Annexure 9.3

Avinashilingam Institute for Home Science and Higher Education for Women

(Deemed to be University Estd. u/s 3 of UGC Act 1956, Category A by MHRD)
Re-accredited with A++ Grade by NAAC. CGPA 3.65/4, Category I by UGC
Coimbatore - 641 043, Tamil Nadu, India

Department of Biochemistry, Biotechnology and Bioinformatics

M.Sc., Bioinformatics

Two years programme (with practical)

Programme Outcomes:

On successful completion of the M.Sc., Bioinformatics programme, the students will be able to

1. Gain fundamental and comprehensive knowledge in specific domain with interdisciplinary perspectives
2. Analyze and interpret data obtained from biological experiments done in practical courses and research projects following Good Laboratory Practices
3. Employ acquired scientific concepts and skills to identify and analyze complex problems by devising suitable protocols, using technical tools and software to achieve valid conclusions
4. Formulate and design appropriate technology-based solutions to tackle academic and industrial challenges and exhibit organizational skills for execution of need-based novel projects
5. Apply critical thinking and integrate innovative solutions from any relevant discipline to overcome local and global problems
6. Develop entrepreneurial skills by facilitating technology transfer and nurture Biopreneurs for sustainable development
7. Enhance effective communicative skills to disseminate domain knowledge to scientific community and society
8. Practice professional and scientific ethics in adherence with moral values
9. Excel at executing tasks individually and as a team in diverse scenarios
10. Assess the societal challenges and intervene through suitable conceptual and contextual ideas and products
11. Engage in independent and life-long learning by adapting strategies for changing environment

Programme Specific Outcomes

The M.Sc. Bioinformatics programme will enable the students to

1. Gain interdisciplinary knowledge and practical skills in computational, mathematical and biological sciences for challenging careers in academics, research and industries.

2. Apply the appropriate programming and analytical skills in data science and makepurposeful predictions to solve industrial and societal problems

3. Design new algorithms and *in-silico* interventions to develop entrepreneurial venturesand become successful professional

Scheme of Instruction and Examinations
(for students admitted from 2023-2024 & onwards)

Part	*Subject Code*	*Name of paper/component*	*Hours of instructions / week*		*Scheme of Examination*				
			T	*P*	*Duration of exam*	*CIA*	*CE*	*Total*	*Credit*
		First Semester							
I	23MBIC01	Basic Biology	3	-	3	40	60	100	3
	23MBIC02	Applied Mathematics in Bioinformatics	3	-	3	40	60	100	3
	23MBIC03	Basics in Computer and C Programming	4	-	3	40	60	100	4
	23MBIC04	Molecular Biology and rDNA Technology	3	-	3	40	60	100	3
	23MBIC05	Biological Databases and Sequence Analysis	4	-	3	40	60	100	4
	23MBIC06	Practical I - C Programming and Web Programming	-	5	3	40	60	100	4
	23MBIC07	Practical II - Biological Databases and Sequence Analysis	-	5	3	40	60	100	4
		Library	1						
II		CSS / Adult Education /Community Engagement and Social Responsibility	2	-	2	-	-	-	-
		Second Semester							
I	23MBIC08	Perl and Python	4	-	3	40	60	100	4
	23MBIC09	Structural Bioinformatics and R Programming	3	-	3	40	60	100	3
	23MBIC10	OMICs Technologies	3	-	3	40	60	100	3
	23MBIC11	Research Methodology and Statistics (Open Book Test)	3	-	-	100	-	100	3
	23MBIC12	Practical III - Perl and Python	-	5	3	40	60	100	4
	23MBIC13	Practical IV- Genomics and Proteomics	-	5	3	40	60	100	4
	23MBIC14	Mini Project	1	-	-	100	-	100	2
		Interdisciplinary course	4	-	3	40	60	100	4
II	23MXCSS1/ 23MXAED1/ 23MXCSR1	CSS / Adult Education /Community Engagement and Social Responsibility	2	-	2	-	-	100	2
II		Professional Certification	-	-	-	-	-	-	2

Part	*Subject Code*	*Name of paper/component*	*Hours of instructions /week*		*Scheme of Examination*				
			T	*P*	*Duration of exam*	*CIA*	*CE*	*Total*	*Credit*
Internship during summer vacation for one month									
Third Semester									
I	23MBIC15	Database Management Systems	3	-	3	40	60	100	3
	23MBIC16	Object Oriented Languages	4	-	3	40	60	100	4
	23MBIC17	Molecular Modeling, Simulation and Drug Designing	3	-	3	40	60	100	3
	23MBIC18	Big Data and Next Generation Sequencing	4		3	40	60	100	4
	23MBIC19	Systems Biology and Machine Learning	4		3	40	60	100	4
	23MBIC20	Practical V- Drug Designing and Next Generation Sequencing Data Analysis		4	3	40	60	100	4
	23MBIC21	Practical VI - Object Oriented Languages and Database Management Systems		4	3	40	60	100	4
	23MBIC22	Environmental Science and Disaster Management (Self Study)	1		3	40	60	100	4
		Multidisciplinary course	2	-	3	100	-	100	2
		Research Project	1	-	-	-	-	-	-
II	23MBIC23	Internship	-	-	-	100	-	100	2
Fourth Semester									
	23MBIC24	Research Project	30			100	100	200	8
		Total						2800	**98**

Minimum 98+2 credits to earn the degree

Other course to be undergone by the students

1. Professional Certificate Course - 2 Credits
2. MOOC Course (Any Semester before 4th Semester) - 2 - 4 Credits

Other Courses offered by the department

- **Inter Disciplinary Course:** 23MBII01 – Bioinformatics in Health
- **Multi-Disciplinary Course:** 23MBIM01 – Applications of EXCEL in Statistics
- **Professional Certificate Course** 23MBIPC1 - R Programming

Basic Biology

Semester I
23MBIC01

Hours of Instruction / week: 3
No. of credits: 3

Course Objectives:

- To understand how a biological system works
- To imbibe the biological concepts fundamental to Bioinformatics
- To prepare the learner to apply bioinformatics tools in research and industry

Unit I ***Chemical basis of life*** **9 hrs**

Composition of living matter; Water–properties, pH, ionization and hydrophobicity; Emergent properties of biomolecules in water; Biomolecular hierarchy; Macromolecules; Molecular assemblies; Structure-function relationships Amino acids – structure and functional group properties; Peptides and covalent structure of proteins; Elucidation of primary and higher order structures; Evolution of protein structure; Structure-function relationships in model proteins like ribonuclease A, expansion and hemoglobin, Tools to characterize expressed proteins.
Self Study : Highly conserved and least conserved proteins with examples

Unit II ***Enzyme catalysis*** **9 hrs**

General principles of catalysis; Quantitation of enzyme activity and efficiency; Enzyme characterization and Michaelis-Menten kinetics; Relevance of enzymes in metabolic regulation, activation, inhibition and covalent modification; Single substrate enzymes. Elucidation of metabolic pathways; Logic and integration of central metabolism; entry / exit of various biomolecules from central pathways; Principles of metabolic regulation; Regulatory steps; Signals and second messengers.
Self Study: Metabolic disorders –Phenylketonuria, Homocystinuria

Unit III ***Bioenergetics*** **9 hrs**

Basic principles; Equilibria and concept of free energy; Zero, first and second order kinetics, Laws of thermodynamics, isothermal process, entropy, reversible and irreversible processes; Concepts of enthalpy, internal energy and potential energy; Interrelation between potential energy and force, heat of formation, Coupled processes; Oxidative phosphorylation; Photosynthesis
Self Study: Glycolytic pathway; Kreb's cycle

Unit IV ***Introduction to Genetics*** **9hrs**

Basic concepts and terminologists, Mendelian principles of inheritance, sex linked inheritance, multiple alleles, polygenic inheritance, concepts of linkage, linkage maps and recombination, phenotype and genotype relationships, role of environment, extra-chromosomal inheritance, study of quantitative traits, genetics of populations, genetics and evolution,
Self study: Mutations: molecular, point and chromosomal mutations, hotspots. X-linked and autosomal disease.

Unit V ***Genome organization*** **9 hrs**

Levels of organization, Basic aspects of prokaryotic and eukaryotic cell, cell membranes. Role of nuclear matrix in chromosome organization and function; Matrix binding proteins; Heterochromatin and Euchromatin; DNA reassociation kinetics (Cot curve analysis); Repetitive and unique sequences; Satellite DNA; DNA melting and buoyant density; Nucleosome phasing; DNase I hypersensitive regions; DNA methylation & Imprinting, Overview of central dogma
Self study: Cell cycle and its regulation events during mitosis and meiosis

Total hours 45.

Text Books:

1. ***Dubey, R.C.*** (2014), ***A text book of Biotechnology,*** Revised Ed. S Chand.
2. ***Satyananarayana, U.,*** (2017), ***Biochemistry,*** 5th Ed.,Elsevier
3. **Snustad, D.P. and Simmons, M.J.** (2016), ***Principles of Genetics,*** 7th Ed, John Wiley & Sons
4. M. R. Duchen (2021) Bioenergetics A Practical Approach - Oxford University Press

Reference books:

1. ***Voet, D. and Voet, J.G.*** (2016), ***Biochemistry***, 5th edition, John Wiley, New York
2. ***Lehninger, A. L.*** (2017), ***Principles of Biochemistry***, 4th edition, W.H Freeman &Company.
3. ***Stryer, L.*** (2015), ***Biochemistry***, 8th edition, W.H. Freeman &Company
4. **Rajshekaran,** (2021), Biomolecules and Cell Biology, Academic Aspirations Publishers.

Course Outcomes: Students will be able to

1. Describe the importance of the basic chemicals of life and their functioning.
2. Explain the integration of metabolic process central to the logical understanding of life
3. Relate the concept of energy metabolism.
4. Differentiate the similarities and dissimilarities between prokaryotic and eukaryotic systems.
5. Demonstrate the evolutionary process of life and analyze how to apply bioinformatics for betterment of life.

