THIRUVALLUVAR UNIVERSITY

SERKKADU, VELLORE–632115

M.SC., BIOINFORMATICS

SYLLABUS

FROM THE ACADEMIC YEAR

2023 – 2024

Programme	**M.Sc. BIO - INFORMATICS**
Programme Code	
Duration	**2 years for PG**
Programme Outcomes (Pos)	**PO1: Problem Solving Skill** Apply knowledge of Management theories and Human Resource practices to solve business problems through research in Global context. **PO2: Decision Making Skill** Foster analytical and critical thinking abilities for data-based decision-making. **PO3: Ethical Value** Ability to incorporate quality, ethical and legal value-based perspectives to all organizational activities. **PO4: Communication Skill** Ability to develop communication, managerial and interpersonal skills. **PO5: Individual and Team Leadership Skill** Capability to lead themselves and the team to achieve organizational goals. **PO6: Employability Skill** Inculcate contemporary business practices to enhance employability skills in the competitive environment. **PO7: Entrepreneurial Skill**

	Equip with skills and competencies to become an entrepreneur. **PO8: Contribution to Society** Succeed in career endeavors and contribute significantly to society. **PO 9 Multicultural competence** Possess knowledge of the values and beliefs of multiple cultures and a global perspective. **PO 10: Moral and ethical awareness/reasoning** Ability to embrace moral/ethical values in conducting one's life.
Programme Specific Outcomes **(PSOs)**	**PSO1 – Placement** To prepare the students who will demonstrate respectful engagement with others' ideas, behaviors, beliefs and apply diverse frames of reference to decisions and actions. **PSO 2 - Entrepreneur** To create effective entrepreneurs by enhancing their critical thinking, problem solving, decision making and leadership skill that will facilitate startups and high potential organizations. **PSO3 – Research and Development** Design and implement HR systems and practices grounded in research that comply with employment laws, leading the organization towards growth and development.

	PSO4 – Contribution to Business World To produce employable, ethical and innovative professionals to sustain in the dynamic business world. **PSO 5 – Contribution to the Society** To contribute to the development of the society by collaborating with stakeholders for mutual benefit.

Template for P.G., Programmes

Semester–I	Credit	Hours	Semester-II	Credit	Hours	Semester-III	Credit	Hours	Semester–IV	Credit	Hours
1.1. Core-I	4	5	2.1. Core-IV	5	6	3.1. Core-VII	5	6	4.1. Core-XI	5	6
1.2 Core-II	4	5	2.2 Core-V	5	6	3.2 Core-VIII	5	6	4.2 Core-XII	5	6
1.3 Core – III	4	6	2.3 Core – VI	4	6	3.3 Core – IX	5	6	4.3 Project with viva voce	7	10
1.4 Discipline Centric Elective -I	3	5	2.4 Discipline Centric Elective – III	3	4	3.4 Core – X	4	6	4.4Elective - VI (Industry / Entrepreneurship) 20% Theory 80% Practical	3	4
1.5 Generic Elective-II:	3	5	2.5 Generic Elective -IV:	3	4	3.5 Discipline Centric Elective - V	3	3	4.5 Skill Enhancement course / Professional Competency Skill	2	4
Value added course I	2	4	2.6 NME I	2	4	3.6 NME II	2	3	4.6 Extension Activity	1	
						3.7 Internship/ Industrial Activity	2	-			
	20	**30**		**22**	**30**		**26**	**30**		**23**	**30**
Total Credit Points -91											

Choice Based Credit System (CBCS), Learning Outcomes Based Curriculum Framework (LOCF) Guideline Based Credits and Hours Distribution System for all Post – Graduate Courses including Lab Hours

First Year – Semester – I

Part	List of Courses	Credits	No. of Hours
	Core – I	4	5
	Core – II	4	5
	Core – III	4	6
	Elective – I	3	5
	Elective – II	3	5
	Value Added Course I	2	4
		20	**30**

Semester-II

Part	List of Courses	Credits	No. of Hours
	Core – IV	5	6
	Core – V	5	6
	Core – VI	4	6
	Elective – III	3	4
	Elective – IV	3	4
	Skill Enhancement Course [SEC] - I	2	4
		22	**30**

