

M.Sc., BIOINFORMATICS

VISION

- Our Vision is to create holistic Bioinformatics professionals who are competitive globally.

MISSION

M1: To provide excellence in Bioinformatics/Computational Biology

M2: To Upgrade and update the techniques involved in Bioinformatics/Computational Biology for reaching global heights

M3: To develop individuals with the knowledge and skill to contribute for a better society

PROGRAMME EDUCATIONAL OBJECTIVES (PEO)

The Graduates of the programme will:

PEO1: Are knowledgeable, innovative, and highly valued professionals in industry, academia, or government

PEO2: Will achieve peer-recognition; as an individual or in a team; through demonstration of good analytical, design and implementation skills

PEO3: Will thrive to pursue life-long learning to become accustomed in the World of emerging Technology

PROGRAMME OUTCOMES (PO)

The Students of Bioinformatics Department will have the ability to:

PO1: Apply mathematics, Statistics and Information Sciences to solve Biological Problems

PO2: Identify, formulate, analyze and solve Biological problems through Algorithm Development

PO3: Design and develop solutions for problems in Biology through program development

PO4: Investigate complex Biological problems through statistical analysis

PO5: Use the Online and Academic licensed Bioinformatics resources for Biological Data Analysis

PO6: Understand and fulfill the needs of the Society

PO7: Develop proposals for developing a sustainable environment

PO8: Understand the professional and ethical responsibility

PO9: Work efficiently as an individual or as a team

PO10: Communicate clearly with the Bioinformatics Community as well as Society

PO11: Entail life-long learning process to keep them updated in the latest innovations in Bioinformatics

PO12: Manage scientific project proposals through financial principles

PROGRAMME SPECIFIC OUTCOMES (PSO)

After the Completion of M.Sc Bioinformatics the students are:

PSO1: Trained in interdisciplinary subjects that require analysis of Biological data, development of algorithms, and implementation of programs to analyze and store Biological data.

PSO2: Provided Hands on Experience in Basic Microbiology, Biochemistry and Genetic engineering, Biotechnology.

PSO3: Well trained to pursue academic careers in research and R&D careers in industry in the areas of Bioinformatics/Computational Biology

MAPPING OF VISION, MISSION AND PROGRAMME EDUCATIONAL OBJECTIVES OF THE DEPARTMENT

Vision	Mission	Programme Educational Objectives (PEO)
<ul style="list-style-type: none"> Our Vision is to create holistic Bioinformatics professionals who are competitive globally. 	<ul style="list-style-type: none"> To provide excellence in Bioinformatics/Computational Biology To Upgrade and update the techniques involved in Bioinformatics/Computational Biology for reaching global heights To develop individuals with the knowledge and skill to contribute for a better society 	Are knowledgeable, innovative, and highly valued professionals in industry, academia, or government Relates to M1
		Will achieve peer-recognition; as an individual or in a team; through demonstration of good analytical, design and implementation skills Relates to M3
		Will thrive to pursue life-long learning to become accustomed in the World of emerging Technology Relates to M2

Mapping of PEOs and POs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
PEO1	2	2	2	2	2	3		3					3		
PEO2	3	3	3	3	3	2			3					3	
PEO3							3			3	3	3			3

(Correlation: 3 – High, 2- Medium, 1- Low)

POST GRADUATE PROGRAMME: M.Sc., Bioinformatics
CHOICE BASED CREDIT SYSTEM (CBCS PATTERN)
(For the candidates admitted from 2023-24 onwards)

Semester	COURSE CODE	TITLE OF THE COURSE	Nature	Instructional Hours/ Week	Credit Points	Exam Duration	MARKS		
							CIA	ESE	Total
I	23PBI1C01	CORE: Fundamentals of Biological Systems	CC	6	5	3	25	75	100
	23PBI1C02	CORE: Computational methods for Sequence Analysis	CC	6	5	3	25	75	100
	23PBI1C03	CORE: Introduction to Computers and Programming in C (<i>Employability</i>)	CC	6	5	3	25	75	100
	23PBI1E01/ 23PBI1E02	ELECTIVE: Molecular Interactions (OR) Biophysics and Crystallography	DSE	4	3	3	25	75	100
	23PBI1CP1	Practical I: Fundamentals of Biological Systems (<i>Skill Development</i>)	CC	4	3	6	25	75	100
	23PBI1CP2	Practical II: Programming in C and Computational Biology (<i>Skill Development & Employability</i>)	CC	4	3	6	25	75	100
II	23PBI2C04	CORE: Genetic Engineering & Bioethics(<i>Employability</i>)	CC	6	5	3	25	75	100
	23PBI2C05	CORE: Molecular Evolution and Phylogenetics	CC	6	5	3	25	75	100
	23PBI2C06	CORE: Database Management Systems(<i>Employability</i>)	CC	6	5	3	25	75	100
	23PBI2E01/ 23PBI2E02	ELECTIVE: Big Data Analytics (OR) Artificial intelligence in Biology	DSE	4	3	3	25	75	100
	23PBI2CP3	Practical III: Genetic Engineering (<i>Skill Development & Employability</i>)	CC	4	3	6	25	75	100
	23PBI2CP4	Practical IV: Database Development and Molecular Phylogenetics (<i>Skill Development & Employability</i>)	CC	4	3	6	25	75	100

III	23PBI3C07	CORE: Genomics and Proteomics (<i>Employability</i>)	CC	6	5	3	25	75	100
	23PBI3C08	CORE: Systems Biology	CC	6	5	3	25	75	100
	23PBI3C09	CORE: Molecular Modelling and Computer Aided Drug Design(<i>Employability</i>)	CC	6	5	3	25	75	100
	23PBI3E01/ 23PBI3E02	ELECTIVE: Pharmacogenomics (OR) Basics of Cheminformatics	DSE	4	3	3	25	75	100
	23PBI3CP5	Practical V: OMICS and Systems Biology (<i>Skill Development</i>)	CC	4	3	6	25	75	100
	23PBI3CP6	Practical VI: Molecular Modeling and Drug Design(<i>Skill Development & Employability</i>)	CC	4	3	6	25	75	100
IV	23PBI4C10	CORE: Biostatistics and BioScripting (<i>Employability</i>)	CC	6	5	3	25	75	100
	23PBI4C11	CORE: Research Methodology	CC	6	5	3	25	75	100
	23PBI4CP7	Practical VII: Scripting (<i>Skill Development & Employability</i>)	CC	4	3	6	25	75	100
	23PBI4PVV	Project work & Viva voce	CC	14	5	-	25	75	100
		Total			90				2200
	-	Summer Internship*		-	2	-	-	-	-
	-	Swayam-MOOC-Online		-	2	-	-	-	-
IV	20PDIS404	Digital Security		2	2	2	-	-	50
		Total		120	90+2				2200
				+2	+2+2				+50

CC – Core Course; DSE – Department Specific Elective

* Summer Internship to be taken by the Students for a duration more than 15 days in an Industry/ Research/Academic Institute by the end of first year and Assessment to be done at the end of fourth Semester

VALUE ADDED COURSE

NAME OF THE COURSE	COURSE CODE	HOURS	TOTAL MARKS
Certificate Course in Computer Aided Drug Discovery	23PCCCAD1	30	100

SEMESTER: I

COURSE CODE: 23PBI1C01

TITLE OF THE COURSE: CORE: FUNDAMENTALS OF BIOLOGICAL SYSTEMS

COURSE OBJECTIVES:

- To recall and introduce the students to the Fundamentals of Biological system such as Cell Biology, Enzymology and Immunology.
- To introduce the students to Molecular Biology.

COURSE OUTCOMES:

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

CO1	Summarize the structure and functions of various cell organelles through Cell biology	K1
CO2	Classify the macromolecules based on their properties	K2
CO3	Interpret the enzymes and immune systems based on enzymology/immunology	K2
CO4	Classify the genetic material and central dogma of life through genome organization	K2
CO5	Examine the different operon concepts and gene mutations through their gene regulation	K4

Syllabus

Total Credits: 5

Instructional hours: 90

UNIT I: Fundamentals of Cell (K1)

18 hours

Cell - Definition, Structure of prokaryotic cells: Bacteria and Viruses, Microbial Physiology- Nutrition and growth. Structure of eukaryotic cells: cell wall - cell membrane – cytoplasm - Structure and function of cellular organelles - Mitochondria, Chloroplast, Endoplasmic Reticulum, Golgi complex, Lysosomes, Ribosomes, Cytoskeleton, Nucleus. Differences and similarities in plant and animal cells. Cell division and cell cycle: Mitosis and meiosis, their regulation, steps in cell cycle, and control of cell cycle.

(Self-study: Microbial Physiology- Nutrition and growth)

UNIT II: Macromolecules (K2)

18 hours

Macromolecules: Introduction to Carbohydrates and Lipids, Proteins: amino acids, single and three letter code and peptides, classification, chemical and physical properties, peptide bond, Conformation of proteins (Ramachandran plot, secondary, tertiary and quaternary structure; domains; motif and folds). Nucleic acids: Physical properties of DNA, Conformation of nucleic acids (A-, B-, Z-DNA)). DNA bending, supercoiling.

UNIT III: Enzymology & Immunology(K2)

18 hours

Enzyme: nomenclature and classification, Types of enzymes- isoenzymes, allosteric enzymes, Ribozyme and Abzyme. Coenzymes & Cofactors, Enzyme inhibitors, kinetics (MM Equation only); Enzyme activity with reference to lysozyme. Hormones-Types, Receptor binding and mechanism of action of insulin hormone. Immune system: Innate and adaptive immunity, Humoral immunity, Antibodies: Immunoglobulins, Immunoglobulin classes and subclasses, Antigen-Antibody Interactions

(Beyond the Curriculum: Membrane receptors - B-cell surface receptor (BCR) - T-cell surface receptor (TCR); major histocompatibility complex (MHC)).

UNIT IV: Central Dogma of Life (K2)**18 hours**

Genetic material- DNA and RNA-mRNA, Rrna & tRNA; Genome organization - Prokaryotic and Eukaryotic & Plastid DNA, extra chromosomal material (Plasmid); Evolution of genetic material, flow of genetic information; Chromosome Structure, C-value paradox; DNA replication. Transcription - prokaryotes/ Eukaryotes, splicing, Post-transcriptional processing; Genetic code, Translation- post translational modifications.

UNIT V: Gene Regulation (K4)**18 hours**

Regulation of gene expression in prokaryotes and eukaryotes; operon concept – *lac*, *trp*– promoter, attenuator – terminator and operator– allosteric enzymes and feedback inhibition – repression; DNA methylation, DNA binding proteins – transcription factors. Translational Control: Riboswitches and Metabolite sensing. Gene mutations – Types, mutagens, Induced Mutations-Environmental, Radiation, Chemical.

TEXTBOOK(S):

1. AjoyPaul(2007)TextbookofCellandMolecularBiology,3rdEdition.Books and Allied (P) Ltd., Kolkata
2. U. Satyanarayana and U. Chakrapani. Biochemistry 4th Edition. Books and Allied (P) Ltd., Kolkata
3. R. Ananthanarayanan& C.K. Paniker (2005), Textbook of Microbiology,7th edition, Orient Longman Private Ltd.,Hyderabad
4. U. Satyanarayana (2005), Biotechnology, Books and Allied (P) Ltd., Kolkata
5. P.K. Gupta (2013) A Text Book of Cell & Molecular Biology, 3rd Edition, Rastogi Publishers, India

REFERENCE BOOK(S):

1. Gerald Karp (2009), Cell and Molecular Biology: Concepts and Experiments, 6th Edition, John Wiley & Sons, NY
2. David L. Nelson and Michael M. Cox (2008), Lehninger Principles of Biochemistry, 5th Edition, WH Freeman and Company, NY
3. T.Palmer (1993), Principles of Enzymology for technological applications, Butterworth- Heinemann Publisher, UK
4. LM Prescott (2005), Microbiology, 6th Ed, JP Harley DA Klein, McGraw Hill, USA
5. J Kuby (2003), Immunology, 5th Ed, WH Freeman and Company, NY.
6. Bruce Alberts (2002), Molecular Biology of the Cell, 4th Edition, Garland Science, NY.
7. Benjamin Lewin (2007), Genes IX, 9th Edition, Jones & Bartlett Learning U.S.A.

BLENDED LEARNING E-RESOURCES**UNIT V: GENE REGULATION**

TOPIC	LINKS
Regulation of gene expression in prokaryotes and eukaryotes	https://youtu.be/AArP63yiG_U
Operon concept	https://youtu.be/EjRXz1xAdow
DNA methylation	https://youtu.be/J-OjEzCaacY
DNA binding proteins	https://youtu.be/vDHZP83SnIk
Riboswitches and Metabolite sensing	https://youtu.be/3bQID8VTeqs
Gene Mutation	https://youtu.be/t_E2dXyHS0w

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1						1	3	3	2	3	3	2	2	1	3
CO2						1	3	3	2	3	3	2	2	1	3
CO3						1	3	3	2	3	3	2	2	1	3
CO4						1	3	3	2	3	3	2	2	1	3
CO5						1	3	3	2	3	3	2	2	1	3

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Group Discussion (Unit V)	Once in a semester

Course Designed by: Mrs. P.J. Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER I**COURSE CODE: 23PBI1C02****TITLE OF THE COURSE: CORE: COMPUTATIONAL METHODS FOR SEQUENCE ANALYSIS****COURSE OBJECTIVES:**

- To introduce the students to the field of Bioinformatics
- To educate the students on database & tools used in Bioinformatics

COURSE OUTCOMES:

At the completion of the course the student will be able to

CO1	Summarize the History of Bioinformatics through Inventions/updates in Biology	K1
CO2	Classify the Biological Databases based on different criteria	K2
CO3	Compare the Protein/Nucleotide sequences by Sequence alignment	K3
CO4	Analyze the Protein/Nucleotide sequences using different tools	K4
CO5	Illustrate about the different algorithms to solve biological problems	K2

Syllabus**Total Credits: 5****Instructional hours: 90****UNIT I: Introduction to Bioinformatics (K1)****18 hours**

Bioinformatics – History, definition, concept, aims, scope and applications; Computational analysis & Molecular biology in Computers, Role of internet in Bioinformatics, Inventions that found the base for Bioinformatics; components and basic tools in Bioinformatics. Application of bioinformatics in various fields. Introduction to single letter code of aminoacids, symbols used in nucleotides.