Mapping of COs with POs & PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1	H		M	M	M						H	H	H	H
CO 2	H		M	H	H						H	M	H	M
CO 3	H		M	H	H						H	H	H	H
CO 4	H			H					M	H	H	H	M	L
CO 5	H			H					M	H	H	M	M	H

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;

H: High M: Medium L: Low

Applied Mathematics in Bioinformatics

Semester I **Hours of Instruction / week: 3**
23MBIC02 **No. of credits: 3**

Course Objectives:

- To understand basic concepts in mathematics that is frequently applied in different areas of bioinformatics
- To gain knowledge about the concepts in differentiation, calculus etc.
- To recognise basic concepts optimization techniques and application in modelling

Unit I ***Matrix Algebra*** **9 hrs**

Properties of Determinants, Minors and Cofactors, Reciprocal, Symmetric Determinants, Cramer's rule, Addition, subtraction, multiplication, transpose, inverse and conjugate of matrix, eigenvalue, eigenvector.
Self study: Properties of Determinants, Minors and Cofactors

Unit II ***Analytical Geometry and Vector*** **9 hrs**

Analytical Geometry: 2D coordinate geometry: equations of line, circle, ellipse, parabola, and hyperbola. Vector: addition, subtraction, dot and cross product.
Self study: equation of line

Unit III ***Numerical Differentiation and Integration*** **9 hrs**

Numerical Differentiation**:** Numerical differentiation – Derivatives through Newton's forward difference formula – Newton's backward difference formula – Maximum and minimum values of a tabulated function.
Numerical Integration: General integration formula – The Trapezoidal rule – Simpson's ⅓ rule – Simpson's ⅜ rule
Self study: Application of numerical differentiation and integration

Unit IV ***Differntial Equations*** **9 hrs**

Numerical solution of Ordinary Differential Equations: Taylor-series method – Euler and Modified Euler methods – Runge- kutta methods (upto third order only).
Self study: Improved Euler method

Unit V ***Linear Systems of Equations*** **9 hrs**

Linear Systems of Equations: Solution of linear systems – Direct Methods: Matrix Inversion Method – Gauss elimination method – Modification of Gauss method – Gauss Jordan method.
Solution of linear systems – Iterative Methods: Gauss – Jacobi method and Gauss – Seidel method.
Self study: Applications in biology

Total hours 45

Text Books:

1. ***Manickavachagom Pillay, T.K., Natarajan. T & Ganapathy, K.S*** (2009), ***Algebra,*** Vol-I
2. **Kandasamy, P.,*Thilagavathy, K. and Gunavathy, K.*** (2015), ***Numerical Methods***, 3rd Edition, S. Chand Co. Ltd., New Delhi
3. ***Rao, V., Krishnamurthy,N., Sarma, B. V. S. S, Sastry, A., and Ranganatham S. (2016). A text Book of B.Sc Mathematics,*** Vol. III, S Chand.

Reference Books:

1. ***Cummins*, J** (2007), ***Algebra: Concepts and Applications,*** McGraw-Hill, Carol Malloy, Glencoe/McGraw-Hill.
2. **Spivak, M** (2006) **Calculus**, 3rd. edition, Cambridge University Press.
3. **Burden, A.M., Burden, R.L., and Faires, J. D**(2016), **Numerical Analysis,** 10th Ed, Thomson Asia Pvt. Ltd., Singapore

Course Outcomes: Students will be able to

1. Use the fundamental concepts of matrix algebra;
2. Demonstrate the principles and applications in analytical geometry and vector functions;
3. Apply the numerical concepts in solving the differentiation and integration;
4. Identify and analyze complex problems in bioinformatics using numerical differential equation;
5. Apply linear equation system for solving challenges in academic, industrial and society

Mapping of COs with POs & PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO 3
CO 1	H	H		L	M							L	L	
CO 2	H	H		L	M							L	L	
CO 3	H	H	L	M	M							L	L	
CO 4	H		H	L	M					M		L	L	
CO 5	H	H		H	M					M		L	L	

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;

H: High M: Medium L: Low

Basics in Computer and C Programming

Semester I
23MBIC03

Hours of Instruction / week: 4
No. of credits: 4

Course Objectives:

- To understand fundamentals of computer
- To develop logic building skills that are used in programming
- To operate on files and file handling

Unit I ***Fundamentals of Computer and Algorithms*** **12 hrs**

History, Organization, Generations, operating system, memory and storage devices; Computer networking: Introduction to LAN, WAN, Intranet, Internet – ISP – VSAT, modem, fiber optics network, email, TCP/IP, WWW; Classification of programming languages; Types of processing: batch, real-time, online, offline. Types of modern computing: workstations, servers, parallel processing computing, cluster computing, grid computing. Characteristics of algorithm, algorithm design and analysis, algorithm complexity: Time and space complexity, Asymptotic notation, dynamic programming algorithm.

Self study: History, Organization and Generations of Computer

Unit II ***Fundamentals of C programme*** **12 hrs**

Character set in C , constants, key words in C, escape sequences, datatypes in C: integer, real, double, character and string; variables: rules for naming and assigning values to variable; Operators: arithmetic, unary, relational, logical, conditional, assignment, increment and decrement operators, library functions, datatype conversion: cast.

Self study: Keywords and History of C

Unit III ***Structure of a C program and Control statements*** **12 hrs**

Entering, saving, compiling and executing a C program: .c, .obj and .exe files, Input and output statements: simple problems with input and output statements; Control statements: if, if – else, nested if statements, unconditional goto, switch-case statements, Loops in C: for loop, while loop and do-while loop,

Self study: Application of numerical differentiation and integration

Unit IV ***Functions*** **12 hrs**

Roles of functions, main function, user-defined functions, parameter passing and return values in functions, structures in C, defining and using structures within structures, arrays: integer arrays. Character arrays, simple programs using functions, structures and arrays. Using simple problems like counting specific nucleotides, identifying type II restriction sites, calculation of Tm of oligonucleotides

Self study: Using character arrays as biological sequences

Unit V ***Pointers*** **12 hrs**

Pointers to functions, linked list, stack, queue, graphs, binary trees, threaded binary trees, File management: defining and opening a file, sequential and random access of files, closing a file; input/output operations on files, Exception handling in C

Self study: Macros, file inclusion and command line arguments in C

Total hours 60.

Text Books:

1. ***Balagurusamy*** (2017), ***Programming in Ansi C*** 7th Ed. McGraw Hill Education.
2. ***Bharihoke D.*** (2012), ***Fundamentals of Information Technology,*** Excel Books
3. ***Brian*** (2015), ***The C Programming Language,*** 2nd Ed. Pearson Education India
4. ***Graham, D.,*** (2016), C Programming: Language A step by step beginner's guide to learn C programming in 7 Days, *3rdEd.*.Great space \ independent Pub.

Reference Books:

1. ***Kanetkar, Y.*** (2016) ***Let us C***; 15th Ed. BPB Publications
2. ***Rajaraman, V.*** (2019), ***Computer programming in C,*** Prentice- Hall of India.
3. ***Ritchie, D.*** (2007), ***The C programming language***; Pearson Education.
4. **Jagadesh B., N., Murty AVSN, Koneti, D.,** (2018), Fundamentals of C Programming, 1st Ed., Himalaya Publishing House.

Course Outcomes: Students will be able to

1. Demonstrate an understanding of concepts in fundamentals of computer
2. Develop Computer programs by applying concepts of data types and control structures.
3. Ability to design and develop Computer programs, analyzes, and interprets the concept of pointers, declarations, initialization, operations on pointers and their usage.
4. Implement the algorithm and develop C Programming to solve problems in bioinformatics.
5. Develop confidence for self-education and ability for life-long learning needed for bioinformatics data analysis.

Mapping of COs with POs and PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1	H	M	H	L	L								H	H
CO 2	H	M	H	L	M							H	H	M
CO 3	H	M	H	L	M							M	M	
CO 4	H	M	H	L	M							M		H
CO 5	H		M		M					L	H			H

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;

H: High M: Medium L: Low

Molecular Biology and rDNA Technology

Semester I
23MBIC04

Hours of Instruction / week: 3
No. of credits: 3

Course Objectives:

- To gain knowledge about the genome organization
- To earn the methods of replication, transcription and translation
- To understand the concepts of rDNA technology and its applications

Unit I ***Genes and Genome complexity*** **9 hrs**

Gene complexity, SNPs, renaturation kinetics and genome complexity, nature of the genetic code, epigenetics; location and packaging of nucleic acids, functions of nucleic acids: DNA replication, Semi-conservative mechanism, enzymes involved in replication, DNA polymerases, helicases, topoisomerases, DNA ligase. Prokaryotic, mitochondrial, chloroplastic and eukaryotic DNA replication, DNA protection and repair system.

Self study: Manipulation of nucleic acids: basic tools and techniques, isolation and separation of nucleic acids.

Unit II ***Transcription and translation*** **9 hrs**

Transcription of DNA: promoter and terminator sequences in DNA, mechanism of transcription in prokaryotes and eukaryotes, inhibitors, post transcriptional processing, translation of mRNA, control of protein production: RNA interference, Molecular analysis of nucleic acid sequences: restriction mapping of DNA fragments, nucleic-acid blotting methods, design and production of gene probes.

Self-study: Labelling DNA

Unit III ***Polymerase Chain Reaction and Gene libraries*** **9 hrs**

PCR: Basic concepts, stages in PCR, primer design and bioinformatics, amplification templates, sensitivity of the PCR, alternative amplification methods, quantitative PCR, TaqMan System; Constructing gene libraries: digesting genomic DNA molecules, ligation, genomic DNA libraries, cDNA libraries.

Self study: cloning PCR products, Gibson Assemble Cloning System.

Unit IV Cloning **9 hrs**

Cloning vectors: plasmids, virus-based vectors, phage mid-based vectors, cosmid-based vectors, large insert-based vectors:
YAC, BAC, MAC, PAC vectors.

Self study: Vectors used in eukaryotes, Applications of gene cloning.

Unit V ***Expression of foreign genes*** **9 hrs**

Prokaryotic expression vectors, expression of eukaryotic genes, phage display technique, identifying and analyzing mRNA (PAGE, RT-PCR), analyzing genes *in situ*, analyzing protein-DNA interaction, transgenics and gene targeting, modulating gene expression by RNAi, CRISPER/cas9-based genome editing.

Self study: Analyzing genetic mutations and polymorphisms.

Total hours 45

Text Books:

1. ***Brown, T.A.,*** (2018), ***Genomes 4,*** Kindle Edition, Garland Science.
2. ***Dubey,*** (2008), ***A text book of Biotechnology,*** S Chand & Company. New Delhi
3. ***Jeyanthi G.P.*** (2009), ***Molecular Biology.*** MJP publishers 4.**Strachan Tom, Read Andrew P**, (2019), Human Molecular Genetics, 5th Ed., CRC press.

