M. Sc. BioInformatics

Syllabus

UNIVERSITY DEPARTMENT

Program Code: BIIA

2021 – 2022 onwards

BHARATHIAR UNIVERSITY

(A State University, Accredited with "A" Grade by NAAC,
Ranked 13th among Indian Universities by MHRD-NIRF,
World Ranking: Times -801-1000,Shanghai -901-1000, URAP - 982)

Coimbatore - 641 046, Tamil Nadu, India

Program Educational Objectives (PEOs)	
The **M. Sc. Bioinformatics** program describe accomplishments that graduates are expected to attain within five to seven years after graduation	
PEO1	Should be aware of available bioinformatics resources and information in databases
PEO2	Apply critical, analytical and problem solving skills to deal with bioinformatics research
PEO3	Gain a deep understanding of the biomolecular systems
PEO4	Attain knowledge to identify the research problems in molecular biology
PEO5	Develop very efficient algorithms to extract biological knowledge from complex dataset
PEO6	Develop programming skills to write their own codes and scripts to resolve research accomplishments
PEO7	Possess drafting and writing skills to enhance scientific communication
PEO8	Update in accordance with recent scientific advancements and technology
PEO9	Gain higher level degrees to pursue a career in academics or scientific organizations
PEO10	Should be able to pursue research and also in industry placement in the sectors of pharmaceutical, agricultural, environmental science and food industries

Program Specific Outcomes (PSOs)	
After the successful completion of M.Sc. Bioinformatics program, the students are expected to	
PSO1	Develop applications to solve biological problems by utilizing the Bioinformatics algorithms and programming languages
PSO2	Manipulate scientific datasets and retrieve and access them through biological databases
PSO3	Develop knowledge and skills to analyse and interpret biological data for research requirements
PSO4	Develop good scientific communication skills
PSO5	Gain knowledge of the tools, frameworks, and libraries for bioinformatics applications
PSO6	Undergo seminars, conferences and hands on workshops to facilitate domain expertise

Program Outcomes (POs)	
On successful completion of the M. Sc. Bioinformatics program	
PO1	Should be able to understand the basic principles and concepts of biology, computer science and mathematics
PO2	Able to apply the knowledge in Bioinformatics such as computational biology, chemical principles that underlie biochemistry, molecular biology and genomics
PO3	Develop and implement software effectively to retrieve information from biological databases and use this information for computation
PO4	Comprehend and provide solution to enable designing and implementing new algorithms and analysis methods
PO5	Understand the concept of intersection of life and information sciences, structure-function relationships, information theory, gene expression, and database queries
PO6	Develop computational techniques and diversified bioinformatics tools for processing data, including statistical, machine learning and data mining techniques
PO7	Design and implement efficient and reliable bioinformatics solutions by optimizing the usage of existing tools and developing new ones
PO8	Analyze and think critically the research methods in Bioinformatics such as dissertation, research, preparation and presentations at scientific meetings, seminars and qualifying examinations
PO9	Develop an insight into scientific methodology and advances in bioinformatics research
PO10	Have an understanding of current technology trends as well as future directions and recognize the need and develop the skills necessary for professional development

BHARATHIAR UNIVERSITY: COIMBATORE 641 046
M. Sc. Bioinformatics
Curriculum (University Department)
(For the students admitted during the academic year 2021 – 22 onwards)

Course Code	Title of the Course	Credits	Hours		Maximum Marks		
			Theory	Practical	CIA	ESE	Total
FIRST SEMESTER							
13A	Molecular Cell Biology and Genetic Engineering	4	60	-	50	50	100
13B	Artificial Intelligence and Applications in Biological Sequence Analysis	4	60	-	50	50	100
13C	Programming in C and C++	4	60	-	50	50	100
13D	Immunology & Immunoinformatics	4	60	-	50	50	100
13P	Practical-I wet lab- Microbial and Phytochemical techniques	4	-	60	50	50	100
1EA	Mathematical & Statistical applications in bioinformatics	4	60		50	50	100
1EB	Biostatistics						
NEW GS???	Supportive-I Advanced Bioinformatics	2	30		25	25	50
	Total	**26**			**325**	**325**	**650**
SECOND SEMESTER							
23A	Perl and Python programming for Bioinformatics	4	60		50	50	100
23B	Molecular interactions	4	60		50	50	100
23C	Biophysics and Crystallography	4	60		50	50	100
23D	Pharmacogenomics and Drug design	4	60		50	50	100
2EA	Biodiversity Informatics						
2EB	Basics of Cheminformatics	4	60		50	50	100
23P	Practical-II Computer Programming	4	-	60	50	50	100
GS125	Supportive-II Principles of Drug Discovery	2	30		25	25	50
Total		**26**			**325**	**325**	**650**
THIRD SEMESTER							
33A	Genomics and NGS	4	60		50	50	100
33B	Proteomics	4	60		50	50	100
33C	Visual Basic.NET with RDBMS	4	60		50	50	100
33D	Molecular Modeling	4	60		50	50	100
3EA	Systems Biology	4	60		50	50	100

3EB	Big Data Analytics						
GS02	Supportive-III Advanced Bioinformatics	2	30		25	25	50
33P	Practical-III Molecular Techniques	4	-	60	50	50	100
33Q	Practical-IV Biological Sequence Analysis and Computer Aided drug Design	4	-	60	50	50	100
Total		**30**			**375**	**375**	**750**
FOURTH SEMESTER							
47V	Project / Dissertation + Viva-voce	8	-	-	100	100	200
Total		**8**	**-**	**-**	**100**	**100**	**200**
Grand Total		**90**			**1125**	**1125**	**2250**
CO-SCHOLASTIC COURSES							
ONLINE COURSES*							
	Swayam, MOOC Course etc.,	2	-	-	-	-	50
JOB ORIENTED COURSES**							
J01	Bioinformatics Algorithms and Machine Learning	4	30	-	50	-	50
J02	IT Tools and Applications	4	30	-	50	-	50
J03	Microbial Genomics	4	30	-	50	-	50
J04	Web Designing	4	30	-	50	-	50
VALUE ADDED COURSES***							
VA1	Communication Skills Enhancement	2	15	-	50	-	50
VA2	Soft Skills Development	2	15	-	50	-	50
VA3	Journal Seminar and Aptitude Skills	2	15	-	50	-	50
VA4	Project Proposal Writing Skills	2	15	-	-	-	50

*** SWAYAM –MOOCs – Online course is mandatory and it should be completed within third semester**

****JOB ORITENTED COURSE - Two courses to be completed, each year one course to be completed**

*****VALUE ADDED COURSE - Minimum two courses to be completed, each year one course to be completed**

Duration of the M.Sc Bioinformatcs course: 2 years

Eligibility:
A pass in any one of the following degree courses of UGC recognized universities.
B.Sc. / B.Tech. in all Science disciplines, B.V.Sc. / B.Pharm / M.B.B.S and B.D.S.

First Semester

Course code	13A	MOLECULAR CELL BIOLOGY AND GENETIC ENGINEERING	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basics of Biology	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Make the students understand the central dogma of molecular biology
2. Familiarize the students to versatile tools and techniques employed in genetic engineering and recombinant DNA technology.
3. Provide an understanding on the different structural form of biomolecules.

Expected Course Outcomes:

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

1	Understand the cell cycle and molecules of life in various aspects.	K1
2	Evaluate the changes in the transcription and translation.	K2
3	Describe the different structures of carbohydrate, lipids, nucleotides, DNA and Protein	K3
4	Know the various components and events of Gene expression	K4
5	Design and conduct experiments involving genetic manipulation.	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Biomolecules	10 hours

Introduction to carbohydrates–Functions, classification-Monosaccharides and their derivatives, Disaccharides, Polysaccharides. Proteins – Structure of aminoacids, Different levels of organization–Properties of proteins, Denaturation and renaturation, Classification of proteins, Biologically important proteins. Nucleic acids – Purines, pyrimidines, Nucleosides and Nucleotides, Different structural form of DNA, denaturation and renaturation of DNA, Structure, function and Types of RNA. Lipids-Structure and function of Fatty acids, Triacylglycerols, steroids, lipoproteins and phospholipids. Enzymes – Classification, properties of enzymes, Factors affecting enzyme activity, Michaelis – Menten kinetics, Line-Weaver Burk plot, Eadie Hofstee plot, Mechanism of enzyme action, Enzyme inhibition: Reversible, Irreversible and allosteric inhibition.

Unit:2	Molecular Biology of the cell	12 hours

Chromatin organization and packaging; DNA Replication in Prokaryotes and Eukaryotes: enzymes involved, replication fork, extrachromosomal replicons, Homologous and non-homologous recombination, site specific recombination. Transcription in Prokaryotes and Eukaryotes: Transcription factors, transcription machinery, activators and repressors of transcription, RNA polymerases, capping, elongation and termination, RNA processing, RNA editing (splicing, polyadenylation), RNA transport in eukaryotes. Translation in Prokaryotes and Eukaryotes: Ribosome, initiation complex, genetic code, aminoacylation of tRNA, post-translational modification of proteins in eukaryotes.

Unit:3	**Genetic Engineering**	**12 hours**

Gene cloning Techniques – Cloning Vectors, types, properties; Enzymes in gene cloning - restriction endonucleases, ligases, reverse transcriptase, polymerase, terminal transferases - Homopolymer tailing, linkers and adaptors. Methods of gene transfer: Microinjection, electroporation, gene gun, liposome and viral- mediated delivery, Agrobacterium-mediated delivery. Strategies for selection and screening- marker and reporter genes, positive and negative selection, insertion inactivation, α complementation. Polymerase chain reaction –Primer design tools, Fidelity of thermostable enzymes, Types of PCR and its applications.

Unit:4	**Sequencing and Cloning strategies**	**12 hours**

DNA sequencing - Sanger‟s method, Maxam and Gilbert method and Automated method, Construction of genomic and cDNA libraries; Cloning strategies – TA cloning, Gateway cloning, DNA fingerprinting by RFLP and RAPD, Site- directed mutagenesis. Gene silencing techniques – siRNA, microRNA, principles and application, Gene knockouts and Gene Therapy, Genome editing by CRISPR/Cas9 system.

Unit:5	**Cell cycle and control**	**12 hours**

Phases of Cell Cycle - Cyclin dependent kinases, Mechanisms of Checkpoint regulation; Signal transduction: Intercellular junctions, signaling by hormones and neurotransmitters; Receptors - GPCR, protein kinases and second messengers. Cell-cell interaction; Cell-matrix interaction - Integration of cellular function - pathways of Apoptosis and Autophagy.

Unit:6	**Contemporary Issues**	**2 hours**

Expert lectures, online seminars - webinars

	Total Lecture hours	**60 hours**

Text Book(s)

1. Lehninger, A. L. 1984. Principles of Biochemistry. CBS publishers and distributors, New Delhi,India.
2. Gene Cloning, an introduction – T. A. Brown, Chapman and Hall, 3rd Edition, 1995.
3. David. E. Sadava Cell Biology: Organelle Structure and Function Jones & Bartlett publishers.

Reference Books

1. An Introduction to Molecular Biotechnology: Molecular Fundamentals, Methods and Applications in Modern Biotechnology - M. Wink. Wiley, ed. 2, 2011.
2. Horton, Moran, Ochs, Rawn, Scrimgeour Principles of Biochemistry Prentice Hall Publishers.

Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]

1. https://nptel.ac.in/courses/102/103/102103013/
2. https://nptel.ac.in/courses/102/103/102103045/

Course Designed By: Prof. P. Shanmughavel

Mapping with Programme Outcomes

COs	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10
CO1	S	S	S	S	M	S	M	S	S	M
CO3	S	M	M	M	S	M	S	M	S	S
CO3	S	S	S	S	S	S	S	S	S	M
CO4	S	S	S	S	S	S	S	M	M	S
CO5	S	M	M	M	M	M	S	M	M	M

*S-Strong; M-Medium; L-Low

Course code	13B	ARTIFICIAL INTELLIGENCE AND APPLICATIONS IN BIOLOGICAL SEQUENCE ANALYSIS	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic Computer and Biology knowledge	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. To understand the various computational techniques with Artificial Intelligence.
2. To analyze biological data with the use of sequence information.
3. To understand the steps involved in Evolutionary analysis.
4. Also helps to start error free sequence analysis investigation successfully.

Expected Course Outcomes:

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

1	To do the sequence analysis and phylogenetic prediction with their own knowledge.	K3
2	Also capable to search the protein/gene sequence and structural information from the any biological databases.	K2
3	Helps to ensure the comparative sequence analysis without any error.	K5
4	To analyze and interpret the biological data through Artificial Intelligence.	K4

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Outline of Bioinformatics and AI	12hours

Introduction and Applications of Bioinformatics. Classification of biological databases, Biological data formats. Introduction to single letter code of amino acids, Symbols used in nucleotides. Data retrieval from Entrez and SRS.

Artificial Intelligence (AI) Introduction: Definition, Challenges and Applications. Role of AI in bioinformatics.

Unit:2	Wide-ranging of Sequence Alignment	12 hours

Outline and Uses of sequence alignment. Similar sequence search using FASTA and BLAST programs in the database. Pairwise sequence alignment and Multiple sequence alignment. Local and Global alignment (Smith-Waterman and Needleman-Wunsch algorithm). Substitution matrices, Scoring matrices - PAM, BLOSUM and Dot plot. Statistics of alignment score and evaluation.

Unit:3	Evolutionary / Phylogenetic Analysis	12 hours

Overview of Tree analysis. Cladistics, Phenetics and Distances. Various tree types. Overview of Bootstrapping. Tools – Clustal Omega, PHYLIP and Mega. Problems and errors in phylogenetic reconstruction. Overview of AI in Phylogenetic analysis.

Unit:4	Genome Exploration & Protein Assessment	12 hours

Gene finding methods. Gene prediction: Analysis and prediction of regulatory regions. Fragment assembly. Genome sequence assembly, Restriction Mapping and Repeat Sequence finder. Primary sequence information. Secondary structure prediction of RNA and Protein. ProtParam, GOR, HNN &Sopma.