(Self-study: Introduction to single letter code of aminoacids)

UNIT II: Biological Databases (K2)**18 hours**

Biological Databases – Classification of biological databases, Characteristics sequence and structure, Biological data formats- SDE, GDE, Genbank, EMBL, Accession codes and identifiers; sequence databases, sequence motif databases, Structure databases- PDB, CATH, SCOP, MMDB and specialized databases- EST, dbSNP, KEGG, BRENDA; Systems for searching, indexing and cross – referencing- Entrez and SRS, compilation of resources.

(Beyond the Curriculum: Architecture of Biological Databases – Details about Front end and back end of the databases)

UNIT III: Sequence Alignment (K3)**18 hours**

Tools – data submission tools, data analysis tools – pairwise and multiple sequence alignments, protein structure alignment, phylogenetic analysis; Scoring matrices: Substitution matrices – PAM and BLOSUM, Local and Global alignment concepts, Dot plot. Dynamic programming methodology: Needleman and Wunsch algorithm. Smith–Waterman algorithm. Statistics of alignment score. Phylogenetic analysis, Multiple sequence alignment- Progressive and hierarchical alignment. Database search for similar sequences using FASTA and BLAST Programs. Application of sequence alignment.

UNIT IV: Protein Sequence Analysis (K4)**18 hours**

Protein prediction tools- Expasy, Computation of Physical, Chemical properties of a protein from sequence. Concepts of secondary structure prediction of Protein – Chou Fasman, GOR, Nearest Neighbour, Neural Networks, Prediction of Transmembrane proteins, Post- translational modifications- Glycosylation, phosphorylation, Ubiquitination, methylation, Acetylation. Proteolysis.

UNIT V: Nucleotide Sequence Analysis (K4)**18 hours**

Softwares included in DNA sequence analysis (EMBOSS) and Primer design using programs from public domain, Prediction of Genes and Regulatory sequences in DNA. Fragment assembly. Genome sequence assembly and annotation, Restriction Mapping, Repeat Sequence finder, Tools for whole genome comparison. Prediction of RNA secondary and tertiary structures.

TEXT BOOKS:

1. S. C. Rastogi, Namita Mendiratta, Parag Rastogi (2006), Bioinformatics methods and applications: Genomics, Proteomics and drug discovery, PHI Learning Pvt. Ltd., India
2. Arthur M. Lesk (2002), Introduction to Bioinformatics, Oxford University Press, UK
3. Teresa K. Attwood and David Parry-Smith (2001), Introduction to Bioinformatics, Pearson Education, NJ

REFERENCE BOOKS:

1. Andreas D Baxevanis and BF Francis Ouellette (2004), Bioinformatics: A Practical guide to the analysis of Genes and Proteins, 3rd Edition, John Wiley & Sons, NY
2. David W Mount (2013), Bioinformatics: Sequence and Genome Analysis, 2nd Edition, Cold Spring Harbor Laboratory Press, USA
3. Krane and Raymer (2002), Fundamental Concepts of Bioinformatics, Pearson, USA
4. Ghosh and Mallik (2008), Bioinformatics: Principles and Applications, OUP India

BLENDED LEARNING E-RESOURCES
UNIT III: Sequence Alignment

TOPIC	LINKS
Sequence Alignment	https://www.youtube.com/watch?v=8XaA_NtPt2o
Multiple Sequence Alignment	https://www.youtube.com/watch?v=TZaA_-4j19w
Dynamic Programming Algorithm	https://www.youtube.com/watch?v=mGVWYT-WBn0
FASTA and BLAST programs	https://www.youtube.com/watch?v=IrHDOEDtwD4

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	3				3		2		1	1	1		2		2
CO2	3				3		2		1	1	1		2		2
CO3	3	3			3		2		1	1	1		2		2
CO4	3	3			3		2		1	1	1		2		2
CO5	3	3			3		2		1	1	1		2		2

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Report writing (Unit V)	Once in a semester

Course Designed by: Dr. S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: I

COURSE CODE: 23PBI1C03

TITLE OF THE COURSE: CORE: INTRODUCTION TO COMPUTERS AND PROGRAMMING IN C (*Employability*)

COURSE OBJECTIVES:

- To introduce the students to programming in C language.
- To train the students to apply C programming to solve problems in Biology.

COURSE OUTCOMES:

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

CO1	Summarize the components of a computer	K2
CO2	Develop a Website using HTML	K3
CO3	Make use of control statements in C	K2
CO4	Create User defined functions in C	K3
CO5	Understand Structures, files and pointers in C	K2

Syllabus

Total Credits: 5

Instructional hours:90

UNIT I: Introduction to Computers (K2)

18 hours

Introduction to computers – Storage devices– Input devices – Output devices – System software – Application software. MS Office & its applications - Operating system concepts – Linux operating system – Linux commands – Linux shell programming.
(Self-study: MS Office and its applications)

UNIT II: Internet and HTML Programming (K3)

18 hours

The Internet: Evolution of the Internet – Internet terminologies: WWW, URL, FTP, HTTP, Gopher, e-mail, browsers, protocol, Archie, Telnet, Search Engines.
HTML Programming: formatting, links, lists, Tables, Forms and Frames. Applications of IT: Computers in education, business, entertainment, science, engineering and medicine.
(Beyond the Curriculum: Dynamic HTML – Features, Usage and Applications)

UNIT III: Introduction to C (K2)

18 hours

Overview of C: Introduction – Basic structure of C programs – constants, Variables, and Data types – Operators and expression – Managing input and output statements - Decision making and branching - Decision making and looping - Arrays (One Dimensional and two Dimensional).

UNIT IV: User defined Functions (K3)

18 hours

Handling of character Strings – User-Defined Functions – Introduction, Need for user- defined functions, A multi-function program, Return values and their types, calling a function, category of functions – No arguments and no return values, Arguments but no return values, Arguments with return values. Scope and life time of variables – Local and Global variables. Storage classes-Static, auto, register, external.

UNIT V: Structures, Files and Pointers (K2)

18 hours

Structures: introduction – structure definition – giving values to members – structure initialization – comparison of structure variables – arrays of structures- Pointers- understanding pointers-Accessing the address of a variable-pointers and arrays- pointer and character strings – pointers and functions- introduction to C files – defining and opening files – closing a file – input/output operations on files.

TEXTBOOK(S):

1. Yashwant Kanetkar (2008), Let Us C, 8th Edition, Jones & Bartlett Learning, USA
2. E. Balagurusamy (2008), Programming in ANSI C, 4th edition, Tata McGraw Hill, India
3. KR Venugopal and SR Prasad (2007), Mastering C, Tata McGraw Hill, India

REFERENCE BOOK(S):

1. Brian W. Kernighan and Dennis M. Ritchie (1988), C Programming Language, 2nd Edition, Prentice Hall, NJ
2. Byron S. Gottfried, Schaum's Outline of Programming with C, 2nd Edition, McGraw Hill Publications, India.

BLENDING LEARNING E-RESOURCES

UNIT I: INTRODUCTION TO COMPUTERS

TOPIC	LINKS
Introduction to Computers	https://www.youtube.com/watch?v=z3KnlfATUek
Storage Devices, Input Devices, Output Devices	https://www.youtube.com/watch?v=luQ3PzcDjhQ
System and Application Software	https://www.youtube.com/watch?v=BTB86HeZVwk
MS Office	https://www.youtube.com/watch?v=yCVy5Kw0l8s
Operating System	https://www.youtube.com/watch?v=RozoeWzT7IM
Linux	https://www.youtube.com/watch?v=v_1zB2WNN14

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	3	3	3				2	1		1	1	1		2	
CO2	3	3	3		3		2	1		1	1	1			
CO3	3	3	3		3		2	1		1	1	1			2
CO4	3	3	3		3		2	1		1	1	1		2	
CO5	3	3	3				2	1		1	1	1	2		

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Code Development using C(Unit V)	Once in a semester

Course Designed by: Dr. S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: I

COURSE CODE: 23PBI1E01

TITLE OF THE COURSE: ELECTIVE: MOLECULAR INTERACTIONS

COURSE OBJECTIVES:

- To educate the students on the different types of interactions between biomolecules.
- To introduce the students to the basics of Spectroscopy and its applications in Biology.

COURSE OUTCOMES:

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

CO1	Relate a thorough and comprehensive understanding of various types of chemical Bonding	K1
CO2	Summarize the various theories behind molecular interactions	K2
CO3	Outline the mechanism of protein folding and mis-folding	K2
CO4	Identify the various types of macromolecular interactions with examples	K3
CO5	Apply the basics of Spectroscopy and the types of Spectroscopy to study macromolecules	K3

Syllabus

Total Credits: 3

Instructional hours: 60

UNIT-I: Chemical Bonding (K1)

12 Hours

Introduction and characteristics: Ionic bond, covalent bond, coordination bond and hydrogen bond. Factors affecting covalent bond strength. Non-bonded interactions - electrostatic interactions and Van der Waals interactions. Hydrophobic interactions and Hydrophilic interactions. Bond stretching interactions and Metallic bond. (*Self-Study: Ionic bond*)

UNIT-II: Theories of Chemical Bonding (K2)

12 Hours

Valence bond Theory - Sigma bond, Pi bond and Hybridization. Types of interaction between atoms - Bond distance, Bond angle, Torsion Angle, Bond energy and Dipole-Dipole interactions. VSEPR theory - Shape of orbitals and orbital hybridization. Molecular orbital theory and its applications.

UNIT-III: Protein Folding (K2) 12 Hours

Principles of protein folding. Role of chaperones, folding pathways. Methods to study protein folding - Phi, Psi & Omega angles with distance. Zwitterion, Disulfide Bridge and Ramachandran Plot. Types of Helices, Beta turns, Gamma turns. FSSP, VAST and DALI. Protein Mis-folding and aggregation: Principles and correlation with disease.

UNIT IV: Macromolecular interactions (K3)

12 Hours

Protein-Protein, Protein-DNA, DNA-Drug, Protein-Lipid, Protein-Ligand, Protein-Carbohydrate interaction, Metalloproteins. Pi... Pi interactions, C-H... Pi interactions.

UNIT V: Fundamentals of Spectroscopy (K3)

12 Hours

Spectroscopy: Principles, Theory, Instrumentation and Application of UV, IR, NMR and Circular dichroism (CD) to macromolecules. Stereochemistry of proteins and nucleic acids. Quantum mechanics - Wave properties - Absorption Spectra - Ultraviolet Spectra of Proteins and Nucleic Acids - NMR Spectroscopy - Chemical Shifts - Spin-Spin Splitting - Magnetic Resonance Imaging - Electron Spin Resonance - Circular Dichroism of Proteins and Nucleic acids - Optical Rotatory Dispersion - Infrared Spectroscopy - Raman Spectroscopy - Structure Determination with Vibrational Spectroscopy - Applications.

TEXT BOOK(S):

1. Puri and Sharma (2020), "Principles of Inorganic Chemistry", Vishal Publishing Co, India
2. Gordon G. Hammes (2005), "Spectroscopy for the Biological Sciences", John Wiley & Sons.
3. David Micha. (2009), "Molecular Interactions", John Wiley & Sons.

REFERENCE BOOK(S):

1. Tewari K.S. Vishnoi N.K. (2006), "A Text book of organic chemistry", Vikas publishing house, India.
2. David W Ball (2001), "Basics of Spectroscopy", SPIE press, Bellingham, WA.

BLENDED LEARNING E-RESOURCES
UNIT II: THEORIES OF CHEMICAL BONDING

TOPIC	LINKS
Valence Bond Theory	https://www.youtube.com/watch?v=nTujP4jCbSg
Types of Interactions between atoms	https://www.youtube.com/watch?v=QdwzMPwPA3I
VSEPR Theory	https://www.youtube.com/watch?v=DBrq31w8vC4
Molecular Orbital Theory	https://www.youtube.com/watch?v=6tB6E6R_XpQ

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1					3	1	1	1	1	1	2	1	3		1
CO2					3	1	1	1	1	1	2	1	3		1
CO3					3	1	1	1	1	1	2	1	3		1
CO4					3	1	1	1	1	1	2	1	3	1	1
CO5					3	1	1	1	1	1	2	1	3		1

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
5	Assignment (Unit I & Unit II)	Twice in a semester
6	Seminar (Unit III & Unit IV)	Twice in a semester
7	Term Paper (Unit V)	Once in a semester

Course Designed by: Mrs. P.J. Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: I**COURSE CODE: 23PBI1E02****TITLE OF THE COURSE: ELECTIVE: BIOPHYSICS AND CRYSTALLOGRAPHY****COURSE OBJECTIVES:**

- To coach the students on the basics of Biophysics.
- To instruct the students on X-ray Crystallography with reference to Protein Structure determination.

COURSE OUTCOMES:

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

CO1	Define the different conformations of Macromolecules	K1
CO2	Explain the physical properties of water	K2
CO3	Extend the basic principles of thermodynamics to Biological processes	K2
CO4	Relate the concepts of crystallography and methods of Crystallization	K1
CO5	Illustrate the different protein structure determination methods	K2

Syllabus

Total Credits: 3

Instructional hours:60

UNIT I: Molecular Biophysics (K1)

12 hours

Conformational parameters of nucleic acids - geometrics - Proteins: Principles of ionization - Predicting properties from amino acid composition - Unusual amino acids, peptides, polypeptides, structural levels of proteins & stabilizing forces, conformational properties of polypeptides, Ramachandran plot, Helical parameters & conformation, organization & interaction angles - Conformational Analysis - Forces that determine protein and nucleic acid structure, basic problems, polypeptide chains geometrics, potential energy calculations, hydrogen bonding, hydrophobic interactions and water structures ionic interactions, disulphide bonds - Statistical thermodynamics and organizational levels of biomacromolecule structure.

