmad Mir, Sheikh Mansoor Shafi, Sajad Majeed Zargar Elsevier (January 25, 2023).

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B : 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

S738BLH33	PYTHON PROGRAMMING	L	T	P	EL	Credits	Total Marks
		2	0	0	2	2	100

COURSE OBJECTIVES

- To introduce students to the basic principles and concepts of bioinformatics and data science.
- To provide a thorough understanding of Python programming and its application in data handling and analysis.
- To train students on using Python to work with various data types, data structures and file handling techniques.
- To familiarize students with the concept of Object-Oriented Programming (OOP) and Graphical User Interface (GUI) creation in Python.
- To apply the learned programming concepts in solving real-world bioinformatics problems.

UNIT 1 INTRODUCTION**12 Hrs.**

Basics of Bioinformatics, Role of Data Science in Bioinformatics, Python Programming Basics, Introduction to Python Libraries for Data Science such as Pandas, Numpy, and Scikit-learn.

PRACTICE PROGRAMS:

1. Write a Python program to calculate the GC content of a DNA sequence.
2. Create a Python script to load a CSV file using Pandas and display the first five records.

UNIT 2 FUNCTIONS AND STRINGS**12 Hrs.**

Python Functions, String Manipulation, Regular Expressions, Error Handling, Lambda Functions, Recursion, Function Decorators.

PRACTICE PROGRAMS:

1. Write a Python function to reverse complement a DNA sequence.
2. Create a Python function to validate an email address using Regular Expressions.

UNIT 3 LIST, TUPLES, AND DICTIONARIES**12 Hrs.**

Lists, Tuples, Dictionaries, List Comprehensions, Dictionary Comprehensions, Iterating over data structures, Sorting, Indexing and Slicing.

PRACTICE PROGRAMS:

1. Write a Python program to store gene expression data in a dictionary and retrieve values based on the gene name.
2. Create a Python script to calculate the frequency of amino acids in a protein sequence using lists and dictionaries.

UNIT 4 FILES AND REGULAR EXPRESSIONS**12 Hrs.**

File Handling, Reading and Writing Files, JSON data, CSV data, XML data, Regular Expressions, Pattern Matching, Searching, Substituting, Parsing Biological Data Files.

PRACTICE PROGRAMS:

1. Write a Python script to parse a FASTA file and output the sequence ID and sequence length.
2. Create a Python script using Regular Expressions to extract all protein-coding gene names from a GenBank file.

UNIT 5 CREATING GUI FORM, CLASSES, AND OBJECTS**12 Hrs.**

Introduction to OOP, Classes and Objects, Inheritance, Polymorphism, Encapsulation, GUI Programming in Python, Event-Driven Programming, Tkinter Library.

PRACTICE PROGRAMS:

1. Write a Python program to implement a class 'DNA', with methods for calculating GC content and reverse complement.
2. Create a Python GUI application using Tkinter to enter a DNA sequence and display its reverse complement and GC content.

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 significance in data science.
- CO2** - Acquire proficiency in Python programming for data analysis and manipulation.
- CO3** - Master the utilization of data structures like lists, tuples, and dictionaries in Python for complex data handling.
- CO4** - Gain skills in file handling and the usage of regular expressions for biological data parsing and processing.
- CO5** - Comprehend the principles of object-oriented programming and use it in the development of bioinformatics software applications.
- CO6** - Develop graphical user interface forms using Python for interactive data input and output in bioinformatics applications.

REFERENCE BOOKS:

1. Zelle, J. (2017). "Python Programming: An Introduction to Computer Science", 3rd Edition, Franklin, Beedle & Associates Inc.
2. Sweigart, A. (2015). "Automate The Boring Stuff With Python", 1st Edition, No Starch Press.
3. McKinney, W. (2017). "Python for Data Analysis", 2nd Edition, O'Reilly Media.
4. Mount, D. (2004). "Bioinformatics: Sequence and Genome Analysis", 2nd Edition, Cold Spring Harbor Laboratory Press.
5. Pevsner, J. (2015). "Bioinformatics and Functional Genomics", 3rd Edition, Wiley-Blackwell.
6. Baker, M. (2021). "Python for Biologists: A complete programming course for beginners", 2nd Edition, CreateSpace Independent Publishing.
7. Bassi, S. (2021). "Bioinformatics for Evolutionary Biologists: A Problems Approach", 1st Edition, Springer.
8. Talele, T. (2022). "Python Machine Learning in Bioinformatics", 1st Edition, Springer.
9. Sefer, E. (2023). "Bioinformatics Algorithms: Design and Implementation in Python", 1st Edition, Wiley.
10. Via, A. (2023). "Bioinformatics and Data Analysis in Python: A Practical Handbook for the Life Sciences", 1st Edition, Cambridge University Press.
11. <https://www.python.org/>

SBIB2301	SYSTEMS BIOLOGY LAB	L	T	P	EL	Credits	Total Marks
		2	0	0	0	2	100

LIST OF SUGGESTED EXPERIMENTS

1. Network Analysis: Analyzing Gene Regulatory Networks
2. Mathematical Modeling: Simulating Metabolic Pathways
3. Omics Data Integration: Integrating Genomics and Transcriptomics Data
4. Systems Biology Visualization: Visualizing Protein-Protein Interaction Networks
5. Biological Pathway Analysis: Identifying Key Pathways in Disease Processes
6. Parameter Estimation: Calibrating Mathematical Models to Experimental Data
7. Dynamical Modeling: Investigating Oscillatory Behavior in Gene Networks
8. Drug Target Identification: Applying Systems Biology Approaches to Identify Potential Therapeutic Targets

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

SBIB1402	MICROBIOME AND METAGENOMICS	L	T	P	EL	Credits	Total Marks
		3	0	0	4	4	100

COURSE OBJECTIVES

- This course provides an in-depth exploration of microbiome research and metagenomics.
- Data analysis module focusing on the analysis of microbial communities and their genetic material.
- Students will learn the underlying principles, techniques, and tools used in microbiome and metagenomic studies and gain hands-on experience with data analysis and interpretation.

UNIT 1 INTRODUCTION TO MICROBIOME**9 Hrs.**

Historical overview: from microorganisms to microbiomes; definition and composition of term microbiome; microbiota: bacteria, archaea, fungi, protist, algae, virus; concept of holobiont; hologenome theory; functions of microbiome.

UNIT 2 GENERATING MICROBIOME DATA**9 Hrs.**

History of sequencing technologies: first, second and third generations; Amplicon (gene marker) sequencing, shotgun metagenomics, whole genome sequencing.

UNIT 3 MICROBIOME DATA ANALYSIS**9 Hrs.**

Pre-processing of data, assembly, taxonomic and functional annotation; useful web servers and tools for data analysis; metadata; key terms: alpha and beta diversity, dysbiosis, rarefaction, core microbiome, phylogenetics and phylogenomics.

UNIT 4 HUMAN MICROBIOME**9 Hrs.**

Human microbiome project; Oral microbiome; Gut microbiome; infectious disease and host microbiome; Viromes and human health, impact of antibiotics on human microbiome, microbiome engineering.

UNIT 5 METAGENOMICS APPLICATION**9 Hrs.**

Metagenomics for i) prevention and control of environmental pollution, ii) pathogenic microbes; iii) biodiscovery; iv) agriculture. Key microbiome projects: earth microbiome projects, Tara Oceans, Indian soil microbiome project; Major stakeholders in metagenomics; Metagenomics and the convention on biological diversity; Biosafety and IPR issues in metagenomics.

Max.45 Hrs.**COURSE OUTCOMES:**

On completion of the course the student will be able to

- CO1** - Understand the basic principles and concepts of microbiome research and metagenomics, including the composition and ecological significance of microbial communities.
- CO2** - Gain proficiency in sample collection techniques for microbiome studies and DNA extraction methods for isolating microbial DNA from different environmental samples.
- CO3** - Familiarize themselves with different metagenomic sequencing technologies and their applications in studying microbial communities.
- CO4** - Develop skills in metagenomic data analysis, including preprocessing, quality control, taxonomic profiling, functional annotation, and comparative analysis of microbial communities.
- CO5** - Analyze and interpret metagenomic data to identify taxonomic composition, functional potential, and ecological relationships within microbial communities.
- CO6** - Understand the interactions between the microbiome and the host organism, including the role of the microbiome in human health and disease.

TEXT /REFERENCE BOOKS:

1. "Metagenomics in Microbiology" edited by Charles Thomas Parker (2017).
2. "The Gut Microbiome: Implications for Human Disease" edited by Gyorgy Abel (2018).