Unit:5	Artificial Intelligence (AI)	10 hours
Practice and implications of AI in Healthcare industry. Algorithms for Bioinformatics prediction: HMM and Neural Network. Case study: AI in computational sequence analysis.		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars - webinars		
	Total Lecture hours	**60 hours**

Text Book(s)	
1	S.C. Rastogi et al. Bioinformatics: Methods and Applications: (Genomics, Proteomics and Drug Discovery) Kindle Edition.
2	Stuart Russel and Peter Norvig, "Artificial Intelligence- A Modern Approach", Prentice Hall, 1995.
Reference Books	
1	Andreas D. Baxevanis and B.F. Francis Ouellette. Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. ISBN: 978-0-471-47878-2.
2	George F Luger, "Artificial Intelligence", Pearson Education, 4th Edition, 2001.
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	Artificial Intelligence Search Methods For Problem Solving By Prof. Deepak Khemani | IIT Madras| SWAYAM
2	Fundamentals of Artificial Intelligence By Prof. Shyamanta M. Hazarika | IIT Guwahati| SWAYAM
3	https://www.ncbi.nlm.nih.gov/books/NBK20261/
4	https://link.springer.com/chapter/10.1007/978-1-4757-3783-7_5
Course Designed By: **Dr. C. Jayaprakash**	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	S	S	S	M	M	S
CO2	M	S	M	M	S	S	M	S	S	S
CO3	S	S	S	M	S	S	M	M	S	S
CO4	S	S	S	S	M	M	S	S	S	S

*S-Strong; M-Medium; L-Low

Course code	13C	PROGRAMMING IN C AND C++	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic Computer Operating skills	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. To make the students understand the basic aspects of programming.
2. Develop an in-depth understanding of functional, logic, and object-oriented programming paradigms.
3. Explain and be able to use fundamental programming constructs such as sequencing, decisions and iteration.
4. To enhance problem solving and programming skills in C & C++.

Expected Course Outcomes:

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

1	Have a good understanding about the concept of C & C++.	K2
2	Be able to explain and make use of data types, variables, constants, assignment statements, and arithmetic and Boolean expressions in writing programs;	K3
3	Understand object-oriented programming using C++	K2
4	Explain and are able to use arrays and structures;	K4
5	Be able to write and read basic codes in C & C++.	K6

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Introduction to Programming Languages	10 hours

Introduction–Programming languages – Problem solving Technique: Algorithm, Flowchart,
Compiling, Testing and Debugging, Documentation – Data structures – Array, Stack, Queue,
Linked List concepts.

Unit:2	Programming in C	12 hours

C language Introduction – Tokens – Keywords, Identifier, Variables, Constants, Operators –
Expression – Data types –Operator precedence – Statement: Input statement, Output statement, Conditional and Unconditional Control Statement – Looping Statement: while, do–while, for –nested loop – Arrays.

Unit:3	Procedural Concepts in C	12 hours

C – Procedural Concepts: Structured Programming – Built-in library function – User defined
functions – Pointer introduction – Passing pointer in a function – Structure – Union – File handle: Read and Write character from a file.

Unit:4	Object Oriented Programming and C++	12 hours

Basic concepts of OOPS– Data hiding–Encapsulation–Inheritance, Polymorphism – Introduction to C++, C vs C++ – data types, variables, constants, operators and statements in C++ – Conditional and looping statements

Unit:5	Programming and C++	12 hours
C++ classes - Classes & Objects – Functions in C++ – function prototype-definition– Different forms of Constructor – Destructor – Copy constructor – Inheritance –Single, Multiple and Multi level inheritance – Function & operator overloading –inline functions – Friend and virtual functions – Overloaded functions.		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars - webinars		
	Total Lecture hours	**60 hours**

Text Book(s)	
1	B.W.Kernighan and D.M. Ritchie, "The C Programming Language", 2nd Edition. Prentice Hall of India.
2	E. Balagurusamy - "Programming in C++ " - Tata McGraw Hill Edition
Reference Books	
1	Byron Gottfried, "Programming with C" (Schaum's Outline Series) - Tata McGraw Hill Publishing Company – 1998
2	Robert Laffore -"Object oriented programming with C++" -Waite series.
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	https://nptel.ac.in/courses/106/105/106105171/
2	Introduction to Programming in C By Prof. SatyadevNandakumar- SWAYAM
3	Programming in C++ By Prof. ParthaPratim Das - SWAYAM
Course Designed By: **Prof. N. Jeyakumar**	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	S	S	S	S	M	S
CO3	M	S	M	S	S	S	M	S	M	M
CO3	S	S	S	M	M	S	S	S	S	M
CO4	S	S	M	M	M	S	M	M	S	S
CO5	S	M	S	S	S	M	S	S	S	M

*S-Strong; M-Medium; L-Low

Course code	13D	IMMUNOLOGY & IMMUNOINFORMATICS	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic knowledge in Biology	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Make the students understand the immune system, its components and their functions.
2. Provide fundamental knowledge in Immunoinformatics databases and tools.
3. Learn the informatics-based approaches for prediction of Epitopes, design of vaccines and immuno-diagnostic tools.

Expected Course Outcomes:

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

1	Describe the mechanism of Immune response and antibody production	K1
2	Understand the molecular interactions between antigen and antibody.	K2
3	Interpret the Methods to predict MHC and B-cell epitopes	K3
4	Knowledge on different tools and servers for vaccine designing.	K4
5	Explain the role of the immune molecules in infectious diseases and cancer	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Immune system and its types	10 hours

Innate and Adaptive Immunity: Cell types and processes involved, Anatomical and Physiological Barriers, Inflammation, Soluble molecules and Toll-like receptors, Innate Immune response and their recognition structures, Humoral and Cell mediated responses of immune system. **Cells of Immune system:** Lymphocytes, Mononuclear phagocytes, Antigen Presenting cells, polymorphs, Natural Killer cells, Granulocytes, Mast cells, Dendritic cells, Cluster designation (CD) and antigen specific receptors. **Organs of Immune system:** Primary lymphoid organs (Bone marrow and Thymus). Secondary Lymphoid organs (Lymph node, spleen and MALT).

Unit:2	Immunoglobulins	12 hours

Immunoglobulins: Structure and function - Clonal selection theory – Ig Classes and subclasses, DR and LDR regions and sequence numbering, Immunogenetics & Immunogenomics, **Monoclonal antibodies:** Hybridoma technology, applications, Humanization of antibodies by design. Membrane receptors for antigen- B-cell generation and differentiation - T-dependent activation of B cells - Recognition of Antigen by B cells, Neutralizing Antibody. **Cytokines:** Cytokine receptors and signal transduction mediated by class I and II cytokine receptors. Complement system- activation, pathways and biological effects.

Unit:3	Immunoinformatics	12 hours

Databases & tools: IMGT & IEDB, BciPep, Epitome, CED, Ag-Ab database, Allergen Databases, Allergenicity Prediction. **Major Histocompatibility Complex:** Structure and functions of MHC class I and II, MHC polymorphism, MHC supertypes, MHC peptides-Specificity, characterization, MHCpeptide designing tool. **HLA:** nomenclature, HLA-peptide interactions, Antigen Processing in the MHC Class I Pathway, Processing of MHC Class II Epitopes, Sequential and Conformational Epitopes, Epitope Prediction algorithms - T cell, B cell epitope prediction tool.

Unit:4	Vaccine Design and Development	12 hours
Rational vaccine design, Reverse vaccinology, Prediction of immunogenicity - Pipeline & workflows, Toxoid as vaccine, Conjugate vaccine, DNA vaccine, Recombinant vector vaccines, Personalised vaccination. **Structure-based Vaccine design** - tools and techniques, Antigenicity modification, Epitope replacement, germline targeting, Epitope focussing, hyperglycosylation, chimeric fusion, epitope scaffold, Conformational stabilization, multimeric scaffolding, stabilizing mutations, Antigen display and delivery platforms - multivalent display, co-display, immunomodulation, Genetic delivery.		
Unit:5	**Immunoinformatics in Health and Diseases**	**12 hours**
Cancer Immunology: Malignant transformation of cells, Oncogenes and cancer induction, Tumors of immune system, Tumor antigens, Tumor evasion of the immune system, Cancer immunotherapy. Secondary **immunodeficiency in AIDS:** Mode of infection, causative agent, HIV infection of target cells and activation of Provirus, Immunological abnormalities associated with HIV infection, Discrete Models of HIV Infection, Simulation of HIV-1 Infection. Emerging and Re-emerging **Infectious Diseases** – Pathogens with antigenic variation, Modifying and Improving Biological Therapeutics, Computational Immunology.		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars - webinars		
	Total Lecture hours	**60 hours**

Text Book(s)	
1	Richard Coico, Geoffrey Sunshine, "Immunology: A short course" 6th Edition. Wiley-Blackwell, 2009.
2	Darren R Flower, "Immunoinformatics: Predicting Immunogenicity in Silico", Humana Press, 2007.
3	Roitt Ivan, Delves Peter. Roitt's Essential Immunology 10th Edition. Publisher: Canada, Blackwell. 2001.
Reference Books	
1	Thomas J. Kindt , Barbara A. Osborne , Richard A. Goldsby , " Kuby Immunology", WH Freeman, Sixth Edition, 2006.
2	Rammensee, "Immunoinformatics - Bioinformatics Strategies for better understanding of Immune Function", Wiley, 2003.
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	https://nptel.ac.in/courses/102/103/102103038/
2	https://nptel.ac.in/courses/102/105/102105083/
Course Designed By:	Dr. V. Hemamalini

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	M	S	S	S	S	M	M	S
CO3	M	S	M	S	M	S	S	S	M	M
CO3	S	M	S	M	M	S	S	S	M	S
CO4	M	M	S	S	S	S	M	S	S	S
CO5	S	M	S	S	M	M	S	M	S	S

*S-Strong; M-Medium; L-Low

Course code	13P	PRACTICAL – I WET LAB – MICROBIAL AND PHYTOCHEMICAL TECHNIQUES	L	T	P	C
Core/Elective/Supportive		Core	-	-	4	4
Pre-requisite		Basic wet lab knowledge	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

4. To understand the isolation of three different microorganisms in a single aspect.
5. To know the collection of microbes, plants and blood samples.
6. To make students understand preliminary phytochemical analysis from plant extracts.

Expected Course Outcomes:

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

1	A step by step procedure describes the isolation methods.	K2
2	Skillful in comparison and interpretation of the result with the standard reports.	K5
3	Able to identify the expected compound present or absent in the taken sample.	K2
4	Capable to prepare the Gel and do the staining processes individually.	K6

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

I	MICROBIOLOGY LAB	30 hours

1. Isolation of bacteria from soil - serial dilution technique
2. Isolation of fungi from soil - serial dilution technique
3. Isolation of actinomycetes from soil - serial dilution technique
4. Screening microbes for antibiotic production
5. Extraction of proteins from microbes, plant and blood
6. Separation of protein and molecular weight determination using SDS-PAGE
7. Staining the gel - CBB and Silver staining

II	PHYTOCHEMISTRY LAB	28 hours

8. Extraction of secondary metabolites from medicinal plants - Cold percolation method
9. Extraction of secondary metabolites from medicinal plants - Soxhlet method
10. Preliminary Phytochemical analysis of plant extracts
11. Antibiotic bioassay-inhibitory activity (Disc Diffusion)
12. Tissue culture - callus induction
13. Tissue culture - cell suspension culture

III	Contemporary Issues	2 hours

Expert lectures, online seminars – webinars

	Total Lecture hours	60 hours

Text Book(s)

1	Dr. Harshal A. Pawar. 2018 A Practical Book on Pharmacognosy and Phytochemistry I (English, Paperback)

Reference Books

1	Sharada L. Deore. Rpt.2019. Pharmacognosy and Phytochemistry : A Companion Handbook.

Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]

1	https://nptel.ac.in/courses/102/103/102103015/

Course Designed By: **Dr. C. Jayaprakash**

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	S	S	S	M	S	S
CO2	S	S	S	M	S	S	M	M	M	S
CO3	M	S	S	S	S	S	S	M	S	S
CO4	M	S	S	S	S	S	S	M	S	S

*S-Strong; M-Medium; L-Low

Course code	1EA	MATHEMATICAL & STATISTICAL APPLICATIONS IN BIOINFORMATICS	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic knowledge in Mathematics, Statistics and Programming	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Achieve skills in mathematics to understand and investigate biological processes
2. Help in analyzing vast amount of datasets generated from genome and related projects using mathematical and statistical frameworks
3. Understand and appreciate computational problems in proper perspective.

Expected Course Outcomes:

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

1	Workout basic mathematical problems in bioinformatics	K2
2	Write R codes and Matlab programs for biological problems	K4
3	Analyse the statistical significance of any biological data	K3
4	Apply the mathematical and statistical knowledge in programming	K5
5	Develop new coding functionalities	K6

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Unit:1	Matrices, Determinants and Vectors	12 hours

Different types of matrices - Matrix Operations - transpose, inverse, and conjugate systems - symmetric and skew symmetric matrices - Diagonalization of Matrices and Characteristic roots - Equality of Matrices - Adjoint of a matrix - Singular and non-singular matrices - Eigen values and Eigen vector – Rank – Determinants - evaluation – Properties - Minors and Cofactors, Multiplication of Determinants, Adjoint, Reciprocal, Symmetric Determinants - Solving Simultaneous equations in three variables using matrices - Solution of a system of linear equations by Cramer‟s rule and by matrix inversion method - Cayley – Hamilton theorem without proof - Consistency of linear equations. Vectors - The concept of a Vector, Vector addition and subtraction, Products of two vectors-Dot product and Cross product, Products of three vectors- scalar triple product and vector triple product, Gradient, Divergence and Curl, equation.

Unit:2	Differential and Integral Calculus	12 hours

Calculus – Differentiation Standard results – Derivatives of simple functions – Product Rule – Quotient Rule - Partial Differentiation – Partial derivative of simple functions (3 variables case only) - Euler‟s Theorem. Integration – Standard results – Integrals of simple functions – Definite Integrals – Indefinite Integrals – Integration by parts – Integration by substitution – Integration by partial fractions.