(Self Study: Proteins)

UNIT II: Biophysics of Water (K2)

12 hours

Association of water through H- bonding, Nature of hydrophobic interactions, physicochemical properties of water, State of water in biostructures& its significance - Small-Molecule Solutes: Hydrophiles, Hydrophobes, Large Hydrophobic Solutes and Surfaces, The Influence of Ions: Structure-Making and Structure-Breaking, Long-Range Hydrophobic Interactions Hydrophilic Surfaces - Protein Hydration- Specific Roles of Water in Structure and Function, Secondary Structure, Protein-Protein Interactions, Mediation of Ligand Binding, Functional Tuning, Allostery - Hydrophobic Cavities, Electron Transfer, Involvement of Bound Water in Catalytic Action, Water and Nucleic Acids

UNIT III: Principles of Thermodynamics (K2)

12 hours

Thermodynamics of solutions - the total free energy of a solution - excluded volume for dilute solutions & flexible polymers - Molecular weight averages and distributions - average dimensions - end-to-end distance - radius of gyration - interaction between polymer segments and solvent molecules - osmotic pressure of protein solutions - membrane potentials – phase equilibria - solubility and freezing point melting points of crystalline polymers - light scattering by macromolecules Zimm plot - estimation of chain dimensions - experimental results on some proteins and nucleic acids - Biophysics of the Immune System - Membrane biophysics: Membrane potentials (energetics of transport across membranes), transporters and channels: classification of ion transport - Energetic of transport across membrane theories.

UNIT IV: Introduction to Crystallography (K1)

12 hours

General concepts, overview of Crystals and their properties - Unit cell, Lattices, Planes and Indices - point groups and space groups. Crystal systems and Symmetry - Bragg's Law and its applications in X-ray diffraction, Atomic scattering factor, Structure factor and Electron density calculations - Fourier series - Fourier Transform and crystal diffraction - Crystallographic statistics – Phase problem - Small molecule and Macromolecular

Crystallography - Crystallization methods, X-ray diffraction data collection, structure determination methods - model building and Validation (Ramachandran Plot), molecular dynamics refinement - Structural and Interaction analysis - Synthetic Compounds - Structure determination using SHELXS program-Electron density map calculation-structure refinement-quality indicator: the Rfactor - Validation method Interpretative of results: PROCHECK, - Ramachandran plot - RMS deviations - structural analysis, conformations and Interaction analysis Structure – Function relationship of some small molecules – Cambridge Structural Database - Deposition of structures in Databases - - Classification and comparison of protein 3D structures – Structural Databases

UNIT V: Structure Determination techniques (K2)

12 hours

Molecular replacement method – Isomorphous replacement method - preparing heavy atom derivatives - Anomalous scattering - Multiwave length anomalous dispersion technique - Synchrotron radiation and its implications in structure determination. Introduction to X-ray Free Electron Laser technology (XFEL), importance and applications - Cryo-electron microscopy, Fiber, Powder and Neutron diffraction - NMR- Importance of NMR in Structural Biology, Cryo- EM - Diffusion: Macromolecular diffusion - Ultracentrifugation - density gradient methods - Light Scattering: Experimental results on some proteins and nucleic acids - determination of radius of gyration and end to end distance Electrophoresis - Chromatography: General principles, types - applications to macromolecules Application of X-ray crystallography in drug design.

TEXT BOOK(S):

1. Cantor, C. R., & Schimmel, P. R. (2008), Biophysical Chemistry: Part II: Techniques for the study of Biological structure and function, Anebooks - W. H. Freeman, India.
2. Gu, J., & Bourne, P. E. (Eds.) (2009), Structural Bioinformatics. John Wiley & Sons, San Diego.

REFERENCE BOOK(S)

1. Banaszak, L. J. (2000). Foundations of Structural Biology. Elsevier, USA
2. Drenth, J. (1994). Laue Diffraction. In Principles of Protein X-Ray Crystallography. Springer, New York, NY

BLENDDED LEARNING E-RESOURCES

UNIT V: STRUCTURE DETERMINATION TECHNIQUES

TOPIC	LINKS
Molecular Replacement methods	https://www.youtube.com/watch?v=uv7au0NWETA
X-ray Free Electron Laser technology	https://www.youtube.com/watch?v=wYPFMKf2TLc
Cryo-electron microscopy	https://www.youtube.com/watch?v=Qq8DO-4BnIY
Electrophoresis	https://www.youtube.com/watch?v=bYwq5oNZmq4
Chromatography	https://www.youtube.com/watch?v=XMtmSz_9umk

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1				3	1	1	1	1	1	1	2		3		1
CO2			3		1	1	1	1	1	1	2		3		1
CO3					1	1	1	1	1	1	2		3		1
CO4		3			1	1	1	1	1	1	2		3		1
CO5					1	1	1	1	1	1	2		3		1

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Term Paper (Unit V)	Once in a semester

Course Designed by: Mrs. P.J. Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER I

COURSE CODE: 23PBI1CP1

TITLE OF THE COURSE: PRACTICAL: FUNDAMENTALS OF BIOLOGICAL SYSTEMS (Skill Development)

COURSE OBJECTIVES:

- To train the students in the basic techniques and experiments of Microbiology and Cell Biology
- To educate the students on the basic techniques and experiments of Biochemistry and Immunology

COURSE OUTCOMES:

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

CO1	Major Experiment: Make use of the instruments/equipments to perform basic experiments in Microbiology, Cell Biology, Biochemistry and Immunology	K3
CO2	Minor Experiment: Estimate/Evaluate using Microbiology, Cell Biology, Biochemistry and Immunology techniques	K5
CO3	Spotters: Identify and explain about the Instruments/Chemicals used in Microbiology, Cell Biology, Biochemistry and Immunology techniques	K3
CO4	Viva: Interpret the results obtained from Microbiology, Cell Biology, Biochemistry and Immunology experiments	K5
CO5	Record: Illustrate and Summarize the experiments in Microbiology, Cell Biology, Biochemistry and Immunology	K2

Syllabus

Total Credits: 3

Instructional hours:60

INSTRUMENTATION

- Good laboratory practices
- Instrumentation – pH meter, Compound Microscope, Cooling Centrifuge, Colorimeter
- Buffer preparation

CELL BIOLOGY

- Isolation and fractionation of cell organelles

- Identification of various stages in mitosis and meiosis in onion roottip

MICROBIOLOGY

- Isolation, identification and Maintenance of pure microbial cultures
- Identify the given strain as Gram positive or Gram Negative bacteria.
- To perform Negative Staining for the given bacterial strain
- Bacterial growth curve

BIOCHEMISTRY

- Estimation of protein by Bradford method
- Estimation of glucose by ortho-toluidine method
- DNA estimation by di-phenyl amine method.
- RNA estimation by Orcinol method
- Separation of Plant Pigments using Thin Layer chromatography

IMMUNOLOGY

- Blood Grouping and Haem agglutination
- Single radial immunoassay

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1			3	3		1	2	2	1	1	2	2			1
CO2			3				2	2	1	1	2	2			1
CO3			3		3		2	2	1	1	2	2			1
CO4		3	3				2	2	1	1	2	2			1
CO5			3			3	2	2	1	1	2	2			1

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	Model Practical Examination	Once in a Semester
	Major Experiment	
	Minor Experiment	
	Spotters	
	Record/Observation	
	Viva	
2.	End Semester Practical Examination	

Course Designed by: Mrs. P.J.Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER I
COURSE CODE: 23PBI1CP2
TITLE OF THE COURSE: PRACTICAL: PROGRAMMING IN C & COMPUTATIONAL BIOLOGY (*Skill Development & Employability*)

COURSE OBJECTIVES:

- To coach the students in the use of Biological databases and perform Sequence analysis
- To train the students on HTML and C Programming

COURSE OUTCOMES:

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

CO1	Major Experiment: Develop C programs/Web pages to analyze protein and nucleotide sequences	K6
CO2	Minor Experiment: Examine the various primary and Secondary Databases in Bioinformatics and analyze the data	K4
CO3	Queries: Create and Execute simple queries to retrieve information from Databases	K6
CO4	Viva: Interpret the results obtained from Sequence Analysis	K5
CO5	Record: Illustrate and Summarize the experiments in Sequence Analysis and C Programming	K2

Syllabus

Total Credits: 3

Instructional hours:60

Biological Databases

- Data retrieval tools and methods- (NCBI-Entrez,SRS)
- Database file formats- (EMBL, Swiss-prot, Genbank, GCG, raw, Fasta)
- Sequence Databases
 - Nucleic acid – GenBank, EMBL, DDBJ
 - Protein – Uniprot, PIR
- Structure Databases – PDB, SCOP,CATH
- Searching metabolic pathway information in KEGG database, BRENDA
- Sequence submission tools – NCBI WGS.
- Derived databases- PROSITE, PRODOM, PFAM.
- Motif searching in derived databases PRINTS and BLOCKS databases

Sequence Analysis

- Sequence similarity searching (NCBI-BLAST).
- Multiple sequence alignment (Clustal X), Tcoffee, mafft
- Sequence analysis using EMBOSS.
- Protein sequence analysis (ExPASy proteomics tools).
- Biological workbench/CLC Workbench/Bioedit
- Gene structure and function prediction (using GenScan, GeneMark).
- Prediction of secondary structure of rRNA & tRNA by mFOLDserver

HTML

- Create a Personal Home page using Tables and Forms
- Create a Website for your Department using Images, Links and frames

C Programming – Simple programs

- Find the nature of the solution based on pH, given the concentration of H⁺ / OH⁻ ions
- Compute the rpm value using RCF value
- Find the molecular weight of a DNA with n base pairs in length
- Find the molecular weight of a given dephosphorylated oligonucleotide sequence
- Find the molecular weight of a given DNA sequence, after checking for phosphorylation
- Calculate sedimentation time (in hrs. & mins.) using clearing factor and sedimentation coefficient
- Read and Display a character array
- To compare two DNA Sequences
- To detect SNP in a DNA Sequence
- Length of the Protein
- To check whether a DNA Sequence is a type II restriction site or not using palindrome concept
- Concatenate two character arrays (String Concatenate)

C Programming - Functions and Files

Functions

- Factorial of an integer.
- Printing the 3-digit number in words.

Files

- Reading from a file.
- Writing to a file.
- Appending a sequence of text to a file.
- Computing base composition of a given nucleotide sequence from file

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	3	3	3	3		1	1	2	1	1	2	1	2		1
CO2	3	3	3			1	1	2	1	1	2	1	2		1
CO3	3	3	3		3	1	1	2	1	1	2	1	2		1
CO4	3	3	3			1	1	2	1	1	2	1	2		1
CO5	3	3	3			1	1	2	1	1	2	1	2		1

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	Model Practical Examination	Once in a Semester
	Major Experiment	
	Minor Experiment	
	Queries	
	Record/Observation	
	Viva	
2	End Semester Practical Examination	

Course Designed by: Dr. S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: II
COURSE CODE: 23PBI2C04
TITLE OF THE COURSE: CORE: GENETIC ENGINEERING AND BIOETHICS
(Employability)

COURSE OBJECTIVES:

- To introduce the students to the field of genetic engineering.
- To educate the students about the techniques and methods used in genetic engineering.

COURSE OUTCOMES:

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

CO1	Make use of the enzyme in genetic engineering	K3
CO2	Classify the protein/nucleotide identification based on different techniques	K2
CO3	Utilize the different gene transfer methods to construct the genomic DNA	K3
CO4	Examine the different GMO and therapies for diseases through the application in genetic engineering	K4
CO5	Summarize to know the guidelines for research and the property rights through biosafety and organizations	K2

Syllabus

Total Credits:5

Instructional hours:90

UNIT I: Enzymes used in genetic engineering (K3)

18 hours

Enzymes used in genetic engineering - DNA modifying enzymes and uses a) Restriction enzymes b) DNA Polymerases - Thermostable DNA polymerases used in PCR – *Taq, Pfu*, c) Reverse Transcriptase d) Terminal Transferases e) T4 Polynucleotide kinases and Alkaline phosphatase f) DNA dependent RNA polymerases g) DNA ligases h) Nucleases: S1 nucleases, DNase I, Ribonucleases., Vectors for gene cloning (Plasmid, phages, cosmids, YAC and BAC) (*Self Study: DNA ligases*)

UNIT II: Techniques in genetic engineering (K2)

18 hours

Techniques in genetic engineering: Isolation of Nucleic acids and Protein, Electrophoresis of nucleic acids (AGE) and proteins (PAGE); PCR – primer designing, types, method and applications. Molecular Markers – RAPD, RFLP, SNP, STS, VNTR, AFLP, SSR. DNA finger printing, DNA footprinting, Blotting techniques: Dot blot, Southern, Northern and Western blotting, Biochips, Autoradiography.

UNIT III: Construction of cDNA library (K3)

18 hours

Construction of genomic DNA & cDNA Library. Cloning & subcloning strategies – Selection of rDNA clones – Gene transfer mechanisms (Transformation, transduction and Transfection); Gene transfer techniques (Direct and Indirect); DNA sequencing – Classical and NextGen Sequencing (Elementary concepts only). Chromosomal walking and Chromosomal jumping; Gene silencing – anti-sense RNA technique – siRNA. Site-directed mutagenesis and protein engineering.

UNIT IV: Applications of Genetic Engineering (K4)

18 hours

Applications of Genetic Engineering – commercial aspects of recombinant proteins, transgenic plants (Bt Cotton, flavr savr tomato); transgenic animals (Silk producing goats, Sheep with more wool, milkier cows); gene knock out Technologies. Gene therapy –

Different strategies for Gene Therapy, Gene therapy for inherited diseases-ADA, Cystic Fibrosis; Therapeutic products for use in human health care – Insulin, and Human growth factor – plantibodies.

(Beyond the Curriculum: Nucleic Acid Hybridization: Principle and application - Preparation of nucleic acid probes, Principle of Nucleic acid hybridization, Nucleic acid hybridization assays, and microarrays).

UNIT V: Biosafety and Bioethics (K2)

18 hours

Biosafety- Introduction: Different levels of Biosafety. Guidelines for rDNA research activities. Good Laboratory Practices (GLP) – Disposal and Management of Biowastes – Bioethics. Property rights – Physical and Intellectual; International Organizations - WTO, WIPO, ISO; Treaties and Agreement (GATT and TRIPS) – different types of IPR and examples in Patents, Trade mark, Trade secret and Copy right; Indian Patent Act, 1970.