Second Year – Semester – III

Part	List of Courses	Credits	No. of Hours
	Core – VII	5	6
	Core – VIII	5	6
	Core – IX	5	6
	Core (Industry Module) – X	4	6
	Elective – V	3	3
	Skill Enhancement Course - II	2	3
	Internship / Industrial Activity [Credits]	2	-
		26	**30**

Semester-IV

Part	List of Courses	Credits	No. of Hours
	Core – XI	5	6
	Core – XII	5	6
	Project with VIVA VOCE	7	10
	Elective – VI (Industry Entrepreneurship)	3	4
	Skill Enhancement Course – III / Professional Competency Skill	2	4
	Extension Activity	1	-
		23	**30**

Total 91 Credits for PG Courses

M.Sc. Bioinformatics
The Course of Study and the scheme of evaluation
Choice Based Credit System

C-Credits, **H**- hours of instruction/week, **Ex**-Exam Hours,
IA- Internal Assessment Marks, **ES**-End Semester Marks, **T**-Total Marks

Subject Type	Title of Course	C	H	Ex	IA	ES	T
SEMESTER I							
Core Course I	Introduction to Bioinformatics	4	5	3	25	75	100
Core Course II	Programming in Linux, C++ and Perl	4	5	3	25	75	100
Core Course III	Cell and Molecular Biology	4	6	3	25	75	100
Generic/Department specific Elective Course (G/DSEC) I	Choose from the list below 1. Immuno informatics 2. Cheminformatics	3	5	3	25	75	100
Generic / Department specific Elective Course (G/DSEC) II	Choose from the list below 1.Structural Bioinformatics 2. Network Biology and visualisation	3	5	3	25	75	100

SEMESTER - I

COURSE	TITLE	CREDITS	HOURS / WEEK	TOTAL TEACHING HOURS
Core I	**Introduction to Bioinformatics**	**4**	**5**	**65**

OBJECTIVES OF THE COURSE

- To provide an integrative approach to the understanding of both theory and practice of bioinformatics
- To apply biological concepts at different levels to study gene / protein analysis, and the proteins implicated in diseases
- To understand the evolution of the life

COURSE LEARNING OUTCOMES

On successful completion of the course, students will be able to

COs	Description	CL
CO1	Recognize and relate the biological databases, tools and softwares to be used in the field of Bioinformatics	K1
CO2	Perceive the different databases, fundamental tools in bioinformatics and infer the required information and acquire hands on practice	K2
CO3	Compare and identify the differences in sequences and structure	K3
CO4	Perform a complete analysis of the genes and protein	K4
CO5	Apply the knowledge obtained from gene and protein sequence analysis to other clinical conditions	K5, K6

UNIT	CONTENT	Hrs	CO
1	**Basics of Bioinformatics** Introduction to Bioinformatics; Computers in Biology to understand Biological System; Concept of open resources in Bioinformatics. Biological databases – NCBI, NCBI, EBI, CMBI, OMIM	12	CO 1-5
2	**Introduction to Biological Databases** Type of Databases, Public Biological Databases –. Primary Nucleotide Sequence Databases: EMBL, GenBank, DDBJ, Secondary Nucleotide Sequence Databases: UniGene, SGD. Sequence Submission Methods	13	CO 1-5

	and Tools (Sequin, Sakura, Bankit), Sequence Retrieval Systems (Entrez & SRS); Sequence File Formats and Conversion Tools. Finding Scientific Articles using Pubmed.		
3	**Introduction to Sequence Alignment** Protein and nucleotide alignment, Homology, Similarity, Identity, Pairwise alignments: Dot Plots, Scoring Matrix-PAM, BLOSUM, Gap Penalty, Dynamics programming - Alignment Algorithms: Global Sequence Alignment: Needleman-Wunch Algorithm. Local Sequence Alignment: Smith –Waterman Algorithm. Rapid, Heuristic Versions of Smith Waterman: FASTA, Basic Local Alignment Search Tool, BLAST Search Steps, Search Strategy, E Value, Raw Scores and Bit Scores, Ensembl BLAST, TIGR BLAST, PSI-BLAST- Practical and theory	15	CO 1-5
4	**Multiple Sequence Alignment and phylogeny** Definition of Multiple Sequence Alignment. Tools of Multiple Sequence Alignment Programs, Clutsal, Phylip, MAFT. Hidden markov models. Evolutionary analysis, Relationship of Phylogenetic Analysis to Sequence Alignment, Genome Complexity. Bootstrap, Tree construction Methods. Neighbor-Joining Method, Unweighted Pair Group Method with Arithmetic Mean (UPGMA), Character based methods: Maximum Parsimony Method and Maximum-Likelihood Method	15	CO 1-5
5	**Specialised databases** Literature databases and biomedical databases – pubmed, OMIM, Metabolic database- KEGG, Metacyc, reactome, Protein domain and motif prediction. Databases and tools to infer STS, EST, CDS, ORF, Domains and motifs- Interpro, Prosite. Protein structure databases - CATH, SCOP, Homologs, paralogs, xenologs, orthologs, COG.	5	CO 1-5
Self study	Concepts from ASRB-NET Bioinformatics related to this course can be discussed and taught	5	