3. "Microbiome Analysis: Advances, Methods, and Applications" edited by Yiming Yang (2019).
4. "Metagenomics: Methods and Protocols" edited by Mark Tangney and George A. O'Toole (2020).
5. "The Human Microbiome Handbook" edited by Jia V. Li and Jun Wang (2021).

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B : 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SB1B1402	MATLAB FOR BIOLOGICAL DATA ANALYSIS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- The objective of this course is to provide undergraduates studying bioinformatics with a solid foundation in using Matlab for analyzing and visualizing biological data.
- The course aims to equip students with the necessary skills to efficiently process, analyze, and interpret biological datasets using Matlab.

UNIT 1 INTRODUCTION TO MATLAB FOR BIOLOGICAL DATA ANALYSIS 9 Hrs.

Introduction to Matlab as a programming and analysis tool for biological data - Understanding the Matlab environment, syntax, and basic data types - Importing, exporting, and manipulating biological data in Matlab.

UNIT 2 DATA VISUALIZATION AND EXPLORATION 9 Hrs.

Visualization techniques for biological data, including plotting functions and customizing plots in Matlab - Exploratory data analysis methods, such as histograms, scatter plots, and box plots - Interactive data exploration using Matlab's graphical user interface (GUI) features.

UNIT 3 STATISTICAL ANALYSIS IN MATLAB 9 Hrs.

Introduction to statistical analysis techniques for biological data in Matlab - Descriptive statistics, hypothesis testing, and statistical inference using built-in functions and toolboxes in Matlab - Linear regression, ANOVA, and other statistical modeling techniques in Matlab.

UNIT 4 IMAGE PROCESSING AND ANALYSIS 9 Hrs.

Fundamentals of image processing and analysis using Matlab - Image enhancement, filtering, and segmentation techniques in Matlab - Quantitative analysis of biological images and feature extraction.

UNIT 5 BIOINFORMATICS APPLICATIONS WITH MATLAB 9 Hrs.

Sequence analysis using Matlab, including sequence alignment and motif discovery - Gene expression analysis and microarray data processing in Matlab - Network analysis and pathway enrichment analysis using Matlab toolboxes.

Max.45 Hrs.**COURSE OUTCOMES:**

On completion of the course the student will be able to

- CO1** - Develop proficiency in using Matlab for biological data analysis tasks.
- CO2** - Apply data visualization techniques in Matlab to explore and interpret biological datasets.
- CO3** - Perform statistical analysis and hypothesis testing on biological data using Matlab.
- CO4** - Apply image processing techniques in Matlab to analyze biological images.
- CO5** - Utilize Matlab for bioinformatics applications, such as sequence analysis and gene expression analysis.
- CO6** - Communicate and present biological data analysis results effectively using Matlab.

TEXT / REFERENCE BOOKS

1. Matlab for Neuroscientists: An Introduction to Scientific Computing in Matlab - Pascal Wallisch, Michael E. Lusignan, Marc D. Benayoun, Tanya I. Baker, Adam Seth Dickey (Academic Press, 2014).
2. Bioinformatics Toolbox User's Guide - MathWorks (MathWorks, Year varies with version).
3. Matlab for Engineers: Applications in Control, Electrical Engineering, IT and Robotics - Clara M. Ionescu (CRC Press, 2019).

4. Data Analysis for the Life Sciences with R - Rafael A. Irizarry, Michael I. Love (Chapman and Hall/CRC, 2019).
5. Introduction to MATLAB for Engineers and Scientists - Sandeep Nagar (Oxford University Press, 2021).

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B : 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

S738BLH44	IMMUNOLOGY AND IMMUNOINFORMATICS	L	T	P	EL	Credits	Total Marks
		2	0	2	2	4	100

COURSE OBJECTIVES

- Understand the key components and functions of the immune system, including innate and adaptive immunity, antigen presentation, and immune cell signaling.
- Explain the mechanisms underlying immune responses, including inflammation, immune memory, and tolerance, and their relevance to health and disease.
- Acquire practical skills in immunological techniques, such as ELISA, flow cytometry, and immunohistochemistry, for experimental analysis in immunology research.
- Explore the field of immunoinformatics and gain knowledge of computational tools and approaches for epitope prediction, antigen selection, and vaccine design.
- Apply immunoinformatics principles to critically analyze and design vaccines, considering factors such as immunogenicity, epitope conservation, and vaccine efficacy.

UNIT 1 INTRODUCTION TO IMMUNOLOGY

12 Hrs.

Overview of the immune system and its components (cells, tissues, organs) - Innate and adaptive immune responses - Major histocompatibility complex (MHC) and antigen presentation - Immunological disorders and diseases.

Lab Exercise: Immune Repertoire Analysis: Analyze immune repertoire sequencing data (e.g., T-cell receptor or B-cell receptor sequences) using tools like IMGT/HighV-QUEST, MiXCR, or VDJtools.

UNIT 2 CELLS AND MOLECULES OF THE IMMUNE SYSTEM

12 Hrs.

Introduction to immune cells (lymphocytes, macrophages, dendritic cells, etc.) and their functions - Antibodies and B cells: structure, antigen recognition, and antibody-mediated immunity - T cells and T cell receptors: activation, effector functions, and T cell-mediated immunity - Complement system and its role in immune responses.

Lab Exercise: Antigen Retrieval and Prediction: Retrieve known antigens from public databases. Predict T-cell epitopes using tools like NetMHC, NetMHCpan, or IEDB epitope prediction tools. B-cell Epitope Prediction: Predict B-cell epitopes within protein sequences using tools like BepiPred, ABCpred, or IEDB B-cell epitope prediction tools.

UNIT 3 IMMUNE RESPONSES AND MECHANISMS

12 Hrs.

Immune signaling and cytokines: communication between immune cells - Inflammation and its role in immune defense and tissue repair - Immune memory and vaccination - Hypersensitivity reactions and immune tolerance - Autoimmunity and immunodeficiency disorders.

Lab Exercises: Allergen databases; Allergen structure prediction, IgE epitope prediction.

UNIT 4 IMMUNOLOGICAL TECHNIQUES AND EXPERIMENTAL METHODS

12 Hrs.

Immunological assays and techniques (ELISA, flow cytometry, western blotting, etc.) - Immunohistochemistry and immunofluorescence for tissue analysis - Animal models and in vitro systems in immunology research - Ethical considerations and experimental design in immunological studies.

Lab exercise: Analyze protein-protein interaction networks involving immune-related molecules using tools like STRING or Cytoscape.

UNIT 5 IMMUNOINFORMATICS AND VACCINE DESIGN

12 Hrs.

Introduction to immunoinformatics and its role in vaccine design - Epitope prediction and antigen selection for vaccine development - Immunogenicity assessment and epitope-based vaccine design - Vaccine informatics databases and tools - Case studies of successful immunoinformatics applications in vaccine development.

Lab exercises: Predict peptide binding to major histocompatibility complex (MHC) molecules using tools like NetMHC, NetMHCpan, or IEDB MHC binding prediction tools.

Max.60 Hrs.

COURSE OUTCOMES:

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

- CO1** - Understand the fundamental principles of immunology, including immune system components and antigen presentation.
- CO2** - Explain the mechanisms of immune responses, including inflammation, immune memory, and tolerance.
- CO3** - Apply practical skills in immunological techniques such as ELISA and flow cytometry.
- CO4** - Utilize immunoinformatics tools for epitope prediction, antigen selection, and vaccine design.
- CO5** - Analyze and interpret immunological data for research and vaccine development.
- CO6** - Design effective vaccines considering immunogenicity, epitope conservation, and efficacy using immunoinformatics principles.

Max.45 Hrs.

TEXT / REFERENCE BOOKS

1. Kuby Immunology by Judy Owen, Jenni Punt, and Sharon Stranford (W.H. Freeman and Company, 2019).
2. Janeway's Immunobiology by Kenneth Murphy, Casey Weaver, and Allan Mowat (Garland Science, 2016).
3. Basic Immunology: Functions and Disorders of the Immune System by Abul Abbas, Andrew H. Lichtman, and Shiv Pillai (Elsevier, 2020).
4. Immunology: A Short Course by Richard Coico and Geoffrey Sunshine (Wiley, 2018)
5. Principles of Immunology by Ivan Roitt, Peter Delves, and Seamus Martin (Wolters Kluwer, 2017).