TEXT BOOK(S)

1. U. Satyanarayana (2005), Biotechnology, Books and Allied (P) Ltd., Kolkata
2. SN Jogdand (2009), Gene Biotechnology, Revised Edition, Himalaya Publishing House, India.
3. Subbaram, N., (2003). Patents. Pharma Book Syndicate, Hyderabad
4. Practical Approach to Intellectual Property Rights - Rachna Singh Puri, Arvind Viswanathan, I K International Publishing House Pvt. Ltd, India

REFERENCE BOOK(S)

1. Molecular Cloning: Laboratory Manual (2001) Sambrook J, Russell DW, Sambrook J Cold Spring Harbor Laboratory Press, New York.
2. Analysis of Genes and Genomes (2004) RJ Reece, John Wiley & Sons, Ltd, NJ, USA
3. SB Primrose and RM Twyman (2006), Principles of Gene Manipulation and Genomics, 7th edition, Blackwell Publishing, USA
4. James D. Watson, Richard M. Meyers, Amy A. Caudy (2007), Recombinant DNA: Genes and Genomes - A Short Course, 3rd Edition, Cold Spring Harbor Laboratory Press, USA
5. TA Brown (2010), Gene Cloning and DNA Analysis-An Introduction, 6th Edition, Wiley Blackwell, USA
6. Adrian Slater, Nigel Scott, Mark Fowler (2008) Plant Biotechnology: The genetic manipulation of plants, 2nd Edition, Oxford Publications, UK
7. Diane O. Fleming, Debra L. Hunt (2006) Biological Safety: Principles and Practices, 4th Edition, ASM Press, USA

BLENDED LEARNING E-RESOURCES UNIT V: BIOSAFETY AND BIOETHICS

TOPIC	LINKS
Biosafety- Introduction: Different levels of Biosafety	https://youtu.be/F7TBfCJTZ54
Guidelines for rDNA research activities	https://youtu.be/GQn7sIZSjg0
Good Laboratory Practices (GLP)	https://youtu.be/IFUVh3eBJWw
Disposal and Management of Biowastes - Bioethics	https://youtu.be/C49tYFwnWR0
Property rights – Physical and Intellectual	https://youtu.be/avSdoMz6OuA
GATT and TRIPS	https://youtu.be/cIpltUN183g
Types of IPR	https://youtu.be/KLJsjVni0Tw

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1						1	2	1	1	1	1	2		3	2
CO2						1	2	1	1	1	1	2		3	2
CO3						1	2	1	1	1	1	2		3	2
CO4						1	2	1	1	1	1	2		3	2
CO5						1	2	1	1	1	1	2		3	2

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Group Discussion (Unit V)	Once in a semester

Course Designed by: Mrs. P.J.Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: II

COURSE CODE: 23PBI2C05

TITLE OF THE COURSE: CORE: MOLECULAR EVOLUTION & PHYLOGENETICS

COURSE OBJECTIVES:

- To instruct the students about Molecular Phylogenetics
- To edify the students about the Classification of Organisms at Molecular level

COURSE OUTCOMES:

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

CO1	Recall the different methods of classifying organisms	K1
CO2	Identify the different parts of a phylogenetic trees	K2
CO3	Understand the types of phylogenetic trees	K3
CO4	Compare different algorithms of phylogenetic analysis	K4
CO5	Summarize the concepts of Population genetics	K2

Syllabus

Total Credits: 5

Instructional hours:90

UNIT I: Introduction to Molecular Phylogenetics (K1)

18 hours

Background Knowledge: Evolutionary Biology – From atoms to molecules to life, Hypothesis of evolution, Darwin's theory of evolution, From taxonomy to molecular phylogenetics – Linnaeus' classification systems- Whittaker's five kingdom system, Carl Woese's three domain system; Gene Duplication, Exon shuffling and Concerted Evolution: Types of gene duplication, Domains and Exons, Domain Duplication and Gene Elongation, Formation of Gene Families and the Acquisition of New Functions, Dating Gene Duplications, Gene Loss, Prevalence of Gene Duplication, Gene Loss and Functional Divergence, Exon Shuffling, The 'Introns – early' vs 'Introns-late' hypothesis, Alternative pathways for producing new functions. (*Self Study: Darwin's theory of evolution*)

UNIT II: Terminologies in Molecular Phylogenetics (K2)

18hours

Traditional Systematics/phylogeny - Molecular data as molecular fossils; Molecular-clock-hypothesis; The terminology of phylogenetics- Trees, Root, branches, Node, Leaf, Clade; lineage sorting, orthology, homology, paralogy, xenology;"basal" lineages, crown vs. stem groups, Phylograms vs. cladograms

UNIT III: Types of Phylogenetic analysis(K3)

18 hours

Molecular phylogeny: Gene phylogeny vs. species phylogeny; Different types of trees rooted vs. unrooted trees, dichotomy vs. polytomy, monophyletic vs. paraphyletic, ultrametric vs. unconstrained; Constructing molecular phylogenetic trees-Choice of molecular markers.

UNIT IV: Phylogenetic Algorithms (K4)

18 hours

Phylogenetic Algorithms: Clustering based methods-UPGMA and neighbor joining, Optimality based: Fitch - Margoliash and minimum evolution algorithm; Character based methods-Maximum Parsimony (MP) and Maximum Likelihood(ML) methods; Evaluation of phylogenetic trees-reliability and significance; Boot strapping; Jack-knifing. Phylogenetic softwares& Applications - ClustalW, Mega, Phylip, Phylodraw, HyPhy, PAUP, PAML, QuickTree. Case studies- Phylip/PAUP.

(Beyond the Curriculum: Evaluation of results from phylogenetic analyses, phylogenetic dating).

UNIT V: Population Genetics (K2) –BLENDEDLEARNING

18 hours

Allied topics: Population genetics. Genetic polymorphism, variations, alleles. Human Y chromosome haplogroups.Mitochondriomics: - Mitochondrial haplogroups, rCRS, SNP, Mitochondrial eve, Human mitochondrial molecular clock, prevalence in mitochondrial haplogroups, Human geographic project, mitochondrial polymorphism, Dysfunction and disease studies.

TEXTBOOK(S)

1. Marco Salemi and Anne-Mieke Vandamme (2009), The Phylogenetic Handbook: A Practical Approach to DNA and Protein Phylogeny, Cambridge University Press, UK
2. Roderick D.M. Page and Edward C. Holmes (1998), Molecular Evolution: A Phylogenetic Approach, Wiley-Blackwell, UK

REFERENCE BOOK(S)

1. Wen-Hsiung Li (1997), Molecular Evolution, Sinauer Associates, USA
2. Dan Graur and Wen-Hsiung Li (2000), Fundamentals of Molecular Evolution, 2nd Edition, Sinauer Associates, USA
3. Masatoshi Nei and Sudhir Kumar (2000) Molecular Evolution and Phylogenetics, Oxford University Press, USA

BLENDLED LEARNING E-RESOURCES UNIT V: POPULATION GENETICS

TOPIC	LINKS
Population Genetics	https://www.youtube.com/watch?v=frvV84FR6K4
Haplogroups	https://www.youtube.com/watch?v=-QdtwRJdVsM https://www.youtube.com/watch?v=gE1kVWRW3D0
Mitochondrial Haplogroups	https://www.youtube.com/watch?v=09GsPp-iIJM
SNP	https://www.youtube.com/watch?v=DE9b1dxy_pE
Mitochondrial Eve	https://www.youtube.com/watch?v=yuT4IC1KXoc
Human Genographic project	https://www.youtube.com/watch?v=WM-3x3tK9n4

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1				3	2	2		2	2	1	1	1		3	1
CO2				3	1	2		2	2	1	1	1	1	3	1
CO3				3	2	2		2	2	1	1	1		3	1
CO4				3	1	2		2	2	1	1	1		3	1
CO5				3	2	2	3	2	2	1	1	1	1	3	1

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Group Discussion (Unit V)	Once in a semester

Course Designed by: Mrs. P.J.Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: II
COURSE CODE: 23PBI2C06
TITLE OF THE COURSE: CORE: DATABASE MANAGEMENT SYSTEMS

COURSE OBJECTIVES:

- To instruct the students about Database Management System
- To guide the students about the creation of Database on the web

COURSE OUTCOMES:

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

CO1	Explain the different models of Databases	K2
CO2	Create relations using SQL	K4
CO3	Understand the concept of Scripting through PHP	K3
CO4	Develop Databases using MySQL	K5
CO5	Summarize the concepts of Data mining	K2

Syllabus

Total Credits: 5

Instructional hours: 90

UNIT I: Introduction to Database Systems (K2)

18 hours

Introduction: Data abstraction, Data models, Instances & schemes E-R Model: Entity and entity sets, Relations and relationship sets, E-R diagrams, Reducing E-R diagrams to tables. Network Data Model: Basic concepts, Hierarchical Data Model: Basic concepts. Introduction to distributed database processing. Introduction to Database Management System – Classification of database system - Database designing & administration.
(Self Study: ER Diagrams)

UNIT II: Introduction to SQL(K4)

18 hours

ORACLE - Introduction to RDBMS, ORDBMS, Data definition languages – Data Manipulation language, Data Control language, Data types in Oracle. Constraints in Oracle, Data and String Functions, Union and Intersect operator, Sub queries, Normal Forms, Introduction to PL / SQL, Simple PL / SQL programs.
(Beyond the Curriculum: Functions, Packages, Triggers and Collections in PL/SQL)

UNIT III: PHP (K3)

18 hours

Basic PHP Syntax: PHP Tags, PHP Statements and Whitespace, Comments, PHP Functions, Variables, Operators, Strings, arrays, comments, Built-in functions, PHP Methods, Functions- User-defined functions, Function arguments, Returning values, Variable functions, PHP looping, Conditional statements.

UNIT IV: MySQL (K5)

18 hours

Introduction to MySQL, MYSQL for Web application, Creating database, Create table, Constraints, Where clause, Alias, Using MySQL from PHP, introduction to MySQL – Query processing & optimization - integration of PHP with database, introduction to WAMP, examples for small database management project.

UNIT V: Data mining (K2)

18 hours

Introduction to data mining: Basics of data mining, related concepts, Data mining

techniques. Data Mining Algorithms: Classification: Overview and Techniques, Clustering: Overview and Techniques, Association rules.

TEXT BOOK(S):

1. Henry F. Korth and Abraham Silbershatz (1992), "Database System Concepts", 2nd edition, McGraw Hill, NY.
2. C.J. Date (2003), An Introduction to Database Systems, 8th Edition, Addison-Wesley, USA

REFERENCE BOOK(S):

1. Ivan Bayros (2010), SQL, PL/SQL the Programming Language of Oracle, 4th Edition, BPB Publications, India.
2. Michael K. Glass, Yann Le Scouarnec, Elizabeth Naramore, Gary Mailer and Jeremy Sto (2004), Beginning PHP, Apache, MySQL Web Development, John Wiley & Sons, USA.
3. Steven Holzner (2007), PHP: The Complete Reference, Mcgraw-Hill Education, USA
4. Gilmore, W Jason (2010), Beginning PHP and MySQL- From Novice to Professional, 4th Edition, Apress, NY

**BLENDED LEARNING E-RESOURCES
UNIT V: DATA MINING**

Introduction to Data Mining	https://www.youtube.com/watch?v=0Q7j7sv4rns
Data mining Techniques	https://www.youtube.com/watch?v=syY4tCAxGfk
Classification	https://www.youtube.com/watch?v=lLg6F_TY8bw
Clustering	https://www.youtube.com/watch?v=2QTeu00C-fY
Association Rule	https://www.youtube.com/watch?v=RiFrbyiYpRs

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	3	3	3	1		1	2	1	2			3		3	
CO2	3	3	3	1		1	2	1	2	2		3		3	
CO3	3	3	3	1		1	2	1	2	2		3		3	
CO4	3	3	3	1		1	2	1	2	2	3	3		3	
CO5	3	3	3	1		1	3	1	3			3		3	

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Database Development (Unit V)	Once in a semester

Course Designed by: Dr. S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: II
COURSE CODE: 23PBI2E01
TITLE OF THE COURSE: ELECTIVE: BIG DATA ANALYTICS

COURSE OBJECTIVES:

- To edify the students on the basics of big data analytics
- To instruct the students on the applications of Big data analytics in Biology.

COURSE OUTCOMES:

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

CO1	Relate the structure of Big Data	K1
CO2	Explain the various environments available in big data analysis	K2
CO3	Summarize the different platforms for big data	K3
CO4	Identify the applications of Big data analysis in various industries	K3
CO5	Experiment with various advanced techniques in bid data analysis	K3

Syllabus

Total Credits: 3

Instructional hours:60

UNIT I: Basics of Big Data (K1)

12 hours

Introduction to Big Data and its Applications. Linear data structures and Non-linear data structures, Algorithm design. (*Self Study: Linear Data Structures*)

UNIT II: Environment and Databases (K2)

12 hours

Distributed Computing Environment for Big Data. No SQL databases for Big Data Storage Applications (HBase). Distributed Processing of data using MapReduce & Pig. In memory distributed processing using Apache Spark. Data Storage on Cloud (Amazon S3 & DynamoDB), Introduction to Apache Hadoop database.

UNIT III: Concepts and Platforms (K2)

12 hours

Performing operations. **Concepts for Big Data, Big Data Platforms (Industry 4.0)**, Workflow management. Batch Processing.

UNIT IV: Applications and Source (K3)

12 hours

Applications of Streaming Data in Industry. Sourcing Streaming data using Apache Flume. Building real-time data pipeline using Apache Storm. Streaming on Apache Spark.

UNIT V: Advances in Big Data (K3)-BLENDED LEARNING

12 hours

Regression, Clustering & Classification using Spark MLlib. Building visualizations using Big Data. Case studies on applications of Big Data Analytics in Biology.

TEXT BOOK(S)

1. Parag Kulkarni, 2016, Big Data Analytics, PHI Learning Pvt Ltd, New Delhi

REFERENCE BOOK(S)

1. Viktor Mayer-Schonberger and Kenneth Cukier. 2013, Big Data: A Revolution That Will Transform How We Live, Work and Think. Hodder And Stoughton, UK

BLENDED LEARNING E-RESOURCES
UNIT V: ADVANCES IN BIG DATA

TOPIC	LINKS
Regression	https://www.youtube.com/watch?v=CtKeHnfK5uA
Clustering & Classification using SparkMLLib	https://www.youtube.com/watch?v=d68VGJ7yAko
Building visualizations using Big Data	https://www.youtube.com/watch?v=WWKxzjKzN3A

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	2		2	3		1	1	1	2	1	1	3	2	1	3
CO2	2		2	3		1	1	1	2	1	1	3	2	1	3
CO3	2		2	3		1	1	1	2	1	1	3	2	1	3
CO4	2	3	2	3		1	1	1	2	1	1	1	2	1	3
CO5	2	3	2	3		1	1	1	2	1	1	2	2	1	3

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Group Discussion (Unit V)	Once in a semester

Course Designed by: Dr. S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: II

COURSE CODE: 23PB12E02

TITLE OF THE COURSE: ELECTIVE: ARTIFICIAL INTELLIGENCE IN BIOLOGY

COURSEOBJECTIVES:

- To enlighten the students on the basics of artificial intelligence
- To train the students on the applications of artificial intelligence in Biology.