Unit:3	Basic Concepts in Statistics	10 hours

Classification and tabulation of Data - Diagrammatic and graphic Presentation - frequency curve and its characteristics - Introduction to Central Tendency - Frequency Distributions and Statistical Measures (Arithmetic Mean, Median, Mode) - Measures of Dispersion - Methods of Studying Variation, Range, Mean Deviation, Standard Deviation, Variance, coefficient of Variation - Correlation and regression – Introduction - Types of correlation, methods of studying correlation - Coefficient of correlation – Probable error -– Regression – Simple linear regression - Principles of least squares, - Relation between regression and correlation - Regression Equations.

Unit:4	Advanced Topics in Statistics	12 hours
Concept and definitions of Probability - Terms used in probability - Probability of events - axioms of probability - Theorem of probability - Properties of probability - Conditional probability - Baye‟s theorem, Problem based on Baye‟s theorem - Random variables: Discrete and continuous random variables, cumulative density function, Probability density and mass functions - Probability distribution- Introduction, binomial distribution, Poisson distribution, Normal distribution - Test of Hypothesis Sampling - Population – Sample – Parameter – Statistic – Standard error - Hypothesis- Null Hypothesis – Alternative Hypothesis – Critical Region – Level of Significance – Errors in Sampling – One tailed and two test statistic-test of significance and its test procedure. Test of significance for small samples: Tests based on normal distribution for Single mean, difference of two means - Tests based on t-distribution for single mean, difference of two means, paired test and observed correlation coefficient – F Test – Parametric and Non parametric tests - Chi-square ($\chi 2$) test for goodness of fit. Analysis of variance: One way and two way classifications - PCA, Factor analysis.		
Unit:5	**Programming in R and Matlab**	**12 hours**
How R works - Data sets included in R - Objects –Operators - The data editor – Useful R functions - Graphics with R – Data frames and lists - File operations - Mathematical operations, Basic matrix computation - Basic graphics (high-level plotting, low-level plotting, interacting with graphics) - Statistical analyses with R - Hypothesis testing and data handling: Parametric and nonparametric tests, Chi-square test, t-tests, ANOVA, Correlation and regression, Principal component Analysis – Packages in R - Bioconductor - Loops and vectorization - Expression Set Class, Data annotation, biomaRt, Network analysis - Writing a program in R - Writing own functions -Matlab- key features, basic functionalities - tool box, data types, variables, operators, vectors, matrix operations, Control structures The Matlab interface - Writing in script files - Importing data – Plotting - Using in-built functions - Creating your own functions - Basic programming in Matlab (including for loops) – Case study with biological examples.		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars – webinars		
	Total Lecture hours	**60 hours**

	Text Book(s)
1	S.C.Gupta and V.K. Kapoor, Fundamentals of Mathematical Statistics.
2	Basic mathematics by Serge A. Lang, 1988, Springer publisher

	Reference Books
1	Gentle, James E.; Härdle, Wolfgang K. Mori, Yuichi (Eds.). Handbook of Computational Statistics
2	Ewens, W.J. and Grant, 2001. Statistical Methods in Bioinformatics: An Introduction, Springer-Verlag

	Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]
1	Biostatistics and Mathematical Biology By Dr. Felix Bast, Central University of Punjab, Bathinda – SWAYAM
2	R By Prof Kannan Moudgalya - Indian Institute of Technology Bombay – SWAYAM
3	https://nptel.ac.in/courses/103/106/103106118/ - Matlab Programming for Numerical Computation IIT Madras

Course Designed By: Dr. S. Usha

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	M	S	M	M	S	M	M
CO2	M	M	M	M	M	M	M	M	M	M
CO3	S	S	S	M	S	M	M	S	M	M
CO4	S	S	S	M	S	M	M	S	M	M
CO5	M	M	M	M	M	M	L	M	M	M

*S-Strong; M-Medium; L-Low

Course code	1EB	BIOSTATISTICS	L	T	P	C
Core/Elective/Supportive		Elective	4	-	-	4
Pre-requisite		Basic knowledge in Statistics	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Enable the students to achieve skills in statistics that are essential for applications in bioinformatics.
2. Introduce basic concepts of probability and statistics.
3. Understand and appreciate computational problems in proper perspective.

Expected Course Outcomes:

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

1	Understand the basics of Biostatistics and data collection & classification methods	K1
2	Know the types of central tendency and dispersion for different data analysis	K2
3	Understand the concept and methods of Correlation and Regression.	K3
4	Understand the types of Distribution, Hypothesis test and Non parametric test.	K4
5	Apply Statistical frameworks to analyze vast amount of datasets generated from genome and related projects.	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Unit:1	Introduction to Statistics and Data collection	12 hours

Statistics – Definition – Statistical methods – Basic principles – Variables – Measurements, functions– Collection of Data – Primary and Secondary – Types and methods of data collection – Procedure – Merits and Demerits – Classification and tabulation of data – Diagrams and graphs.

Unit:2	Central Tendency and Dispersion	10 hours

Measures of Central tendency – Mean, Median, Mode, Geometric Mean – Merits and Demerits – Dispersion and measure of dispersion – Range, Standard deviation, quartile deviation – Merits and Demerits – Co-efficient of variations.

Unit:3	Correlation and Regression	12 hours

Skewness and Kurtosis – Correlation – Types and method of correlation – Regression – Simple regression equation fitting – Prediction, similarities and dissimilarities of correlation and regression.

Unit:4	Distribution and Hypothesis tests	12 hours

Distribution – Binomial, Poisson, Normal – Statistical inference – Sampling methods – Simple hypothesis testing – Students “t”- test – Chi square test.

Unit:5	Non Parametric Test	12 hours

Sign test, Wilcoxon signed rank test, one sample Run Test, Median test, Kruskal Wallis H test, Kolmogorov Smirnov test, Mann Whitney U test.

Unit:6	Contemporary Issues	2 hours

Expert lectures, online seminars - webinars

	Total Lecture hours	60 hours

1	An introduction to Bio-Statistics by N.Gurumani.2009 – MJP Publications.
2	Principles of Biostatistics, Marcello Pagano, Kimberlee Gauvreau, 1993, CRC Press.
Reference Books	
1	Schaum‟s Outline Statistics by Murray.R, Spiegel, Larry.J.Stephens, 4th edition, McGraw Hill Companies.
2	Zar, J. - Bio-statistical Analysis, Prentice Hall of India.
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	https://nptel.ac.in/courses/102/101/102101056/
Course Designed By: Dr. S. Usha	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	M	S	M	S	S	S	M	M	M	S
CO3	S	S	M	S	S	M	S	S	M	M
CO3	S	S	S	S	S	M	S	M	S	S
CO4	M	S	M	S	M	S	S	M	S	S
CO5	S	S	M	M	M	M	M	S	M	S

*S-Strong; M-Medium; L-Low

Course code	GS02	ADVANCED BIOINFORMATICS	L	T	P	C
Core/Elective/Supportive		Supportive I	2	-	-	2
Pre-requisite		Basic knowledge in Biology	Syllabus Version	2021-22		

Course Objectives:

The main objectives of this course are to:

1. Make the students understand the basic aspects and applications of Bioinformatics.
2. Know the computational methods for Sequence Alignment and the related scoring algorithms.
3. Understand the steps in Evolutionary analysis.

Expected Course Outcomes:

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

1	Describe the file formats, nomenclature of macromolecules and have an idea of Databases.	K1
2	Interpret the algorithms, scoring functions involved in the sequence alignment.	K2
3	Evaluate the phylogenetic relationship of an organism and identify genes, repeats,domains from sequences using bioinformatics tools.	K3
4	Model 2D and 3D structure of a target from the sequence.	K4
5	Exploit the information in the sequences for further research.	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Sequence Alignment	6 hours

Introduction to sequence alignment, PAM - BLOSUM, Local and Global alignment, Needleman- wunsch algorithm, Smith-waterman algorithm, Multiple sequence alignment, FASTA, BLAST.

Unit:2	Phylogenetic Analysis	6 hours

Evolutionary analysis – steps and construction of Phylogenetic tree- Cladistic, and Phenetic methods- Clustering methods - Rooted and Unrooted tree representation.

Unit:3	Gene Prediction Analysis	5 hours

Gene Prediction – methods and tools - similarity based and ab-initio prediction- GENSCAN, GRAIL, FGENES- Protein Domain analysis - Pfam, MOTIF search, SMART.

Unit:4	Protein structure prediction	5 hours

Structure prediction methods: Chou-Fasman, GOR method, Neural Network, Threading and Fold recognition, Modeling and Docking.

Unit:5	Genome Analysis	6 hours

Genome Projects- Genome sequencing technologies and analysis methods - Analysis of gene expression data - Function, gene set enrichment and pathway analysis.

Unit:6	Contemporary Issues	2 hours

Expert lectures, online seminars - webinars

	Total Lecture hours	30 hours

Text Book(s)	
1	David. W. Mount (2001): Bioinformatics Sequence and Genome Analysis, Cold spring Harbor Lab. NY.USA.
2	Genomes T.A Brown, 2001, Taylor and Francis Group.
	Comparative Genomics Ann Gibbons, 1998, Science.
Reference Books	
1	Understanding Bioinformatics, Jeremy O. Baum, Marketa J. Zvelebil. 2007, Garland Science, USA
2	Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Andreas D. Baxevanis, B. F. Francis Ouellette, 1998, Wiley Publishers
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	Bio-Informatics: Algorithms and Applications- SWAYAM
2	https://nptel.ac.in/courses/102/103/102103044/
Course Designed By: Dr. V. Hemamalini	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	M	S	M	S	M	S	S	S
CO3	S	S	S	M	S	S	M	S	M	S
CO3	M	M	M	S	S	M	M	S	S	S
CO4	S	S	M	M	M	S	S	S	M	M
CO5	M	S	S	M	S	S	S	M	S	M

*S-Strong; M-Medium; L-Low

Second Semester

Course code	23A	PERL AND PYTHON PROGRAMMING FOR BIOINFORMATICS	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic Computer Programming Skills	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Utilise the UNIX/LINUX environment effectively to perform a range of system-level tasks
2. Analyse, write and apply shell and Perl scripts to solve bioinformatics problems and form an appropriate skill set
3. Provide a thorough understanding of the Python and provide an exposure of effective Python programming for biological research

Expected Course Outcomes:

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

1	Understand the interpreter in Perl and Python	K2
2	Apply abstraction, mathematics and/or discipline fundamentals to analysis, design and operation	K3
3	Implement and test solutions	K4
4	Design components, systems and/ or processes to meet required specification	K5
5	Develop Perl and Python modules for bioinformatics applications	K6

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	UNIX/LINUX Operating System	12 hours

UNIX - File system - Overview - Text processing - Commands and Operation - UNIX filenames and file protections - working with directories - loops and IF statements - Different File Editors - Mastering the special features of the UNIX system - Advanced Unix commands - Configuring services in Unix - - Networking Utilities Introduction to Linux - System Processes - User Management - Types of users, Creating users- Granting Rights - File Quota, File-System Management and Layout - Login Process- Linux shells (bash and tcsh) - Shell Programming Networking on Linux - Printing and print sharing- ftp service, http service.

Unit:2	PERL Basics	10 hours

Data types – Operators – variables –Variable Interpolation- Cont–Scalars, Lists, Hashes - Arrays – Array functions – Hash Functions, Using Hashes for the Genetic Code, Gene Expression Data Using Hashes - PERL Subroutines, Modules & Objects - Subroutines - for calculation, Reference to subroutine - Arguments, Passing Data to Subroutines - Passing arrays and hashes to subroutines. Modules - Perl standard modules-Library - Object oriented Perl – Working with objects - Perl and Databases – Perl and DBM

Unit:3	Advanced Topics in PERL	12 hours

Pattern-matching - Substitutions, Transliteration, Split and join functions - Quantifiers - File handling concepts - Writing to Files - Opening and Closing a File handle - Directory Manipulation - Common Gateway Interface - CGI.pm Module - Simple CGI programs, Passing Parameters via CGI, Perl and the Web - Perl control statements - PERL programs for Sequences and Strings – Representing Sequence data, store a DNA sequence, concatenating DNA fragments, Transcription. Motifs – Finding motifs, counting nucleotides. Genbank – Files and libraries. Protein Data Bank – files and folders, PDB files. Blast – String matching and homology, blast output files - BioPERL: 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:4	**Introduction to Python**	**12 hours**
Installing Python - Environment Setup - Python interpreter - Identifiers, Keywords and Indentation - Comments - Python Data Types - Python variables - Operators - Lists in Python - operations, methods, parameters – Iterators - Generators, Comprehensions and Expressions - Tuples - Python Dictionaries and Sets - operations and methods		
Unit:5	**Advanced Concepts in Python Programming**	**10 hours**
Files - reading and writing files, command line arguments - Exception handling - Modules and Packages - Functions - Control Statements and Regular Expression - string functions and methods - Web Programming with Python - Using Databases in Python - Introduction to Biopython - Sequence objects - Database search using Biopython, Advanced modules in Biopython - Python For Data Analysis - Array Function, Processing, Input and Output		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars - webinars		
	Total Lecture hours	**60 hours**

Text Book(s)	
1	Tisdall, J. (2001). Beginning Perl for Bioinformatics. O'Reilly Media, Inc.
2	Martelli, A. (2006). Python in a Nutshell. O'Reilly Media, Inc.
Reference Books	
1	Thomas, R. A., & Yates, J. (1987). Advanced Programmer's Guide to Unix System. V. McGraw-Hill Book Company
2	Cozens, S., & Wainwright, P. (2000). Beginning Perl. Wrox Press.
3	Sedgewick, R., Wayne, K., & Dondero, R. (2015). Introduction to programming in Python: An interdisciplinary approach. Addison-Wesley Professional
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	Operating Systems By Dr. S. Sasikala, University of Madras - SWAYAM
2	https://www.perltutorial.org/
3	https://nptel.ac.in/courses/106/106/106106182/
Course Designed By: Dr. S. Usha	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	M	S	S	S	M	S	S	M
CO2	S	S	S	S	S	S	S	S	S	S
CO3	S	S	S	S	S	S	S	S	S	S
CO4	S	S	M	S	S	S	M	S	S	M
CO5	S	S	M	S	S	S	L	S	S	M

*S-Strong; M-Medium; L-Low

Course code	23B	MOLECULAR INTERACTIONS	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic chemistry and Biology knowledge	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. To acquire a thorough and comprehensive understanding of various types of chemical bonding.
2. To impart advanced knowledge on protein Structure, its characteristics property and significance in biological systems.
3. To introduce the concepts on structure of chemical compounds that is considered important in understanding the interaction of biomolecules.
4. To understand the structural and dynamic properties of biomolecules with special emphasis on stereochemistry and conformational analysis.
5. To gain knowledge on principles of spectroscopy for structural elucidation.
6. To understanding the structural properties and energy minimization in protein folding process.