Reference books:

1. ***Brown, T. A.,*** (2016), ***Gene cloning and DNA analysis: An introduction, 7th Ed.*** Wiley-Blackwell.
2. ***Stryer, L., et al.,*** (2019), ***Biochemistry,*** *9*th Kindle edition, Blackwell Scientific Publication, USA.
3. ***Hofmann, A. and Clokie, S.,*** (2018), ***Wilson and Walker's -Principles and Techniques of Biochemistry and Molecular Biology,*** 8th Ed. Cambridge.
4. **Prabhakar, S., Banerjee S,** (2019), Molecular Biology, 1st Ed., Wisom Press.

Course Outcomes:

Students will be able to

1. Interpret the prokaryotic and eukaryotic genome structure and replication;
2. Explain the transcription and translation and apply in the analysis of nucleic acid sequences;
3. Outline the method of polymerase chain reaction and apply in the development of gene libraries;
4. Illustrate the method and applications of cloning.
5. Apply rDNA technology in analyzing genes.

Mapping of COs with POs& PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1	H			H						H	H		H	H
CO 2	H										H	H		M
CO 3	H	H	H		H				M	H		M	M	
CO 4		H	H	H	H			H	M			M		H
CO 5		H	H	H	H				M					

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;

H: High M: Medium L: Low

Biological Databases and Sequence Analysis

Semester I
23MBIC05

Hours of Instruction / week: 4
No. of credits: 4

Course Objectives:

- To build a strong background and potential in bioinformatics
- To give a detailed knowledge about biological databases and make the students familiar with various bioinformatics tools.
- To master the computational techniques used in biological sequence and structure analysis.

Unit I ***Introduction to bioinformatics and databases*** **12 hrs**

Bioinformatics: definition, aim, scope/research areas, branches and applications; Introduction to Biological databases: importance and functioning; types of biological databases: nucleic acid databases, protein sequence and structure databases, specialized databases, genome databases, mapping databases, carbohydrate databases, model organism databases, literature databases; Sequence and molecular file formats, information retrieval systems - Entrez and SRS.

Self study: History of Bioinformatics, Hybridoma databank structure, Virus information system, Cell line information systems.

Unit II ***Sequence alignment*** **12 hrs**

Molecular sequence alignment: Importance, homology, identity, similarity; Scoring matrices: PAM and BLOSUM; Pairwise alignment algorithm: global (Needleman and Wunsch) and local alignment (Smith and Waterman), statistical analysis of pairwise alignment; BLAST: introduction, types and steps, BLAST algorithm for local alignment search and gene discovery, megablast, PSI-BLAST, DELTA-BLAST, PHI-BLAST; FASTA search algorithm and types; Multiple sequence alignment: Progressive alignment methods, Iterative method (DIALIGN, MultiAlin), Genetic algorithm, HMM, Pfam, SMART, InterPro and iProClass, Profilescan, PROBE, Clustal.

Self-study: DNA alignment via UCSC, Galaxy, Ensemble

Unit III ***Molecular phylogeny and evolution*** **12 hrs**

Molecular Phylogeny: Goals, historical background, molecular clock hypothesis; properties and types of phylogenetic trees; Stages of phylogenetic tree construction and methods: distance-based (UPGMA, NJ), phylogenetic inference (Maximum parsimony), model-based phylogenetic inference (Maximum Likelihood), Tree inference (Bayesian method), tree evaluation (Bootstrapping).

Self study: Software packages for phylogenetic analysis

Unit IV ***Analysis of nucleotide sequence*** **12 hrs**

Gene prediction and regulation of prokaryotes and eukaryotes: ORFs, promotor and regulatory region; gene finding methods: Neural Network, problems in gene finding, constructing restriction maps; RNA – types, level of organization and prediction of secondary structure of RNA; searching RNA specific genes and importance with case studies.

Self study: transcriptional elements, primer design and probe synthesis, algorithms for Tm calculation

Unit V ***Analysis of protein sequence*** **12 hrs**

Protein sequence analysis: ExPASy tools, protein property prediction, tools for peptide cleavage and mapping; Protein structure and classification; protein structural analysis: alignment and significance, DALI; Protein secondary structure prediction methods: Neural Network, HMM.

Self study: Molecular visualization tools: RasMol, DeepView.

Total hours 60

Text Books:

1. ***Pevsne. J.,*** (2019), *Bioinformatics and Functional Genomics*, 3rd Ed. Wiley Blackwell.
2. ***Xiong,J.,*** (2006), *Essential Bioinformatics*, Cambridge University Press.
3. ***Lesk, M.A.*** (2014), *Introduction to Bioinformatics*, 4th Ed. Oxford University Press, New York

Reference books:

1. ***Baxevanis, A,.***(2009), *Bioinformatics- A practical guide to the analysis of Genes and proteins, 3rd Ed.*. Willey
2. ***Campbell, A.M. and Heyer, L.J.*** (2013), *Discovering Genomics, Proteomics and Bioinformatics, 2nd Ed.* pearson Education INC, India
3. ***Mount.*** (2005) *Bioinformatics - Sequence and Genome analysis*. Cold Spring Harbor Laboratory Press
4. ***Mohiuddin,A., Sakibkhan, P.,*** *(2019), Data Analytics: concepts, techniques and applications,* CRC Press Taylor and Francis Group.

Course Outcomes: Students will be able to

1. explain types of data available from the most common sequence and structure databases;
2. elucidate the theories underlying sequence searches and alignment;
3. demonstrate the different approaches of creating phylogenetic trees and evaluating them;
4. Illuminate the nucleotide sequence and structure with various bioinformatics tools;
5. analyse protein sequence and structure with relevant methods and algorithms.

Mapping of COs with POs& PSOs

CO / PO	**PO 1**	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PO 9**	**PO 10**	**PO 11**	**PSO 1**	**PSO 2**	**PSO3**
CO 1	H	H		L	M							L	L	L
CO 2	H	H		L	M							L	L	L
CO 3	H	H	L	M	M							L	L	L
CO 4	H		H	L	M					M		L	L	M
CO 5	H	H		H	M					M		L	L	H

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;

H: High M: Medium L: Low

Practical I - C Programming and Web Programming

Semester I
23MBIC06

Hours of Instruction / week: 5
No. of credits:4

Course Objectives:

- To get exposure in operating system and data processing
- To understand programming concepts and develop logic building skills in programming
- To operate on functions, structures, pointers and file handling

Expt. No.	**Content**
1	Programs with conditional statements
2	Programs with looping statements
3	Programs with functions
4	Programs with structures
4	Programs using arrays
5	Programs using character arrays as biological sequences: simple problems like counting specific nucleotides, identifying restriction sites and calculation of Tm of oligonucleotides
6	Programs using pointers
7	Programs to construct and use linked list, stack, queus
8	Simple programs on file management
9	Working with MS Office
10	Working with DOS – internal and external commands
11	Working with Linux architecture, basic commands and Text Editors
12	Creating web pages using HTML and XML

Total hours 75

Text Books:

1. **Gómez et al.,** (2022), Red Hat Enterprise Linux 9 Administration - Second Edition, Packt Publishing
2. **Balagurusamy** (2017), Programming in Ansi C 7th Ed. McGraw Hill Education.
3. **Brian** (2015), The C Programming Language, 2nd Ed. Pearson Education India

Reference Books:

1. **Kanetkar, Y.** (2016) Let us C; 15th Ed. BPB Publications
2. **Rajaraman, V.** (2019), Computer programming in C, Prentice- Hall of India
3. **Kernighan, B., Ritchie, D.,** (2019), The C Programming Language, Third Edition, Pearson Paperback

Course Outcomes: Students will be able to

1. Work and execute programs in Linux platform
2. Develop Computer programs by applying concepts of HTML.
3. Design and develop Computer programs, analyzes, and interprets the concept of pointers, declarations, initialization, operations on pointers and their usage.
4. Implement the algorithm and develop C Programming tool for biological data analysis.

Develop confidence and ability for life-long learning needed for bioinformatics.

Mapping of COs with POs& PSOs

CO/PO	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PSO1	PSO2	PSO3
CO 1	H		H		L	L							H	H
CO 2	H		H	L	M							H		M
CO 3	H		H	L	M							M	M	
CO 4	H	H	M		L							M		H
CO 5	H				M					L	H			

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes; H: High M: Medium L: Low

Practical II - Biological Databases and Sequence Analysis

Semester I **Hours of Instruction / week: 5**
23MBIC07 **No. of credits: 4**

Course Objectives:

1. To understand nucleotide and protein sequence analysis
2. To acquire knowledge about the algorithms in analysis
3. To realize the applications of bioinformatics

Expt. No.	Content
1	Biological databases, Information retrieval using Entrez, SRS
2	Nucleotide BLAST, Protein blast, PSI-BLAST, DELTA-BLAST, PHI-BLAST, MegaBLAST, HMMER, BLAT
3	FASTA algorithm
4	Near and Far relative sequence identification using BLAST
5	Multiple sequence alignment : Clustal, NJ plot
6	PHYLIP – construction of rooted and unrooted phylogenetic trees
7	Sequence analysis using UCSC Genome Browser, Ensembl browser, Galaxy
8	Gene finding programs (GeneMark, GenScan)
9	Protein sequence analysis : ExPASy Proteomic tools
10	Molecular visualization: downloading atom coordinates from PDB: using the coordinate files to view the molecules using molecular visualization tools
11	Structure analysis using DeepView (Swiss PDB Viewer). Selecting display, measuring bond length, distance between specific atom, bond angle, torsion angle, construction of Ramachandran plot

Total hours 75.

Text Books:

1. **Pevsner,. J.** (2019), **Bioinformatics and Functional Genomics,** 3rd Ed. Wiley Blackwell.
2. **Xiong, J.,** (2006), **Essential Bioinformatics,** Cambridge University Press
3. **Lesk, M.A.** (2014), **Introduction to Bioinformatics,** 4th Ed. Oxford University Press, New York

Reference books:

1. **Baxevanis, A.** (2009), **Bioinformatics- A practical guide to the analysis of Genesand proteins,** 3rd Ed.. Willey
2. **Campbell, A.M. and Heyer, L.J.** (2013), **Discovering Genomics, Proteomics and Bioinformatics,**
   2nd Ed. pearson Education INC, India
3. **Mount.** (2005) **Bioinformatics - Sequence and Genome analysis.** Cold Spring HarborLaboratory Press

Course Outcomes: Students will be able to

1. Explain types of data available from the most common sequence and structure databases;
2. Apply different database search tools for searching data;
3. Analyse tools for sequence analysis and interpret the data effectively;
4. Understand the free online tools for phylogenetic analysis;
5. Understand the importance of biomolecules structure and interpret data.