BOOKS FOR STUDY

- Richard Blum, Linux Command Line and Shell Scripting Bible, 3rd Edition, Wiley, 816
- Pevsner, Jonathan. Bioinformatics and Functional Genomics. USA: John Wiley,2009.
- Baxevanis, Andreas, D. and Francis B.F. Ouellette, Bioinformatics- A Practical Guide to the Analysis of Genes and Proteins. NewYork: John Wiley, 2004.
- David W.Mount. Bioinformatics Sequence and Genome Analysis. :CBS Publishers,2003.

BOOKS FOR REFERENCE:

- Baldi, P. and Brunak, S. Bioinformatics: Machine Learning Approach.USA: MIT Press, 2003.
- Chen and Yi-Ping Phoebe. Bioinformatics Technologies. Germany: Springer, 2005.
- Durbin, R., S. Eddy, A. Krogh and G. Mitchison. Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. USA: Cambridge University Press, 2005.
- Higgins, Des and Willie Taylor. Bioinformatics –Sequence, Structure and Databanks – Practical Approach. London: Oxford University Press, 2001.
- Lesk, Arthur M. Introduction to Bioinformatics. UK: Oxford University Press, 2014.

JOURNALS

BMC Bioinformatics
Bioinformatics
Journal of Bioinformatics and Computational Biology
Journal of Biomedical Informatics
Journal of Integrative Bioinformatics

WEB RESOURCES

http://bioinformaticsweb.net/tools.html
https://www.bits.vib.be/index.php/training/122-basic-bioinformatics
http://bioinformaticssoftwareandtools.co.in/
http://www.genscript.com/tools.html

	POs						PSOs		
	1	2	3	4	5	6	1	2	3
CLO1	3	2	3	2	1	3	3	3	2
CLO2	1	1	2	2	2	2	1	2	2
CLO3	2	2	2	1	3	3	1	3	3
CLO4	3	3	3	3	3	3	1	3	3
CLO5	3	3	3	3	3	3	2	3	3
Weightage	12	11	13	11	12	14	8	14	13
Weighted percentage of Course Contribution to	2.4	2.2	2.6	2.2	2.4	2.8	1.6	2.8	2.6

PSOs									

Method of Evaluation

Internal Assessment			End semester exams	Total
Test 1	**Test 2**	**Other components (Seminars/quiz/assignments)**		
10	10	5	75	100

Methods of assessment:

Recall (K1) - Simple definitions, MCQ, Recall steps, Concept definitions.

Understand/ Comprehend (K2) - MCQ, True/False, Short essays, Concept explanations, short summary or overview.

Application (K3) - Suggest idea/concept with examples, Solve problems, Observe, Explain.

Analyse(K4) – Problem-solving questions, Finish a procedure in many steps, Differentiate between various ideas.

Evaluate (K5) - Longer essay/ Evaluation essay, Critique or justify with pros and cons

Create (K6) – Check knowledge in specific or offbeat situations, group discussions.

COURSE	TITLE	CREDITS	HOURS / WEEK	TOTAL TEACHING HOURS
Core II	**Programming in Linux/Unix, C++ and Perl**	**4**	**5**	**65**

OBJECTIVES OF THE COURSE

- To facilitate the students in gaining programming skills with both linux and windows operating systems.
- To enable the students to design and execute C++ and Perl scripts
- To interpolate biological demands through programming

COURSE LEARNING OUTCOMES

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

COs	Description	CL
1	Recognize and recall the basics of programming in biology	K1, K2
2	Relate the necessity of using Linux based operating systems	K3,K4
3	Access biological concepts with C++ and Perl scripts	K4
4	Apply programing to analyse genomic sequences and process them	K5, K6
5	Utilise the BioPerl knowledge to solve complex problems in Bioinformatics	K5, K6