Expected Course Outcomes:

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

1	Predict and justify the changes in the subcomponents of a biological polymer affect the functionality of the molecule.	K5
2	Define models that illustrate the interactions between biomolecules.	K3
3	Analyze data to identify how molecular interactions affect structure and function of the biological molecules.	K4

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Chemical Bonding	10 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.

Unit:2	Theories of Chemical Bonding	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:3	Protein Folding	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:4	Macromolecular interactions	12 hours

Protein-Protein, Protein-Nucleic acids, Protein-Carbohydrates, Protein-Drug or Small

molecule interactions. Metalloprotein, Sequence and structure based methods to predict protein-protein interaction. Stereochemistry of proteins and nucleic acids.		
Unit:5	**Fundamentals of Spectroscopy**	**12 hours**
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.		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars – webinars		
	Total Lecture hours	**60 hours**

Text Book(s)	
1	Tewari K.S. Vishonoi N.K. (1998) "A Text book of organic chemistry", Vikhyas publishing house.
2	Gordon G. Hammes. (2005) "Spectroscopy for the Biological Sciences", John Wiley& Sons.
3	David Micha. (2009) "Molecular Interactions" John Wiley & Sons.
Reference Books	
1	Creighton T.E. (1993) "Proteins-structures and molecular properties", Freeman WH.
2	Carl Branden & John Tooze. (1999) "Introduction to Protein Structure" Garland Publishing, New York & London.
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	Molecular BiologyBy Dr. Nayan K. Jain -SWAYAM
2	https://ww2.chemistry.gatech.edu/~lw26/structure/molecular_interactions/mol_int.html
3	https://www.cambridgemedchemconsulting.com/resources/molecular_interactions.html
4	https://www.ebi.ac.uk/training/online/course/protein-interactions-and-their-importance/protein-protein-interactions/importance-molecular-i
Course Designed By: **Dr. C. Jayaprakash**	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	S	S	S	M	S	S
CO2	S	S	M	M	M	S	M	M	S	S
CO3	S	S	S	S	S	S	M	M	S	S
CO4	S	M	M	S	S	S	S	S	S	M
CO5	S	M	M	S	S	M	S	S	S	M
CO6	M	S	S	S	M	M	S	S	S	M

*S-Strong; M-Medium; L-Low

Course code	23C	BIOPHYSICS AND CRYSTALLOGRAPHY	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic knowledge in Physics and Biomolecules	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Make the students understand the structural and energetic aspects of macromolecular association
2. Provide knowledge about basic aspects such as crystal and solution structure determination of biomolecules and its applications in crystallography
3. Utilize different scientific resources for structural and functional analysis of biomolecules

Expected Course Outcomes:

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

1	Describe the Physical and chemical properties of nucleic acids and amino acids and model 2D and 3D structure of a target from the sequence	K1
2	Interpret the model refinement and validation of macromolecular structures	K2
3	Development of new methods for novel structure determination of macromolecules	K3
4	Structure-based designing of new therapeutic molecules for various disease targets	K4
5	Visualize and compare the protein structures using bioinformatics tools	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Molecular Biophysics	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, Ramchandran 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.

Unit:2	Biophysics of Water	10 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:3	Principles of Thermodynamics	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 membranes theories		
Unit:4	**Introduction to Crystallography**	**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 - Braggs' 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:5	**Structure Determination Techniques**	**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		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars - webinars		
	Total Lecture hours	**60 hours**

Text Book(s)	
1	Cantor, C. R., & Schimmel, P. R. (1980). Biophysical Chemistry: Part II: Techniques for the study of Biological structure and function. Macmillan
2	Gu, J., & Bourne, P. E. (Eds.). (2009). Structural Bioinformatics. John Wiley & Sons
Reference Books	
1	Banaszak, L. J. (2000). Foundations of Structural Biology. Elsevier
2	Drenth, J. (1994). Laue Diffraction. In Principles of Protein X-Ray Crystallography. Springer, New York, NY
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	https://www.uib.no/en/rg/biss/111704/structural-biology - UNIVERSITY OF BERGEN
2	https://www.biophysics.org/education-careers/education-resources - Biophysical Society
3	https://pdb101.rcsb.org/learn/guide-to-understanding-pdb-data/methods-for-determining-structure

Course Designed By: Dr. Usha/Prof. N. Jeyakumar

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	S	M	M	S	S	S
CO2	S	S	S	S	S	S	S	S	S	S
CO3	S	S	S	S	S	M	L	S	M	S
CO4	S	S	S	S	S	M	M	S	M	S
CO5	S	S	S	S	S	S	S	S	S	S

*S-Strong; M-Medium; L-Low

Course code	23D	PHARMACOGENOMICS AND DRUG DESIGN	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic knowledge in Biology	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Provide the basics of pharmacogenomics, Pharmacodynamics, and toxicogenomics
2. Familarise the students to the stages in drug development.
3. know the concept of drug interactions and drug metabolism in the host
4. Model the target and to use computational tools and software to design a drug.

Expected Course Outcomes:

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

1	Describe the metabolism of the drug right from administration to excretion and biotransformation.	K1
2	Understand the genes affecting the efficacy of the drugs in the treatment of some important diseases.	K2
3	Relate the traditional medicinal system to the modern scientific results through Ayugenomics; apply modern research tools in the area of Pharmacogenomics.	K3
4	Model and validate the target structures	K4
5	*In silico* identification of lead molecules through docking.	K5,K6

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Introduction to Pharmacogenomics	12 hours

Introduction to pharmacogenomics, 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.

Unit:2	Drug Metabolism and Ayugenomics	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. Ayugenomics (integration of Ayurveda & genomics). Microsatellite in studying genetic variation. Microarray in herbal drug research, Pharmacodynamics, Pharmacogenomics and Pharmacognosy.

Unit:3	Pharmacogenomics in the Disease Treatment	10 hours

Pharmacogenomics in the treatment of cancer, neurodegenerative diseases, cardiovascular diseases. Pharmacogenomics in pharmaceutical industry, Ethical issues related to Pharmacogenomics, Pharmacogenomics and ethanopharmacology.

Unit:4	Ligand Designing	12 hours

2-D and 3-D database searching, Structure-based and Ligand based drug design for all classes of targets, SPROUT, LUDI. Structure Activity Relationship studies. QSAR studies, 3D QSAR, CoMFA, Verlot Algorithm, Craig Plot, Topliss scheme. Pharmacophore identification and novel drug design. ADME prediction - SwissADME, PreADMET.

Unit:5	Modeling and Docking	12 hours
Druggable Targets, Macromolecular modeling- Ab initio modeling; Phyre 2 server. Homology Modeling; Modeller. Threading; RAPTOR. Validation of the Model – Ramachandran Plot. PROCHECK. Binding site; Q-Site finder, Catalytic site atlas. Molecular docking; ArgusLab, AutoDock, GLIDE. Drug-receptor interaction. Pymol, Rasmol viewer.		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars - webinars		
	Total Lecture hours	**60 hours**

Text Book(s)	
1	B.Patwaradhan.2007. Drug discovery and development. New India publishing agency, New Delhi.
2	Andrew R. Leach Molecular Modeling: Principles and Applications.
3	L.Shargel and A.B.C.Yu.1999. Applied Biopharmaceutics and Pharmacology. McGraw-Hill, New York.
4	Jin Xiong. Essential Bioinformatics. Cambridge University Press.
Reference Books	
1	J.H. Block and J.M. Beale Jr. 2004. Organic medicinal and Pharmaceutical chemistry. Lippincott Williams and Wilkins, New York.
2	Rothstein, Pharmacogenomics: Social, ethical and clinical dimensions, Wiley Less.
3	D.M. Brown.2004. Drug delivery systems in Cancer therapy. Humana press, Totowa, New Jersey.
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	https://dth.ac.in/medical/courses/pharmacology/3/13/index.php
2	https://dth.ac.in/medical/courses/pharmacology/3/4/index.php
Course Designed By: Dr. V. Hemamalini	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	M	M	M	S	S	S
CO2	M	S	S	M	S	S	S	M	M	M
CO3	S	S	M	M	S	S	S	S	S	S
CO4	S	M	M	S	S	M	S	M	S	S
CO5	M	M	S	S	M	S	M	S	S	M

*S-Strong; M-Medium; L-Low

Course code	2EA	BIODIVERSITY INFORMATICS	L	T	P	C
Core/Elective/Supportive		Elective	4	-	-	4
Pre-requisite		Basic knowledge in Biology	Syllabus Version			2021-22

Course Objectives:

The main objectives of this course are to:

- To make the students understand the basic Biological diversity of life.
- To know the distributed databases and web- accessible resources
- To analyze the software for identification of Assessing existing biodiversity databases
- To understand the probabilistic and deterministic method for analyzing biodiversity data.

Expected Course Outcomes:

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

1	Describe the role of information technology in distributing biodiversity information.	K1
2	Involve the biodiversity assessments and inventorying programmes.	K2
3	Interpret the morphological and molecular characterization of biodiversity	K3
4	Evaluate the Red data books and Biodiversity registers.	K4
5	Global biodiversity information system	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Biological Diversity of Life	10 hours

Methods for species identification & classification- Information needs in biodiversity assessments and inventorying programmes- Role of information technology in distributing biodiversityinformation..

Unit:2	Introduction to Biodiversity Informatics	12 hours

Assessing, analyzing and documenting biodiversity- Morphological and molecular characterization of biodiversity- Introduction to biodiversity database: endangered animals, endemism and Red data books- Biodiversity registers.

Unit:3	Network and Databases	12 hours

Designing information systems to support biodiversity conservation- Networks for distributing information- Distributed Databases and Web- Accessible Resources.

Unit:4	Software for Biodiversity Informatics	12 hours

Software for identification of Assessing existing biodiversity databases on the world-wide web- Probabilistic and deterministic identification, Delta, MicroIS, AVIS, ICTV.

Unit:5	Global Biodiversity Information System	12 hours

Overview of the UNEP/GEF biodiversity data management project (BDM) – CBD and bioethics– General agreement on trade andtraffics.

Unit:6	Contemporary Issues	2 hours

Expert lectures, online seminars - webinars

	Total Lecture hours	**60 hours**
Text Book(s)		
1	Biodiversity: Measurement & Estimation -Hawkswoth, D.I. (Ed.) (1995), Chapman & Hall, London.	
2	Alice, 1990. A Biodiversity database system. Alice software partnership. Cnhos, D.A.L. Canhos, V.P and Kirsop, B.E (eds) 1994. Linking Mechanisms for biodiversity information, Tropical foundation, Tropical Foundation, Campinas, Brazil.	
Reference Books		
1	GlobalBiodiversity:StatusoftheEarth‟sLivingResources.WaterConservationMonitoring Centre (1992), Chapman & Hall,London.	
2	Systematics and Conservation Evaluation- Forey, P.L., C.J. Humphries and R.I Vane-Wright (eds) (1994), Clarendon press, Oxford.	
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]		
1	https://www.biologydiscussion.com/biodiversity/biodiversity-concept-types-and-other-details-with-diagram/7132	
Course Designed By: Prof. P. Shanmughavel		

Mapping with Programme Outcomes

COs	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10
CO1	S	S	S	S	M	S	M	S	S	M
CO3	S	M	M	M	S	M	S	M	S	S
CO3	S	S	S	S	S	S	S	S	S	M
CO4	S	S	S	S	S	S	S	M	M	S
CO5	S	M	M	M	M	M	S	M	M	M

*S-Strong; M-Medium; L-Low

Course code	2EB	BASICS OF CHEMINFORMATICS	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic knowledge in Chemistry and Computer Science	Syllabus Version	2021-22		

Course Objectives:

The main objectives of this course are to:

- To make the students understand the basics of cheminformatics and their application.
- To aware the various chemical information sources.
- To analyze the pharmacokinetic properties of small molecules using ADMETcalculation.
- To understand the steps in pro drug design.
- To utilize the bioinformatics tools and software in different aspects.

Expected Course Outcomes:

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

1	To make the students understand the basics of cheminformatics and their application.	K1
2	To aware the various chemical information sources.	K2
3	To analyze the pharmacokinetic properties of small molecules using ADMETcalculation.	K3
4	To understand the steps in pro drug design.	K4
5	To utilize the bioinformatics tools and software in different aspects.	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Basic Mathematics and Statistics	10 hours

Graph theory and molecular numerology; Logic, sets and functions; Algorithms, integersand matrices; Mathematical reasoning, induction and recursion; Counting; graphs, trees and sets, basic probability and statistics; Markovprocesses..

Unit:2	Foundations of Chemistry and Biology	12 hours

Basic Stereochemistry, Group Theory, 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. Physical properties of proteins - charge, size, hydrophobic, protein binding – structural aspects; antibodies; transport; nucleotide binding; catalytic enzymes; basic concepts of combinatorial chemistry. Introduction to drug action, pro drug design and applications.