COURSE OUTCOMES:

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

CO1	Summarize on the basics of Artificial Intelligence	K2
CO2	Choose the appropriate search techniques for the artificial intelligence problems	K3
CO3	Experiment with different machine learning algorithms	K3
CO4	Make use of Expert systems for Artificial Intelligence	K3
CO5	Relate the different algorithms with their applications in Biology	K2

Syllabus

Total Credits: 3

Instructional hours: 60

UNIT I: Basics of Artificial Intelligence (K2)

12 hours

Introduction to AI-Problem formulation, Problem Definition-Production systems, Control strategies, Search strategies. Problem characteristics, Production system characteristics - Specialized productions system- Problem solving methods – Problem graphs, Matching, Indexing and Heuristic functions -Hill Climbing-Depth first and Breath first, Constraints satisfaction – Related algorithms, Measure of performance and analysis of search algorithms. (*Self Study: Problem formulation*)

UNIT II: Search techniques (K3)

12 hours

Game playing – Knowledge representation, Knowledge representation using Predicate logic, Introduction to predicate calculus, Resolution, Use of predicate calculus, Knowledge representation using other logic-Structured representation of knowledge. Knowledge representation -Production based system, Frame based system. Inference – Backward chaining, Forward chaining, Rule value approach, Fuzzy reasoning – Certainty factors, Bayesian Theory- Bayesian Network-Dempster – Shafer theory.

UNIT III: Planning and Machine learning (K3)

12 hours

Basic plan generation systems – Strips -Advanced plan generation systems – K strips - Strategic explanations -Why, Why not and how explanations. **Learning-Machine learning, adaptive Learning. (Industry 4.0)**

UNIT IV: Expert systems (K3)

12 hours

Architecture of expert systems, Roles of expert systems – Knowledge Acquisition – Meta knowledge, Heuristics. Typical expert systems – MYCIN, DART, XOON, Expert systems shells.

UNIT V: Algorithms in Biology (K2)

12 hours

Algorithms – Data analysis algorithms and Prediction algorithms, Artificial Intelligence – problems, approaches and tools; Neural networks Technology, Implementation and application of Artificial neural networks. Probabilistic models: Markov chain, Hidden Markov Models and its applications.

TEXT BOOK(S):

1. Kevin Night and Elaine Rich, Nair B., “Artificial Intelligence (SIE)”2008, McGraw Hill- USA.
2. Dan W. Patterson, “Introduction to AI and ES”, 2007, Pearson Education, UK.

REFERENCE BOOK(S):

1. “Artificial Intelligence: A Modern Approach”, 2002 by Stuart Russell and Peter Norvig, Pearson,UK.
2. “Artificial Intelligence: A New Synthesis”, 2003 by Nils J Nilsson, Elsevier,India

BLENDED LEARNING E-RESOURCES**UNITV: ALGORITHMS IN BIOLOGY**

Design and analysis of Algorithms	https://www.youtube.com/watch?v=GQNT0v5zKhE&list=PLrjKTqL3jnm8wGQyNhgdm2gkoa8CXCml
Prediction Algorithms	https://www.youtube.com/watch?v=n5yKDyedUes
Artificial Intelligence	https://www.youtube.com/watch?v=kmeaG_BOZ7M
Neural Networks	https://www.youtube.com/watch?v=airAravnKk
Artificial Neural Networks	https://www.youtube.com/watch?v=g9coqhm5CUM&list=PLhdVEDm7SZ-PdtzOkXWb6xyAPxFInnpx-
Probabilistic Models	https://www.youtube.com/watch?v=Yo2Mse_qi5w

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	3	3	2	3		1	2	1	1	1	1	1	3		3
CO2	3	3	2	3		1		1	1	1	1	1	3		3
CO3	3	3	2	3		1		1	1	1	1	1	3		3
CO4	3	3	2	3		1		1	1	1	1	1	3		3
CO5	3	3	2	3		1		1	1	1	1	1	3		3

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Group Discussion (Unit V)	Once in a semester

Course Designed by: Dr. S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER II**COURSE CODE: 23PBI2CP3****TITLE OF THE COURSE: PRACTICAL: GENETIC ENGINEERING***(Skill Development & Employability)***COURSE OBJECTIVES:**

- To educate the students on the techniques of genetic Engineering
- To offer hands-on exposure to experiments in genetic Engineering

COURSE OUTCOMES:

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

CO1	Major Experiment: Make use of the instruments/equipments to carry out demonstration and experiments in Genetic Engineering	K3
CO2	Minor Experiment: Estimate/Evaluate using Genetic Engineering techniques	K5
CO3	Spotters: Identify and explain about the Instruments/Chemicals used in Genetic Engineering	K3
CO4	Viva: Interpret the results obtained from Genetic Engineering experiments	K5
CO5	Record: Illustrate and Summarize the experiments in Genetic Engineering	K2

Syllabus

Total Credits: 3

Instructional hours: 60

- Isolation of Genomic DNA
- Isolation of plasmid DNA
- Agarose Gel Electrophoresis of given DNA sample
- PCR Amplification of DNA
- RAPD
- SDS PAGE
- Restriction analysis
- Ligation
- Competent cells preparation
- Transformation of vector into *E.coli*
- Southern Blotting(Online Demo)
- Primer Designing using primer3
- Cloning vector construction by FastPCR, pDRAW software, WebCutter server and Plasmid Genome Database
- Recombination frequency analysis by MEGA software
- Identification of mutations in genes by GeneSNP-VISTA software

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1				3	3	1	2	2	1	1	2	2		3	1
CO2			3		3	1	2	2	1	1	2	2		3	1
CO3					3	1	2	2	1	1	2	2		3	1
CO4		3			3	1	2	2	1	1	2	2		3	1
CO5					3	1	2	2	1	1	2	2		3	1

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	Model Practical Examination	Once in a Semester
	Major Experiment	
	Minor Experiment	
	Spotters	
	Record/Observation	
	Viva	
2	End Semester Practical Examination	

Course Designed by: Mrs. P.J.Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER II

COURSE CODE: 23PBI2CP4

TITLE OF THE COURSE: PRACTICAL: DATABASE DEVELOPMENT & MOLECULAR PHYLOGENETICS
(Skill Development & Employability)

COURSE OBJECTIVES:

- To coach the students in Database Development and web hosting
- To edify the students about the Tools and Databases in Molecular Phylogenetics

COURSE OUTCOMES:

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

CO1	Major Experiment: Develop databases to store protein/nucleotide information	K6
CO2	Minor Experiment: Examine the various Molecular Phylogenetics tools to analyze the data	K4
CO3	Queries: Create and Execute simple queries to retrieve information from SQL Databases	K6
CO4	Viva: Interpret and explain the results obtained from Database Development and Molecular Phylogenetics	K5
CO5	Record: Illustrate and Summarize the experiments in Database Development and Molecular Phylogenetics	K2

Syllabus

Total Credits: 3

Instructional hours: 60

Database Development

- Query processing using SQL DDL Commands
- SQL DML Commands
- SQL DCL Commands
- Query processing using MySQL
- Modifying Database using MySQL

- Creating database connection using PHP
- Creating Registration form using PHP
- Creating login form using PHP
- Creating password reset form using PHP
- Web Interface using PHP
- Small Database Management Project using WAMP
- CSS basics

Molecular Phylogenetics

- Phylogenetic tree construction (Neighbor Joining & UPGMA method)
- To perform phylogenetic analysis by neighbor joining method using the Kimura two-parameter model for a set of nucleotide sequences.
- To perform phylogenetic analysis by neighbor joining method using the Dayhoff PAM matrix for a set of amino acid sequences (ribonucleases)

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	3	3	3	3		1	1	1	1	1	2		1	3	1
CO2	3	3	3			1	1	1	1	1	2		1	3	1
CO3	3	3	3		3	1	1	1	1	1	2		1	3	1
CO4	3	3	3			1	1	1	1	1	2		1	3	1
CO5	3	3	3			1	1	1	1	1	2		1	3	1

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	Model Practical Examination	Once in a Semester
	Major Experiment	
	Minor Experiment	
	Queries	
	Record/Observation	
	Viva	
2	End Semester Practical Examination	

Course Designed by: Dr. S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER III

COURSE CODE: 23PBI3C07

TITLE OF THE COURSE: CORE: GENOMICS AND PROTEOMICS
(Employability)

COURSE OBJECTIVES:

- To demonstrate on the techniques in Genomic and Proteomic analysis to the students
- To edify the concepts and techniques in genomics and Proteomics to the students

COURSE OUTCOMES:

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

CO1	Summarize the basics of genomics through the map elements and the map repositories	K2
CO2	Illustrate the structure of human genomes through the structural annotation	K2
CO3	Experiment with Next generation Sequencing techniques	K3
CO4	Outline the tools and techniques in proteomics	K2
CO5	Construct the applications of Proteomics in various fields	K3

Syllabus

Total Credits: 5

Instructional hours:90

Unit I: Basics of Genomics (K2)

18 hours

Introduction to Genomics: Definition of Genome, Genome sequencing & Human Genome project. Map elements, Types of maps - Cytogenetic, Linkage map, Physical map, Comparative map, STS content maps, Genome map: Types and their uses, High and low-resolution map, Map repositories: NCBI – Entrez Human genome map viewer, OMIM – Online Mendelian Inheritance in Man, Linkage map resources: CEPH reference pedigree, CHLC – Cooperative human linkage center, Radiation hybrid map resources. Current updates in Genomic databases and browsers – NCBI, TIGR, KEGG. SAGE: Strategies for generating ESTs and full length inserts; EST clustering and assembly; EST databases (DBEST, UNIGENE). (*Self Study: Types of maps*)

Unit II: Human genome and Comparative genomics (K2)

18 hours

Structure of Human genome – sequence repeats, transposable elements, gene structure, pseudo genes – Gene analysis – gene order – chromosome rearrangement – compositional analysis – clustering of genes – composite genes. Computational Sequence Analysis - Comparative Genomics of pathogens and non-pathogens. - Gene Ontology: Purpose and Methods of comparison, Tools for genomic comparison. Genome projects and Model Organism research -Yeast; Drosophila; C. elegans; and Mouse – a comparative analysis. Comparative genomics as an aid to gene mapping and in the study of human diseases.

(Beyond the Curriculum: Gene prediction in prokaryotes and eukaryotes, Evaluation of gene prediction methods, Prediction of promoter sequences).

Unit III: NGS(K3)

18 hours

What is Next Generation Sequencing? How is it different from traditional sequencing/Microarrays? Various NGS technologies/platforms. Experiment types and applications. Workflows for various NGS experiments (variant discovery and expression profiling). Algorithms and tools for NGS read alignment, SNP calling. Various file formats - SAM, VCF, BED, WIG, and PILEUP. DNaseq genetic variations.NGS and personal genome sequencing. Whole genome sequencing. Target sequencing. Sequencing Mappability. Refined

alignment. Base quality Recalibration. Variants identification. Four different workflows for mutation discovery (CrossBow, Bowtie, BWA, MAQ).

UNIT IV: Introduction to Proteomics (K2)

18 hours

Proteomes: definition of proteomes; genome-proteome relationship; deducing proteome from genome. Tools for Proteomics: Separation of proteins – Chromatography-Principle and types (HPLC and GLC). Electrophoresis: General principles, Electrophoresis of proteins: SDS- PAGE, Native gels, Isoelectric focusing, 2-D gel electrophoresis; Detection, estimation and recovery of proteins, Mass Spectrometry for protein and peptide analysis: MALDI-TOF Analyzers, Tandem mass spectrometry and protein sequencing and peptide fingerprinting.

Unit V: Applications of Proteomics (K3)

18 hours

Proteomics Applications: Protein Network Mapping, SALSA, Proteome applications and Protein array: Protein expression profiling, Protein Biochips, Protein-protein interaction –Motifs & Patterns, Shotgun Proteomics and its application to yeast proteome, Forward and Reverse Proteomics, Integrated Proteome Analysis - Phage antibody as tool, Proteomics in plant breeding: Genetic diversity analysis, Distribution of varieties, lines and cultivars, Mutant characteristics, Variability between organ and developmental stage, Identification of abiotic stress, Genetic mapping of protein markers.

TEXT BOOK(S):

1. TA Brown (2006), Genomes 3, 3rd Edition, Garland Science, USA
2. Arthur M Lesk (2012), Introduction to Genomics, 2nd Edition, Oxford University Press, UK
3. Stuart M. Brown. Next-Generation DNA Sequencing Informatics, Second Edition. New York University School of Medicine (ISBN-13:978-1621921236).
4. Proteomics: From Protein Sequence to Function, S. R. Pennington, Michael J. Dunn, 2001, BIOS Scientific Publishers, England

REFERENCE BOOK(S):

1. Jonathan Pevzner (2009), Bioinformatics and Functional Genomics, 2nd edition, Blackwell Wiley Publishing House, USA
2. William H. Majoros, Computational methods for gene prediction, 1st edition, Cambridge University Press, USA
3. Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme Mitchison (1998), Biological Sequence Analysis: Probabilistic models of proteins and nucleic acids, Cambridge University Press, USA
4. Principles of Proteomics, Richard Twyman, 2001, BIOS Scientific Publishers, England.
5. Introduction to Proteomics: Principles and Applications, Nawin C. Mishra, 2011, Wiley Publishers, USA
6. Introduction to Proteomics: Tools for the New Biology, Daniel Liebler, 2001, Humana Press, NJ, USA.