UNIT	CONTENT	Hrs	CO
1	**Introduction to Programming language and Linux/Unix** Machine/Assembly Language, Higher Level Languages. Operating systems - Windows and Linux/Unix. Properties of Linux/Unix, Desktop Environment, Linux basics commands. Working with Files, Text Editors, I/O Redirections, Pipes, Filters, and Wildcards. Changing Access Rights. Bash scripting, loops, text mining, Awk, sed and grep. Editors- vim, nano, gedit.	12	CO 1-5
2	**Introduction to C++** Simple and Compound Data, Code: Syntax and Semantics, Programming in C++: C++ Characteristics, Tokens, Keywords, Identifiers and Constants, Basic Data Types, User Defined Data Types, Derived Data Types, Expressions and Control Structures, Functions and Variables: Scope, Declaration and Definition, Arrays and Strings in C++.	13	CO 1-5
3	**Object Oriented Programming**		

	Using Objects, Classes, Encapsulation, Inheritance, Abstraction and Polymorphism. Friend functions, String and file operations– creating string objects, Standard Streams – string and Files, Open, close, EOF, updating files and error Handling, String manipulation- String operators Manipulating String, String characteristics, Comparing and Swapping.	10	CO 1-5
4	**Introduction to Perl Programming** Introduction, Statements and Declarations, Default Variable, Expressions, Statements, Operators in Perl, Control Structures, Variable Types and Data types– Scalar, Arrays, Hashes. Functions- split, join, length, lcfirst, ucfirst, index and exists, Creating Regular Expressions- Characters, Character Classes, Alternative Match Patterns, Quantifiers, Assertions, Back References, Modifiers and Translator. Subroutines.	13	CO 1-5
5	**File Handling and Bioperl** Files- Overview and working with File handles, Closing the files, printing, renaming files, Various Ways of Opening a Perl File Handles. **Bioperl** Introduction to Bioperl: Installation Procedures, Architecture, Uses of Bioperl, Modules of bioperl- seq, seqio, alignio, db, Modules of Bioperl – Annotation, location, tools - practical	12	CO 1-5
Self study	Concepts from ASRB-NET Bioinformatics related to this course can be discussed and taught	5	

BOOKS FOR STUDY

- E. Balagurusamy. *Object Oriented Programming with C++*. New Delhi: Tata McGraw-Hill, 2017.
- Tisdall James D. *Beginning Perl for Bioinformatics.* USA: O'Reilly and Associates, 2014.
- Jason Cannon, Linux for Beginners: An Introduction to the Linux Operating System and Command Line, 1st edition, 204 pages.

BOOKS FOR REFERENCE

- Conrod Bessant, Ian Shadforth and Darren Oakley. *Building Bioinformatics Solutions with Perl, R and MySQL***.** New York: Oxford University Press, 2014.
- Bjarne, Stroustrup. *The C++ Programming Language*. India: Addison Wesley, 2013.
- Holzner and Steven. *Perl Black Book*. India: Dream Tech Press, 2006.
- Hubbard, John. *Programming with C++, Schaum's Outline Series*. New Delhi: Tata McGraw Hill, 2003.

- Tisdall James D. *Beginning Perl for Bioinformatics.* USA: O'Reilly and Associates, 2003.
- Ellen Siever, Weber, Stephen Figgins, Robert, Arnold Robbins *Linux in a Nutshell-ADesktop Quick Reference.* USA: O'Reilly and Associates, 2006
- Sanjeev Sofat. *Object Oriented Programming Using C++,* India : Cyber Tech. Publication, 2009.

JOURNALS

C/C++ Users Journal

International Journal of Computer Applications

Computer Methods and Programs in Biomedicine

Perl in communities

WEB RESOURCES

http://www.cplusplus.com/doc/tutorial/

http://www.cprogramming.com/

http://www.stroustrup.com/4th.html

	POs						PSOs		
	1	2	3	4	5	6	1	2	3
CLO1	1	3	1	3	1	3	1	3	2
CLO2	3	1	2	1	2	2	1	3	2
CLO3	3	2	2	2	2	3	3	3	3
CLO4	3	3	3	3	3	3	3	3	3
CLO5	3	3	3	3	3	3	3	3	3
Weightage	14	12	11	12	11	14	11	15	13
Weighted percentage of Course Contribution to PSOs	2.8	2.4	2.2	2.4	2.2	2.8	2.2	3	2.6

Method of Evaluation

Internal Assessment			**End semester exams**	**Total**
Test 1	**Test 2**	**Other components (Seminars/quiz/assignments)**		
10	10	5	75	100

Methods of assessment:

Recall (K1) - Simple definitions, MCQ, Recall steps, Concept definitions.