Unit:3	Chemical information sources	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:4	Bioinformatics	12 hours

Introduction; Experimental sources of biological data; Publicly available databases; Gene expression monitoring; Genomics and Proteomics; Metabolomics; Visualization of sequence data; Visualization of structures using Rasmol or SPDB

Viewer or CHIME; Genetic basis of disease; Personalized medicine and gene-based diagnostics; Legal, ethical and commercial ramifications of bioinformatics.		
Unit:5	**Pharmaceutical applications of molecular modeling**	**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 receptors. Drug design target interaction. Prediction of Binding Modes, Protein–ligand binding free energies, Fragment-Based Drug Design; Absorption, Distribution, Metabolism, Excretion & Toxicology (ADMET) prediction; Calculation of Physico-Chemical Properties, Biological and Physico-Chemical Predictive Model Building.		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars – webinars		
	Total Lecture hours	**60 hours**

Text Book(s)	
1	"Mathematical Methods for Physicists" Arfken, Academic Press1985
2	Molecular Modeling: Basic Principles and Applications, 3rd Edition,Hans-Dieter Höltje, Wolfgang Sippl, Didier Rognan,GerdFolkers
Reference Books	
1	Introduction to Bioinformatics, Teresa K. Attwood, DavidParry-Smith
2	Combinatorial Chemistry and Molecular Diversity in Drug Discovery, Eric M. Gordon , James F.Kerwin
3	Introduction to Protein Structure: Second Edition ,Carl Branden , JohnTooze
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	https://chem.libretexts.org/Courses/Intercollegiate_Courses/Cheminformatics_OLCC_(2019)
Course Designed By: Prof. P. Shanmughavel	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	S	S	S	S	S	S
CO3	M	S	S	S	S	S	S	S	S	S
CO3	S	M	M	M	S	M				
CO4	S	S	S	S	M	S	S	S	S	S
CO5	S	M	M	S	M	M	S	S	S	S

*S-Strong; M-Medium; L-Low

Course code	23P	PRACTICAL II - COMPUTER PROGRAMMING	L	T	P	C
Core/Elective/Supportive		Core	-	-	4	4
Pre-requisite		Basic programming knowledge	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. To make the students understand the basic aspects of programming.
2. Practice the use of conditional and looping statements.
3. Gain skills to handle strings and files.
4. Explain and be able to use fundamental programming constructs such as sequencing, decisions and iteration.
5. To program with advanced features of the C, C++ and PERL.

Expected Course Outcomes:

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

1	Have a good understanding about the concepts of C & PERL.	K2
2	Be able to write and read basic codes in C.	K3
3	Be able to explain and make use of data types, variables, constants, assignment statements, and arithmetic and Boolean expressions in writing programs.	K4
4	Explain and are able to use arrays and structures.	K6

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

I	Programming in C	30hours

I. Character array manipulations

1) Read and Display a character array
2) Reverse print the array (Sting Reverse)
3) Length of the array
4) Copying the contents of one array to another (String Copy)
5) Copy the Uppercase character of one array as Lowercase character to another array
6) Checking whether a string is a palindrome or not
7) Copy the left 'n' characters of one array to another
8) Copy the last 'n' characters of one array to another
9) Copy the middle 'n' characters of one array to another
10) Concatenate two character arrays (String Concatenate)
11) Counting the numbers of Words, Lines and characters in an array
12) Counting the numbers of Uppercase and Lowercase Alphabets, Digits and special characters in an array
13) Check the number of occurrences of a pattern
14) Check the occurrences of a pattern and skip the same
15) Check the occurrences of a pattern and replace it with a different pattern

II. Pointers and Character Array

16) Pattern Counting
17) Pattern Skipping
18) Pattern Replacing

III. Files and Command Line Arguments

19) Read data from the keyboard and write it in the file (char by char)
20) Read data from the file and display it on the screen (char by char)
21) Display the content of all the files(Cat all the files)
22) Copy data from one file to another
23) Pattern Count

24) Line in which the pattern occurs with line number 25) Grep all files (Pattern match all the files)		
II	**Programming in PERL**	**30 hours**
I PERL Basics 1. Program to print the elements of a array 2. Program to take an element off the end of an array 3. Program to take an element off the beginning of an array 4. Program to put an element at the beginning of an array 5. Program to put an element at the end of an array 6. Program to reverse an array 7. Program to get the length of an array 8. Program to insert an element at a random position in an array **II PERL Bioinformatics Programming** 9. Program to store a DNA sequence 10. Program to concatenate DNA fragments 11. Program to convert DNA to RNA. 12. Program to calculate reverse compliment of DNA sequence 13. Program to read protein sequence data from a file 14. Program to find motifs in a protein sequence 15. Program to count nucleotides in a sequence 16 Program to find the percentage of hydrophobic amino acids in a sequence 17 Program to find the percentage of G and C in a DNA sequence 18. Program to append ATGC to a DNA sequence using subroutines 19. Program to concatenate two strings using subroutines 20. Program to count the number of given motifs 21. Program to convert DNAto RNA using subroutines 22. Program to find if a DNA is stable or not		
	Total Lecture hours	**60 hours**
Text Book(s)		
1	B.W.Kernighan and D.M. Ritchie, "The C Programming Language", 2nd Edition. Prentice Hall of India.	
2	E. Balagurusamy - "Programming in C++ " - Tata McGraw Hill Edition	
Reference Books		
1	Byron Gottfried, "Programming with C" (Schaum's Outline Series) - Tata McGraw Hill Publishing Company – 1998	
2	Robert Laffore -"Object oriented programming with C++" -Waite series.	
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]		
1	https://www.programiz.com/c-programming/examples	
2	https://www.tutorialspoint.com/learn_c_by_examples/simple_programs_in_c.htm	
Course Designed By: **Prof. N. Jeyakumar**		

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	S	S	S	S	M	S
CO3	M	S	M	S	S	S	M	S	M	M
CO3	S	S	S	M	M	S	S	S	S	M
CO4	S	S	M	M	M	S	M	M	S	S
CO5	S	M	S	S	S	M	S	S	S	M

*S-Strong; M-Medium; L-Low

Course code	GS125	PRINCIPLES OF DRUG DISCOVERY	L	T	P	C
Core/Elective/Supportive		Supportive	2	-	-	2
Pre-requisite		Basic knowledge in Biology	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Model the protein target and use computational tools and software to design a drug.
2. Acquire knowledge on the computational softwares to visualize and analyze the structure and sequences.
3. Analyze the conformational properties of protein using Ramachandran plot.

Expected Course Outcomes:

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

1	Perform molecular docking with ligands	K2
2	Model and validate the target structures and identification of lead molecules through docking.	K3
3	Evaluate the ligand binding and interaction with the target using bioinformatics tools.	K4
4	Analyze the conformational properties of protein using Ramachandran plot.	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Unit:1	Introduction to Drug Discovery	6 hours

History of drug design, Drug properties, likeness; Principles of Protein structure - Helix, Sheet, Strand, Loop and Coil, Torsion angles, Active site, Domains, Fold, Motif, PSSM; Structural databases- PDB, CATH, SCOP; Chemical Databases – ZINC, Pubchem, Chembl..

Unit:2	Macromolecular modeling	6 hours

Ab initio modeling; Homology Modeling; Threading; Fold Recognition. Model refinement and validation – Ramachandran Plot, PROCHECK. Prediction of Binding site; ADME prediction; Rasmol viewer.

Unit:3	Quantitative Structure Activity Relationship (QSAR)	6 hours

SAR, QSAR, Types of physicochemical parameters, experimental and theoretical approaches for the determination of physicochemical parameters. 3D-QSAR software COMFA.

Unit:4	Molecular docking and Virtual screening	5 hours

Structure-based drug design and Ligand based drug design; Virtual Screening, Pharmacophore design and identification. Molecular docking- AutoDock, Drug-receptor interaction.

Unit:5	Molecular Mechanics and Dynamics	5 hours

General features of molecular mechanics; Energy Minimization - local and global energy minima, applications. Molecular dynamics simulation.

Unit:6	Contemporary Issues	2 hours

Expert lectures, online seminars – webinars

	Total Lecture hours	30 hours

Text Book(s)	
1	Molecular Modeling: Basic Principles and Applications, 3rd Edition,Hans-Dieter Höltje, Wolfgang Sippl, Didier Rognan, Gerd Folkers•
2	Andrew R. Leach Molecular Modeling: Principles and Applications.
Reference Books	
1	Textbook of Drug Design and Discovery, Kristian Stromgaard, Povl Krogsgaard-Larsen, Ulf Madsen, 2009, CRC Press.
2	Drug Design and Discovery: Methods and Protocols, Volume 716, Seetharama D. Satyanarayanajois, Humana Press, 2011.
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	https://nptel.ac.in/courses/102/106/102106070/
Course Designed By: Dr. V. Hemamalini	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	M	S	S	M	S	S	M	S	M
CO3	S	S	M	M	S	S	S	S	S	S
CO3	S	S	M	S	S	S	S	M	M	S
CO4	S	S	S	S	M	M	M	S	S	S

*S-Strong; M-Medium; L-Low

Third Semester

Course code	33A	GENOMICS AND NGS	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic Bioinformatics knowledge	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. To understand the genome architecture with gene function and regulation.
2. To provide students with the skills of genomic data analysis.
3. To get clear idea about the Computational trancriptomics and epigenomics part.
4. To provide general and unique aspects of Next Generation Sequencing (NGS) through various tools.
5. To understand the basics and applications of big data.

Expected Course Outcomes:

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

1	Explain genomic technologies and the ways in which genomic data are stored.	K2
2	Have hands-on experience on various bioinformatics tools available for analyzing genes and genomes.	K3
3	To handle biological big data generated by the sequencing projects and its analysis.	K4
4	Adequate awareness on plant and clinical trancriptomics and epigenomics evaluation.	K5
5	Get the clear idea in theories of various NGS technologies.	K1

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Unit:1	Genome Organization	10hours

Anatomy of the Eukaryotic and Prokaryotic Genome, Repetitive DNA Content of Genomes. Gene-protein relations, Mutational sites Complementation. Genome Mapping – Mapping Genomes, Genetic and Physical Maps, Sequencing Genomes, Methodology for DNA Sequencing, Assembly of a Contiguous DNA Sequence, understanding a Genome Sequence, Locating the Genes in a Genome Sequence, Determining the Functions of Individual Genes.

Unit:2	Genome Analysis, Gene Prediction & Genome Rearrangement	12 hours

DNA Sequencing databases, Sequence analysis programs. The first complete genome sequence and database. DNA sequencing, sequencing cDNA Libraries of expressed genes, Accuracy and computers storage of sequence, Conversions of one sequence format to others.
ORF Prediction, gene prediction methods and tools. Analyzing Genomes, Applications to Complex Genomes. Comparative Genomics – Completed genomes, Sequence assembly and gene identification, functional classification of genes.

Unit:3	Transcriptomics and Epigenomics	12 hours

Transcriptomics: Introduction and Importance, Data collection and processing. Applications and Candidate genes. Significance of Transcriptomics. Different types of RNA transcripts and, Single-cell transcriptomics.
Epigenomics: What is epigenomics?Challenges and opportunities of computational epigenomics. Introduction of plant epigenomics. Clinical Applications of Epigenomics.

Unit:4	Introduction to Next Generation Sequencing	12 hours

What is Next Generation Sequencing? How it is 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:5	**NGS related Theories with Experiments and Big Data**	**12 hours**

RNAseq - Biological theories on RNAseq experiments. Major scientific advance using RNAseq. Alignment - Gene expression analysis, Differential expression analysis. Alternative splicing - TopHat and Cufflinks for RNAseq.

ChIPseq - Introduction and biological theories on ChIPseq analysis. DNA fragment evaluation. Peak identification. Two condition comparison. Saturation analysis. Motif finding and related theories.

Big Data- Overview and its Applications in genomics. Platforms for Big Data. Utilization in Biological Industry.

Unit:6	**Contemporary Issues**	**2 hours**

Expert lectures, online seminars – webinars

	Total Lecture hours	**60 hours**

Text Book(s)

1	Brown, T.A. 2002 Genome. John Wiley Press, US.
2	Campbell, A.M. & Heyer, L.J. 2002 Discovering Genomics, Proteomics and Bioinformatics. Benjamin/Cummings.
3	Stuart M. Brown. Next-Generation DNA Sequencing Informatics, Second Edition. New York University School of Medicine (ISBN-13: 978-1621921236).
4	Xinkun Wang. Next Generation Sequencing Data Analysis, CRC Press. (ISBN13: 9781482217889).

Reference Books

1	Primrose and Twyman 2003 Principles of Genome Analysis & Genomics. Blackwell.
2	Pasternak 2000 An Introduction to Molecular Human Genetics. Fitzgerald.
3	Dale and Schartz 2003 From Genes to Genomes. Humana.

Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]

1	Applied Optimization for Wireless, Machine Learning, Big DataBy Prof. Aditya K. Jagannatham | IIT Kanpur| SWAYAM
2	Big Data ComputingBy Prof. Rajiv Misra | IIT Patna| SWAYAM
3	https://nptel.ac.in/courses/102/104/102104056/
4	https://nptel.ac.in/courses/102/103/102103017/

Course Designed By: **Dr. C. Jayaprakash**

Mapping with Programme Outcomes

COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	S	S	S	M	S	S
CO2	S	S	S	M	S	S	M	M	M	S
CO3	M	S	S	S	S	S	S	M	S	S
CO4	S	M	S	S	M	M	S	S	S	S
CO5	S	S	S	M	S	S	S	S	S	M

*S-Strong; M-Medium; L-Low

Course code	33B	PROTEOMICS	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic knowledge in Biology	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Understand the structure of cellular proteins and methods for structure prediction.
2. Analyze the methodology of MALDI-TOF analyzers and perform functional proteome analysis.
3. Predict the protein secondary structure using different algorithm.

Expected Course Outcomes:

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

1	Describe the different secondary structure of protein.	K1
2	Interpret the properties of protein in solution and in membranes.	K2
3	Evaluate the variability between organ and developmental stage.	K5
4	Identify the immobilized pH gradient and describe the digital imaging, Spot detection and quantification.	K3
5	Perform functional proteome analysis	K4

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Unit:1	Protein classification	10 hours

Structural elements and terminology: Helix, Sheet, Strand, Loop and coil, Active site, Architecture, Blocks, Class and Domains, Fold, Motif, PSSM. Principles of classification: Based on structural features, Phylogenetic relationship. Properties of protein in solution and in membranes. Interaction with other molecules like lipids, carbohydrates, metal Ions.

Unit:2	Protein structure prediction	12 hours

Use of sequence pattern, leucine zipper, coiled coil, transmembrane, signal peptide, cleavage site. Secondary structure prediction: Chou – Fasman / GOR method, Neural network, nearest neighbor method, tertiary structure prediction, threading profile, contact potential, modeling.