SBIA2401	MATLAB FOR BIOLOGICAL DATA ANALYSIS LAB	L	T	P	EL	Credits	Total Marks
		0	0	4	0	2	100

MATLAB EXERCISES:**EXERCISE 1: EXPLORATORY DATA ANALYSIS (EDA)**

Load a gene expression dataset and perform basic EDA tasks such as histogram plotting, box plots, and scatter plots to understand the distribution and relationships among different genes.

EXERCISE 2: PRINCIPAL COMPONENT ANALYSIS (PCA)

Implement PCA on a multi-dimensional gene expression dataset to reduce the dimensionality and visualize the data in a lower-dimensional space. Analyze the results and discuss the principal components' importance.

EXERCISE 3: CLUSTERING ANALYSIS

Apply K-means clustering to group genes based on their expression patterns. Evaluate the clustering results using various metrics like silhouette scores and visualize the clusters.

EXERCISE 4: MACHINE LEARNING CLASSIFICATION

Use a machine learning algorithm (e.g., Support Vector Machine, Random Forest) to predict a biological outcome (e.g., disease status) based on gene expression data. Evaluate the model's performance using cross-validation and ROC curves.

EXERCISE 5: DIFFERENTIAL GENE EXPRESSION ANALYSIS

Perform a differential gene expression analysis between two conditions (e.g., control vs. treatment) using tools like limma or DESeq2. Identify significantly upregulated/downregulated genes and visualize the results using heatmaps or volcano plots.

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

SBIB2402	MICROBIOME AND METAGENOMICS LAB	L	T	P	EL	Credits	Total Marks
		0	0	4	4	2	100

LIST OF EXERCISES

1. Output file formats from different sequencers.
2. Data visualization and quality control for microbial amplicon sequence generated through Sanger Sequencer.
3. Exploration of publicly available genome and metagenome databases.
4. Amplicon sequence (16S rRNA) data analysis using MOTHUR- from sequence to annotation
5. Webservers and tools for metagenome sequence analysis.

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

SBIB1501	NEXT GENERATION SEQUENCING	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVE

- To enable student to understand the latest technology in sequencing of DNA.
- To understand NGS technology, algorithms, and data formats.
- To use bioinformatics tools for handling sequencing data and visualization.
- To perform downstream analyses for studying gene expression and genetic variations.
- To realize the utility of NGS in several areas of research.

UNIT 1 INTRODUCTION TO SEQUENCING**9 Hrs.**

Over view of sequencing, Need and applications. Generations in sequencing – first generation sequencing – Sangers method and Maxam Gilbert method. Second generation sequencing –NGS platforms - Roche/454, Illumina/Solexa, Ion torrent, SOLiD system. Third generation sequencing.

UNIT 2 NGS WORKFLOW**9 Hrs.**

Library preparation – Template enrichment – Emulsion and Bridge PCR, Sequencing: NGS platforms; Comparison of NGS platforms. Data analysis- Data acquisition - Reads and quality check, Base calling. Read alignment and refinement, Sequence assembly. Variant calling. File formats used in NGS.

UNIT 3 RNA SEQUENCING**9 Hrs.**

Data acquisition- Read alignment – Transcriptome assembly - Differential expression analysis – Alternative splicing - Allele- specific expression - RNA editing – smRNA.

UNIT 4 CHIP SEQ**9 Hrs.**

Basics on immune precipitation, Types of Chips Seq – XchIP and NChIP. Workflow – isolation, mapping, peak finding – functional analysis and annotation.

UNIT 5 APPLICATIONS OF NGS**9 Hrs.**

Whole-genome sequencing, Exome sequencing, Targeted sequencing, Pooled sequencing, methylome sequencing. Next generation sequencing applications in Agri-Biotech, health care, metagenomics, GWAS.

Max.45 Hrs.**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 steps involved in a general NGS data analysis.
- CO3** - Explain key theoretical concepts in RNA sequencing.
- CO4** - Understand and analyze DNA protein sequencing strategies.
- CO5** - Appreciate the applications of this technology.
- CO6** - Independently create a basic NGS data analysis workflow.

TEXT BOOKS/REFERENCE BOOKS

- Next-Generation Sequencing Data Analysis by Xinkun Wang CRC Press; 1st edition (24 February 2016).
- Next Generation Sequencing and Data Analysis Melanie Kappelman-Fenzl Springer <https://doi.org/10.1007/978-3-030-62490-3> 2021.
- 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 EXAM QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B : 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB1502	R PROGRAMMING FOR BIOLOGIST	L	T	P	EL	Credits	Total Marks
		3	0	0	0	3	100

COURSE OBJECTIVES

- The objective of the R programming paper for undergraduates studying bioinformatics and data science is to provide a comprehensive understanding of R programming and its applications in the field.
- The course aims to equip students with the necessary skills to effectively analyze and manipulate biological data using R programming.

UNIT 1 INTRODUCTION TO R PROGRAMMING**9 Hrs.**

Introduction to the R programming language, its syntax, and its advantages in data analysis - Understanding basic data types, variables, and functions in R - Exploring data structures such as vectors, matrices, data frames, and lists in R - Importing and exporting data from various file formats (e.g., CSV, Excel) using R - Data manipulation and transformation techniques using built-in functions and packages in R.

UNIT 2 EXPLORATORY DATA ANALYSIS WITH R**9 Hrs.**

Data visualization techniques using popular R packages such as ggplot2 and lattice - Summarizing and exploring data using descriptive statistics, including measures of central tendency and variability - Handling missing data and outliers in R - Preprocessing data by cleaning, filtering, and transforming variables - Exploring relationships between variables using scatter plots, histograms, and other graphical representations.

UNIT 3 STATISTICAL ANALYSIS WITH R**9 Hrs.**

Introduction to statistical concepts and hypothesis testing - Performing t-tests, chi-square tests, and ANOVA using R - Calculating p-values and interpreting statistical results in R - Building and interpreting regression models in R, including linear regression and logistic regression - Understanding how to handle assumptions and interpret model outputs.

UNIT 4 DATA MINING AND MACHINE LEARNING WITH R**9 Hrs.**

Introduction to data mining concepts, including supervised and unsupervised learning - Implementing popular machine learning algorithms in R, such as decision trees, random forests, and k-means clustering - Evaluating and comparing models using performance metrics like accuracy, precision, recall, and ROC curves - Feature selection and dimensionality reduction techniques in R - Handling imbalanced datasets and performing resampling techniques (e.g., cross-validation) in R.

UNIT 5 BIOINFORMATICS APPLICATIONS WITH R**9 Hrs.**

Analyzing biological sequences (DNA, RNA, protein) using Bioconductor packages in R - Exploring genomics data, including DNA sequencing and genomic variations, using R - Analyzing and visualizing gene expression data, including differential gene expression analysis and heatmaps, in R - Understanding functional enrichment analysis and pathway analysis using R packages - Integrating bioinformatics data with statistical analysis and machine learning techniques in R.

Max.45 Hrs.**COURSE OUTCOMES:**

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

CO1 - Demonstrate proficiency in R programming language and its syntax.

CO2 - Apply exploratory data analysis techniques using R to gain insights from biological datasets.

CO3 - Perform statistical analysis and hypothesis testing in R for biological data.

- CO4** - Utilize data mining and machine learning techniques in R for bioinformatics applications.
CO5 - Apply R programming to analyze and interpret genomic and gene expression data.
CO6 - Communicate and present data analysis results effectively using R.

TEXT / REFERENCE BOOKS

1. R for Data Science - Hadley Wickham, Garrett Golemund (O'Reilly Media, 2016).
2. R Cookbook - Paul Teetor (O'Reilly Media, 2011).
3. Bioinformatics Data Skills: Reproducible and Robust Research with Open-Source Tools - Vince Buffalo (O'Reilly Media, 2015)
4. Hands-On Programming with R: Write Your Own Functions and Simulations - Garrett Golemund (O'Reilly Media, 2014)..
5. Practical Computing for Biologists - Steven H. D. Haddock, Casey W. Dunn (Sinauer Associates, 2010).

END SEMESTER EXAM QUESTION PAPER PATTERN**Max. Marks: 100****Exam Duration: 3 Hrs.****PART A :** 10 Questions of 2 marks each uniformly distributed – No choice**20 Marks****PART B :** 2 Questions from each unit of internal choice, each carrying 16 marks**80 Marks**

SBIB1503	DEEP LEARNING FOR BIOINFORMATICS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- This course introduces students to the principles and applications of deep learning techniques in the field of bioinformatics.
- Students will learn how to apply deep learning algorithms to analyze biological data, including genomics, proteomics, transcriptomics, and medical imaging.
- The course will cover both theoretical concepts and hands-on practical sessions using popular deep learning frameworks.