Understand/ Comprehend (K2) - MCQ, True/False, Short essays, Concept explanations, Finding errors from the script.

Application (K3) - Suggest idea/concept with examples, Write a code to solve biological problems, Observe, Explain.

Analyse(K4) – Problem-solving questions, Finish a procedure in many steps, Differentiate between various ideas.

Evaluate (K5) - Longer essay/ Evaluation essay, Critique or justify with pros and cons/ writing codes and scripts

Create (K6) – Check knowledge in specific or offbeat situations, group discussions.

COURSE	TITLE	CREDITS	HOURS / WEEK	TOTAL TEACHING HOURS
Core III	**Cell and Molecular Biology**	**4**	**6**	**65**

OBJECTIVES OF THE COURSE

- To understand the general principles of gene organisation and expression
- To explore various levels of gene regulation and protein function
- To analyse various genetic and molecular changes that occur in a normal cell

COURSE LEARNING OUTCOMES

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

COs	Description	CL
CO1	Grasp the functions of the prokaryotic and eukaryotic cell and cell cycle mechanisms at the molecular level	K1
CO2	Explore and analyse the structural organisation of genes and the control of gene expression	K2
CO3	Interpret the significance of central dogma of life	K3
CO4	Appreciate the molecular mechanisms involved in cancer signalling	K4
CO5	Link the concepts of cell and molecular biology to a better understanding of diseases, including cancer	K5, K6

UNIT	CONTENT	Hrs	CO
1	**Cellular Organisation** Prokaryotic and Eukaryotic cell - Characteristics, Membrane structure and function - lipid bilayer, osmosis, ion channels, active transport, membrane pumps, Structural organisation and function of intracellular organelles, Cell division - Mitosis and meiosis, Cell cycle regulation, Check points.	12	CO 1-5
2	**Structural organisation of Chromosomes and Genes** DNA-Structure and Conformations, Chromosomes – Functions, Organisation of Genomes - Coding Sequences, Repetitive Sequences, transposons, Mitochondria and Chloroplast Genome - Organisation and Function, Bacteria - Cells structure and bacterial genetics, Virus - Structure, Viral genome, Viroids and Prions.	15	CO 1-5

3	**Replication and Transcription** DNA replication, Mutations, DNA damage and repair mechanisms in prokaryotes and eukaryotes, Transcription- Transcriptional Control by Regulatory Proteins, RNA polymerases, Post Transcriptional Regulation - DNA Methylation, Histone Modification, - capping, RNA editing, splicing, and polyadenylation.	10	CO 1-5
4	**Translation** RNA- Types, structure and functions,Ribosomes – Structure and Assembly, Translational Regulation - Regulation of gene expression in Prokaryotes (Operon) and Eukaryotes, Genetic code, Gene Silencing, Post-translational modification of proteins.	10	CO 1-5
5	**Cell Signalling and Cancer** Cell signalling – Signalling molecules, Receptors - Hormones receptors, cell surface receptor, G-protein coupled receptors, signal transduction pathways, Cancer Biology- Characteristics and genetic basis of cancers, Proto-oncogene, Oncogenes, Tumour Suppressor Genes, Oncogenesis - Cancer Immunotherapy, Regulation of Cell Death, Apoptosis.	13	CO 1-5
Self study	Concepts from CSIR NET (lifesciences) and ASRB-NET Bioinformatics related to this course can be discussed and taught	5	

BOOKS FOR STUDY

- Harvey Lodish, Arnold Berk, Chris A. Kaiser, Monty Krieger, Anthony Bretscher, Hidde Ploegh. *Molecular Cell Biology.* USA: W. H. Freeman, Eighth edition, 2016.
- Wolfe, Stephen L. *Molecular and Cellular Biology.* USA: Wadsworth, 2005.
- Watson, James, D. *Molecular Biology of the Gene***.** USA: The Benjamin Cummings Publishing Company, 2007.