Mapping of COs with POs& PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO 3
CO 1	H	H									H		H	H
CO 2		M									L	H		M
CO 3		H	H		M	M			L			M	M	
CO 4		H	H								L	M		H
CO 5			H		M				L		M			

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;
H: High M: Medium L: Low

Perl and Python

Semester II **Hours of Instruction / week: 4**
23MBIC08 **No. of credits: 4**

Course Objectives:

- To obtain the basic knowledge in Perl and Python programming
- To write powerful Perl and python scripts for bioinformatics applications
- To write modules in Bioperl and Biopython

Unit I Introduction to Perl **12 hrs**

Features of perl; Input/output operations in Perl, Scalar Data and Operators, Control Structures, Lists and Arrays, Hashes.

Self study: Perl control structures.

Unit II Regular expressions and File handling **12 hrs**

Regular Expressions in Perl, Subroutines, Packages and Modules; File handling, Files and Directories in Perl.

Self-study: CGI programming using Perl.

Unit III *Introduction to Python* **12 hrs**

Basic Syntax, Datatypes, String Processing, Simple input and output operations, Control Structures, Exceptions, Lists, Tuples, Dictionaries

Self study: Control structures

Unit IV Python programming **12 hrs**

Functions and modules. Classes and Objects, Regular expressions in Python, Libraries, Debugging, Exception Handling.

Self study: Debugging

Unit V *Bio Perl and BioPython* **12 hrs**

Basics in BioPerl, writing and executing small modules in BioPerl.
Simple programs in Biopython - Fetch a PDB entry from the RCSB Web server, Extracting the complete CDS from a GenBank entry.

Self study: Installation of Perl and Python

Total hours 60.

Text Books:

1. ***Bhattacharya* , *S.*** *et al., (2003) Beginning Red Hat Linux 9,* Wiley Dream Tech India. Wiley Blackwell.
2. ***Christiansen T., Foy B. D., and Wall L.*** *(2015), Programming Perl,* 4th Ed. O'REILLY
3. ***Chan J.,*** (2017), *Learn Python in One day and Learn it well, 2nd Ed.* #1 Best Seller
4. **Joel,, G.** (2019), Data Science from Scratch: First principles with python, 2nd Ed., Shroff Publishers and Distributors.

Reference books:

1. ***Lutz M.,*** (2019), *Learning Python,* 5th Ed. O'REILLY
2. ***Mount.*** (2005) *Bioinformatics - Sequence and Genome analysis.* Cold Spring Harbor Laboratory Press
3. ***Petersen and Richard*** (2006), Linux: *The Complete Reference, 6th Ed.*. MacGraw Hill
4. **Kenneth, L., Martin, O,** (2020), Fundamentals of Python, Cengage Learning India.

Course Outcomes: Students will be able to

1. Understand the Perl scripts for demonstrating data manipulations
2. Develop substantial Python scripts using data structure for representing biological data.
3. Write the regular expressions in perl and python to solve scientific problems
4. Explain the fundamental concepts of the foundations of Python and Perl their role in data science and big data
5. Use the bioperl and biopython modules for tackling challenges, analyze and interpret biological data.

Mapping of COs with POs& PSOs

CO / PO	**PO 1**	**PO 2**	**PO 3**	**PO 4**	**PO 5**	**PO 6**	**PO 7**	**PO 8**	**PO 9**	**PO 10**	**PO 11**	**PSO 1**	**PSO 2**	**PSO3**
CO 1	H	H	L	L	M				M			H	H	H
CO 2	H	H	L	L	M				H			H		M
CO 3	H	M	H	M	H				L	L		M	M	H
CO 4	H	H	M	L	L				L	L		M	H	H
CO 5	M	H	H	M	M	L				L	L			

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;
H: High M: Medium L: Low

Structural Bioinformatics and R Programming

Semester II **Hours of Instruction / week: 3**
23MBIC09 **No. of credits: 3**

Course Objectives:

- To understand the knowledge on the basics of bonding and structure of macromolecules.
- To gain knowledge on the structures prediction and interaction of macromolecules.
- To realize the basics in R programming

Unit I ***Chemical bonding and Stereochemistry*** **9 hrs**

Chemical bonding: definition, types, Non-bonded interactions: Van der Waals, electrostatic, different types of hydrogen bonding and hydrogen bond like interactions, hydrophobic interaction. Valence bond theory: sigma, pi bond and hybridization. Molecular orbital theory and its applications;
Stereoisomerism: geometrical and optical isomerism, racemization and optical rotation, asymmetric centers, enantiomers, diastereomers, meso compounds. Rotational isomers and concept of hindered rotation; anti, syn, gauche conformations.
Self study: Structure of water; solvent - solute interaction, Cahn-ingold priority rules, Symmetry elements and operations.

Unit II ***Carbohydrates and lipids*** **9 hrs**

Carbohydrates: The various building blocks (monosaccharides), configurations and conformations of the building blocks; formations of polysaccharides and structural diversity due to the different types of linkages.
Lipids: definition, classification of lipids on backbone structure. Structure and biological importance of glycosaminoglycans. Structure of fat- and water-soluble vitamins.
Self-study: Glyco-conjugates: various types of glycolipids and glycoproteins, lipoproteins.

Unit III ***Nucleic acids and proteins*** **9 hrs**

Nucleic acids – Structure of bases and nucleotides. Level of organization, Types of base pairing in DNA and RNA. Watson- Crick and Hoogsteen; types of double helices (A, B, Z), triple and quadruple stranded DNA structures
Proteins – structure and classification of amino acids, level of organization. Motifs and domains. Conformational properties of proteins.
Protein folding - fundamental principles, methods to study protein folding – phi, psi and omega angles. Ramachandran plot. Factors determining protein folds – helices, strands, turns, loops, disulfide linkages. Mechanism of protein folding, role of chaperons, factors determining protein stability.
Molecular interactions – protein-protein, protein-DNA, DNA-drug, protein-lipid, protein-ligand, protein-carbohydrate. **Self study**: Physical and Chemical properties of nucleic acids, Metal coordination in metalloproteins, inter- and intra- molecular interactionsk

Unit IV ***Protein folding and molecular interactions*** **9 hrs**

Experimental methods of structure determination: Fundamentals of X-ray diffraction, NMR spectroscopy and Cryo-electron microscopy.
Computational methods of protein tertiary structure prediction methods: Homology Modeling, Fold Recognition, *Ab-intio* method.
Motif and Domain: Motif databases and analysis tools. Domain databases and Analysis tools. HMM (Hidden Markov Model): Introduction to HMM, its application in Sequence alignment and HMM based Softwares. Role of neural network in structure prediction.
Self study: Protein structure analysis and validation tools.

Unit V *R Programing* **9 hrs**

Essentials of R-Package and libraries, mathematical operations, string operations, Data structures: vectors, data frames, lists, matrices, Control loops: if, else, while for loops. File Input/Output operations. R plots and the graphics library. . Data representation: Qualitative and quantitative data types, Tabulation and visual display of data, plotting line plot, scatter plot, frequency histograms, pie-chart, heat map and 3D plots.

Self study: Applications in statistics

Total hours 45.

Text Books:

1. ***Bourne, P.,*** (2009), ***Bioinformatics, 4th Edition,*** 2^{nd} Ed. Wiley-Blackwell
2. ***Fisher, J, Arnold, J., Fisher, J., Arnold, J.,*** (2012), ***BIOS Instant Notes in Chemistry for Biologists***, Taylor & Francis, London
3. ***Negi A. S., & Anand, C. S.,*** (2023), ***A Textbook Of Physical Chemistry***, 3 Rd Edition , New age international (p) ltd
4. ***Zumel, N., Mount., J.,*** (2019) ***Practical Data Science with R, Second Edition.*** Manning

Reference books:

5. ***Baxevanis, A.D.*** (2020), *Bioinformatics. A practical guide to the analysis of genes and proteins.*
6. ***Burkowski, F.,*** (2008) *Structural Bioinformatics: An algorithmic Approach.* 1^{st} Ed. Chapman and Hall
7. ***Rastogi et al.,*** (2022) B***ioinformatics, Fifth edition,*** PHI Learning Pvt. Ltd
8. ***Upadhyay, A.*** (2020), ***Biophysical Chemistry,*** Himalaya Publishing House Pvt. Ltd..

Course Outcomes: Students will be able to

1. Explain bonding and their arrangements in a molecules.
2. Define the structure of carbohydrate, lipids and its importance
3. Realize the structure of nucleic acids, proteins and its importance
4. Describe the basic principles of experimental methods for the determination of macromolecules structure an duse of different types of protein prediction tools
5. Acquire the knowledge of R programming for data analysis and plotting

Mapping of COs with POs and PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO 3
CO 1	M	M	H	M		M	L			M			H	H
CO 2	H	H	H	H		M				M		H		M
CO 3	H	H	H	H			M			M		M	M	
CO 4	H	H	H	H		H	M			M		M		H
CO 5	H			H		H	H			M				

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes; H: High M: Medium L: Low

OMICs Technologies

Semester II
23MBIC10
Hours of Instruction / week: 3
No. of credits: 3

Course Objectives:

- To provide a broad overview of the goals, methods, and applications for OMICs in life sciences.
- To familiarize the terminology, underlying principles and strategies, and the technical methodologies involved
- To enable the students to compare and contrast the strengths and limitations of the methodology.

Unit I ***Genomics*** **9 hrs**

Introduction: Overview of Genomics and Genome Architecture (Genome maps), C value Paradox, Genome diversity, Genome sequencing strategies (Shotgun, massive parallel sequencing), assembly and annotation; Genome Projects: Human Genome Project, HapMap Project, GWAS, Evolutionary Genomics, Metagenomics

Self study: ENCODE; Genome Browsers: Ensembl, UCSC

Unit II ***Transcriptomics*** **9 hrs**

Transcriptomics: EST, SAGE, Microarray: Designing and producing microarray, types of microarray: cDNA micoarray and oligonucleotide array, analysis of microarray data: normalization, detecting differential gene expression, correlation of gene expression data to biological process, clustering with case studies

Self study: Database: GEO and ArrayExpress.