UNIT 1 INTRODUCTION TO DEEP LEARNING**9 Hrs.**

Basics of neural networks and deep learning-Activation functions, loss functions, and optimization algorithms-Introduction to popular deep learning frameworks (e.g., TensorFlow, PyTorch).

UNIT 2 DEEP LEARNING FOR GENOMICS**9 Hrs.**

DNA sequence analysis using convolutional neural networks (CNNs)-Variant calling and genomic variant interpretation using deep learning-Predicting gene expression and splicing using recurrent neural networks (RNNs).

UNIT 3 DEEP LEARNING FOR PROTEOMICS**9 Hrs.**

Protein structure prediction and folding using deep learning models-Protein function prediction using deep learning architectures-Analysis of protein-protein interactions and protein-ligand binding using deep learning approaches. Deep Learning for Drug Discovery (2 weeks).

UNIT 4 DEEP LEARNING FOR DRUG DISCOVERY**9 Hrs.**

Deep learning applications in virtual screening and drug target prediction-Drug toxicity prediction using deep learning algorithms. Generative models for drug design and molecular generation.

UNIT 5 ETHICAL CONSIDERATIONS AND CHALLENGES IN DEEP LEARNING FOR BIOINFORMATICS**9 Hrs.**

Ethical issues in using deep learning for biological data-Challenges and limitations of deep learning in bioinformatics-Future directions and emerging trends in deep learning for bioinformatics.

Max.45 Hrs.**COURSE OUTCOMES:**

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

- CO1** - Understand the principles and concepts of deep learning, including neural networks, activation functions, loss functions, and optimization algorithms.
- CO2** - Comprehend the applications of deep learning techniques in various domains of bioinformatics, such as genomics, proteomics, transcriptomics, and medical imaging.
- CO3** - Gain hands-on experience with popular deep learning frameworks, such as TensorFlow or PyTorch, and be able to implement deep learning models for bioinformatics tasks.
- CO4** - Apply deep learning algorithms to analyze biological data, including DNA sequences, protein structures, gene expression profiles, and medical images.
- CO5** - Evaluate and interpret the results obtained from deep learning models in bioinformatics applications, such as variant calling, gene expression analysis, protein function prediction, and medical image classification.
- CO6** - Explore the use of deep learning in drug discovery and understand its potential in virtual screening, toxicity prediction, and molecular generation.

TEXT / REFERENCE BOOKS

1. Deep Learning for the Life Sciences: Applying Deep Learning to Genomics, Microscopy, Drug Discovery, and More" by Bharath Ramsundar, Peter Eastman, Patrick Walters, and Vijay Pande.
2. Bioinformatics Data Skills: Reproducible and Robust Research with Open Source Tools" by Vince Buffalo.
3. Deep Learning for Genomics: A Concise Guide to Applying Deep Learning to Genomics Data Analysis and Interpretation" by Jason T. L. Wang, Yanjun Qi, and Xinghua Shi.
4. Deep Learning in Python: Master Data Science and Machine Learning with Modern Neural Networks Written in Python, Theano, and TensorFlow" by Francois Chollet.
5. Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach" edited by D. Higgins and W. Taylor.

END SEMESTER EXAM QUESTION PAPER PATTERN**Max. Marks : 100****Exam Duration : 3 Hrs.****PART A :** 10 Questions of 2 marks each uniformly distributed – No choice**20 Marks****PART B :** 2 Questions from each unit of internal choice, each carrying 16 marks**80 Marks**

S738BLH55	MICROARRAY DATA ANALYSIS	L	T	P	EL	Credits	Total Marks
		2	0	2	2	4	100

COURSE OBJECTIVE

- This course provides students with a comprehensive understanding of microarray technology and the computational methods used for analyzing microarray gene expression data.
- Students will learn the fundamental concepts, techniques, and tools required for preprocessing, normalization, differential expression analysis, and functional interpretation of microarray data.

UNIT 1 INTRODUCTION TO MICROARRAY TECHNOLOGY**12 Hrs.**

Overview of microarray technology and its applications in gene expression analysis-Different types of microarrays (e.g., cDNA microarrays, oligonucleotide microarrays) and their characteristics-Experimental design considerations for microarray experiments.

LAB EXERCISES: Microarray dataset retrieval and documentation about the platform-Explore the sample details

UNIT 2 PREPROCESSING AND QUALITY CONTROL**12 Hrs.**

Data preprocessing steps: raw data handling, background correction, normalization, and summarization
Quality control techniques and outlier detection-Data transformation and filtering for downstream analysis
Data Preprocessing and Quality Control:

LAB EXERCISES: Perform background correction and normalization on raw microarray data-Assess data quality using quality control measures and detect outlier-Generate summary statistics and visualizations to explore the pre-processed data.

UNIT 3 DIFFERENTIAL GENE EXPRESSION ANALYSIS**12 Hrs.**

Statistical concepts and methods for identifying differentially expressed genes-Popular statistical tests (e.g., t- test, ANOVA) for detecting differential expression-Multiple testing correction and controlling false discovery rate (FDR)-Practical implementation of differential expression analysis using software like R/Bioconductor

LAB EXERCISES: Perform differential expression analysis to identify genes that are significantly differentially expressed between experimental conditions. Apply statistical tests (e.g., t-test, ANOVA) to determine statistical significance. Adjust for multiple testing and control false discovery rate (FDR).

UNIT 4 CLUSTERING AND DIMENSIONALITY REDUCTION**12 Hrs.**

Unsupervised learning techniques: hierarchical clustering, k-means clustering, and principal component analysis (PCA)-Visualization methods for cluster analysis and PCA-Interpretation and biological validation of clustered gene expression patterns.

LAB EXERCISES: Apply clustering algorithms (e.g., hierarchical clustering, k-means clustering) to identify groups of genes with similar expression patterns. Use dimensionality reduction techniques (e.g., principal component analysis - PCA) to visualize and interpret the clustering results. Create heatmaps and other visualizations to represent gene expression patterns.

UNIT 5 FUNCTIONAL ENRICHMENT ANALYSIS**12 Hrs.**

Introduction to functional annotation databases (e.g., Gene Ontology, KEGG pathways)-Enrichment analysis methods for identifying overrepresented biological functions and pathways-Software tools for functional enrichment analysis (e.g., Gostats, DAVID, Enrichr)

LAB EXERCISES: Perform functional enrichment analysis to identify overrepresented biological functions or pathways associated with differentially expressed genes. Utilize Gene Ontology (GO) or pathway databases to assess functional annotations. Interpret and visualize enrichment analysis results using enrichment plots and gene set network diagrams.

Max.60 Hrs.

COURSE OUTCOMES:

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

- C01** - Understand the principles of microarray technology, including its applications in gene expression analysis and the types of microarrays available.
- C02** - Gain proficiency in preprocessing and quality control techniques for microarray data, including background correction, normalization, summarization, and outlier detection.
- C03** - Develop skills in conducting differential gene expression analysis using statistical tests and understanding the interpretation of statistical significance.
- C04** - Learn clustering algorithms and dimensionality reduction techniques to identify gene expression patterns and visualize microarray data.
- C05** - Perform functional enrichment analysis to identify overrepresented biological functions and pathways associated with differentially expressed genes.
- C06** - Gain knowledge of integrating microarray data with other omics data types, such as RNA-seq or proteomics data, and understand how to perform network analysis and visualization.

TEXT/REFERENCE BOOKS:

1. Microarray Analysis: Methods and Applications- edited by Sarbani Pal, Debashis Ghosh, and Jinze Liu (2019).
2. Analysis of Microarray Data: A Network-Based Approach" by Shu-Qi Zhao (2019).
3. DNA Microarrays: Methods and Protocols" edited by John N. Abelson and Melvin I. Simon (2020).
4. Microarray Data Analysis: Methods and Applications" edited by Pietro Hiram Guzzi (2021).