BOOKS FOR REFERENCE

- Cooper, Geoffrey M. and Robert E. Hausman**.** *The Cell, A Molecular Approach***.** USA: Sinauer Associates, 2004.
- Harvey Lodish, Arnold Berk, Chris A. Kaiser, Monty Krieger, Matthew P. Scott, Anthony Bretscher, Hidde Ploegh and Paul Matsudaira. *Molecular Cell Biology.* USA: W.H.freeman, 2008.
- Watson, James, D. *Molecular Biology of the Gene***.** UK: Pearson, Seventh edition, 2017.
- Darnell, James, Harvey Lodish and David Baltimore. *Molecular and Cell Biology*, Scientific American Books, USA: W.H. Freeman, 2004.
- Karp and Gerald. *Cell and Molecular Biology- Concepts and Experiments*, USA: John Wiley, 2013.
- Lewin and Benjamin. *Genes IX*, UK: Oxford University Press, 2009.

- Roitte, Ivan M., Brostoff, Jonathan and Male, David K. *Immunology.* Philadelphia: J.B. Lippincott, 1990.
- Purvis, William K, David Sadava, Craig Heller and Gordan H. Orians. *Life: The Science of Biology.* USA: Sinauer, 2004.

JOURNALS

Journal of Molecular Biology

Molecular Biology

Journal of Genetics and Genomics

BMC Cell Biology

WEB SOURCES

www.cellbio.com

www.molbiolcell.org

www.sciencedirect.com

http://www.nature.com/scitable/topic/cell-biology-13906536

http://www.biology.arizona.edu/cell_bio/cell_bio.html

http://ghr.nlm.nih.gov/

	POs						PSOs		
	1	2	3	4	5	6	1	2	3
CLO1	1	2	1	1	2	3	1	1	3
CLO2	2	2	3	2	1	2	2	2	3
CLO3	3	3	3	3	3	2	2	3	3
CLO4	3	1	2	3	2	3	2	2	3
CLO5	3	2	3	2	3	2	3	2	3
Weightage	13	10	13	11	11	12	10	10	15
Weighted percentage of Course Contribution to PSOs	2.6	2	2.6	2.2	2.2	2.4	2	2	3

Method of Evaluation

Internal Assessment			**End semester exams**	**Total**
Test 1	**Test 2**	**Other components (Seminars/quiz/assignments)**		
10	10	5	75	100

Methods of assessment:

Recall (K1) - Simple definitions, MCQ, Recall steps, Concept definitions.

Understand/ Comprehend (K2) - MCQ, True/False, Short essays, Concept explanations, short summary or overview.

Application (K3) - Suggest idea/concept with examples, Solve problems, Observe, Explain.

Analyse(K4) – Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

Evaluate (K5) - Longer essay/ Evaluation essay, Critique or justify with pros and cons

Create (K6) – Check knowledge in specific or offbeat situations, group discussions.

COURSE	TITLE	CREDITS	HOURS / WEEK	TOTAL TEACHING HOURS
Generic DESC I Elective	**Immunoinformatics**	**3**	**5**	**65**

OBJECTIVES OF THE COURSE

- To be familiar with the use of a wide variety of internet applications and biological database
- To understand the immune system, its components and their functions
- To impart knowledge of immune responses to various pathogens by integrating genomics and proteomics with bioinformatics strategies
- To provide information about the methods used in immunological bioinformatics
- To understand the application of information technology to immunology

COURSE LEARNING OUTCOMES

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

Cos	Description	CL
1	Understand the application of information technology to immunology	K1, K2
2	Understand informatics-based approaches for prediction of epitopes and immuno-diagnostic tools	K2
3	Apply the immunological data and to the sophisticated computational solutions available for immunological research	K3
4	Emphasise the application of bioinformatics and biological databases to problem solving in real research problems	K4
5	Comprehend knowledge about computer aided vaccine design and reverse vaccinology	K5, K6

UNIT	CONTENT	Hrs	CO
1	**Immune System** Introduction to Immune System - Adaptive and Innate Immunity. Cells of the Immune System, Soluble Mediators of Immunity, Cell and Antibody mediated immunity. Immune Responses - Inflammation, Immunopathology, Autoimmune diseases, Vaccines	7	CO 1-5
2	**Antigens and Antibodies** Immunoglobulin classes and subclasses, Major Histocompatibility Complex (MHC) its Polymorphism, Causes for Polymorphism, MHC Supertypes. Antigen types – Epitope, Affinity Maturation, Epitope mapping. B-cell and T-cell Epitope Prediction, Recognition of Antigen by B cells. Neutralising Antibody.	8	CO 1-5