Unit III ***Metabolomics*** **9 hrs**

Introduction to metabolites, Classic analysis method – capillary electrophoresis, chromatography, spectrophotometry, use of GC/MS and NMR in metabolomics. Metabolomic data analysis tool, metabolic pathways resources: KEGG, Biocart; Applications, Glycomics, Lipidomics, global systems biology

Self study: databases in metabolomics: HMDB, GMD, METLIN

Unit IV ***Proteomics*** **9 hrs**

Classicapproachinproteomeresearch–gelbased,separationtechniques,Proteinsequencing–Chemicalandenzymaticprotein fragmentation, Amino acid sequence analysis - Edman degradation, Mass spectrometry in proteomics and description of mass spectrometer, Mass spectral analysis, Complex peptide mixture analysis: liquid chromatography coupled to mass spectrometer (LC-MS), *de novo* protein sequencing by mass spectrometry, proteomic approach to posttranslational modification analysis, protein-protein interactions: experimental methods, Co-immune precipitation, affinity purification, yeast two-hybrid assays, FRET, computational methods: gene neighbor and gene cluster methods, phylogenetic profile method, rosette stone method, sequence co-evolution method, classification methods, protein-protein interaction database: STRING, 2D-PAGE, PDBrs.

Self study: Vectors used in eukaryotes, Applications of gene cloning.

Unit V ***Integrating OMICs and its applications*** **9 hrs**

Integrating Omics data – Computational methods; Meta analysis, Bayesian graphical model for integrative analysis, Applications - Evolutionary Genomics, Comparative genomics, Personal genomics – Ethical, legal and Social issues – Metagenomics, CRISPR spacer

Self study: Integration of cancer – omics data on a whole-cell pathway model

Total hours 45 .

Text Books:

1. ***Brown, T.A.***, (2018), ***Genomes 4,*** Kindle Edition, Garland Science.
2. ***Campbell, A.M. and Heyer, L. J.*** (2006) ***Discovering Genomics, Proteomic and Bioinformatics,*** 2nd Edition, Cold Spring Laboratory Press
3. ***Pevesner, J.*** (2019) ***Bioinformatics and Functional Genomics,*** 2ndEditon, Wiley-Blackwell publisher

Reference books:

1. ***Brown, T. A.,*** (2016), ***Gene cloning and DNA analysis: An introduction, 7th Ed.*** Wiley-Blackwell.
2. ***Stryer, L., et al.,*** (2019), ***Biochemistry, 9th*** Kindle edition, Blackwell Scientific Publication, USA.
3. ***Wilson and Walker's*** (2018), ***Principles and Techniques of Biochemistry and Molecular Biology,*** 8th Ed. Hofmann and Clokie

Course Outcomes: Students will be able to

1. Outline genomics and genome database and genome browsers;
2. Plan experiments with the knowledge gained;
3. Illustrate key technologies involved in metabolomics;
4. Explain key technologies in proteomics;
5. Apply omics data in understanding and the management of disease.

Mapping of COs with POs& PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1	H	H	H	M	M	L						H	H	H
CO 2		H	H	M	M	M			L	L		H		M
CO 3	H	M	H	H	M	L				L		M	M	
CO 4	H	M	H	H	M							M		H
CO 5				H	H	M	L	H		M	M		H	M

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;

H: High M: Medium L: Low

Research Methodology and Statistics (Open Book Test)

Semester II **Hours of Instruction / week: 3**
23MBIC11 **No. of credits: 3**

Course Objectives:

- To understand the statistical tools, concepts of hypothesis testing and its importance in biological research
- To know the aspects fundamental to research and to understand the methods of research
- To know the nuances of technical writing of scientific documents like thesis and journal articles

Unit I ***Statistical survey and data collection*** ***9* hrs**

Statistical survey – Organization of a statistical survey, methods of data collection, data representation, diagrammatical and graphical representation of data. Sampling fundamentals – need for sampling, properties of an ideal sample, sampling procedures.
Self study: Frequency distributions, sampling distributions, standard error

Unit II Measures of central tendency, deviation, correlation and regression ***9 hrs***

Measures of central tendency – arithmetic mean, median, mode. Measures of deviation – range, quartile deviation, variance, standard deviation Correlation and regression – correlation analysis and regression analysis

Self study: Relationship between mean, median and mode; pros and cons of the measures of central tendency and deviation; applications of correlation and regression

Unit III ***Probability and hypothesis testing*** ***9* hrs**

Probability and theoretical distributions – probability definition, types, binomial, Poisson and normal distributions, large and small samples, degrees of freedom. Hypothesis testing – Formulation of null and alternate hypotheses, testing the hypothesis, Student's *t* test, Chi square test and goodness of fit, Analysis of Variance (one way and two way only), acceptance and rejection of hypothesis.
Self study: Simple problems on probability, theoretical distributions, hypothesis testing; importance of hypothesis testing

Unit IV ***Research methodology*** ***9* hrs**

Research methodology – meaning of research, objectives of research, types of research, research methodology and research designs, single blind and double blind trials. Inclusion and exclusion criteria – importance of inclusion and exclusion criteria in animal and human research with special reference to clinical research (elementary concepts only), examples and case studies
Self study: Random block design; importance of single blind and double blind studies

Unit V ***Report Writing*** ***9* hrs**

Writing a thesis – layout of the thesis, preparing the components of the thesis – hypothesis, abstract, introduction, review of literature, methodology, results, discussion, summary and conclusion, references. Writing a journal article – format of an article – journal requirements – differences between the thesis components and article components; abstract preparation – concise presentation, outline of work presented; keywords – list of important technical terms; main article – introduction, materials and methods, results, discussion, presentation of tables, figures and graphs, conclusion, acknowledgement, references, conflicts of interest. Avoiding plagiarism – definition of plagiarism, ethical issues, copyright issues
Self study: Different formats of thesis; plagiarism-detection software; ShodhGanga and ShodhGangotri
Conceive the best presentation mode for their results in the form of a thesis and journal article(s)

Total hours 45.

Text Books:

1. ***Gupta, S.P.*** (2010) ***Statistical methods***, Sultan Chand and Sons, New Delhi
2. ***Day, R.A.*** (2006) ***How to write and publish a scientific paper***, Cambridge University Press, UK
3. ***Banerjee, P.K.*** (2008) ***Introduction to Biostatistics***, S. Chand and Co., New Delhi

References:

1. ***Kothari, C.R.*** (2019) ***Research Methodology, Methods and Techniques***, 6th Edition, New Age International Publishers, New Delhi
2. ***Alred, G.J., Bursaw, C.T. and Oliu, W.E.*** (2003) ***The Handbook of Technical Writing***, McGraw Hill Publishers, NewJersey
3. ***Arumugam N.*** (2016), Research Methodology for life sciences, Saras Publications, India

Course Outcomes: Students will be able to:

1. Understand basics of survey, sampling and data collection
2. Ascertain whether a given set of biological data are statistically significant or not by applying the appropriate hypothesis testing method
3. Devise the research methodology for their dissertation and design a project based on the research problem presented to them by their supervisor
4. Compile their results from the dissertation work and integrate the interpretation in relation to the published literature in their area of research

Mapping of COs with POs& PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1	H		H	M			L				L	H	L	L
CO 2	H		M	L			L				L	H	L	L
CO 3	H		M	M		M	L				M	H	L	L
CO 4	H		L	M		M	L				M	H	L	L
CO 5	H		L	M		M	L				M	H	L	L

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;

H: High M: Medium L: Low

Practical III - Perl and Python

Semester II
23MBIC12

Hours of Instruction / week: 5
No. of credits: 4

Course Objectives:

- To provide skills in writing Perl and Python programming.
- To apply the Perl and Python programming skill in biological data analysis
- To enable the students to write module using BioPerl and BioPython

Expt. No.	**Content**
1	Simple programs using Input/output operations using Perl
2	Simple program using loops, list and array strings in Perl
3	Simple programs using Hashes, Regular Expressions and Subroutines
4	Simple programs using File handling in Perl
5	Simple programs using Bioperl
6	Simple programs using Control structures in Python
7	Simple programs using Lists in Python
8	Simple programs using Functions and modules in Python
9	Simple programs using Classes and Objects, Regular expressions in Python and Biopython
10	CGI concept using Perl and Python

Total hours 75.

Text Books:

1. ***Bhattacharya , S. et al., (2003) Beginning Red Hat Linux 9,*** Wiley Dream Tech India. Wiley Blackwell.
2. ***Christiansen T., Foy B. D., and Wall L. (2015), Programming Perl,*** 4th Ed. O'REILLY
3. ***Chan J.,*** (2017), ***Learn Python in One day and Learn it well, 2nd*** *Ed.* #1 Best Seller
4. **Lambert Kenneth A, Osborne Martin,** (2020), Fundamentals of Python, Cengage Learning India.

Reference books:

1. ***Lutz M.,*** (2019), ***Learning Python***, 5th Ed. O'REILLY
2. ***Mount.*** (2005) ***Bioinformatics - Sequence and Genome analysis***. Cold Spring Harbor Laboratory Press
3. ***Petersen and Richard*** (2006), **Linux:** ***The Complete Reference, 6th Ed.***. MacGraw Hill

Course Outcomes: Students will be able to

1. Design the Perl scripts for demonstrating data manipulations
2. Analyse the substantial Python scripts using data structure for representing biological data.
3. Demonstrate ability to think, analyze and write programs to solve biological problem.
4. Develop and use modules of BioPerl and BioPython for tackling challenges and analyze biological data.
5. Understand and explain the fundamental concepts of the foundations of Python and Perl their role in data science and big data

Mapping of COs with POs and PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1	H	H	L	L	M				M				H	H
CO 2	H	H	L	L	M				H			H	H	M
CO 3	H	M	H	M	H				L	L		M	M	
CO 4	H	H	M	L	L				L	L		M		H
CO 5	M	H	H	M	M	L				L	L	H		

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;

H: High M: Medium L: Low

Practical IV - Genomics and Proteomics

Semester II
23MBIC13

Hours of Instruction / week: 5
No. of credits: 4

Course Objectives:

1. To isolate and purify the protein and DNA from bacteria
2. To learn tools for data analysis
3. To know about high-throughput technology

Expt. No.	**Content**
1	Genomic Sequence Analysis tool
2	Comparative genomics – VISTA
3	Microarray Data Analysis – DNA and Protein
4	Isolation of DNA – Bacteria and Plants
5	Isolation of RNA and Quantitation
6	Blotting Techniques – Demo
7	Isolation of Protein – Demo
8	Purification of Protein – Demo
9	SDS PAGE – Demo
10	2D PAGE– Demo

Total hours 75.