Unit:3	Bioanalysis of protein and peptides	12 hours

Complex protein and peptide mixtures, Extracting proteins from biological samples, Protein separation before digestion: 1D and 2 D Electrophoresis, Immobilized pH gradient, Sample preparation, First dimension criteria, second dimension criteria, Stabilization, Detecting protein on gel: Electro blot, Image analysis, Digital imaging, Spot detection and quantification, Gel matching. Data Analysis – Database for 2D gel.

Unit:4	Tool of Proteomics	12 hours

Mass Spectrometry for protein and peptide analysis: MALDI-TOF Analyzers, ESI Tandem MS instrument, Tandem Mass Analyzers, The Triple Quadrupole Mass Analyzer, The Ion Trap Mass Analyzer, Q-TOF & Fourier Transform–Ion Cyclotron Resonance, MS Instrument.

Unit:5	Functional Proteome Analysis	12 hours

Integrated Proteome Analysis - Phage antibody as tool, Protein expression analysis, High throughput analysis for proteomics. Automation of proteomic analysis. Proteomics in plant

breeding: Objectives, principles and methods, 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.		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars – webinars		
	Total Lecture hours	**60 hours**

Text Book(s)	
1	Introduction to Proteomics: Principles and Applications, Nawin C. Mishra, 2011, Wiley Publishers
2	Introduction to Proteomics: Tools for the New Biology, Daniel Liebler, 2001, Humana Press.
Reference Books	
1	Proteomics: From Protein Sequence to Function, S. R. Pennington, Michael J. Dunn, 2001, BIOS Scientific Publishers.
2	Principles of Proteomics, Richard Twyman, 2001, BIOS Scientific Publishers.
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	https://nptel.ac.in/courses/102/103/102103017/
2	https://swayam.gov.in/nd1_noc19_bt26/preview
Course Designed By: Dr. V. Hemamalini/Prof. N. Jeyakumar	

Mapping with Programme Outcomes

COs	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10
CO1	S	M	S	S	S	M	S	S	S	M
CO3	M	S	S	S	M	S	S	S	M	S
CO3	S	M	S	M	M	S	S	M	S	S
CO4	S	S	S	S	S	S	M	M	M	S
CO5	M	S	M	S	S	M	S	S	S	M

*S-Strong; M-Medium; L-Low

Course code	33C	VISUAL BASIC.NET WITH RDBMS	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic Computer Programming Skills	Syllabus Version		2021-2022	

Course Objectives:

The main objectives of this course are to:

1. To gain knowledge on relational data and its management
2. To design Logical Database Schema and Mapping it to implementation level schema through Database Language Features.
3. To provide knowledge of incorporating SQL/ PL/SQL with programming languages
4. To understand the practical problems of Concurrency control and its solutions Gain knowledge about failure and Recovery mechanisms
5. To inculcate knowledge on RDBMS concepts and Programming with Visual Basic.NET

Expected Course Outcomes:

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

1	To analyze Relational Data Base design methodology.	K4
2	Acquire knowledge in fundamentals of Relational Data Base Management System.	K2
3	Able to handle different Data Base languages.	K3
4	Beable to effectively develop applications with full functionality and a graphical user interface using the language Visual Basic.NET.	K3
5	Create database applications by connecting VB.NET with databases	K6

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Unit:1	Introduction	10 hours

Data Abstraction, Schemas and & Instances- Data Models: Data modeling using Entity Relationship (ER) Model -entity and entity sets, relations and relationship sets, E-R diagrams - Reductions of ER Schema to Tables - Overview of the QBE Language-Hierarchical and Network Model Relational Model- Object Oriented Model - Introduction to distributed database processing.

Unit:2	Recovery and Security	12 hours

Database Recovery Techniques - Database Security - Distributed databases and Client-Server Architecture - Concepts for Object Database - Enhanced Data Models for Advanced Application Emerging Database Technologies and Application

Unit:3	Database Languages	12 hours

Data definition languages – Data Manipulation language, Data Control language, Data and String Functions, Union and intersect operator, Sub queries, Normal Form – 1NF, 2NF, 3NF & Boyce-Codd NF, Introduction to PL/SQL - Basics concepts of SQL and SQL commands - Nested Queries- Aggregate Functions- Null Values - PL/SQL interface - Data types in SQL, Simple PL/SQL programs.

Unit:4	Visual Basic.NET	12 hours

Introduction to VB.NET, Understanding the development Environment – IDE Components- Data Types – Variables – Conditional and Looping Statements – Modular Coding – Subroutines – Functions – Argument-Passing. - Application development using VB.NET

framework- Working with Forms-Components, Controls and Their Properties, Methods and Events.		
Unit:5	**Working with ADO.NET and database connectivity**	**12 hours**
ADO.NET: overview - Architecture - DataSet - DataGrid Control- File I/0 Operations Introduction to database connectivity: Data Access with ADO.NET-Binding Controls to Databases- Handling Databases in Code.		
Unit:6	**Contemporary Issues**	**4 hours**
Expert lectures, online seminars – webinars		
	Total Lecture hours	**60 hours**

Text Book(s)	
1	Database System Concepts. Silberschatz, Tata McGraw-Hill Publications.
2	Database system organization. J.M.Martin, Princeton-Hall.
3	The Complete Reference Visual Basic .NET. Jeffery R. Shapiro, TataMcGraw-Hills.
Reference Books	
1	Introduction to Database Systems. C.J.Date
2	Introduction to Database Systems. J.M.Martin, Princeton-Hall.
3	Using Microsoft Visual Basic.NET. Brian Siler and Jeff Spotts, Pearson Education
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	https://nptel.ac.in/courses/106/106/106106095/
2	https://www.guru99.com/vb-net-tutorial.html

Course Designed By: **Prof. N. Jeyakumar**

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	M	S	M	M	S	S	M	S	S
CO3	M	S	M	S	S	M	M	S	M	M
CO3	M	S	S	S	S	S	M	S	M	M
CO4	S	S	S	M	M	S	M	M	S	S
CO5	S	M	S	S	S	M	S	S	S	S

*S-Strong; M-Medium; L-Low

Course code	33D	MOLECULAR MODELING	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basics of Chemistry and Biology	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Provide knowledge about the structure of the protein molecule and modeling
2. Make a deep understanding about the electron atom types and biomolecular properties
3. Create a strong view on force field and interactions of molecular assemblies

Expected Course Outcomes:

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

1	Understand the molecular structure and its functional importance	K1
2	Clear view on computations quantum mechanics and methods for calculating molecular properties	K2
3	Understand the Physical properties of macromolecular structure and broader concept of energy minimization and its applications	K3
4	Protein structural stability, atoms movement in a molecule by Molecular Dynamics	K4
5	Develop innovative ideologies with optimal solutions	K6

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Unit:1	Molecules and Its Properties	10 hours

Introduction - Nomenclature, terms and atom-numbering used in molecular modelling - Model-building and calculations - Molecular geometry and conformation - Steric criteria - Molecular Representations and Search connectivity matrix - Molecular Graphics surfaces – Applications of Molecular Graphics - Co-ordinate system, Potential energy surfaces, Applications of molecular modelling – Protein-Ligand Interactions, Protein-Protein Interactions, Virtual Screening, Pharmacophore modelling, Ligand based and structure based virtual screening/ drug design, Fragment based approaches

Unit:2	Quantum Mechanics	12 hours

Quantum chemistry for Modeling of small molecules - Variation method and Time independent Perturbation theory - Computational quantum mechanics - Wave properties - Schrodinger equation - Born Oppenheimer approximation - Hartree fock approximation - One electron atoms, poly electronic atoms and molecules - Molecular orbital calculations - Basic sets - Molecular orbital theory, Huckel theory - Types of quantum mechanics - Electron correlation - Energy component analysis - Density functional theory - Fragment molecular orbital method

Unit:3	Molecular Mechanics	12 hours

General features of MM force field - Free energy calculations - Potentials of mean force - Molecular surface area and solvent accessible surface area - Solvation models - Non-bonded interactions and types - Types of potentials and their functions - Calculating thermodynamic property using force field - Derivatives of molecular mechanic energy function - Force field parametrisation and transferability - Calculations of molecular mechanics parameter involves amino acids and DNA base pair - Calculate property for molecular mechanics trajectories – Tools

Unit:4	**Energy Minimization**	**12 hours**
Introduction - Non-derivation minimization, Derivative minimization method - First order minimization method – Steepest Descent Method, Conjugate Gradients - Second order method – Newton – Raphson, Block Diagonal Newton - Raphson, Quasi- Newton Method, The Fetcher- Powell Algorithm, Choice of method - Global conformational minima determination - approaches and problems - Bioactive vs. global minimum conformations - Applications of energy minimization. Determination of transition structure and reaction pathways - Geometry Optimization Procedures – Tools		
Unit:5	**Molecular Dynamics**	**12 hours**
Introduction - Molecular dynamics using simple methods, Newtonian dynamics - Continuous potentials - Setting and running a molecular dynamics simulations; Implicit and explicit Solvation models, Periodic boundary conditions, Time dependent properties - Molecular dynamics at constant temperature and pressure - Trajectory quality, Initial system setting simulation protocol high speed implementation - Numerical integration - Computational complexity - Verlet algorithm, MD Ensembles – types - Monte Carlo simulation methods - Simulated annealing		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars – webinars		
	Total Lecture hours	**60 hours**

Text Book(s)

1. Molecular Modeling: Principles and Applications, 2nd Edition,Andrew R. Leach
2. Basic principles and applications Hans-x

Reference Books

1. Molecular Modelling for Beginners, Alan Hinchliffe, UMIST, Manchester,UK, John Wiley &Sons, Ltd.
2. Computational Chemistry- Introduction to the Theory and Applications of Molecular and Quantum Mechanics, Errol Lewars, Kulwar Acedemics Publishers

Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]

1. https://www.schrodinger.com/schrodinger-online-learning
2. https://homepage.univie.ac.at/Franz.Vesely/simsp/jsm/c1_intro_s1_intro.html-Molecular Simulation-By Franz J. Vesely, University of Vienna
3. https://nptel.ac.in/noc/courses/noc18/SEM2/noc18-cy13/ - Computational Chemistry and Classical Molecular Dynamics

Course Designed By: Dr. S. Usha

Mapping with Programme Outcomes

COs	PO1	PO2	PO3	PO4	PO5	PO6	PO7	PO8	PO9	PO10
CO1	S	S	S	S	S	S	S	S	S	S
CO2	S	S	S	S	S	S	S	S	S	S
CO3	S	S	S	M	S	S	M	S	S	S
CO4	S	S	S	S	S	S	S	S	S	S
CO5	S	S	M	M	S	M	M	S	M	S

*S-Strong; M-Medium; L-Low

Course code	3EA	SYSTEMS BIOLOGY	L	T	P	C
Core/Elective/Supportive		Core	4	-	-	4
Pre-requisite		Basic knowledge in Biology and Computers	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

To make the students understand the basic aspects and applications of Systems Biology.

- To know the micro array analysis, hierarchical clustering, and self-organizing maps.
- To analyze the virtual erythrocytes and the levels of simulation.
- To understand the steps in yeast two hybrid system and peptide mass fingerprinting.
- To utilize the information from various pathway database for further research.

Expected Course Outcomes:

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

1	Describe the microarray technique and analyze the result in various aspects	K1
2	Interpret the various metabolic pathways.	K2
3	Reorganize the pattern using neural network method.	K3
4	Understand the concept of Quantification of receptor signaling.	K4
5	Know about primer design and epitope identification	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** - Create

Unit:1	Introduction to Systems Biology	10 hours

What is Systems Biology? Integrating Networks. Methods of study: Micro array – definition, types of array, Micro array analysis: Hierarchical clustering, Self-organizing maps. Applications of Micro Array in systems biology.

Unit:2	Metabolomics	12 hours

Digestion of proteins and protein metabolism, Urea Cycle, Transport metabolism, Carbohydrate metabolism – metabolism of glucose – glycolysis, TCA cycle, glycogenesis, Pentose phosphate shunt, Electron transport. Lipid metabolism: beta oxidation. Interconnection of pathways, metabolic regulations. Interconnection of pathways, metabolic regulation, Phylogeny, RNA secondary Structure, Gene Prediction

Unit:3	Computational Cell Biology	12 hours

Principle and levels of simulation – Virtual Erythrocytes, Pathological analysis. Flux Balance Analysis; Graphical Biological Network Editor and Simulator (Cell Designer).

Unit:4	Location Proteomics	12 hours

Protein subcellular location- Pattern Recognition. Predicting ligand-binding function, Use of gene cluster, detecting protein – protein interaction. Methods for Protein-Protein Interaction Analysis- Yeast Two Hybrid System (Y2H); Peptide Mass Fingerprinting (PMF).

Unit:5	Creative Bioinformatics	12 hours

Novel use for database. Use of EST database – Unigene, gene discovery, Primer

design, Restriction mapping, Position specific cloning, KEGG, SNP database, Target identification, Epitope identification. Spatial Signaling Dynamics – Methods and Quantification of receptor signaling.		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars - webinars		
	Total Lecture hours	**-- hours**

Text Book(s)	
1	Foundation of Systems Biology – Hi Roaki Kitano
2	Introduction to Systems Biology – Sangdun Choi
3	Shanmughavel, P. 2005. Principles of Bioinformatics, Pointer Publishers, Jaipur, India.
Reference Books	
1	Shanmughavel, P. 2006. Trends in Bioinformatics, Pointer Publishers, Jaipur, India
2	Towards metabolic phenomics: Analysis of Genomics Data Using Flux Balances. Christopher H. Schilling *et. al*. 1999. *Biotechnology. Prog.* 15: 288-295.
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	https://nptel.ac.in/courses/102/106/102106035/
2	
4	
Course Designed By: Prof. P. Shanmughavel	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	M	S	M	S	S	M
CO3	S	M	M	M	S	M	S	M	S	S
CO3	S	S	S	S	S	S	S	S	S	M
CO4	S	S	S	S	S	S	S	M	M	S
CO5	S	M	M	M	M	M	S	M	M	M

*S-Strong; M-Medium; L-Low

Course code	3EB	BIG DATA ANALYTICS	L	T	P	C
Core/Elective/Supportive		Elective	4	-	-	4
Pre-requisite	Programming and Database Management Knowledge		Syllabus Version	2021-22		

Course Objectives:

The main objectives of this course are to:

1. Able to select and implement appropriate data structures to solve big data problems and also write Map and Reduce codes for distributed processing of data.
2. Interested students will also have an opportunity to learn the basics of functional programming in Scala.
3. Capable to perform batch processing operations on Big data on your own computer as well as on an Amazon EC2 instance.