BLENDED LEARNING E-RESOURCES

UNIT III: NGS

TOPIC	LINKS
What is Next Generation Sequencing	https://www.youtube.com/watch?v=jFCD8Q6qSTM
How is it different from traditional sequencing/Microarrays	https://www.youtube.com/watch?v=2c3t3tDEmsU
Various NGS technologies/platforms	https://www.youtube.com/watch?v=zBPKj0mMcDg
Workflows for various NGS experiments	https://www.youtube.com/watch?v=MJaBfqF0lds

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	1			3			1	2	1	1	1	1	2	3	3
CO2	1		3				1	2	1	1	1	1	2	3	3
CO3	1				3		1	2	1	1	1	1	2	3	3
CO4	1	3					1	2	1	1	1	1	2	3	3
CO5	1					3	1	2	1	1	1	1	2	3	3

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Term paper (Unit V)	Once in a semester

Course Designed by: Mrs. P.J.Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER III

COURSE CODE: 23PBI3C08

TITLE OF THE COURSE: CORE: SYSTEMS BIOLOGY

COURSE OBJECTIVES:

- To introduce the field of Systems Biology to the Students
- To illuminate the students about Cell Simulation

COURSE OUTCOMES:

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

CO1	Illustrate the basics of Systems Biology with applications	K2
CO2	Experiment with various tools and databases available in Systems Biology	K3
CO3	Summarize the concept and objectives of system biology database based on different criteria	K3
CO4	Categorize the whole metabolisms and functions through the different biological pathways	K3
CO5	Illustrate the different biological process and cell simulation through the <i>Insilico</i> Modeling and simulation methods	K2

Syllabus

Total Credits: 5

Instructional hours:90

Unit I: Introduction to Systems biology (K2)

18 hours

What is Systems Biology? Integrating Networks. Methods of study: Micro array – definition, types of array, Micro array data analysis: Hierarchical clustering, Self-organizing maps. Applications of Micro Arrays in systems biology. Gene expression analysis by cDNA micro arrays, Global Gene Expression Analysis, Microarray analysis, Comparative Transcriptomics, Differential Gene Expression- Sporulation Vs Vegetative condition in yeast and Bacillus (*Self Study: Integrating Networks*)

Unit II: Tools and Databases in Systems Biology(K3)

18 hours

Basic concepts & objectives of System biology Databases for Systems biology - Developments and trends of Systems biology, Long and medium-term goals of Systems biology, the potential applications of Systems biology, - Natural language processing and ontology- enhanced biomedical literature mining for Systems Biology.

Unit III: Metabolomics & Metabolic Pathways (K3)

18 hours

Membrane transport - Overview, Digestion of proteins and protein metabolism, Carbohydrate metabolism – metabolism of glucose – glycolysis, TCA cycle, glycogenesis, Pentose phosphate shunt, Electron transport, Interconnection of pathways, metabolic regulation. Translating biochemical networks into linear algebra.

Metabolomite, Metabolome, metabolomic separation and analysis techniques - metabolic profiling/ fingerprinting, Metabolome informatics - Resources/databases of metabolomics. (*Beyond the Curriculum: Pathways to Networks – cAMP and G-Protein pathways, MAP- Kinase Pathways/Network*)

Unit IV: Cytomics (K3)

18 hours

Strategies relating to *Insilico* Modeling of biological processes - Gene Expression Patterns. - Microarray analysis and gene networks, BRB Array tool - Applications of Systems Biology Markup language (SMBL), Spatio-temporal Systems biology, Cytomics-from Cell States to predictive medicine, The IUPS Physiome project. Genesis tool and its applications

Unit V - Whole cell simulation (K2)

18 hours

Principle and levels of simulation –E.cell and V- cell Simulations and Applications, Virtual Erythrocytes, Pathological analysis. Flux Balance Analysis. Relationship analysis: Predicting ligand-binding function, Use of gene cluster, detecting protein – protein interaction.

TEXTBOOK(S):

1. Uri Alon (2006), An Introduction to Systems Biology: Design Principles of Biological Circuits, Chapman and Hall/CRC,USA
2. Walhout Marian, Marc Vidal, Job Dekker (2012), Handbook of Systems Biology: Concepts and Insights, Academic Press, UK

REFERENCE BOOK(S):

1. EberhardVoit (2012), A First Course in Systems Biology, Taylor & Francis group, USA
2. Jens Nielsen and Michael C. Jewett (2007), Metabolomics: A Powerful Tool in Systems Biology, Springer, Germany
3. Robert K. Murray, David A. Bender, Kathleen M. Botham, Peter J. Kennelly, Victor W. Rodwell and P. Anthony Weil (2012), Harpers Illustrated Biochemistry, 29th Edition, McGraw-Hill Medical, USA

**BLENDED LEARNING E-RESOURCES
UNIT V: WHOLE CELL SIMULATION**

TOPIC	LINKS
Gene Expression Patterns - Microarray analysis and gene networks	https://youtu.be/Hv5flUOsE0s
The IUPS Physiome project	https://youtu.be/MxZqJobgam4
Principle and levels of simulation	https://youtu.be/Wp3jyLkfBQs
Virtual Erythrocytes	https://youtu.be/GSrPe04NkcI
Flux Balance Analysis	https://youtu.be/eNo7NeQPA2c
Predicting ligand-binding function	https://youtu.be/5-hLq8DmtZs
Detecting protein – protein interaction	https://youtu.be/9IrPVXn-x5k

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	1				2	1	1	1	1	1	1	1	2	3	3
CO2		2			2	1	1	1	1	1	1	1	2	3	3
CO3			3		2	1	1	1	1	1	1	1	2	3	3
CO4				1	2	1	1	1	1	1	1	1	2	3	3
CO5					2	1	1	1	1	1	1	1	2	3	3

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Term paper (Unit V)	Once in a semester

Course Designed by: Mrs. P.J.Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by:
	Principal

SEMESTER: III

COURSE CODE: 23PBI3C09

**TITLE OF THE COURSE: CORE: MOLECULAR MODELING & COMPUTER
AIDED DRUG DESIGN (*Employability*)**

COURSE OBJECTIVES:

- To introduce the students to Molecular Modeling
- To educate the students about the Computer Aided Drug Designing

COURSE OUTCOMES:

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

CO1	Outline the concepts in Molecular Modeling	K2
CO2	Compare different techniques of Simulation for Conformational analysis	K2
CO3	Understand the types of Drug targets	K3
CO4	Appraise the technique of Molecular Modeling	K5
CO5	Establish CADD using Molecular Docking	K5

Syllabus

Total Credits: 5

Instructional hours:90

UNIT I: Introduction to the concepts of molecular modeling (K2) 18 hours

Introduction to the concepts of molecular modelling- Coordinate System; potential energy surfaces Molecular structure and internal energy. Empirical representation of molecular energies. Use of force fields and the molecular mechanics method. Molecular Mechanics: Features of molecular mechanics, force fields; Bond structure and bending angles, electrostatic, van der Waals and non-bonded interactions, hydrogen bond; Derivatives of molecular mechanics energy function; Transferability of force field parameters, delocalized pi system; Energy minimization of small molecules: Application of energy minimization. Discussion of local and global energy minima. Application of molecular graphics (*Self Study: Coordinate System*)

UNIT II: Simulation for conformational analysis (K2) 18 hours

Simulation for conformational analysis. *Ab initio*, dft and semi empirical methods. Molecular Dynamics: Simulation Methods using simple models; continuous potentials; Time dependent properties; Solvent effects; Conformational changes from simulation, Monte Carlo Simulation.

UNIT III: Drug Targets (K3) 18 hours

Drug targets: Cell surface receptors, GPCR's, Kinases, Channel proteins, Enzymes, Ubiquitin, DNA and cytosolic receptors with mode of action. Finding new drug targets to treat disease, new targets for anti-cancer drugs, Role of p53 – Oncogene changes, Drugs that rescue mutant p53. Chemogenomics: Effect of chemicals on genes – delayed mutations – Interaction of molecules (small & Big) with DNA intercalation – case study with copper deficiency leading to diseases.

(Beyond the Curriculum: Drug targets for Inflammation, Diabetes and Arthritis – mechanism of action and therapies).

UNIT IV: Macromolecular Modeling (K5) 18 hours

Macromolecular modeling. Protein structure modeling: Homology modeling, Threading, *Abinitio*, Vector based method, neural network. Model refinement and validation. Small Molecule Modelling: Lipinski's rule, Design of ligands for known macromolecular target sites, Classical SAR / QSAR studies and their implications to the 3-D modeler. 2-D and 3-D database searching. Pharmacophore identification and novel drug design. ADMET properties.

UNIT V: Structure based Drug Design(K5) 18hours

Structure Based Drug Design: Steps involved, Inside Out and Outside In approaches. Enzyme inhibition Strategies: competitive, non-competitive and uncompetitive enzyme inhibition. Docking: Principles of Docking, Drug – receptor interaction, Steps in Docking, Types of Docking - Rigid and Flexible, Protein-Protein Docking and Protein-Ligand Docking, applications of docking.

TEXT BOOKS:

1. Andrew Leach (2001), Molecular Modelling: Principles and Applications, 2nd Edition, Prentice hall, NJ
2. Alan Hinchliffe (2008), Molecular Modelling for Beginners, 2nd Edition, John-Wiley Inc, NY

REFERENCE BOOKS:

1. Kukol, Andreas (Ed.) (2008), Molecular Modeling of Proteins, Humana Press, NJ
2. Johann Gasteiger and Thomas Engel (2003), Chemoinformatics: A Textbook, Wiley VCH, NY
3. Rajarshi Guhaand Andreas Bender (2012), Computational Approaches in Cheminformatics and Bioinformatics, Wiley-Blackwell, NY
4. Andrew R. Leach (2007), An Introduction to Chemoinformatics, Springer, Germany.

BLENDED LEARNING E-RESOURCES**UNIT II: SIMULATION FOR CONFORMATIONAL ANALYSIS**

TOPIC	LINKS
Quantum Mechanics	https://www.youtube.com/watch?v=7kb1VT0J3DE
Ab initio, dft and Semi-empirical methods	https://www.youtube.com/watch?v=YkFE8h3S89g
Molecular Dynamics	https://www.youtube.com/watch?v=_TiQYNWJwYg

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1				1	3	1	1	2	1	1	1	3		3	2
CO2				1	3	1	1	2	1	1	1	3		3	2
CO3				1	3	1	1	2	1	1	1	3		3	2
CO4				1	3	1	1	2	1	1	1	3		3	2
CO5				1	3	1	1	2	1	1	1	3		3	2

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Review Paper (Unit V)	Once in a semester

Course Designed by: Dr. S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: III**COURSE CODE: 23PBI3E01****TITLE OF THE COURSE: ELECTIVE: PHARMACOGENOMICS****COURSEOBJECTIVES:**

- To introduce the students to the field of Pharmacogenomics
- To train the students on the methods of study of Pharmacogenomics

COURSE OUTCOMES:

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

CO1	Outline the concepts of pharmacogenomics	K2
CO2	Compare different polymorphisms involved in pharmacogenomics study	K2
CO3	Interpret the factors affecting drug response	K2
CO4	Explain the various methods of biotransformation	K2
CO5	Apply the Pharmacogenomics tools for personalized medicine research	K3

Syllabus

Total Credits: 3

Instructional hours: 60

Unit I: Pharmacogenomics (K2)

12 hours

Introduction, basic concepts about genetics diseases. Personalized medicine-introduction and importance. The genetics of therapeutic targets and gene-based targets. Pharmacogenomics necessity in drug designing

Unit II: Polymorphisms(K2)

12 hours

Introduction, types and importance in Drug targets. Introduction to pharmacodynamics, pharmacokinetics, toxicogenomics and ADME properties. Process of drug development-clinical trials phase I, II, III and IV. Route of drug administration. Nature of cell membrane, physiological factors related to drug absorption and drug distribution. (*Self Study: Drug targets*)

Unit III: Factors affecting drug response (K2)

12 hours

Drug response to patients, Structural influence in the Drug response.Efficacy and metabolism of drugs.Pharmacogenomics vs. Structural Pharmacogenomics.Drug metabolism pathways and adverse drug reactions.Prediction of structural changes among sequences by the influence of polymorphisms.

Unit IV: Biotransformation (K2)

12 hours

Biotransformation (Metabolism) of drugs and related organic compounds - General pathways, sites of drug biotransformation. Oxidative reactions, reductive reactions, hydrolytic reactions, conjugation reactions, factors affecting drug metabolism and variability in drug response. Ayurgenomics (integration of Ayurveda & genomics).Microsatellite in studying genetic variation.Microarray in herbal drug research, Pharmacodynamics, Pharmacogenomics and Pharmacognosy.

Unit V: Tools for pharmacogenomics analysis (K3)

12 hours

Pharmacokinetics (PK), Pharmacodynamics (PD).Process in Structural Pharmacogenomics - Target Structure optimization, Validation, lead identification, ADME prediction, synthesis, assays and Clinical trials.Pharmacogenomics in the treatment of cancer, neurodegenerative diseases, cardiovascular diseases. Pharmacogenomics in pharmaceutical industry, Ethical issues related to Pharmacogenomics, Pharmacogenomics and ethno pharmacology,CTD and PharmGKB.

TEXT BOOK(S):

1. Rothstein, Pharmacogenomics: Social, ethical and clinical dimensions, Wiley Lisspublisher,NJ.
2. B.Patwaradhan.2007. Drug discovery and development. New India publishing agency, NewDelhi.

REFERENCE BOOK(S):

1. J.H. Block and J.M. Beale Jr. 2004. Organic medicinal and Pharmaceutical chemistry. Lippincott Williams and Wilkins, NewYork.

BLENDED LEARNING E-RESOURCES
UNIT IV: BIOTRANSFORMATION

TOPIC	LINKS
Biotransformation (Metabolism) of drugs	https://www.youtube.com/watch?v=guJeisEYM2I
Oxidative reactions, reductive reactions	https://www.youtube.com/watch?v=dF5lB7gRtcA
Conjugation reactions	https://www.youtube.com/watch?v=gSGt6Nyyfy8
Ayurgenomics	https://www.youtube.com/watch?v=5NC7SPvmDOE

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	3	3		2				1	1	1	1	1		3	3
CO2	3	3		2				1	1	1	1	1		3	3
CO3	3			2				1	1	1	1	1		3	3
CO4	3		3	2				1	1	1	1	1		3	3
CO5	3		3	2		3	3	1	1	1	1	1		3	3

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Group Discussion (Unit V)	Once in a semester

Course Designed by: Dr.S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: III

COURSE CODE: 23PBI3E02

TITLE OF THE COURSE: ELECTIVE: BASICS OF CHEMINFORMATICS

COURSEOBJECTIVES:

- To introduce the students to the field of Cheminformatics
- To train the students on the methods of study of Cheminformatics

COURSE OUTCOMES:

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

CO1	Outline the concepts of graph theory	K2
CO2	Infer the stereochemistry of proteins	K2
CO3	Extend various chemical databases available for cheminformatics research	K2
CO4	Relate the tools used in Cheminformatics for drug design applications	K2
CO5	Summarize various drug design methods	K2

Syllabus

TotalCredits:3

Instructional hours:60

UNIT I: Introduction(K2)

12hours

Graph theory and molecular numerology; Logic, sets and functions; Algorithms, integers and matrices; Mathematical reasoning, induction and recursion; Counting; graphs, trees and sets, basic probability and statistics; Markov processes. Chemical data File Format, Chemical Drawing Softwares.(*Self Study: Algorithms*)

UNIT II: Stereochemistry (K2)

12 hours

Basic Stereochemistry, Amino acids and Proteins and Properties; pKa, pH and ionization of acids and bases; Protein structure - Primary structure, Secondary structure - helix & sheet; Tertiary structure; Quaternary structure; covalent and non-covalent forces that maintain structures.Introduction to drug action, pro drug design andapplications.