Text Books:

1. ***Brown, T.A.,*** (2006), ***Gene COning- An Introduction,*** 5th Edition, Blackwell Publishing Company, USA
2. ***Cambell, A. M. and Heyer, L.J.*** (2006) ***Discovering Genomics, Proteomic and Bioinformatics,*** 2nd Edition, Cold Spring Laboratory Press
3. ***Pevesner, J.*** (2019) ***Bioinformatics and Functional Genomics, 3rd*** Editon, Wiley-Blackwell publisher

Reference books:

1. ***Rinaldis, E.D. and Lahm, A.*** (2007) ***DNA Microarrays, Horizon Bioscience,*** Causton H.C
2. ***Primrose S.B. and Twyman R.*** (2008) ***Principles of Genome Analysis and Genomics***, Blackwell Publishing
3. ***Croline et al.,*** (2014) ***Fundamentals of Omics Technologies Vol 63 of Comprehensive Analytical Chemistry***, Newnes, Spain

Course Outcomes: Students will be able to:

1. Design the genomics and genome database and genome browsers;
2. Apply the techniques related with genomics, proteomics, and transcriptomic;
3. Estimate DNA, RNA and proteins from the sample;
4. Use isolation techniques to design experiments;
5. Realize omics data in understanding and the management of disease

Mapping of COs with POs& PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1	H	H	M	M	L							H	H	H
CO 2					M	M	M	H	H	L	L	H		M
CO 3	H	M	H	H	M	L						M	M	
CO 4			H	M	H	H	M					M		H
CO 5				H	H	M	L	H		M	M		H	H

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes; H: High M: Medium L: Low

Mini Project

Semester II
23MBIC14 **No. of credits: 2**

Database Management Systems

Semester III
23MBIC15

Hours of Instruction / week: 3
No. of credits: 3

Course Objectives:

- To obtain knowledge in the concepts of data, data models and relationships.
- To impart the fundamental concepts of database design, database languages, and database system implementation.
- To make the students familiar with MS-Access, Oracle and SQL and to become an entrepreneur.

Unit I ***Fundamentals of DBMS concept*** **9 hrs**

Purpose of database systems, data, data abstraction, instances and Schemas, data independence, data models, E-R model basic concepts: Entity sets, relationship sets, mapping constraints, keys, E-R schema to tables. Relational model: basic structure, relational algebra, tuple relational calculus, domain relational calculus. assertions, triggers, functional dependencies

Self study: Data Mart and Data Warehouse, Design of an E-R database schema.

Unit II *Normalization* **9 hrs**

Informal design guidelines for relational schemas, functional dependencies, normal forms based on primary keys, general definitions of second and third normal forms, Boyce-Codd normal form, Concurrency control Techniques-Two phase locking, Time stamp ordering.

Self study: Network and Hierarchical data model.

Unit III *SQL* **9 hrs**

Introduction to Oracle, SQL Features, Types of SQL Commands: DDL, DML and TCL commands. Integrity Constraints, Operators, GROUP BY and HAVING Clause, Sub Queries, Joins, Character Functions, Numeric Functions, Date Functions, Conversion Functions, Aggregate Functions, Roles and Privileges, Data Control Language: GRANT, REVOKE.

Self study: Roles and Privileges.

Unit IV ***PL/SQL*** **9 hrs**

Overview of PL/SQL, Advantages of PL/SQL, PL/SQL Character Set, Data Types, Basic Structure, Variables, Constants, If- then-else Structure, Attribute: %type, %rowtype. Iteration in PL/SQL: For loop, While loop. Cursors: Basics, Using a cursor for a multirow SQL query.

Self study: Stored procedures: Procedures, Functions, Exception Handling: Predefined and User defined. Triggers.

Unit V ***PHP and MySQL*** **9 hrs**

Introduction to PHP - Configuring and installation-Apache, PHP, MySQL - Handling html form with PHP - Structure and syntax- Constant, Variable, Superglobals, Data types, Operators, Expression and PHP tag–ECHO and PRINT Statements - Decisions and loop – Function – String – Array – Numeric, Associative, Multidimensional- Forms – Filters - Cookies and Sessions - Setting cookies with PHP, Using cookies with sessions, Deleting cookies, Registering session variables - Working with file and directories–Exception Handling

Self study: Connecting to MySQL - Selecting the Database - Executing Simple Queries - Retrieving Query Results

Total 45 hrs

Text Books:

1. ***Elmasri, R and Navathe, B. S.*** (2016), ***Fundamentals of Database Systems***, Seventh Edition, Tata McGraw Hill Publications.
2. ***Leon, A. and Leon, M.*** (2008), ***SQL: A Complete Reference***, Sixth edition, Tata McGraw Hill.
3. ***Nixon,*** R. (2018), ***Learning PHP, MySQL, JavaScript***, CSS & HTML5, Paperback, O'reilly, 5th Edition.

Reference books:

1. ***Silberschatz, A., Korth, H. F. and Sudarshan, S.*** (2019), ***Database System Concepts***, Seventh Edition, Tata McGraw Hill Publications.
2. ***Date, C.J.*** (2006). ***An Introduction to database systems***, Addison Wesley, Third Edition. Total hours : 60 Page 46 of 80
3. ***Deshpande, P. S.*** (2008). ***SQL/PL SQL for Oracle 9i***, Reprint Edition, Dream Tech Press

Course Outcomes: Students will be able to

1. Outline the database management system;
2. Plan and design relational database by understanding functional dependencies;
3. Illustrate the basics of SQL and constructs queries using SQL
4. Design a relational database schema using SQL for a given problem-domain;;
5. Apply the concept of concurrency control of database processing.

Mapping of COs with POs and PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1	H	M	M	M	L							H	M	H
CO 2	H	M	M	M	L							H	M	H
CO 3	H	M	M	M	L							H	M	H
CO 4	H	M	M	M	L							H	M	H
CO 5	H	H	H	M	M	M	L		H	H	H	H	H	H

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes; H: High M: Medium L: Low

Object Oriented Languages

Semester III
23MBIC16

Hours of Instruction / week: 4
No. of credits: 4

Course Objectives:

1. To identify the benefits of using C++ and object-oriented programming techniques for application development
2. To understand the fundamental Object Oriented Concepts
3. To solve simple and moderately complex problems using C++ and Java for execution of need-based novel projects in industries

Unit I *Introduction to Object Oriented Programming* **12 hrs**

Concepts: Encapsulation, Abstraction, Polymorphism, Classes, Messages Association, Interfaces. Introduction to C++: Features of C++, Basics of C++, Data Types and sizes, User defined Data Types, Variables, Constants and its types: Character Constants, String Constant, Operators.
Self study: OOP vs. procedure-oriented programming, Difference between C and C++.

Unit II *Object and Classes in C++* **12 hrs**

Implementation of class in C++, Friend functions and inline function. Different forms of Constructor, Destructor, Abstract class.
Self study: Control structures, Operator overloading

Unit III *Inheritance and polymorphism* **12 hrs**

Type of Inheritance - Virtual base classes – pointers to derived classes – Virtual functions – Polymorphism - formatted I/O – I/O manipulators - File Handling– Templates and Exception Handling.
Self study: File I/O Basics – Binary I/O – Random access.

Unit IV *Introduction to Java* **12 hrs**

Comparison in Java and C++, Simple Java program. Data types, Keywords, Modifiers, Variables, Constants, Operators and Separators, Control Structures, String handling, Interfaces, Garbage Collection.
Self study: History of Java, Features of Java and Packages.

Unit V *Multithreading and GUI* **12 hrs**

Multithreading, Exception Handling, Input Stream & Output Stream, Java Applets Basics.
Self study: BioJava – Installation and basic sequence manipulation (Nucleic acids).

Total 60 hrs

Text Books:

1. ***Schildt, H.*** *(2007). Java - A Beginners Guide (4th Ed.), Tata Mc-Graw-Hill publication*
2. ***Balagurusamy, E.*** *(2003), Object Oriented Programming with C++,PHI*
3. ***Bloch, J.*** (2017) *Effective Java.* 3rd ED. Addison-Wesley professional

Reference books:

1. ***Horstmann, C.S.*** *(2000). Computing Concepts with Java 2 Essentials (2nd Ed.) by John Wiley Publishers.*
2. ***Bhave, O.M.P. and Patekar, S.*** *A. (2004). Object Oriented Programming with C++, Pearson Education, Singapore Pvt Ltd.*
3. ***Kaladhar*** (2012). *BioJava: A programming Guide.* Lap Lambert

Course Outcomes: Students will be able to:

1. Discuss the basic concepts in OOPs;
2. Apply classes in writing program;
3. Design the Inheritance and file handling in OOPs;
4. Know how to apply Java and Biojava and sequence analysis;
5. Demonstrate Java Applets and GUI.

Mapping of COs with POs and PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1	H	H	M	M			L					H	H	M
CO 2	H	H	M	M			L					H	H	M
CO 3	H	H	M	M			L					H	H	M
CO 4	H	H	M	M			L					H	H	M
CO 5	H	H	H	H	H	H	L	L		L		H	H	H

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes; H: High M: Medium

Molecular Modeling, Simulation and Drug Designing

Semester III
23MBIC17

Hours of Instruction/week :3
No. of credits:3

Course Objectives:

- To provide students with a comprehensive understanding of quantum mechanical methods in solving electronic structure of molecule
- To impart knowledge on the basic concepts and principles of molecular mechanics
- To develop broad knowledge and conceptual base in the field of drug design and discovery

Unit I *Basics in molecular modeling and Quantum mechanics method* 9hrs

Molecular structure and internal energy, types of movements, Schrödinger equation, One-electron atoms, Poly electronic atoms and molecules, The Born-Oppenheimer approximation, The Hartree-fock approximation Basis sets, Roothaan-Hall approach (Concepts only). Semi-empirical Methods, potential energy calculation using *ab initio* method.

Self Study: Input formats for computation: Z matrix, MIME, GAUSSIANZ matrix, GAMES format

Unit II *Molecular Mechanics and Energy minimization* 9hrs

Molecular mechanics: General features of molecular mechanics force field bonded interaction: bond stretching, angle bending, torsional terms. Non- bonded interactions, force field parametrization and transferability, Types of Force Field: AMBER, CHARM and MM. Energy Minimization: Potential energy surfaces, Convergence Criteria, Characterizing Stationary Point, Optimization methods: Non derivative (Golden section search, parabolic method and downhill simplex method) Global Minimization: simulated annealing, Genetic algorithm

Self study: Derivative methods: First-order- Steepest descent minimization, Conjugate gradient method, second-order–Newton-Raphson and Quasi-Newton method.

Unit III *Molecular Dynamics and Simulation methods* 9hrs

Phase space, ensembles and ergodic hypothesis (concepts only), Newtonian dynamics, Integrating the equation of Motion: Leapfrog and Verlet algorithm, predictor-corrector algorithm, potential truncation and shifted-force potentials, Implicit and explicit Solvation models, Periodic boundary condition, Monte Carlo simulation methods.