3	**Computational Immunology** Computational Immunology **-** Databases in Immunology, dbMHC-MHC database at NCBI. T-cell epitope databases, B-cell epitope databases, SYFPEITHI MHC-presented epitopes. IMGT Immunoinformatics, IMGT International ImMunoGeneTics Information System. HLA Nomenclature and the IMGT/HLA Sequence Database	8	CO 1-5
4	**Vaccine Design** From immunome to Vaccine – Prediction of immunogenicity, Vaccine design tools. Reverse Vaccinology and Immunoinformatics, Peptides with Antimicrobial Activity or Antibiotic Peptides. Functional Prospecting of Genes and Transcripts, Future of Computational Modelling and Prediction Systems in Clinical Immunology.	8	CO 1-5
5	**Viral Bioinformatics** Viral Bioinformatics - Computational Views of Hosts and Pathogens using VIDA. Virus- human protein interaction databases. Virus- NCBI. GISAID database. Virus mint, Virus host database. Viral zone- Expasy	8	CO 1-5

BOOKS FOR STUDY

- Darren R. Flower. *Bioinformatics forImmunomics (Immunomics Reviews).* New York: Springer-Verlag, 2010.
- Abul K. Abbas, Andrew H. H. Lichtman, and Shiv Pillai. *Cellular and Molecular Immunology* USA: Elsevier, 2017.
- Andrew R. Leach, Valerie J. Gillet. *An Introduction to Chemoinformatics*.UK: Springer, 2007.

BOOKS FOR REFERENCE

- Christian Schönbach, ShobaRanganathan, and Vladimir Brusic. *Immunoinformatics (Immunomics Reviews)* USA: Humana Press, 2010.
- Kenneth Murphy. *Janeway's Immunobiology*, UK: Garland Science, 2014.
- Bunin, Barry A. Dordrecht. *Chemoinformatics: Theory, Practice, and Products*.UK: Springer, 2010.
- Malay Das , Liuyin Ma , Amita Pal , Chittaranjan Kole , "Genetics, Genomics and Breeding of Bamboos (Advances in Agri-Genomics) 1st Edition", by CRC Press

JOURNALS

The Pharmacogenomics Journal

Pharmacogenomics and Personalized Medicine
Pharmacogenetics and Genomics
Immunoinformatics
BMC Genomics
Journal of Computational Biology
Chemoinformatics: Concepts, Methods, and Tools for Drug Discovery
International Journal of Chemoinformatics and Chemical Engineering
BMR Bioinformatics & Cheminformatics

WEB RESOURCES

http://www.imgt.org/Immunoinformatics.html
http://rsob.royalsocietypublishing.org/content/3/1/120139
http://ghr.nlm.nih.gov/handbook/genomicresearch/pharmacogenomics
https://www.pharmgkb.org/
http://cheminformatics.org/
http://www.emolecules.com/info/molecular-informatics
https://www.illumina.com/areas-of-interest/agrigenomics.html
https://center-forward.org/genomics-agricultural-innovation/
http://www.pmjournal.ir/

	POs						PSOs		
	1	2	3	4	5	6	1	2	3
CLO1	3	2	2	1	2	3	3	1	2
CLO2	3	2	2	3	1	3	3	1	3
CLO3	3	3	3	3	2	3	3	1	3
CLO4	3	3	3	3	2	3	3	1	3
CLO5	3	3	3	3	3	3	3	1	2
Weightage	15	13	13	14	10	15	15	5	13
Weighted percentage of course contribution to PSOs	3	2.6	2.6	2.8	2	3	3	1	2.4

Method of Evaluation

Internal Assessment			**End semester exams**	**Total**
Test 1	**Test 2**	**Other components (Seminars/quiz/assignments)**		
10	10	5	75	100

Methods of assessment:

Recall (K1) - Simple definitions, MCQ, Recall steps, Concept definitions.

Understand/ Comprehend (K2) - MCQ, True/False, Short essays, Concept explanations, short summary or overview.

Application (K3) - Suggest idea/concept with examples, Solve problems, Observe, Explain.

Analyse(K4) – Problem-saving questions, Finish a procedure in many steps, Differentiate between various ideas.