SBIB2501	NEXT GENERATION SEQUENCING LAB	L	T	P	EL	Credits	Total Marks
		0	0	4	0	2	100

LIST OF EXERCISES:

1. Quality Control (QC) and Preprocessing: Perform quality control checks on raw sequencing data using tools like FastQC. Trim or filter low-quality reads, remove adapter sequences, and remove any artifacts or contaminants using tools like Trimmomatic or Cutadapt.
2. Read Alignment: Align the processed reads to a reference genome or transcriptome using alignment algorithms such as Bowtie, BWA, or HISAT2 for DNA-seq or TopHat, STAR, or HISAT2 for RNA-seq.
3. Generate a mapping file (SAM/BAM format) containing aligned reads and their positions.
4. Variant Calling (for DNA-seq): Identify genetic variations (e.g., single nucleotide polymorphisms SNPs, insertions, deletions) in the sequenced DNA sample compared to the reference genome. Use variant calling tools such as GATK, FreeBayes, or SAMtools to identify and filter variants based on quality, coverage, and other parameters.
5. Transcript Quantification (for RNA-seq): Estimate gene expression levels by quantifying the abundance of RNA transcripts. Use tools like feature Counts, HTSeq, or Salmon to assign reads to genes or transcripts and calculate their expression values (e.g., in counts or transcripts per million - TPM).
6. Differential Gene Expression Analysis (for RNA-seq): Compare gene expression between different conditions (e.g., control vs. treatment, disease vs. normal) to identify differentially expressed genes. Utilize tools such as DESeq2, edgeR, or limma-voom to perform statistical tests and generate lists of significantly differentially expressed genes.
7. Functional Analysis: Annotate and interpret the obtained results by identifying enriched gene ontology (GO) terms, pathways, or functional categories associated with the differentially expressed genes. Use tools like DAVID, Enrichr, or clusterProfiler to perform functional enrichment analysis and visualize the results.

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

SBIB2502	R PROGRAMMING FOR BIOLOGIST LAB	L	T	P	EL	Credits	Total Marks
		3	0	0	3	100	

LIST OF EXERCISES

EXERCISE 1: DATA MANIPULATION WITH DPLYR

Load and preprocess a large biological dataset. Use dplyr package functions to filter, arrange, group, and summarize data for exploratory analysis.

EXERCISE 2: DATA VISUALIZATION WITH GGLOT2

Create different types of plots (e.g., scatter plots, bar plots, box plots) to visualize gene expression patterns and compare different biological samples using ggplot2.

EXERCISE 3: STATISTICAL HYPOTHESIS TESTING

Perform t-tests and ANOVA to compare gene expression levels between multiple groups. Interpret the results and discuss the biological implications.

EXERCISE 4: DIMENSIONALITY REDUCTION WITH T-SNE

Apply t-distributed Stochastic Neighbor Embedding (t-SNE) on gene expression data to visualize high-dimensional data in a 2D/3D space and explore cluster formations.

EXERCISE 5: GENE SET ENRICHMENT ANALYSIS (GSEA)

Use the clusterProfiler package to perform GSEA to identify enriched gene sets or pathways in a given gene list. Interpret the enriched pathways' biological significance.

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

SBIB1601	COMPUTER AIDED DRUG DESIGN	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVE

- To make the students aware of knowledge and skills needed for computer aided drug design.
- To know how computer aided drug design is executed at advanced levels.
- To perform the process of ligand based and structure-based drug design.
- To understanding the basic principles of rational drug design to aid the drug discovery process.
- To apply skills related to in silico drug design on various drug targets.

UNIT 1 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.

UNIT 2 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 3 MODELLING MOLECULES**9 Hrs.**

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

UNIT 4 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 5 DATABASES AND TOOLS**9 Hrs.**

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

Max.45 Hrs.**COURSE OUTCOMES:**

On completion of the course the student will be able to

- CO1** - Understand the fundamentals of drugs and their pharmacokinetic properties.
- CO2** - Identify the drug development process and lead molecule discovery.
- CO3** - Understand the basics of modeling strategies.
- CO4** - Analyze the role of simulation studies and perform them.
- 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. Molecular Modelling: Principles and Applications, 2e Andrew Leach Pearson India; 2nd edition (1 January 2009).
2. Computer Assisted Drug Designing Pushpendra Kumar Vishwakarma, Vikash Gupta, Leela Maharaj LAP Lambert Academic Publishing (17 March 2012).

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

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100

Exam Duration: 3 Hrs.

PART A: 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B: 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB2601	COMPUTER AIDED DRUG DESIGN-LAB	L	T	P	EL	Credits	Total Marks
		3	0	0	0	3	100

LIST OF EXPERIMENTS

1. Visualization of molecules.
2. Protein 3D structure generation and validation; Energy minimization.
3. **Ligand-based Virtual Screening:** Perform ligand-based virtual screening using molecular fingerprints and similarity search methods. Retrieve a database of compounds and screen them against a known active compound or target protein. Rank the compounds based on their similarity scores and potential activity.
4. **Structure-based Virtual Screening:** Utilize the 3D structure of a target protein to perform structure-based virtual screening. Use docking or other structure-based methods to screen a database of compounds and identify potential hits or lead compounds. Analyze the docking scores and interactions to prioritize the selected compounds.
5. Pharmacophore Modeling: Construct pharmacophore models based on known active compounds or protein-ligand interactions. Use software like Discovery Studio or MOE to generate pharmacophore hypotheses. Apply the pharmacophore models for virtual screening or compound design.
6. Molecular Docking: Perform molecular docking of a ligand into a target protein; Analyze the docking results to understand the binding mode and interactions between the ligand and the protein's active site; Evaluate the docking poses and calculate binding affinities.
7. ADMET Prediction: Predict the absorption, distribution, metabolism, excretion, and toxicity (ADMET) properties of drug candidates. Use computational models or software tools to assess drug-likeness, bioavailability, and potential toxicity. Evaluate the properties of the compounds before experimental testing.

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

SBIB3001	CANCER BIOLOGY	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To educate students on the basis of cancer.
- To provide information on various genetic and molecular changes that normal cells undergo
- To describe factors that contribute to cancer development.
- To understand the mechanism of metastasis.
- To presents an overview on cancer prevention and currently available therapeutic treatments.

UNIT 1 FUNDAMENTALS OF CANCER BIOLOGY**9 Hrs.**

Definition, Hall marks of cancer, Types of Cancer, Common Symptoms. Cell signaling in carcinogenesis- Growth factors and their receptors. Cellular oncogenes, Tumor suppressor genes. Causes of cancer- Mutations and cancer, Viral causes of cancer.

UNIT 2 CARCINOGENESIS**9 Hrs.**

The main stages of carcinogenesis – an overview, Early steps characterized in cancer, Cellular principles of invasion and metastasis, Stromal micro environment and carcinogenesis.

UNIT 3 PRINCIPLES OF CARCINOGENESIS**9 Hrs.**

Chemical Carcinogenesis -Metabolism of Carcinogenesis, Natural History of Carcinogenesis, Targets of Chemical Carcinogenesis. Physical Carcinogenesis- X - Ray radiation – mechanism of radiation Carcinogenesis.

UNIT 4 CANCER METASTASIS**9 Hrs.**

Clinical significance of invasion, heterogeneity of metastatic phenotype, Metastatic cascade, Basement Membrane disruption, Three-step theory of Invasion, Proteinases and tumor cell invasion.

UNIT 5 DETECTION OF CANCER AND CANCER THERAPY**9 Hrs.**

Detection of Cancers, Prediction of aggressiveness of Cancer, Advances in Cancer detection. Different forms of therapy, Chemotherapy, radiation therapy, and Immunotherapy: advantages and limitations.

Max.45 Hrs.**COURSE OUTCOMES:**

At the end of the course the students will

- CO1** - Identify the six hall marks of cancer.
- CO2** - Analyze the mechanism of carcinogenesis and evaluate the effect of chemical carcinogens and assess the role of physical carcinogens.
- CO3** - Identify the ways in which the oncogenes are activated and outline the current state of knowledge about the biochemical and molecular basis of cancer.
- CO4** - Describe the multistage nature of cancer and be able to discuss factors which influence this process.
- CO5** - List out the various cancer treatment strategies and their suitability.
- CO6** - Discuss contemporary approaches to the development of therapies, including specific molecular alterations in cancer as therapeutic targets and prognostic factors to guide treatment.

TEXT BOOKS/REFERENCE BOOKS

1. Karp's Cell Biology, Gerald Karp, Janet Iwasa, Wallace Marshall, Wiley; 8th Edition, Global.
2. Karp's s Cell and Molecular Biology 9th Edition by Gerald Karp, Janet Iwasa, Wallace Marshall Wiley; 9th edition (February 19, 2020).