Self study: Application of Molecular dynamics.

Unit IV *Computer Aided Drug Discovery* 9hrs

Three dimensional structure of macro molecular targets, active site of a target molecule, lead compound. Computer-aided molecular Design, Analog Based drug design:-Pharmacophores, 3D database searching, conformation searches, deriving and using 3D Pharmacophore, constrained systematic search, detection techniques, maximum likelihood method. Structure based drug design:-receptor based, ligand based Docking. types of search methods, docking algorithm and scoring functions, *De Novo* Drug Design: Fragment Placements, Connection Methods, Sequential Grow, Virtual screening.

Self study: Drug design: stages in Drug discovery process. Target identification and validation, lead optimization and validation with case studies, Pharmacognosy.

Unit V *Structure Activity Relationship and Cheminformatics*

9hrs

Introduction to 2D/3D QSAR, Various Descriptors used in QSAR, Regression Analysis, The Significance and Validity of QSAR Regression Equations, Partial Least Squares (PLS) Analysis, Multi Linear Regression Analysis. Steps in QSAR. Cheminformatics: conventions for representing molecules 2D and 3D–application of cheminformatics in drug design -AI in drug design.

Self study: Principle Components Analysis in the QSAR equations.

Total hours 45

Text Books:

1. ***Bloch, J.*** (2017) ***Effective Java.*** 3rdED. Addison-Wesley professional
2. ***Schildt, H.*** *(2007)* ***.Java- A Beginners Guide*** *(4thEd.), Tata Mc-Graw- Hill publication*
3. ***Balagurusamy, E.*** *(2003),**ObjectOrientedProgrammingwithC++**,PHI*

Reference books:

1. ***Horstmann, C.S.*** *(2000).* ***Computing Concepts with Java 2 Essentials*** *(2ndEd.) by John Wiley Publishers.*
2. ***Bhave, O.M.P. and Patekar, S.A.*** *(2004).* ***Object Oriented Programming with C++,*** *Pearson Education, Singapore Pvt Ltd.*
3. ***Kaladhar*** (2012). ***Bio Java: A programming Guide.*** Lap Lambert
4. ***Deshpande, P.S.*** (2008) ***.SQL/PLS QL for Oracle 9i,*** Reprint Edition, Dream Tech Press

Course Learning Outcomes: Students will be able to:

1. Identify the complexity of different quantum mechanical methods
2. Illustrate the basic concept of molecular mechanics
3. Infer the outcomes of molecular dynamics simulation
4. Relate the molecular structure and biological activity
5. Solve their own research problems by applying the concept computational methods of drug discovery

Mapping of COs with Pos

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	O 8	PO 9	PO 10	PO 11	PSO 1	PS O2	PS O3
CO 1	H		H	M		M						H		M
CO 2	M	H	H	H		H				M		H	M	M
CO 3	M	H	H	H		H				M		H	H	H
CO 4	H	H	H	H		M				M		H	H	H
CO 5	H	H	H	L		H				M			H	H

CO- Course Outcomes; PO- Program Outcomes; PSO- Program Specific Outcomes;
H: High M: Medium L: Low

Big Data and Next Generation Sequencing

Semester III
23MBIC18
Hours of Instruction / week:4
No. of credits:4

Course Objectives:

- To introduce advances in sequencing technology
- To gain knowledge about the basic concepts in big data
- To understand the role of bioinformatics in large data analysis and get insights in the field of health sciences industry

Unit I ***Introduction to Big Data*** **12 hrs**

Introduction to Big Data platform, challenges of conventional systems, intelligent data analysis,, nature of data – analytic process and tools. Sources and Uses of Big data, Analyzing Big data- Cluster Computing, Map Reduce, Hadoop & Cloud Computing. Types of big data in biological science. Internet Based consumer health information – telehealth and telemedicine, biomedical data: acquisition, storage and use, Electronic health records, information retrieval form digital libraries, imaging systems in radiology and picture archiving.
Self Study: Big data Challenges in Bioinformatics

Unit II ***DNA sequencing and NGS platform*** **12 hrs**

DNAsequencingtechnologies:Sanger,chemicalmethod,Pyrosequencing.,NextGenerationSequencing:Introduction,NGSplatfor ms(basicconceptsonly):Roche/454FLX, Illumina/Solexa Analyzer, SOLiD system, Helicos Heliscope, Pacific Bioscience/single molecule real time, biological application of NGS: whole genome sequencing, Exome Sequencing, Transcriptome sequencing, Epigenome sequencing, Interactome sequencing and methyl mesequencing (basic concepts only). File/Data formats overview: FASTA, FASTQ, FNA, CSFASTA, GFF. QC and preprocessing of NGS data. fastX and fastQC tools for data filtering, read trimming, adapter clipping.
Selfstudy: NGS Database: SRA, DRA, ENA.

Unit III ***Genome assembly algorithm*** **12 hrs**

Reference based assembly: Indexing the genome – Hash table, Suffix tree, BWA, FM Index; Sequence assembly concepts and challenges in assembling short reads; De-novo assembly: Greedy algorithm, shortest superstring problem. overlap-layout-consensus, de Bruijin and Euler path approach, String graph assembler. Sequence alignment formats: SAM and BAM format. Assembly Tools and its Parameters, Scaffolding and Constructing Draft Genome Genome alignment and analysis tools- BWA (Burrows-Wheeler Aligner), SAM tools, GATK, HISAT, StringTie, Cuffcompare, Velvet, Oases, Trinity
Self study: SOP denovo, Velvet

Unit IV ***RNA-Seq / Chip Sequence Data analysis*** **12 hrs**

RNA-Seq Data Analysis: Introduction to RNA-Seq Sequencing Alignment, Alignment Tools and its Parameters, Alignment quality Assessment, Statistical Analysis and genome Visualization, Qualitative & Quantitative Gene Expression Profiling, Gene Modifications & Alternative Splicing Analysis.

Differential Gene Expression Profiling, Gene Ontology and Pathway Analysis; ChIP Sequencing Aligning ChIPSeq data to genome, Peak Calling Analysis, Peak Annotation and Visualization tools, Motif Analysis
Self study: Bioconductor libraries in R

Unit V *Variant* and Exome Analysis **12 hrs**

Identification somatic and germline variations from genome resequence: SNPs, SNVs, translocation, copy number variation. Variation Analysis, Variation analysis to identify SNV / MNV / SV, dbSNP Annotation / Variation Effect Prediction, Variation Frequency Analysis. Genome wide association studies. Exome sequencing - Exome Enrichment Analysis, Target
/Non-Target Enrichment Analysis, Exome Copy Number Variation Analysis

Self study: Genome wide association studies (GWAS)

Total 60 hrs

Text Books:

1. *Brown, S.M.* (2013) *Next generation DNA sequencing Informatics,* Cold spring harbor laboratory
2. Wang, X. (2016) Next Generation Sequencing Data Analysis; CRC Press.
3. Kappelmann-Fenzl, M. (2021) Next Generation Sequencing and Data Analysis, Sprinker link
4. Kim. J.H. (2019) Genome data anlaysis, Springer Nature Singapore
5. Melanie Kappelmann-Fenzl (2021) ***Next Generation sequencing and data analysis***, Springer

Reference books:

1. Low, L.W.Y. and Tammi, M.T. (2017) Bioinformatics: A Practical Handbook Of Next Generation Sequencing And Its Applications, World Scientific Publishing company
2. Wing-Kin Sung (2017) Algorithms for Next-Generation Sequencing, CRC Press
3. Ortutay, C and Ortutay, Z (2017) Molecular Data analsis using R, Wiley Publisher
4. Xianyong Wang, Zhenghua Wang (2023) *Sequence Analysis and Parallel Computing,* Tsinghua University
5. Shili Lin, Denise Scholtens, Sujay Datta (2022) *Bioinformatics Methods: From Omics to Next Generation Sequencing,* Chapman and Hall/CRC; 1st edition

Course Outcomes: Students will be able to

1. Acquire knowledge on big data and health information
2. Illustrate the principles and types of NGS platforms
3. Compare and contrast the different formats and tools for NGS;
4. Gain skills on different types of NGS data analysis
5. Obtain skills in extracting knowledge from NGS data

Mapping of COs with POs and PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO 3
CO 1	H	H	H	H	M	M	M	M				H	H	H
CO 2	H	H	H	H	M	M	M	M				H	H	H
CO 3	H	H	H	H	M	M	M	M	M	H		H	H	H
CO 4	H	H	H	H	M	M	M	M	M	H	M	H	H	H
CO 5	H	H	H	H	H	H	M	M	M	H	M	H	H	H

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;
H: High M: Medium L: Low

Systems Biology and Machine Learning

Semester III
23MBIC19

Hours of Instruction / week:4
No.ofcredits:4

Course Objectives:

- Biology is moving from molecular to modular. To understand how these molecules interact each other to form modules that act as functional systems
- To understand and to predict cellular behaviors leading to disease states and drug response
- To apply machine learning strategies in data analysis for applications in industries

Unit I ***Introduction to systems biology*** ***12*** **hrs**

The need for systems analysis in biology, importance. Biological networks: Basic concepts, Links to network. Measurement techniques: Time series comprehensiveness, Item comprehensiveness, Next Generation experimental system. System structure identification: Bottom-up approach, Top-down approach.

Self study: SYSTOME project.

Unit II ***Modeling Biochemical reactions*** ***12*** **hrs**

Deterministic models: Michaelis-Menton modeling, Quasi-steady state approximation, Allosteric reaction, regulation of enzymatic reaction -Stochastic models: Stochastic derivative, Gillespie algorithms

Metabolic networks: Basic features, reconstruction methods. Transcriptional regulatory networks: basic properties, lac operon in E coli, Gal regulation in yeast, determining the basic building blocks and structural properties, reconstruction of regulatory networks. Signaling networks: cell signaling pathway-cAMP and MAP-kinase, Signal flow- Pathway to network

Self study: Protein-protein interaction, Regulation of metabolic network

Unit III ***Cellular simulations*** ***12*** **hrs**

Simulation analysis methods: FBA, MCA, Computational cell biology: the stochastic approach

Modules to functions: control systems. Module boundaries: sharp and fuzzy, interaction between subcellular modules, emergence of cellular functions from subcellular modules - SBML models, MathSBML, Cell Designer, Systems biology workbench, DBRF- MEGN

Self study: Computer simulation of the cell: Human erythrocyte model and its applications

Unit IV ***Introduction to Machine learning*** ***12 hrs***

Introduction of machine learning - Hypothesis, Version space, MAP, Maximum likelihood.