Expected Course Outcomes:

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

1	Competent to retrieve and store data in HDFS &Hbase using MapReduce & Apache Pig.	K3
2	Learn to choose and use tools to ingest structured and unstructured data into big data processing systems and use Hive to perform data transformations.	K3
3	Process Big Data on Cloud using Amazon EMR and use OOZIE for managing your workflow.	K2
4	Gifted to build real time data processing systems using Apache Storm and Apache Spark.	K6
5	Talented to perform analytics on the big data using Spark MLLib and get knowledge of tools to visualize results.	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Unit:1	Basics of Big Data	10 hours

Introduction to Big Data and its Applications. Linear data structures and Non-linear data structures. Algorithm design.

Unit:2	Environment and Databases	12 hours

Distributed Computing Environment for Big Data. NoSQL 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 & Dynamo DB).

Unit:3	Concepts and Platforms	12 hours

Performing operations. Concepts for Big Data. Big Data Platforms. Workflow management. Batch Processing.

Unit:4	Applications and Source	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:5	Advances in Big Data	12 hours

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

Unit:6	Contemporary Issues	2 hours
Expert lectures, online seminars – webinars		
	Total Lecture hours	60 hours
Text Book(s)		
1	Parag Kulkarni, Big Data Analytics (Kindle Edition).	
Reference Books		
1	Viktor Mayer-Schonberger and Kenneth Cukier.Big Data: A Revolution That Will Transform How We Live, Work and Think. 2013.	
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]		
1	https://nptel.ac.in/courses/106/104/106104189/	
2	https://nptel.ac.in/courses/106/106/106106142/	
Course Designed By: **Prof. N. Jeyakumar**		

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	S	S	S	S	M	S
CO3	S	S	M	S	M	S	M	S	M	M
CO3	S	S	S	M	M	S	S	M	L	M
CO4	S	S	M	M	M	S	M	M	S	L
CO5	S	M	S	S	S	S	S	S	S	M

*S-Strong; M-Medium; L-Low

Course code	GS02	ADVANCED BIOINFORMATICS	L	T	P	C
Core/Elective/Supportive		Supportive	-	-	2	2
Pre-requisite		Basic knowledge in Biology	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Make the students understand the basic aspects and applications of Bioinformatics.
2. Know the computational methods for Sequence Alignment and the related scoring algorithms.
3. Understand the steps in Evolutionary analysis.

Expected Course Outcomes:

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

1	Describe the file formats, nomenclature of macromolecules and have an idea of Databases.	K1
2	Interpret the algorithms, scoring functions involved in the sequence alignment.	K2
3	Evaluate the phylogenetic relationship of an organism and identify genes, repeats,domains from sequences using bioinformatics tools.	K3
4	Model 2D and 3D structure of a target from the sequence.	K4
5	Exploit the information in the sequences for further research.	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Unit:1	**Sequence Alignment**	**6 hours**

Introduction to sequence alignment, PAM - BLOSUM, Local and Global alignment, Needleman- wunsch algorithm, Smith-waterman algorithm, Multiple sequence alignment, FASTA, BLAST.

Unit:2	**Phylogenetic Analysis**	**6 hours**

Evolutionary analysis – steps and construction of Phylogenetic tree- Cladistic, and Phenetic methods- Clustering methods - Rooted and Unrooted tree representation.

Unit:3	**Gene Prediction Analysis**	**5 hours**

Gene Prediction – methods and tools - similarity based and ab-initio prediction- GENSCAN, GRAIL, FGENES- Protein Domain analysis - Pfam, MOTIF search, SMART.

Unit:4	**Protein structure prediction**	**5 hours**

Structure prediction methods: Chou-Fasman, GOR method, Neural Network, Threading and Fold recognition, Modeling and Docking.

Unit:5	**Genome Analysis**	**6 hours**

Genome Projects- Genome sequencing technologies and analysis methods - Analysis of gene expression data - Function, gene set enrichment and pathway analysis.

Unit:6	**Contemporary Issues**	**2 hours**

Expert lectures, online seminars – webinars

	Total Lecture hours	**30 hours**

Text Book(s)

1	David. W. Mount (2001): Bioinformatics Sequence and Genome Analysis, Cold spring Harbor Lab.

	NY.USA.
2	Genomes T.A Brown,2001, Taylor and Francis Group.
	Comparative Genomics Ann Gibbons, 1998, Science.
Reference Books	
1	Understanding Bioinformatics, Jeremy O. Baum, Marketa J. Zvelebil. 2007, Garland Science, USA
2	Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins, Andreas D. Baxevanis, B. F. Francis Ouellette, 1998, Wiley Publishers
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	Bio-Informatics: Algorithms and Applications- SWAYAM
2	https://nptel.ac.in/courses/102/103/102103044/
Course Designed By: Dr. V. Hemamalini	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	M	S	S	S	S	S	M	S	S
CO3	S	S	S	S	M	M	M	S	S	S
CO3	S	S	M	M	S	S	S	M	S	S
CO4	M	S	S	M	S	M	S	S	M	S
CO5	S	M	S	S	S	S	S	M	S	M

*S-Strong; M-Medium; L-Low

Course code	33P	PRACTICAL – III: MOLECULAR TECHNIQUES	L	T	P	C
Core/Elective/Supportive		Core	0	0	4	4
Pre-requisite		Basic Wet lab knowledge	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Provide hands on training in the basic techniques that is essential for genetic engineering and recombinant DNA technology.
2. Develop their skills in the isolation, identification and quantification of macromolecules.
3. Experience in the handling of macromolecules (DNA and RNA).

Expected Course Outcomes:

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

1	Have technical expertise on versatile techniques in Recombinant DNA technology.	K2
2	Perform various types of practical laboratory work (chemical, biochemical and molecular methods) in a safe way	K3
3	Analyse, interpret and present the results with theoretical background	K4
4	Have hands-on experience on various basic biotechnological techniques for analyzing biomolecules.	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Experiments	**60 hours**

1. Sterilization techniques and Media preparation
2. Preparation and Maintenance of Microbial Culture
3. Plasmid and Chromosomal DNA Preparation from E. coli
4. Pure microbial culture techniques
5. pH measurements and preparation of buffers
6. Spectrophotometric Analysis of DNA
7. Agarose Gel Electrophoretic Analysis of DNA
8. Restriction digestion of bacterial genomic DNA and plasmid DNA
9. Ligation of DNA fragment with plasmid DNA
10. Animal Genomic DNA isolation
11. Plant Genomic DNA isolation
12. Amplification of DNA by PCR
13. Maintenance of Cell lines
14. Cell Viability assay
15. BCA Protein assay

Total hours	**60 hours**

Text Book(s)

1	Life Science Laboratory Manual, DST, 2017
2	Bansal. MP, Molecular biology and biotechnology: basic experimental protocols, The Energy and Resources Institute (TERI), 2012

Reference Books

1	Laboratory Manual Sambrook and Russell, "Molecular Cloning – A Laboratory Manual", CSHL Press, 2002.

Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]	
1	Virtual Lab of Amrita Laboratories - https://vlab.amrita.edu/?sub=3
Course Designed By: Dr. V. Hemamalini	

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	M	S	M	S	M	S	M
CO3	S	M	S	S	S	S	S	S	S	M
CO3	S	S	S	S	S	S	S	S	S	S
CO4	M	S	M	S	M	S	S	S	S	S

*S-Strong; M-Medium; L-Low

Course code	33Q	PRACTICAL IV - BIOLOGICAL SEQUENCE ANALYSIS AND COMPUTER AIDED DRUG DESIGN	L	T	P	C
Core/Elective/Supportive		Core	-	-	4	4
Pre-requisite		Basic knowledge in Biology	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

- To make the students understand the basic aspects and applications of Bioinformatics.
- To know the computational methods for Sequence Alignment.
- To analyze relatedness of the proteins of an organism with that of other organisms.
- To understand the steps in Evolutionary analysis.
- To utilize the information in the sequences for further research.

Expected Course Outcomes:

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

1	To make the students understand the basic aspects and applications of Bioinformatics.	K1
2	To know the computational methods for Sequence Alignment.	K2
3	To analyze relatedness of the proteins of an organism with that of other organisms.	K3
4	To understand the steps in Evolutionary analysis.	K4
5	To utilize the information in the sequences for further research	K5

K1 - Remember; **K2** - Understand; **K3** - Apply; **K4** - Analyze; **K5** - Evaluate; **K6** – Create

Unit:1	Biological Databases	10 hours

Biological Databanks Sequence Databases, Structure Databases, SpecializedDatabases
Data retrieval tools and methodsand Database file formats.

Unit:2	Gene Prediction and Analysis	12 hours

Molecular visualization
Gene structure and function prediction (using GenScan,GeneMark)
Sequence similarity searching (NCBIBLAST)

Unit:3	Multiple Sequence Alignment and Phylogenetic Analysis	12 hours

Protein sequence analysis (ExPASy proteomicstools)
Multiple sequence alignment(Clustal)
Molecular phylogeny(PHYLIP)

Unit:4	Sequence Alignment	12 hours

Analysis of protein and nucleic acids sequences,
Sequence analysis using EMBOSS or GCG WisconsinPackage

Small molecule building, using ISIS DRAW and CHEMSKETCH

Unit:5	Macromolecular Structure Prediction and Validation	12 hours

Homology Modeling using SPDBV

Model structure refinement using SPDBV Model validation using What Check and ProCheck Docking using DOCK or AUTODOCK orAMBER		
Unit:6	**Contemporary Issues**	**2 hours**
Expert lectures, online seminars – webinars		
	Total Lecture hours	**60 hours**
Text Book(s)		
1	K. Mani and N. Vijayaraj, Bioinformatics a Practical Approach, Aparna Publications, Coimbatore.	
Reference Books		
1	Shanmughavel.P and GulshanWadhwa (2009), Practicals in Bioinformatics, Pointers Publishers.	
Related Online Contents [MOOC, SWAYAM, NPTEL, Websites etc.]		
1	https://www.ebi.ac.uk/Tools/	
Course Designed By: Prof. P. Shanmughavel		

Mapping with Programme Outcomes										
COs	**PO1**	**PO2**	**PO3**	**PO4**	**PO5**	**PO6**	**PO7**	**PO8**	**PO9**	**PO10**
CO1	S	S	S	S	M	S	M	S	S	M
CO3	S	M	M	M	S	M	S	M	S	S
CO3	S	S	S	S	S	S	S	S	S	M
CO4	S	S	S	S	S	S	S	M	M	S
CO5	S	M	M	M	M	M	S	M	M	M

*S-Strong; M-Medium; L-Low

Elective papers

Semester	Code No.	Paper Name
I	1EA	Mathematical & Statistical applications in bioinformatics
	1EB	Biostatistics
II	2EA	Biodiversity Informatics
	2EB	Basics of Cheminformatics
III	3EA	Systems Biology
	3EB	Big Data Analytics

Supportive papers

Semester	Code No.	Paper Name
I & III	NEW GS???	Advanced Bioinformatics
II	GS125	Principles of Drug Discovery

JOB-ORIENTED COURSES

S.No	Course code	Title of the Course	Total Hours	Credits
1.	JO1	Bioinformatics Algorithms and Machine Learning	30	4
2.	JO2	IT Tools and Applications	30	4
3.	JO3	Microbial Genomics	30	4
4.	JO4	Web Designing	30	4

Job Oriented Certificate Course

Course code	JO1	BIOINFORMATICS ALGORITHMS AND MACHINE LEARNING	L	T	P	C
Core/Elective/Supportive		Certificate course	4	-	-	4
Pre-requisite		Basic computer and statistics knowledge	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Understand any typical algorithm design problem for efficiently implementing the algorithm
2. Provide an overview on the main approaches of machine learning.
3. Apply various clustering and classification algorithms for bioinformatics problems.

Unit:1	Introduction to Algorithms	5 hours

Biological algorithms versus computer algorithms - The 'Change Big-O Notations – Algorithm design techniques and the different types of algorithms - Molecular Biology Primer - Exhaustive Search: Mapping Algorithms – Motif Finding problem - Search Trees - Finding a Median String.

Unit:2	Alignment algorithms	5 hours

Greedy Algorithms: Genome Rearrangements - A Greedy Approach to Motif Finding - DNA Sequence comparison - Manhattan Tourist Problem - Edit Distance and Alignments - Global Sequence Alignment - Scoring Alignment - Local Sequence Alignment - - Multiple Alignment.

Unit:3		6 hours

Algorithms and Complexity- Clustering And Trees- Hierarchical clustering-k-means clustering - Evolutionary Trees - Distance-based tree reconstruction - Character-based tree reconstruction - Small and large Parsimony Problem - Hidden Markov Models

Unit:4	Machine Learning	6 hours

Introduction of machine learning - Basic concept of machine learning - Supervised learning - Semi-supervised learning - Unsupervised learning - Machine Learning Techniques - Introduction to Support Vector Machines and their applications.

Unit:5	Neural Networks	6 hours

Introduction to Neural Networks - Applications of ANN, SVM etc. Basic structure for deep learning models - Training of deep learning models - Applications of deep learning in structural bioinformatics

Unit:6	Contemporary Issues	2 hours

Expert lectures, online seminars – webinars

	Total Lecture hours	30 hours

Reference Books

1. Jones, N. C., Pevzner, P. A., & Pevzner, P. (2004). An introduction to bioinformatics algorithms. MIT press.
2. Gusfield, D. (1997). Algorithms on strings, trees, and sequences Cambridge University Press.
3. Kerlavage, A. R. (1996). DM128. 00 Computing in the biosciences, Molecular Bioinformatics - Algorithms and Applications, Steffen Schulze-Kremer, Walter de Gruyter (Eds.)
4. Goldberg, D. (1999). Genetic algorithms in search optimization and machine learning. 570 pp.
5. Bishop, C. M. (1995). Neural networks for pattern recognition. Oxford university press.
6. Haykin, S. (1998). Neural Networks: A Comprehensive Foundation, Prentice Hall PTR. Upper Saddle River, NJ, USA.