3. Genomes 5th Edition by Terry A. Brown CRC Press; 5th edition (April 28, 2023).
4. Molecular Cell Biology (842581) Ninth Edition by Harvey Lodish (Author), Arnold Berk (Author), Chris A. Kaiser (Author), Monty Krieger (Author), Anthony Bretscher et al W. H. Freeman; Ninth edition (January 27, 2021).
5. Cell Biology by Verma and Agarwal S CHAND & Company limited 2022.

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100

Exam Duration: 3 Hrs.

PART A: 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B: 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB3002	EPIGENOMICS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- Understand the principles of epigenetics and its role in gene regulation and inheritance.
- Gain knowledge of different types of epigenetic modifications and their impact on gene expression.
- Develop proficiency in experimental techniques for studying epigenetic modifications.
- Learn data analysis methods for interpreting epigenomic datasets.
- Explore the connection between epigenetics and human diseases, including biomarker discovery.

UNIT 1 INTRODUCTION TO EPIGENETICS**9 Hrs.**

Overview of epigenetics and its importance in gene regulation - Epigenetic modifications and their role in gene expression - Key epigenetic marks and modifications (DNA methylation, histone modifications) - Epigenetic inheritance and its implications.

UNIT 2 DNA METHYLATION**9 Hrs.**

DNA methylation and its impact on gene regulation - DNA methylation patterns in different genomic regions - Techniques for DNA methylation analysis (bisulfite sequencing, methylation-specific PCR) - Epigenetic changes in DNA methylation associated with diseases.

UNIT 3 HISTONE MODIFICATIONS**9 Hrs.**

Histone proteins and their modifications - Role of histone modifications in chromatin structure and gene regulation - Techniques to study histone modifications (ChIP-seq, immunohistochemistry) - Histone modification patterns in different cell types and diseases.

UNIT 4 EPIGENOMICS TECHNIQUES**9 Hrs.**

Introduction to epigenomics and high-throughput technologies - Genome-wide profiling of epigenetic marks (ChIP-seq, DNA methylation arrays) - Data analysis and interpretation of epigenomics datasets - Integration of epigenomics data with other omics data.

UNIT 5 EPIGENETICS AND DISEASE**9 Hrs.**

Epigenetic alterations in human diseases (cancer, neurological disorders, etc.) - Epigenetic biomarkers for disease diagnosis and prognosis - Epigenetic therapies and their potential for disease treatment - Ethical considerations and challenges in epigenetics research.

Max.45 Hrs.**COURSE OUTCOMES:**

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

- CO1** - Understand the fundamental concepts and principles of epigenetics and their role in gene regulation.
- CO2** - Acquire knowledge and practical skills in performing epigenomic experiments and analyzing epigenomic data.
- CO3** - Demonstrate proficiency in interpreting and integrating epigenomic data with other omics data to gain comprehensive insights into gene regulation.
- CO4** - Develop an understanding of the impact of epigenetic modifications on human health and disease, and their potential as diagnostic and therapeutic targets.
- CO5** - Explore the ethical considerations and societal implications of epigenetics research and its applications.

CO6 - Apply critical thinking and problem-solving skills to design and conduct independent research projects in the field of epigenomics.

TEXT / REFERENCE BOOKS

1. Epigenetics: How Environment Shapes Our Genes - Richard C. Francis (W.W. Norton & Company, 2012).
2. Epigenetics: A Reference Manual - Jeffrey M. Craig and Nicholas C. Wong (Caister Academic Press, 2011).
3. Epigenomics: From Chromatin Biology to Therapeutics - Anjana Rao and Sriharsa Pradhan (Cambridge University Press, 2015).
4. Epigenetics: Current Research and Emerging Trends - Brian P. Chadwick (Caister Academic Press, 2015).
5. Epigenetic Regulation and Epigenomics - Kresimir Gjuracic (InTech, 2012).

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B : 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB3003	METABOLOMICS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- Solid understanding of metabolomics principles like Role of metabolites, metabolic pathways, and analytical techniques in metabolomics research.
- Proficiency in metabolomics data analysis: Hands-on experience in preprocessing, feature extraction, and statistical analysis of metabolomics data.
- Metabolite identification and annotation: Familiarity with techniques for identifying metabolites using spectral databases and interpretation of mass spectrometry/NMR spectra.
- Awareness of challenges and limitations: Understanding issues like batch effects, missing values, and strategies for quality control in metabolomics data.
- Exploration of metabolic pathway analysis: Mapping data onto pathways, enrichment analysis, and interpretation of metabolic changes and their biological implications.

UNIT 1 INTRODUCTION TO METABOLOMICS

9 Hrs.

Overview of metabolomics and its applications in biological research. Introduction to metabolites, metabolic pathways, and their role in cellular processes. Comparison of metabolomics with other omics technologies (genomics, transcriptomics, proteomics).

UNIT 2 DATA PREPROCESSING AND ANALYSIS

9 Hrs.

Preprocessing techniques for metabolomics data, including baseline correction, peak alignment, and normalization. Multivariate statistical analysis methods, such as principal component analysis (PCA), partial least squares-discriminant analysis (PLS-DA), and hierarchical clustering.

UNIT 3 METABOLITE IDENTIFICATION AND ANNOTATION

9 Hrs.

Strategies for metabolite identification using spectral databases, molecular networking, and annotation tools. Interpretation of MS and NMR spectra for metabolite identification. Prediction of metabolite properties and biological activities.

UNIT 4 METABOLIC PATHWAY ANALYSIS

9 Hrs.

Introduction to metabolic pathway databases, such as KEGG and MetaboAnalyst. Mapping and visualization of metabolomics data onto metabolic pathways. Pathway enrichment analysis and interpretation of metabolic changes.

UNIT 5 ADVANCED TOPICS IN METABOLOMICS

9 Hrs.

Advanced metabolomics techniques, such as imaging mass spectrometry and single-cell metabolomics. Metabolomics in personalized medicine and precision nutrition. Emerging trends and future directions in metabolomics research.

COURSE OUTCOMES:

On completion of the course the student will be able to

- CO1** - Knowledge of metabolomics principles: Students will acquire a comprehensive understanding of the fundamental concepts, principles, and methodologies used in metabolomics research.
- CO2** - Proficiency in metabolomics data analysis: Students will develop skills in preprocessing, analyzing, and interpreting metabolomics data using appropriate statistical and bioinformatics techniques.

- C03** - Competence in metabolite identification and annotation: Students will gain knowledge and practical experience in identifying and annotating metabolites using spectral databases, fragmentation analysis, and annotation tools.
- C04** - Understanding of metabolomics data integration: Students will learn strategies for integrating metabolomics data with other omics data, such as genomics or proteomics, to gain a systems-level understanding of biological processes.
- C05** - Familiarity with metabolic pathway analysis: Students will be able to map metabolomics data onto metabolic pathways, perform pathway enrichment analysis, and interpret metabolic changes in the context of biological pathways.
- C06** - Ability to address challenges and limitations in metabolomics: Students will learn to recognize and address common challenges in metabolomics data, such as batch effects, missing values, and data integration issues.

TEXT / REFERENCE BOOKS

1. Introduction to Metabolomics: Tools for the Analysis of Metabolic Pathways" by Matej Oresic (2013).
2. Metabolomics: From Small Molecules to Big Data" edited by Ute Roessner, Chamindu K. C. K. Herath, and Oliver Kohlbacher (2018).
3. Practical Metabolomics: Methods and Protocols" edited by Ralf Weber and Melanie M. Schulz (2019).
4. Metabolomics: A Powerful Tool in Systems Biology" by Ines Thiele and Ronan M. T. Fleming (2019).
5. Metabolomics: The Science of Systems Biology and Omics Integration" edited by Matej Oresic (2020).

SBIB3004	DATA MINING AND MACHINE LEARNING	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- This course introduces students to the principles and techniques of data mining and machine learning for analyzing and extracting useful insights from large datasets.
- Students will learn various algorithms and methods used in data mining and machine learning.
- Students will get the theoretical foundations, and gain practical experience through hands-on exercises and projects.

UNIT 1 INTRODUCTION TO DATA MINING AND MACHINE LEARNING 9 Hrs.

Overview of data mining and machine learning concepts, applications, and challenges-Introduction to key terminologies, such as supervised learning, unsupervised learning, and feature selection.

UNIT 2 DATA PREPROCESSING AND FEATURE SCREENING 9 Hrs.

Data cleaning and transformation techniques, handling missing values, and dealing with outliers. Feature selection and dimensionality reduction methods to improve model performance. Exploratory data analysis (EDA) techniques for understanding data patterns and relationships.