Classification: Preliminaries; General approach to solving a classification problem; Decision tree induction; Rule-based classifier;

Nearest-neighbor classifier, SVM.

Self study: use of ML in drug discovery and gene expression analysis

Unit V ***Machine learning analysis*** ***12*** **hrs**

Association Analysis: Problem Definition; Frequent Item set generation; Rule Generation; Compact representation of frequent item sets; Alternative methods for generating frequent item-sets, Neural Networks, Cluster Analysis: Overview, K-means, Agglomerative hierarchical clustering, DBSCAN with case studies

Self study: Image analysis with case study

Total 60 hrs

Text Books:

1. ***Kitan, H..*** (2001). *Foundations of systems biology.,* The MIT Press. Cambridge
2. ***Cho, S..*** (2007). *Introduction to systems biology*, Humara Press, New Jersey
3. ***Voit*** (2013) *A first course in systems biology.* Garland Science

Reference books:

1. ***Alon, Y.*** (2007). *An introduction to Systems Biology*. Chapman &Hall.
2. ***Barillo, E.,*** *et al.* (2012).*Computational Systems Biology*. CRC Press, Taylor & Francis group

Course Outcomes:

Students will be able to:

1. Comprehend the basic concepts and measurement techniques in system biology analysis
2. Understand the mathematical modeling of biochemical reactions and pathways construction
3. Apply simulation techniques and perform basic data processing and analysis
4. Realize the basics in machine learning
5. Apply machine learning in data analysis with example

Mapping of COs with POs and PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1												H	H	H
CO 2	H	H	H	H	M	M	M		M	H	H	H	H	H
CO 3	H	H	H	H	M	M	M		M	H	H	H	H	H
CO 4	H	H	H	H	M	M	M		M	H	H	H	H	H
CO 5	H	H	H	H	H	H	M	M	M	H	H	H	H	H

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;
H: High M: Medium L: Low

Practical V

Drug Designing and Next Generation Sequencing Data Analysis

Semester III
23MBIC20

Hours of Instruction / week: 4
No. of credits: 4

Objectives:

- To obtain knowledge about the Molecular docking and dynamics
- To gain knowledge in R and apply NGS data analysis
- To develop drug using Molecular docking

Expt. No	Content
1	Assembling short reads from an organism, computing N50/L50, coverage and length of longest contig
2	Identification of SNPs; annotating the SNPs using UCSC browser; subtracting and intersecting vcf files from various samples using bedtools.
3	RNA-Seq Data analysis – identifying differentially expressed genes –Gene Enrichment and Pathway analysis
4	CHiP sequence data analysis – Peak Identification – Motif analysis
5	Computer-aided drug design – Lead compound optimization, ADME studies and Docking
6	Quantitative Structure Activity Relationship (QSAR)
7	Molecular dynamics using Gromacs

Total 60 hrs

Text Books:

1. ***Gupta and Prakash, S.*** (2013) *QSAR and Molecular modelling* Springer, I edition
2. RNAseq Data Analysis: A Practical Approach; CRC Press, 2014
3. Big Data Analysis for Bioinformatics and Biomedical Discoveries; CRC Press (2015)

Reference Books:

1. ***Ramachandran, K. I. Deepa,G. and Namboori, K*** (2008) *Computational Chemistry and Molecular Modelling: Principles and Application,* Springer
2. ***Schlick,T.*** (2010) *Molecular modelling and simulations: An interdisciplinary guide.* Springer.
3. ***Merz., K*** (2010) *Drug design: Structure- and ligand –based Approaches.* 1st Ed. Cambridge University Press

Course Outcomes:

Students will be able to

1. Create database and querying and creating reports;
2. Apply the basic concept in drug discovery;
3. Demonstrate the HTVS in drug discovery process;
4. Solve their own research problems by applying the concept computational methods of drug discovery;
5. Plan placement in pharmaceutical and biotech companies.

Mapping of COs with POs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO3
CO 1		H	L	L	M				M			H	H	H
CO 2	H	H	L	L	M				H			H	H	H
CO 3	H	M	H	M	H				L	L		H	H	H
CO 4	H	H	M	L	L				L	L		H	H	H
CO 5	M	H	H	M	M	L				L	L	H	H	H

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;
H: High M: Medium L: Low

Practical VI - Object Oriented Languages and Database Management Systems

Semester III **Hours of Instruction / week: 4**
23MBIC21 **No. of credits: 4**

Course Objectives:

- To get exposure in OOPs concept.
- To gain program knowledge in C++, Java and BioJava
- To develop software using C++ and java programming

Expt No	Content
1.	C++ programming – simple programs using class and inheritance.
2.	C++ programming – simple programs using operator overloading, file handling.
3.	C++ programming – simple programs using exception handling
4.	Simple programming with objects, arrays and loops in Java
5.	Simple programming with inheritance and multithreading
6.	Simple programming in Java Applets
7.	Creating database using data definition language
8.	Modifying database using data manipulation language
9.	Data control language in RDBMS
10.	Transaction control in RDBMS

Total 60 hrs

Text Books:

1. *Schildt, H. (2007). Java - A Beginners Guide (4th Ed.), Tata Mc-Graw-Hill publication*
2. *Balagurusamy, E. (2003), Object Oriented Programming with C++, PHI*
3. *Joshua Bloch* (2017) *Effective Java.* 3rd ED. Addison-Wesley professional

Reference books:

1. *Horstmann, C.S. (2000). Computing Concepts with Java 2 Essentials (2nd Ed.) by John Wiley Publishers.*
2. *Bhave, O.M.P. and Patekar, S. A. (2004). Object Oriented Programming with C++, Pearson Education, Singapore Pvt Ltd.*
3. *Kaladhar* (2012). *BioJava: A programming Guide.* Lap Lambert

Course Outcomes: Students will be able to

1. Apply the basic concepts of C++ in data analysis;
2. Demonstrate the basic concepts in Java in data analysis
3. Write program using C++, Java and BioJava in data handling
4. Derive the java applets in designing
5. Able to create databases and creating reports

Mapping of COs with POs and PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO 3
CO 1	H	H	H	H	H				M	H	H	H	H	H
CO 2	H	H	H	H	H				M	H	H	H	H	H
CO 3	H	H	H	H	H	H			M	H	H	H	H	H
CO 4	H	H	H	H	H	H			M	H	H	H	H	H
CO 5	H	H	H	H	H	H			M	H	H	H	H	H

CO- Course Outcomes; PO- Programme Outcomes; PSO- Programme Specific Outcomes;
H: High M: Medium L: Low

Environmental Science and Disaster Management (Self Study)

Semester III **Hours of Instruction / week: 1**
23MBIC22 **No. of credits: 4**

Course Objectives:

- To enhance knowledge skill and attitude to environment
- To provide knowledge on various local environmental aspects
- To provide knowledge on disaster management

Unit I *Introduction* 3 hrs

Multidisciplinary nature of environmental studies: Definition, scope and importance, Need for public awareness.

Natural Resources: Renewable and non renewable resources, Role of individual in conservation of natural resources, equitable use of resources for sustainable lifestyles

Unit II *Environmental pollution and Environmental legislation* 3 hrs

Pollution: Causes, effects and control measures of air, water, soil, marine, noise, thermal and nuclear hazards. Solid waste management, pollution case studies

Climate change, global warming, acid rain, ozone layer depletion and nuclear accidents. Case Studies.

Environment Protection Act, Issues involved in enforcement of environmental legislation, Public awareness.

Unit III *Biodiversity and conservation* 3 hrs

Introduction & definition: genetics, species and ecosystem diversity, Biogeographical classification of India, value of biodiversity, biodiversity at global, national and local level, India as a mega-diversity nation, hot-spots of biodiversity, threats to biodiversity, endangered and endemic species of India, Conservation of biodiversity: In-situ and Ex-situ conservation of biodiversity

Unit IV *Disaster management* 3 hrs

Types of Disasters (Natural and Manmade - Floods, earthquake, landslide, cyclone, heat waves, lightning and fire)

Vulnerability Assessment and Risk Analysis: Vulnerability to various disasters (Flood, Cyclone, Earthquake, Heat waves and Lightning)

Unit V *Institutional Framework in Disaster Management* 3 hrs

Institutional Framework: Institutional arrangements for disaster management (National DisasterManagement Authority (NDMA), State Disaster Management Authority (SDMA), District Disaster Management Authority (DDMA), National Disaster Response Force (NDRF)

Preparedness Measure: Disaster Management Cycle, Early Warning System, Pre-Disaster and Post-Disaster Preparedness, Strengthening of SDMA and DDMA, Community Preparedness, Stakeholder Participation, Corporate Social Responsibility (CSR)

Survival Skills: Survival skills adopted during and after disaster Flood, Cyclone, Earthquake, Heatwaves and Lightning.

Total hours 15.

Text Books:

1. ***Boersema***(2009), ***Principles of Environmental Sciences,*** Springer
2. ***Kapoor, S.K*** (2011) ***International Law and Human Rights,*** Jain Book Depot
3. ***Bharucha, E*** (2004) ***Textbook for Environmental Studies for Undergraduate Courses of all Branches of Higher Education,*** University Grants Commission
4. **IGNOU** (2012)**Conceptual and Institutional Framework of Disaster Management** IGNOU, New Delhi

Reference Books:

1. ***Schoc, M.R.*** (2012). ***Case Studies in Environmental Science,*** Jones & BartlettPublishers
2. ***Miller, T and Spoolman, S*** (2012). *Environmental Science*, Brooks / Cole

Course Outcomes:

Students will be able to

1. Understand the core concepts of environmental studies and the significance of conservation of ecosystem
2. Comprehend the concepts of different ecosystems and the impact of pollution on environment and their management
3. Develop knowledge about biodiversity and its conservation
4. Learn about the different types natural disasters and their risk assessment
5. Comprehend the institutional framework in disaster management in India

Mapping of COs with POs and PSOs

CO / PO	PO 1	PO 2	PO 3	PO 4	PO 5	PO 6	PO 7	PO 8	PO 9	PO 10	PO 11	PSO 1	PSO 2	PSO 3
CO 1	H		L		L				H	H	H	H	L	L
CO 2	H		L		L				H	H	H	H	L	L
CO 3	H		L		L				H	H	H	H	L	L
CO 4	H		L		L				H	H	H	H	L	L
CO 5	H		L		L				H	H	H	H	L	L

CO- Course Outcomes; PO- Programme Learning Outcomes; PSO- Programme Specific Outcomes

H: High M: Medium L: Low