UNIT III: Chemical Databases (K2)

12 hours

History of scientific information communication-chemical literature-chemical information- chemical information search-chemical information sources-chemical name and formula searching-analytical chemistry-chemical history-biography-directories and industry sources

UNIT IV: Tools in Cheminformatics (K2)

12hours

Introduction; Experimental sources of biological data; Publicly available databases; Gene expressionmonitoring;GenomicsandProteomics;Metabolomics;Visualisationofsequencedata; Visualization of structures using Rasmol or SPDB Viewer or CHIME; Genetic basis of disease; Personalized medicine and gene-based diagnostics.

UNIT V: Introduction to Drug Design (K2)

12 hours

Introduction to drugs, structure-based drug design. QSAR and 3D-QSAR Methods.Pharmacophore Design, Ligand-Based Design and *De Novo* Drug Design Virtual screening/docking of ligands.Protein structure, Drug action & enzymes. Drug action and receptors. Prediction of binding modes, Protein-Ligand binding, binding free energies, Fragment based drug design, ADMET prediction.

TEXT BOOK(S):

1. Andrew. R. Leach, 2007, An introduction to Cheminformatics, Springer, Germany

REFERENCE BOOK(S):

1. Rajarshi Guhaand Andreas Bender, 2011, Computational Approaches towards Cheminformatics and Bioinformatics, John Wiley & Sons, USA

**BLENDED LEARNING E-RESOURCES
UNIT V: INTRODUCTION TO DRUG DESIGN**

Introduction to Drug Design	https://www.youtube.com/watch?v=FioRil-0bZE
Ligand based Drug Design	https://www.youtube.com/watch?v=6WgxKV5odks
De novo Drug Design	https://www.youtube.com/watch?v=xjzVx1jp4Gg
QSAR	https://www.youtube.com/watch?v=SEXT6Pulxrc

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1		3		3		1	1	2	1					3	3
CO2		3		3		1	1	2	1					3	3
CO3		3		3		1	1	2	1					3	3
CO4		3		3		1	1	2	1		3			3	3
CO5		3		3		1	1	2	1					3	3

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Group Discussion (Unit V)	Once in a semester

Course Designed by: Dr.S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER III

COURSE CODE: 23PBI3CP5

**TITLE OF THE COURSE: PRACTICAL: OMICS AND SYSTEMS BIOLOGY
(Skill Development)**

COURSE OBJECTIVES:

- To provide hands-on training in Proteomics and genomics tools and Databases
- To Coach the students on Databases and Tools in Systems Biology

COURSE OUTCOMES:

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

CO1	Major Experiment: Make use of the OMICS Databases and retrieve data	K3
CO2	Minor Experiment: Evaluate different OMICS databases for data analysis	K5
CO3	Spotters: Identify and explain about the different OMICS databases and Tools	K3
CO4	Viva: Interpret the results obtained from OMICS data Analysis	K5
CO5	Record: Illustrate and Summarize the experiments in OMICS data analysis	K2

Syllabus

Total Credits: 3

Instructional hours: 60

GENOMICS

- Genome Databases: NCBI, EMBL-ENA, Ensembl, GRAMENE
- Model organism database- TAIR, flybase
- Repositories for high throughput genomic sequences – EST, SRA, NCBI Assembly
- Specialized Databases- GSDB, FSSP
- Comparative genomic analysis by Integrated Microbial Genomes and Microbiomes tools and HGT-DBtools, Byss, RAST.
- Comparative genome annotation by VISTA tools
- Bacterial operon prediction by OperonDB tools
- Gene prediction by WebGene, ORF finder and COG database, Augustus
- Identification of coding region by CRITICA/ Genscan
- Promoter and regulatory region prediction by Virtual FootPrint
- Sequence assembly and finishing by EG assembler/PHRED/PHRAP software, Velvet
- Other Databases – OMIM
- NGS data analysis using galaxy server
 - Quality check - FastQC
 - Reference genome Assembly
 - De novo genome Assembly – Soap denovo
 - Genome Annotation – Local Blast/KAAS

PROTEOMICS

- Protein network prediction by Sting, KEGG Net servers and Cytoscape
- Protein bulk properties prediction by WinGene/WinPep software
- 2D gel data analysis by SWISS-2D GELDB
- Mass spectroscopy data analysis by MSDB and Mascot/ PeptIdent

SYSTEMS BIOLOGY

- Metabolic pathway prediction by UM-BBD and Pathway Hunter Tool
- Molecular visualization- Rasmol, Cn3D, DeepView
- Metabolic reaction and pathway construction by KASS and e-ZYME software
- Microarray data analysis by NCBI-OMNIBUS, TIGR Archive Viewer and TH4/BioConductor/BASE software

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1			3	3		1	1	1	1	1	2	2	3		1
CO2			3	3		1	1	1	1	1	2	2	3		1
CO3			3	3	3	1	1	1	1	1	2	2	3		1
CO4		3	3	3		1	1	1	1	1	2	2	3		1
CO5			3	3		1	1	1	1	1	2	2	3		1

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	Model Practical Examination	Once in a semester
	Major Experiment	
	Minor Experiment	
	Queries	
	Record/Observation	
	Viva	
2	End Semester Practical Examination	

Course Designed by: Mrs. P.J.Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER III

COURSE CODE: 23PBI3CP6

TITLE OF THE COURSE: PRACTICAL: MOLECULAR MODELLING AND DRUG DESIGN
(Skill Development & Employability)

COURSE OBJECTIVES:

- To train the students in the tools and databases for Molecular Modeling
- To educate the students in the tools and databases for Drug designing

COURSE OUTCOMES:

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

CO1	Major Practical: Model Protein Structure from Sequence/Apply Docking to understand Protein-Ligand Interactions	K3
CO2	Minor Practical: Analyze protein Structure / Docked Conformation	K4
CO3	Spotters: Identify and explain about the different Modeling and Docking tools	K3
CO4	Viva: Interpret the results obtained from Modeling and Docking tools	K5
CO5	Record: Illustrate and Summarize the experiments in Modeling and Docking tools	K2

Syllabus

Total Credits: 3

Instructional hours: 60

- Protein structure calculations - bond lengths, bond angles, torsion angles and hydrogen bonds.
- Molecular surface calculations.
- Ramachandran plot
- Structural superposition
- Homology modeling – Swiss-Model, CPH, Modeller
- Homology Modeling and structure refinement using SPDBV
- Model validation using What Check and ProCheck.
- Data mining for retrieval of chemical information from Pubchem and chemspider

- Retrieving pharmacological information from Pharma base and MSDchem (PDBechem) database
- Small molecule building- small peptides or nucleic acids, using CHEMSKETCH.
- Prediction of binding affinity of ligand by protein-ligand interaction/ReLiBase database tools
- Target – Ligand from PDB Sum.
- Binding site identification of target by Q-site finder server
- Generating 3D coordinates –CORINA.
- Molecular Visualisation System –Pymol/VMD.
- Molecular docking –Hex/ArgusLab/VEGA.
- Molecular properties prediction by VEGAZ software
- Molecular dynamics simulation by GROMOS software
- Molecular force field analysis by TINKER software
- Drug activity test by ADMETox tools
- Analysis of hydrophobic features of target by BioEdit software

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	3			3	3	1	1	1	1	1	2	1	3		1
CO2	3		3	3	3	1	1	1	1	1	2	1	3		1
CO3	3			3	3	1	1	1	1	1	2	1	3		1
CO4	3	3		3	3	1	1	1	1	1	2	1	3		1
CO5	3			3	3	1	1	1	1	1	2	1	3		1

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	Model Practical Examination	Once in a semester
	Major Experiment	
	Minor Experiment	
	Queries	
	Record/Observation	
	Viva	
2	End Semester Practical Examination	

Course Designed by: Dr. S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: IV
COURSE CODE: 23PBI4C10
TITLE OF THE COURSE: CORE: BIostatISTICS AND BIOScriptING
(Employability)

COURSE OBJECTIVES:

- To disseminate the students about the concepts and techniques in Scripting
- To prepare the students to solve statistical problems

COURSE OUTCOMES:

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

CO1	Solve statistical problems manually as well as using softwares	K3
CO2	Develop programs using PERL	K3
CO3	Construct programs using BioPERL	K3
CO4	Appraise Biological algorithms using BioPERL	K5
CO5	Compose programs using Python	K3

Syllabus

Total Credits: 5

Instructional hours:90

UNIT I: Statistical Methods (K3)

18 hours

Statistical Methods: Measures of central tendency and dispersion; Simple correlation - correlation coefficient. Regression - simple linear regression; Probability distributions (Binomial, Poisson and normal); sampling distribution; parametric statistics; confidence interval; errors; levels of significance; regression and correlation; t-test; analysis of variance; Chi Square test; F- test (Simple problems only).

Statistical Analysis using SPSS. R – Package - Introduction: Installing R; R as a deluxe calculator, creating objects and assigning values; graphics; working with data sets; statistical distributions. (Industry 4.0) (Self Study: Measures of Central tendency)

UNIT II: PERL (K3)

18 hours

PERL: Introduction – Scalar variables, array variables; Lists, Hashes, Basic control structures- File handling data types; Pattern Matching & Regular expression & string handling features of PERL; substitution & translation, split, subroutines.
(Beyond the Curriculum: References, Modules, Packages and Libraries in PERL).

Unit III: Object Oriented PERL (K3)

18 hours

Basic concepts of OOPS: classes, objects, methods, member functions, constructors and destructors, abstraction, polymorphism, data hiding, encapsulation, inheritance, dynamic binding. Creating Objects, Attributes, Classes, Methods, Constructors & Destructors using PERL; demonstrating Polymorphism, Encapsulation, Inheritance using PERL; OO programs. - Introduction to Bio PERL.

General Bioperl classes, Sequences (Bio::Seq Class, Sequence Manipulation), Features and Location Classes (Extracting CDS), Alignments (AlignIO), Analysis (Blast, Genscan), Databases (Database Classes, Accessing a local Database)

Unit IV: Perl programming for bioinformatics (K5)

18 hours

Introduction to Biological algorithms; Exhaustive search algorithm-Restriction

mapping; Dynamic Programming Algorithm- sequence alignment techniques, statistical approach to gene prediction.

Unit V: Python (K3)

18 hours

Introduction to PYTHON – Working with data – Program organization & functions – Modules & libraries – Classes & Objects – Inside the Python Object system – Testing, debugging & Software development practice – Iterators & generators – Working with text – Binary data handling – Working with processors – Python integration primer.

TEXT BOOKS:

1. A.K. Sharma (2005), Text Book Of Biostatistics I, Discovery Publishing House, New Delhi
2. A.K. Sharma (2005), Text Book Of Biostatistics II, Discovery Publishing House, New Delhi
3. SP Gupta (2011), Statistical Methods, Sultan Chand & Sons, New Delhi
4. David Medinets (1996), Perl 5 by Example, Que Publications, UK
5. Harvey M. Deitel, Paul J. Deitel, Tem R. Nieto and D. C. McPhie (2001), Perl How to Program: Introducing CGI & Python, Prentice Hall, NJ

REFERENCE BOOKS:

1. James Tisdall (2001), Beginning Perl for Bioinformatics, O'Reilly Media, USA
2. Mark Lutz (2011), Programming Python, 4th Edition, Shroff/O'Reilly, USA
3. Mark Lutz (2013), Learning Python: Powerful Object-Oriented Programming, 5th Edition, USA
4. Magnus Lie Hetland (2010), Python Algorithms: Mastering Basic Algorithms in the Python Language, Apress, NY
5. Mark Gardener (2013), Beginning R : The Statistical Programming Language, Wiley, USA

BLENDDED LEARNING E-RESOURCES

UNIT V: PYTHON

TOPIC	LINKS
Introduction to Python	https://www.youtube.com/watch?v=WvhQhj4n6b8
Program Organization and Functions	https://www.youtube.com/watch?v=oSPMmeaiQ68
Modules and Libraries	https://www.youtube.com/watch?v=7GXaobCrBb4
Classes and Objects in Python	https://www.youtube.com/watch?v=_uYorV9ebLg
Testing and debugging in Python	https://www.youtube.com/watch?v=QZKgQravBw4
Iterators and Generators in Python	https://www.youtube.com/watch?v=zLqkC7COSCc
Binary data handling	https://www.youtube.com/watch?v=FfKUNijU-dg

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	1		3	3	3	2	2	2	2	1	1	1		3	2
CO2	1		3	3	3	2	2	2	2	1	1	1		3	2
CO3	1		3	3	3	2	2	2	2	1	1	1		3	2
CO4	1		3	3	3	2	2	2	2	1	1	1		3	2
CO5	1		3	3	3	2	2	2	2	1	1	1		3	2

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Code Development in Python(Unit V)	Once in a semester

Course Designed by: Dr.S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER: IV
COURSE CODE: 23PBI4C11
TITLE OF THE COURSE: CORE: RESEARCH METHODOLOGY

COURSE OBJECTIVES:

- To introduce the students to the methods of doing research
- To educate the students on research writing

COURSE OUTCOMES:

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

CO1	Relate the procedure of doing research	K2
CO2	Explain about research design	K2
CO3	Extend the various data collection methods	K2
CO4	Outline the different methods of research writing	K2
CO5	Plan the ethical considerations while doing research	K3

Syllabus

Total Credits: 5

Instructional hours:90

Unit I – Science and Research: (K2)

18 hours

Definition – History – Evolution of Scientific Inquiry, Scientific Research: Definition, Characteristics, types, need of research. Identification of the problem, assessing the status of the problem, formulating the objectives, preparing design (experimental or otherwise), Actual investigation. (*Self study: Evolution of Scientific inquiry*)

Unit II - Introduction to Research Methodology (K2)

18 hours

Meaning and importance of Research – Types of Research – Selection and formulation of Research Problem Research Design – Need – Features – Inductive, Deductive and Development of models Developing a Research Plan – Exploration, Description, Diagnosis, Experimentation, Determining Experimental and Sample Designs. Analysis of

Literature Review – Primary and Secondary Sources, Web sources –critical Literature Review Hypothesis – Different Types Significance – Development of Working Hypothesis, Null hypothesis Research Methods:Scientific method vs Arbitrary Method, Logical Scientific Methods: Deductive, Inductive, Deductive-Inductive, pattern of Deductive – Inductive logical process – Different types of inductive logical methods.