UNIT 3 SUPERVISED LEARNING ALGORITHMS 9 Hrs.

Linear regression and logistic regression for regression and classification tasks. Decision trees and random forests for classification and feature selection. Support Vector Machines (SVM) for classification and regression. Evaluation metrics and model selection techniques.

UNIT 4 UNSUPERVISED LEARNING ALGORITHMS 9 Hrs.

Clustering algorithms such as k-means, hierarchical clustering, and DBSCAN. Dimensionality reduction techniques, including principal component analysis (PCA) and t-SNE. Association rule mining and frequent pattern analysis.

UNIT 5 ENSEMBLE LEARNING AND MODEL EVALUATION 9 Hrs.

Ensemble methods, including bagging, boosting, and stacking. Model evaluation techniques, including cross-validation, overfitting, and model selection. Evaluation metrics for classification, regression, and clustering tasks.

Max.45 Hrs.**COURSE OUTCOMES:**

On completion of the course the student will be able to

- CO1** - Understand the fundamental concepts, principles, and techniques of data mining and machine learning.
- CO2** - Gain knowledge of various data preprocessing techniques and feature engineering methods to prepare data for analysis.
- CO3** - Familiarize themselves with supervised learning algorithms, including linear regression, logistic regression, decision trees, random forests, and support vector machines.
- CO4** - Learn unsupervised learning algorithms, such as clustering and dimensionality reduction methods, including k-means, hierarchical clustering, PCA, and t-SNE.
- CO5** - Develop proficiency in evaluating and selecting models, using metrics and cross-validation techniques.
- CO6** - Gain exposure to ensemble learning techniques and understand their advantages and applications.

TEXT /REFERENCE BOOKS:

1. Machine Learning: A Probabilistic Perspective" by Kevin P. Murphy (2018).
2. Data Mining: Practical Machine Learning Tools and Techniques" by Ian H. Witten, Eibe Frank, and Mark A. Hall (2016).
3. Pattern Recognition and Machine Learning" by Christopher M. Bishop (2018).
4. Hands-On Machine Learning with Scikit-Learn, Keras, and TensorFlow: Concepts, Tools, and Techniques to Build Intelligent Systems" by Aurélien Géron (2020).

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B : 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB3005	DATABASE MANAGEMENT SYSTEMS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- Solid understanding of DBMS concepts: Develop a strong grasp of core principles, architecture, and key concepts of database management systems.
- Proficiency in SQL and database operations: Acquire skills in SQL, including data definition, manipulation, and control statements, enabling complex queries and basic database operations.
- Relational database design and normalization: Understand the process of designing a relational database schema, including ER modeling, relational schema design, and normalization, for efficient and data-integrity-focused database structures.
- Database implementation and management skills: Gain practical knowledge in implementing and managing databases, including structure creation, user access control, security management, and database administration tasks.
- Explore advanced DBMS concepts: Explore advanced topics like indexing, query optimization, transaction management, and concurrency control, essential for optimizing database performance and ensuring data consistency.

UNIT 1 INTRODUCTION TO DBMS**9 Hrs.**

Overview of DBMS and its importance in bioinformatics. Relational database concepts and architecture. Introduction to SQL (Structured Query Language).

UNIT 2 RELATIONAL DATA MODEL**9 Hrs.**

Entities, attributes, and relationships in the context of bioinformatics data. Relational schema design and normalization. Entity-Relationship (ER) modelling and mapping to relational schemas.

UNIT 3 SQL AND DATA MANIPULATION**9 Hrs.**

Querying and retrieving data using SQL. Data modification operations (insert, update, delete). Join operations and complex queries.

UNIT 4 DATABASE DESIGN AND IMPLEMENTATION**9 Hrs.**

Conceptual, logical, and physical database design for bioinformatics applications. Indexing and optimization techniques for efficient query processing. Transaction management and concurrency control.

UNIT 5 ADVANCED DATA MODELS AND DATA INTEGRATION**9 Hrs.**

Introduction to non-relational (NoSQL) databases and their relevance to bioinformatics. Overview of graph databases, document stores, and key-value stores. Comparison of different data models for bioinformatics data. Data Integration and Warehousing: Techniques for integrating data from multiple sources in bioinformatics. Data warehousing concepts and implementation. Extract, Transform, Load (ETL) processes for data integration.

Max.45 Hrs.**COURSE OUTCOMES:**

On completion of the course the student will be able to

- CO1** - Understand the fundamental concepts of database management systems.
- CO2** - Gain familiarity with SQL (Structured Query Language) for data retrieval and manipulation.
- CO3** - Understand entity-relationship (ER) modeling and its mapping to relational schemas.
- CO4** - Apply advanced SQL concepts for handling complex queries and aggregating data.
- CO5** - Explore advanced data models beyond the relational model, such as NoSQL databases.

C06 - Understand the relevance of graph databases, document stores, and key-value stores in bioinformatics.

TEXT/REFERENCE BOOKS

1. Database Systems: A Practical Approach to Design, Implementation, and Management" by Thomas M.Connolly, Carolyn E. Begg, and Peter Rob (7th Edition, 2020).
2. Modern Database Management" by Jeffrey A. Hoffer, V. Ramesh, and Heikki Topi (14th Edition, 2019).
3. Database System Concepts" by Abraham Silberschatz, Henry F. Korth, and S. Sudarshan (7th Edition, 2020)
4. Fundamentals of Database Systems" by Ramez Elmasri and Shamkant B. Navathe (8th Edition, 2021).
- 5 Database Systems: The Complete Book" by Hector Garcia-Molina, Jeffrey D. Ullman, and Jennifer Widom (3rd Edition, 2020).

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B : 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB3006	NATURAL LANGUAGE PROCESSING BIOMEDICAL DATA	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- Understand NLP concepts and techniques for analyzing biomedical data.
- Learn about challenges and unique characteristics of processing biomedical text.
- Acquire practical skills in text preprocessing and feature extraction for biomedical text analysis.
- Gain hands-on experience in Biomedical Named Entity Recognition (NER).
- Learn text classification methods for biomedical data.
- Explore advanced topics in biomedical text mining and information extraction.

UNIT 1 INTRODUCTION TO NATURAL LANGUAGE PROCESSING**9 Hrs.**

Basics of NLP: concepts, techniques, and applications - Introduction to biomedical data and its unique characteristics - Challenges and opportunities in processing biomedical text.

UNIT 2 TEXT PREPROCESSING AND REPRESENTATION**9 Hrs.**

Text preprocessing techniques: tokenization, stemming, stop word removal, etc. - Feature extraction methods for biomedical text - Word embeddings and distributed representations.

UNIT 3 BIOMEDICAL NAMED ENTITY RECOGNITION (NER)**9 Hrs.**

Introduction to Named Entity Recognition (NER) - Biomedical NER: entity types, annotation, and evaluation metrics - Techniques for biomedical NER: rule-based, dictionary-based, machine learning-based approaches.

UNIT 4 BIOMEDICAL TEXT CLASSIFICATION**9 Hrs.**

Introduction to text classification in the biomedical domain - Feature engineering and selection for biomedical text classification - Machine learning algorithms for biomedical text classification: SVM, Naive Bayes, etc.

UNIT 5 BIOMEDICAL TEXT MINING AND INFORMATION EXTRACTION**9 Hrs.**

Relation extraction from biomedical text - Event extraction and knowledge base population - Biomedical text summarization and information retrieval.

Max.45 Hrs.**COURSE OUTCOMES:**

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

- CO1** - Apply NLP techniques to extract information from biomedical text data effectively.
- CO2** - Address challenges in processing biomedical text and handle domain-specific language and data heterogeneity.
- CO3** - Demonstrate proficiency in Biomedical Named Entity Recognition (NER) for accurate entity extraction.
- CO4** - Utilize text classification methods for categorizing biomedical texts based on relevant classes.
- CO5** - Analyze advanced topics in biomedical text mining, including relation extraction, event extraction, and knowledge base population. **CO6**: Critically evaluate and apply NLP techniques to solve real-world bioinformatics problems.

TEXT / REFERENCE BOOKS

1. Biological Text Mining and its Applications (2009) by K. Bretonnel Cohen and D. R. Leaman.
2. Text Mining for Biology and Biomedicine (2006) edited by Sophia Ananiadou and John McNaught.
3. Biomedical Natural Language Processing (2014) by Kevin Bretonnel Cohen.

4. Introduction to Biomedical Natural Language Processing (2018) by Nizlem Uzuner and Stephanie Beth M. Kagetsu.
5. Text Mining in Practice with R (2017) by Ted Kwartler.