Course Designed By: Dr. S. Usha

Course code	JO2	IT TOOLS AND APPLICATIONS	L	T	P	C
Core/Elective/Supportive		Certificate course	4	-	-	4
Pre-requisite		Basic computer knowledge	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Understand the concept of Information Technology
2. Learn the functioning of computer Software and hardware
3. Gain experience in the basic operations of computer

Unit:1	Introduction to Computers	5 hours

Hardware & Software , Characteristics - Application of computer / information technology - Parts of a computer: Input unit – Output – Storage – CPU - Functioning of Computer/ Computer Operation: Instruction set - main memory organization, I/O buses - BIOS, booting, Instruction Cycle - memory interleaving, Virtual Memory.

Unit:2	Computer Arithmetic	5 hours

Information, Data and its logical & physical concept - Coding system- What is the need for coding? BCD, EBCIDIC, ASCII code, Unicode - Computer Arithmetic - Number systems, binary, Octal, Hexadecimal, Binary Addition, Subtraction and Multiplication. Binary, decimal, hexadecimal number system conversion - Introduction to logic gates & circuits and Boolean algebra.

Unit:3	Software	6 hours

Relationship between hardware and software, need for S/w, system & application & free domain - S/W, Embedded Software - Computer Language - Different generations of languages, High Level Language and Low Level Language, name of some computer languages, compiler, interpreter. Testing and Debugging. - Application Software and its types - Word-processing, Spreadsheet, Presentation Graphics, Data Base Management Software, characteristics and Uses - Virus, Types of viruses, virus detection and prevention - Some file formats - Operating System-Functions of the Operating system - Overview of different operating systems- DOS ,windows, Linux.

Unit:4	Communication Technology	6 hours

Concept of Analog and Digital Signal - Communication types - Duplex - Network components - Bridges, HUB, Routers, Repeater and Gateways - Transmission techniques - wired & wireless - Transmission Media – Bandwidth - Transmission Impairments - Encoding/ Decoding.

Unit:5	Computer Networks	6 hours

Type of Networks, Network configuration- Network protocols **Internet**: Introduction to Internet, requirements, applications and Protocol - WWW, web page, web site, web browsers, HTTP, e-mail, Search engine, Domain name.

Unit:6	Contemporary Issues	2 hours

Expert lectures, online seminars – webinars

	Total Lecture hours	30 hours

Text Book(s)

1	P.K. Sinha and P.Sinha, “Foundations of Computing”, Third Edition, BPB Publication, 2010.
2	“Introduction to Information technology”, ITL Education Solutions Ltd., Pearson Education, 2012
3	Operating System Concepts, Sixth Edition : Abraham Silberschatz, Peter Baer Galvin, Greg Gagne, 2019
4	Data and Computer Communications”, eighth Edition, William Stallings, 2007

Course Designed By: Dr. N. Jeyakumar

Course code	JO3	MICROBIAL GENOMICS	L	T	P	C
Core/Elective/Supportive		Certificate course	4	-	-	4
Pre-requisite		Basic knowledge in Biology	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Provide knowledge about the normal microbial flora and interactions.
2. Understand the methods to clone, propogate and maintain metagenomic libraries
3. Study the functioning of microbial communities using metagenomic approaches.

Unit:1	Microbes and Environment	5 hours

Diversity of Microorganisms, Comparison of three domains – Bacteria, Protista, Fungi, Viral and Algae diversity, Microbial habitats, Metagenomics, Microbe-microbe interactions, Microbe-host interactions, Microbial communities- Biofilms, Quorum sensing, Bioremediation.

Unit:2	Microbial Identification and Characterization	5 hours

Bacterial genome characterisation and dynamics- Sequence alignments to Phylogenetic relationships- Prediction of Genes in prokaryotic genomes- Prediction of Operons, Regulons, transcription signals and Biological pathways- Detection of Viruses using NGS - Reverse vaccinology: from genome to vaccine, Microbial genomics for antibiotic target discovery.

Unit:3	Microbial Genome Sequencing and Characterization	6 hours

Genome sequence analysis- Sequence assembly, Annotation of genomes from sequence to functional annotation, Atlas visualisation of genome-wide information - Comparative genomics and metagenomics- Genome-wide gene expression analyses- Representational display analysis of genome comparisons - Whole genome phylogenetic analysis.

Unit:4	16s rRNA based metagenome profiling	6 hours

16S rRNA microbiome – study design - Sample collection, extraction and library prep - 16S rRNA bioinformatics pipelines- Reads quality and processing - Normalization- - Hierarchical clustering- Taxonomic classification and profiling of bacterial communities - Downstream analysis in R - phyloseq, NMF, vegan, metagenomeSeq.

Unit:5	Whole Metagenome profiling	6 hours

Metagenome sequencing: Cloning the metagenome, Preprocessing of raw sequence data, Downstream sequence analysis – community analysis in R, Shotgun sequencing - Sequencing errors and Diversity estimates, Functional and Pathway annotation- MetaCyc, BioCyc and KEGG, Genomic approaches to study Human microbiome – CRISPR-CAS9/TN-seq.

Unit:6	Contemporary Issues	2 hours

Expert lectures, online seminars – webinars

	Total Lecture hours	30 hours

References

1. Wren, B Dorrell, N, Functional Microbial Genomics: Methods in Microbiology, Academic Press Inc, 2002.
2. Streit, Wolfgang, Daniel, Rolf (Eds.) Metagenomics, Methods and Protocols, Springer, 2010.
3. Fraser C.M., Read T. and Nelson K.E. (2004) Microbial Genomes, Springer.
4. Norman Grossblatt, (Ed), The new science of metagenomics, National Academic Press, Washington, 2007.
5. https://nptel.ac.in/courses/102/103/102103015/

Course Designed By: Dr. V. Hemamalini

Course code	JO4	WEB DESIGNING	L	T	P	C
Core/Elective/Supportive		Certificate course	4	-	-	4
Pre-requisite		Basic knowledge in Computers	Syllabus Version		2021-22	

Course Objectives:

The main objectives of this course are to:

1. Provide knowledge about the web technologies
2. Understand the working of various web development softwares
3. Gain experience in the web designing

Unit:1	Introduction to Web Technologies	5 hours

Careers in Web Technologies and Job Roles - How the Website Works? - Client and Server Scripting – Languages - Domains and Hosting - Responsive Web Designing - Types of Websites (Static and Dynamic - Websites) - **Introduction to HTML** - Tags - Structure - Create and View an HTML document - Editing HTML - Elements - Comments - Alignment - Color and Size - Headings and Paragraphs - Text Formatting - Lists - Hyperlinks - Images – Tables.

Unit:2	Dreamweaver	5 hours

Introduction to Dreamweaver - Tutorials - Dreamweaver Basics - Preparing to Build Dynamic Sites - Working with Page Code - Designing the Page Layout - Adding Content - Working with Behaviors and Animations - Working with Multiple Pages - Making Pages Dynamic - Developing Applications Rapidly – Appendixes – Help.

Unit:3	Photoshop	6 hours

Introduction to Photoshop- An Overview of Adobe Photoshop - What's New in Photoshop - Looking at the Work Area - Getting Images into Photoshop and ImageReady - Working with Color - Producing Consistent Color (Photoshop) - Making Color and Tonal Adjustments - Selecting - Transforming and Retouching - Drawing - Painting - Using Channels and Masks - Using Layers - Applying Filters for Special Effects - Using Type - Designing Web Pages - Creating Rollovers and Animations (ImageReady) - Preparing Graphics for the Web - Saving and Exporting Images - Printing (Photoshop) - Automating Tasks - Macintosh Shortcuts - Windows Shortcuts – Help.

Unit:4	Cascading Style Sheets	6 hours

Introduction to Cascading Style Sheets - Types of CSS - CSS Selectors - CSS Properties - Type Properties - Background Properties - Realtime Implementation - CSS Menu Design (Horizontal, Vertical) - Form Designing. F**lash** : Introduction to flash - Animation - Getting started overview - System requirements for Flash authoring - System requirements for the Flash Player - Installing Flash - Components - Properties Layers - timeline - Tools - Scene - Size - Framerate – Background.

Unit:5	SwiSHmax	6 hours

Introduction - What's New in SwiSHmax - Getting Started - Sample SWiSH Movies - Fundamentals - Movies - Templates - Scenes - Timeline and Frames. Web Hosting: Web Hosting Basics - Types of Hosting Packages - Registering domains - Defining Name Servers - Using Control Panel - Creating Emails in Cpanel - Using FTP Client - Maintaining a Website.

Unit:6	Contemporary Issues	2 hours

Expert lectures, online seminars – webinars

	Total Lecture hours	30 hours

Reference Book(s)	
1	Jon Duckett, “Beginning HTML, XHTML, CSS, and JavaScript”, Wrox, 2019.
2	David Sawyer McFarland, “Dreamweaver CS3: The Missing Manual”, O'Reilly Media, 2007.
3	Scott Kelby, “The Adobe Photoshop CS5 Book for Digital Photographers”, Peachpit Press; First edition, 2010.
4	James English, “Macromedia Flash 8: Training from the Source”, Macromedia Press, 2011.
5	Donna L. Baker and Donna Baker,“Official SWiSHmax Bible”, Wiley, 2019.
Course Designed By: Dr. N. Jeyakumar	

VALUE-ADDED COURSE

S.No	Course code	Title of the Course	Total Hours	Credits
1.	VA1	Communication Skills Enhancement	15	2
2.	VA2	Soft Skills Development	15	2
3.	VA3	Journal Seminar and Aptitude Skills	15	2
4.	VA4	Project Proposal Writing Skills	15	2

Value Added Course

Title of the course:

COMMUNICATION SKILLS ENHANCEMENT

Course Code: VA1 **No. of Credits: 2**

Total hours: 15

Objectives of the course:

This course is designed to aid candidates in their preparation for recruitment and will enable students to be a better professional through effective communication. Students will learn skills to present themselves in an effective manner while facing interviews for placements.

Course Contents:

- Effective Communication Skills
- Reasoning Ability
- Verbal Ability
- Group Discussion
- Team communication
- Personal Grooming
- Personality Development
- Resume Writing Skills
- Interview Techniques

Methods of Instruction

Lecture, Class discussion, Role plays, Guest speakers, Written assignments, Videos

Title of the course:

SOFT SKILLS DEVELOPMENT

Course Code: VA2 **No. of Credits: 2**

Total hours: 15

Objectives of the course:

This course is designed to develop a wide variety of soft skills starting from communication, to developing emotional sensitivity, learning creative and critical decision making, developing awareness of how to work with and negotiate with people and to resolve stress and conflict in ourselves and others.

Course Contents:

- Public Speaking and Extempore speaking
- Assertiveness and self confidence
- Intepersonal Skills
- Basic Book keeping skills
- Leaderstip and influence
- Writing skills
- Developing key traits - Creativity, critical thinking and problem solving

Methods of Instruction

Lecture, Class discussion, Role plays, Guest speakers, Written assignments, Videos

Title of the course:

JOURNAL SEMINAR AND APTITUDE SKILLS

Course Code: VA2 **No. of Credits: 2**

Total hours: 15

Objectives of the course:

This course is designed to encourage the students to use various teaching aids such as over head projectors, power point presentation and demonstrative models. Students will learn skills in quantitative and verbal ability, data interpretation, logical reasoning and other abilities required while facing interviews as well as competitive exams.

Course Contents:

- **Seminar Presentation skills:** Preparing the Contents, Speaking Skills, Essentials for Dynamic Presentations and Speeches, Maintain confidence and handle nerves.
- **Verbal Ability**: English grammar, sentence completion, verbal analogies, word groups, critical reasoning and verbal deduction.
- **Numerical Ability**: Ratio and proportion, Permutation and Combination, Probability, Odd man out series, Time & work, Time-Speed & Distance, etc
- **Numerical reasoning and data interpretation:** Blood Relationships, Coding and Decoding, Cubes and Dices, Line graph, tables, Bar graph and Pie-chart.

Methods of Instruction

Lecture, Class discussion, Role plays, Guest speakers, Written assignments, Videos

Title of the course:

PROJECT PROPOSAL WRITING SKILLS

Course Code: VA4 **No. of Credits: 2**

Total hours: 15

Objectives of the course:

This course is designed to assist students in the completion of their research paper or final project. Students will acquire the skills and guidance in the final completion of the research paper/proposal and to prepare students for the oral defense. Students will be able to conduct academic research in the specific area of interest by collecting original data and analyzing the data to draw conclusions, reviews the literature on the topic, and the depth of knowledge in that discipline is enhanced and academic skills in writing and research are refined.

Course Contents:

- Introduction to the Research Process and determining a plausible study;
- Identifying Appropriate Research Problems;
- Writing the problem statement and Hypotheses;
- Reviewing the Literature and working with databases;
- Introduction Section of a Proposal – components, format
- Writing in a technical manner - APA Style; Review of literature,
- Planning a Study: Decisions on design, validity and reliability.
- Methodology –methods of collecting qualitative data,
- Analyzing the data and Finalizing the Proposal.

Methods of Instruction

Lecture, Class discussion, Role plays, Guest speakers, Written assignments, Videos

Annexure

M. Sc. Bioinformatics

Syllabus
(With effect from 2021)

Program Code:

DEPARTMENT OF BIOINFORMATICS
Bharathiar University
(A State University, Accredited with "A" Grade by NAAC and 13th Rank among Indian Universities by MHRD-NIRF)
Coimbatore 641 046, INDIA

BHARATHIAR UNIVERSITY: COIMBATORE 641046
DEPARTMENT OF BIOINFORMATICS

MISSION

Promote bioinformatics teaching, training and research in excellence
Contribute to biotech and pharma industrial development as per global standards