Unit III - Data Collection and Analysis (K2)

18 hours

Sources of Data – Primary, Secondary and Tertiary – Types of Data – Categorical, nominal & Ordinal. Methods of Collecting Data: Observation, field investigations, Direct studies – Reports, Records or Experimental observations. Sampling methods – Data Processing and Analysis strategies- Graphical representation – Descriptive Analysis – Inferential Analysis- Correlation analysis – Least square method - Data Analysis using statistical package – Hypothesis – testing – Generalization and Interpretation –Modeling.

Unit IV – Scientific Writing (K2)

18 hours

Structure and components of Scientific Reports – types of Report – Technical Reports and Thesis – Significance – Different steps in the preparation – Layout, structure and Language of typical reports - Illustrations and tables – Bibliography, Referencing and foot notes – Importance of Effective Communication. Preparing Research papers for journals, Seminars and Conferences – Design of paper using TEMPLATE, Calculations of Impact factor of a journal, citation Index, ISBN & ISSN. Preparation of Project Proposal - Title, Abstract, Introduction – Rationale, Objectives, Methodology – Time frame and work plan – Budget and Justification – References Documentation and scientific writing Results and Conclusions, Preparation of manuscript for Publication of Research paper, Presenting a paper in scientific seminar, Thesis writing. Structure and Components of Research Report, Types of Report: research papers, thesis, Research Project Reports, Pictures and Graphs, citation styles, writing a review paper, Bibliography.

Unit V – Ethics & Computer applications (K3)

18 hours

Ethical Issues – Ethical Committees – Commercialization – copy right – royalty – Intellectual Property rights and patent law – Track Related aspects of intellectual property Rights – Reproduction of published material – Plagiarism – Citation and Acknowledgement – Reproducibility and accountability. Use of word processing, spread sheet and database software. Plotting of graphs. Internet and its application: E-mail, WWW, Web browsing, acquiring technical skills, drawing inferences from data. (*Beyond the Curriculum: Scholarly publishing- IMRAD concept and design of research paper, Citation and acknowledgement, plagiarism, reproducibility and accountability*).

TEXT BOOK(S):

1. Kothari, C.R. (2008). Research Methodology: Methods and Techniques. Second Edition. New Age International Publishers, New Delhi.

REFERENCE BOOK(S):

1. Garg.B.L., Karadia, R., Agarwal, F. and Agarwal, U.K., 2002. An introduction to Research Methodology, RBSA Publishers, Rajasthan.
2. Sinha, S.C. and Dhiman, A.K., 2002. Research Methodology, Ess Ess Publications, New Delhi

- Gupta S.P. (2008). Statistical Methods. 37th ed. (Rev) Sultan Chand and Sons. New Delhi.
- Leon & Leon (2202). Internet for everyone, Vikas Publishing House, India.
- Wadehra, B.L.2000. Law relating to patents, trade marks, copyright designs and geographical indications. Universal Law Publishing, New Delhi.
- Research Methodology Dr P M Bulakh, Dr P. S. Patki and Dr A S Chodhary 2010 Published by Expert Trading Corporation Dahisar West, Mumbai.

BLENDED LEARNING E-RESOURCES
UNIT III: DATA COLLECTION AND ANALYSIS

TOPIC	LINKS
Sources of Data	https://www.youtube.com/watch?v=bbgDaRtKRQE
Types of Data	https://www.youtube.com/watch?v=7bsNWq2A5gI
Methods of Collecting Data	https://www.youtube.com/watch?v=HvbClOwK9c0
Sampling Methods	https://www.youtube.com/watch?v=10OnonAIEcK

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	2			3					1			1	3	2	2
CO2	2			3					1			1	3	2	2
CO3	2			3					1			1	3	2	2
CO4	2			3					1	3		1	3	2	2
CO5	2			3		3	3		1			1	3	2	2

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	End semester Examination	Once in a semester
2	CIA I	Once in a semester
3	CIA II	Once in a semester
4	Model	Once in a semester
4	Assignment (Unit I & Unit II)	Twice in a semester
5	Seminar (Unit III & Unit IV)	Twice in a semester
6	Review paper (Unit V)	Once in a semester

Course Designed by: Mrs. P.J.Buvaneshwari	Verified by HOD: Dr. S. Sivashankari
Checked by CDC: Dr. G. Chitra	Approved by: Principal

SEMESTER IV
COURSE CODE: 20PDIS404
TITLE OF THE COURSE: COMPULSORY COURSE: DIGITAL SECURITY
Syllabus

Total Credits: 2

Instructional hours: 30

UNIT-I: Cyber Security

5 Hours

Introduction to Cyber Security- Attacks- security goals – Vulnerabilities – Methods of defense controls – Authentication – Malwares.

UNIT –II: Information Security

6 Hours

Components of an Information System – Program Security: Secure Programs - File Production Mechanisms – Database Security: Concepts of Database- Sensitive Data - Inference– Administrating Security: Security Planning – Protecting Programs and Data.

UNIT- III: Network Security

7 Hours

What is Network Security? : Types of Attacks - Networks concepts: Types of Transmission Media- Protocols – Types of Computer Networks- Network Security Controls – Firewalls: Software and Hardware Firewalls- Antivirus – Content Filtering- Web Security: Understanding the Risks - Security Awareness- Securing most Common Social Networking Sites- Encryption Techniques.

UNIT – IV: Cyber Crime and Terrorism

6 Hours

Introduction to Cyber Crime –Where does the Cyber Crime Come From?- Types of Cyber Crime: Identity Theft- Psychological Tricks -Social Media Related Attacks- Digital Banking Frauds - Attacks through Mobile Application - Virus Attack on Personal Computer – Other Types of Attacks - General Tips to keep you safe – Cyber Terrorism and Security Measures.

UNIT –V: Cyber Law and Case Studies

6 Hours

Overview of Cyber Law- Cyber Law in E-Commerce- Digital Signatures and Certificates- Information Technology Acts – Case Studies: Business Frauds- Bank Frauds – Facebook Frauds.

TEXTBOOK:

1. Digital Security for Post graduate Courses, Published by Nirmala College for Women, Coimbatore

SEMESTER IV
COURSE CODE:23PBI4CP7
TITLE OF THE COURSE: PRACTICAL: SCRIPTING
(Skill Development and Employability)

COURSE OBJECTIVES:

- To teach the students about scripting using PERL and Python
- To train the students in Statistical Data analysis using SPSS and R

COURSE OUTCOMES:

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

CO1	Major Experiment: Develop programs in PERL and Python for Biological Data Analysis	K6
CO2	Minor Experiment: Examine the various options in SPSS and analyze the data	K4
CO3	Queries: Create and Execute simple queries in R to analyze data	K6
CO4	Viva: Interpret the results obtained from Scripting using PERL/Python	K5
CO5	Record: Illustrate and Summarize the Scripting experiments in PERL/Python	K2

Syllabus

Total Credits: 3

Instructional hours:60

- Introduction to SPSS -ANOVA Studies
- **PERL:**
 - Program to store a DNA sequence
 - Program to concatenate DNA fragments
 - Program to convert DNA to RNA
 - Program to calculate reverse compliment of DNA sequence
 - Program to read protein sequence data from a file
 - Program to find motifs in a protein sequence
 - Program to count nucleotides in a sequence
 - Program to find the percentage of hydrophobic amino acids in a sequence
 - Program to find the percentage of G and C in a DNA sequence
 - Program to append ATGC to a DNA sequence using subroutines
 - Program to concatenate two strings using subroutines
 - Program to count the number of given motifs
 - Program to convert DNA to RNA using subroutines
 - Program to find if a DNA is stable or not
- **PYTHON**
 - Simple programming
 - Variables & programs in script
 - Loops & conditionals
 - Functions
 - Tuples, lists & dictionaries
 - For loop
 - Classes
 - Importing modules
 - Files Input & output
- **R PACKAGE**
 - R as a deluxe calculator
 - Creating objects & assigning values
 - Graphics presentation using R
 - Working with datasets
 - Statistical distribution using R.

MAPPING OF COs WITH POs AND PSOs

	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10	PO11	PO12	PSO1	PSO2	PSO3
CO1	3			3		1	1	1	1	1	2	1	1		1
CO2	3		3	3		1	1	1	1	1	2	1	1		1
CO3	3			3	3	1	1	1	1	1	2	1	1		1
CO4	3	3		3		1	1	1	1	1	2	1	1		1
CO5	3			3		1	1	1	1	1	2	1	1		1

(Correlation: 1- Low; 2- Medium; 3- High)

ASSESSMENT TOOLS

S. No	Assessment methods	Frequency of Assessment
1	Model Practical Examination	Once in a semester
	Major Experiment	
	Minor Experiment	
	Queries	
	Record/Observation	
	Viva	
2	End Semester Practical Examination	

Course Designed by: Dr. S. Sivashankari	Verified by HOD: Dr. S. Sivashankari
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**SEMESTER IV
COURSE CODE: 23PBI4PVV
PROJECT WORK**

**QUESTION PAPER PATTERN FOR PRACTICAL END SEMESTER
EXAMINATION**

1. Major Experiment	1*30 marks = 30 marks
2. Minor Experiment	1*15 marks = 15 marks
3. Queries/Spotters	5 * 2 marks = 10 marks
4. Viva	10 marks
5. Record	10 marks
TOTAL	75 marks

**VALUE ADDED COURSE
COURSE CODE: 23PCCAD1**

**TITLE OF THE COURSE: CERTIFICATE COURSE IN COMPUTER AIDED DRUG
DISCOVERY**

COURSE OBJECTIVES:

- To educate the students on Different CADD techniques and their applications
- To impart knowledge on Various strategies to design and develop new drug like molecules

COURSE OUTCOMES:

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

CO1	Summarize the physicochemical parameters related to QSAR	K2
CO2	Identify and explain the Components of QSAR equation	K3
CO3	Apply the features of Molecular Docking for Drug Discovery	K3
CO4	Analyse the properties of an effective drug	K4
CO5	Identify and apply the concept of pharmacophore mapping for Drug Discovery	K3

Syllabus

Instructional hours: 30

UNIT I

6 Hrs

Introduction to Computer Aided Drug Design (CADD), History, different techniques and applications, Quantitative Structure Activity Relationships: Basics, History and development of QSAR: Physicochemical parameters and methods to calculate physicochemical parameters: Hammett equation and electronic parameters (σ), lipophilicity effects and parameters ($\log P$, π substituent constant), steric effects (Taft steric and MR parameters) Experimental and theoretical approaches for the determination of these physicochemical parameters.

UNIT II

6 Hrs

Quantitative Structure Activity Relationships: Applications Hansch analysis, Free Wilson analysis and relationship between them, Advantages and disadvantages; Deriving 2D-QSAR equations 3D-QSAR approaches and contour map analysis Statistical methods used in QSAR analysis and importance of statistical parameters.

UNIT III

6 Hrs

Molecular Modeling and Docking: Molecular and Quantum Mechanics in drug design, Energy Minimization Methods: comparison between global minimum conformation and bioactive conformation, Molecular docking and drug receptor interactions: Rigid docking, flexible docking and extra-precision docking. Agents acting on enzymes such as DHFR, HMG-CoA reductase and HIV protease, Choline esterase (AChE & BChE).

UNIT IV

6 Hrs

Molecular Properties and Drug Design: Prediction and analysis of ADMET properties of new molecules and its importance in drug design. De novo drug design: Receptor/enzyme-interaction and its analysis, Receptor/enzyme cavity size prediction, predicting the functional components of cavities, Fragment based drug design. Homology modeling and generation of 3D-structure of protein.

UNITV**6 Hrs**

Pharmacophore Mapping and Virtual Screening Concept of pharmacophore, pharmacophore mapping, identification of Pharmacophore features and Pharmacophore modeling, Conformational search used in pharmacophore mapping, *In Silico* Drug Design and Virtual Screening Techniques, Similarity based methods and Pharmacophore based screening, structure based *In silico* virtual screening protocols

TEXT BOOK(S):

1. Computational and structural approaches to drug discovery, Robert M Stroud and Janet.F Moore, RCS Publishers.
2. An Introduction to Medicinal Chemistry –Graham L. Patrick, Oxford University Press.

REFERENCE BOOK(S):

1. Introduction to Quantitative Drug Design by Y.C. Martin, CRC Press, Taylor & Francis group.
2. Drug Design by Ariens Volume 1 to 10, Academic Press, 1975, Elsevier Publishers.
3. Principles of Drug Design by Smith and Williams, CRC Press, Taylor & Francis.
4. The Organic Chemistry of the Drug Design and Drug action by Richard B. Silverman, Elsevier Publishers.
5. Medicinal Chemistry by Burger, Wiley Publishing Co, NJ, USA
6. Wilson and Gisvold's Text book of Organic Medicinal and Pharmaceutical Chemistry, Ippincott Williams & Wilkins.
7. Comprehensive Medicinal Chemistry – Corwin and Hansch, Pergamon Publishers.
8. Computational and structural approaches to drug design edited by Robert M Stroud and Janet. F Moore

BLENDED LEARNING E-RESOURCES**UNIT IV:**

TOPIC	LINKS
Prediction and analysis of ADMET properties	https://www.youtube.com/watch?v=9NDzRlxBLhI
De novo drug design	https://www.youtube.com/watch?v=xjzVx1jp4Gg&t=24s
Homology modeling and generation of 3D structure of protein.	https://www.youtube.com/watch?v=kfMpOnnBjP8
Fragment based drug design	https://www.youtube.com/watch?v=FRFeC4JoF4o

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CO3	2			3		1			1	1		1	3	2	2
CO4	2			3		1			1	1	3	1	3	2	2
CO5	2			3		1	3		1	1		1	3	2	2

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