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B : 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB3007	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 approach for research.
- To introduce students the ways to design methodologies to address research problems.
- To understand the criteria in sample collection and design.
- To know the ethics in research.

UNIT 1 INTRODUCTION**9 Hrs.**

Meaning of Research, Objectives of Research, Motivation in Research, Types of Research - Descriptive, Analytical, Applied, Fundamental, Quantitative, Qualitative, Conceptual, Empirical. Research Approaches - Quantitative and qualitative approach. Significance of Research, and Research Methods versus Methodology.

UNIT 2 RESEARCH PROBLEM AND DESIGN**9 Hrs.**

Selecting the Problem, Necessity of Defining the Problem Technique Involved in Defining a Problem. Meaning of Research Design, Need for Research Design Features of a Good Design, Important Concepts Relating to Research Design, Different Research Designs-Exploration/ descriptive/ experimental/ Survey/ Case Study.

UNIT 3 SAMPLING DESIGN**9 Hrs.**

Census and Sample Survey, Implications of a Sample Design, Steps in Sampling Design, Criteria of Selecting a Sampling Procedure, Characteristics of a Good Sample Design, Different Types of Sample Designs, Random Sample from an Infinite Universe, Complex Random Sampling Designs.

UNIT 4 DATA COLLECTION**9 Hrs.**

Methods and tools for Data collection: Collection of primary data: Observation method, Interview method, Questionnaire method, case study method. Collection of secondary data. Data processing and management: Processing operations: Editing, coding, classification, tabulation, Use of data entry software (MS Excel & SPSS).

UNIT 5 BIOETHICS**9 Hrs.**

Bioethics: Definition – 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.

Max.45 Hrs.**COURSE OUTCOMES:**

On completion of the course the student will be able to

- CO1** - Decide on the type of research they wish to carry out in project.
- CO2** - Identify the research gap and design the research problem.
- CO3** - Devise sample collection strategy.
- CO4** - Effectively preprocess and handle data.
- CO5** - Create an approach to address research problem with ethical consideration.
- CO6** - Carry out the project more effectively.

TEXT BOOKS/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 EXAM QUESTION PAPER PATTERN

Max. Marks: 100

Exam Duration: 3 Hrs.

PART A: 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B: 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB3008	ETHICAL GUIDELINES FOR CLINICAL TRIALS	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- Understand the significance of ethical guidelines in clinical trials and their role in protecting participant rights.
- Familiarize students with fundamental ethical principles in clinical research, including informed consent and participant welfare.
- Explore major international and national ethical guidelines for clinical trials and their regulatory implications.
- Analyze ethical challenges in clinical trials, such as vulnerable populations and conflicts of interest.
- Develop ethical decision-making skills through case studies, applying guidelines to resolve ethical dilemmas in clinical research.

UNIT 1 INTRODUCTION TO CLINICAL TRIALS AND ETHICS**9 Hrs.**

Overview of clinical trials: purpose, phases, and significance - Introduction to research ethics and its importance in clinical trials - Historical development of ethical guidelines for clinical trials.

UNIT 2 ETHICAL PRINCIPLES IN CLINICAL TRIALS**9 Hrs.**

Informed consent: its significance, components, and challenges - Beneficence and non-maleficence: ensuring participant welfare and minimizing harm - Justice and fairness: considerations of access, equity, and distribution of benefits and burdens in clinical trials.

UNIT 3 ETHICAL GUIDELINES AND REGULATIONS**9 Hrs.**

Exploration of major international and national ethical guidelines for clinical trials - Understanding regulations and oversight mechanisms governing clinical research - Ethical review boards and their role in ensuring participant protection.

UNIT 4 VULNERABLE POPULATIONS IN CLINICAL TRIALS**9 Hrs.**

Ethical considerations when involving vulnerable populations, such as children, pregnant women, and the elderly - Inclusion and exclusion criteria: ethical challenges and implications - Ethical considerations for clinical trials conducted in low-resource settings.

UNIT 5 EMERGING ETHICAL ISSUES IN CLINICAL TRIALS**9 Hrs.**

Placebo use and randomization: ethical dilemmas and alternatives - Data sharing and publication ethics in clinical trials - Conflict of interest and financial considerations in clinical research.

COURSE OUTCOMES:

On completion of the course the student will be able to

- CO1** - Understand the purpose and importance of research ethics in clinical trials.
- CO2** - Apply ethical principles to evaluate participant protections in clinical trial protocols.
- CO3** - Interpret and apply major international and national ethical guidelines and regulations.
- CO4** - Evaluate ethical considerations when involving vulnerable populations in clinical trials.
- CO5** - Analyze and propose ethical solutions for emerging issues in clinical trials.
- CO6** - Understand the role of ethics review boards in participant protection and compliance.

Max.45 Hrs.**TEXT / REFERENCE BOOKS**

1. Ethics in Clinical Research: A Guide for Investigators (2014) by Robert J. Levine.
2. Principles and Practice of Clinical Research (2018) by John I. Gallin and Frederick P. Ognibene.

3. The Ethics of Research with Human Subjects: Protecting People, Advancing Science, Promoting Trust (2010) by Ezekiel J. Emanuel.
4. Ethics and Regulation of Clinical Research (1986) by Robert J. Levine.
5. The Oxford Textbook of Clinical Research Ethics (2008) edited by Ezekiel J. Emanuel, Christine Grady, Robert A. Crouch, Reidar K. Lie, Franklin G. Miller, and David Wendler.

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks : 100

Exam Duration : 3 Hrs.

PART A : 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B : 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks

SBIB1302	ANALYTICAL TECHNIQUES IN BIOLOGY	L	T	P	EL	Credits	Total Marks
		3	0	0	2	3	100

COURSE OBJECTIVES

- To provide scientific understanding of the principle and applications of various instruments.
- To impart the theoretical knowledge about various analytical techniques used in biotechnology.
- To make the students aware of the various instrumentations that are used in the analytical laboratories.
- To understand the applications of the instruments in characterization of biomolecules.
- To make the student possess basic knowledge on the theory, operation and function of analytical instruments.

UNIT 1 BASIC INSTRUMENTATION**9 Hrs.**

Cell disruption techniques, Basics of microscopy, Principle and working of calorimeter, pH meter. Autoclave, Hot air oven, Laminar air flow, Incubator.

UNIT 2 SPECTROSCOPIC TECHNIQUES**9 Hrs.**

Laws of absorption of light, Beer-Lambert's Law, Absorption spectra, Measurement of absorption of light, Factors affecting the absorption properties of chromophores, Ultraviolet-visible absorption spectroscopy: Principle, Instrumentation and application, Fluorescence spectrophotometry: Principle, Instrumentation and application.

UNIT 3 CENTRIFUGATION TECHNIQUES**9 Hrs.**

Basic principles of sedimentation, Types of centrifuges, Types of rotors, Preparative centrifugation (Differential & density gradient), Analytical ultracentrifugation.

UNIT 4 CHROMATOGRAPHIC TECHNIQUES**9 Hrs.**

Principles of chromatography (Adsorption and Partition chromatography), Planar chromatography (Paper and Thin-layer chromatography), Column chromatography, Gas chromatography, Gel permeation chromatography, Ion exchange chromatography, Affinity chromatography, HPLC.

UNIT 5 ELECTROPHORETIC TECHNIQUES**9 Hrs.**

General principles, Electrophoresis of nucleic acids Agarose gel. Electrophoresis of proteins; SDS-PAGE, two dimensional gels, Blotting techniques; Southern, northern, Western blotting.

COURSE OUTCOMES:

On completion of the course the student will be able to

- CO1** - Possess an understanding on the basic techniques and instrumentation in biology labs.
- CO2** - Analyse the quantification of biomolecules by using different spectroscopic techniques.
- CO3** - Understand the separation of molecules based on gravity.
- CO4** - Realize the different chromatographic techniques used for separation of micro molecules.
- CO5** - Develop knowledge on separation of biomolecules like DNA and proteins.
- CO6** - Create the various techniques in molecular biology to analyse micro and macromolecules.

Max.45 Hrs.**TEXT BOOKS/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-Inter science; 1st edition (1 June 2000).

END SEMESTER EXAM QUESTION PAPER PATTERN

Max. Marks: 100

Exam Duration: 3 Hrs.

PART A: 10 Questions of 2 marks each uniformly distributed – No choice

20 Marks

PART B: 2 Questions from each unit of internal choice, each carrying 16 marks

80 Marks