Evaluate (K5) - Longer essay/ Evaluation essay, Critique or justify with pros and cons

Create (K6) – Check knowledge in specific or offbeat situations, group discussions.

COURSE	TITLE	CREDITS	HOURS / WEEK	TOTAL TEACHING HOURS
Generic DESC I Elective	**Cheminformatics**	**3**	**5**	**65**

OBJECTIVES OF THE COURSE

- To introduce the basic concepts of using chemical structure databases
- To apply the concepts and learn the use of Cheminformatics tools
- To understand the applications of Cheminformatics in drug design

COURSE LEARNING OUTCOMES

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

COs	Description	CL
1	Gain skills to analyse the properties of small molecules	K1, K2
2	Design the biological targets and properties of the small molecule under investigation	K3,K4
3	Better understanding of the drug discovery and development process	K4
4	Apply the concepts to create novel leads	K5
5	Compare the molecular data with drugs to predict therapeutic lead molecules	K6

UNIT	CONTENT	Hrs	CO
1	**Introduction** Introduction to Cheminformatics, History and Evolution of Cheminformatics, Use of Cheminformatics, Prospects of Cheminformatics. Databases: Chemical Structure Databases (PubChem, Drug bank). Modelling of small molecules and Structure Elucidation	8	CO 1-5
2	**Representation of Molecules** Representation of Molecules and Chemical Reactions. Different Types of Notations, SMILES Coding, Structure of Mol files and Sdf files (Molecular converter, SMILES Translator). Similarity Search of the Molecule	8	CO 1-5
3	**Cheminformatics databases** Structure databases; Reaction Databases; Literature Databases; Medline; GenBank. PIR; CAS Registry; National Cancer Institute (NCI) Database. Databases of Small Molecules (ZINC), pubchem,	7	CO 1-5

	chemspider.		
4	**Searching Chemical Structure** Searching Chemical Structure: Full Structure Search; SubStructure Search; Similarity Search. Three dimensional Search Methods. Structure Visualisation. Drawing the Chemical Structure: 2D and 3D Drawing Tools (ACD Chemsketch) Structure Optimization	8	CO 1-5
5	**Cheminformatics in drug design** Definition of drugs, Structure-Based Drug Design, QSAR. Pharmacophore Design, Ligand-Based Design, De Novo Drug Design Virtual Screening / Docking of Ligands. Protein structure-Fragment-Based Drug Design, ADMET Prediction.	8	CO 1-5

BOOKS FOR STUDY

- Johann Gasteiger and Thomas Engel. *Chemoinformatics -A Textbook*. Germany: Wiley-VCH, 2003.
- Johann Gasteiger. *Handbook of Chemoinformatics-From Data to Knowledge,* Germany: Wiley-VCH, 2003.

BOOKS FOR REFERENCE

- Andrew R. Leach, Valerie J. Gillet. *An Introduction to Chemoinformatics*.UK: Springer, 2007.
- Bunin, Barry A. Dordrecht. *Chemoinformatics: Theory, Practice, and Products*.UK: Springer, 2010.
- Bajorath, Juergen,Totowa, N.J. *Chemoinformatics: Concepts, Methods, and Tools for Drug Discovery.* USA: Humana Press, 2004.
- Ekins, Sean, Hoboken, N.J. Computer *Applications in Pharmaceutical Research and Development.*Germany: Wiley, 2006.

JOURNALS

Journal of Cheminformatics
Chemoinformatics: Concepts, Methods, and Tools for Drug Discovery
International Journal of Chemoinformatics and Chemical Engineering
BMR Bioinformatics & Cheminformatics
The Journal of Chemical Information and Modeling

WEB RESOURCES

http://cheminformatics.org/
http://www.emolecules.com/info/molecular-informatics
http://accelrys.com/products/informatics/cheminformatics/

http://www.rasalsi.com/services_drugdis.html

Method of Evaluation

Internal Assessment			**End semester exams**	**Total**
Test 1	**Test 2**	**Other components (Seminars/quiz/assignments)**		
10	10	5	75	100

	POs						PSOs		
	1	2	3	4	5	6	1	2	3
CLO1	2	3	3	2	1	3	2	1	3
CLO2	3	2	3	3	1	3	2	1	3
CLO3	3	2	3	3	2	2	2	1	3
CLO4	3	3	3	2	2	3	2	1	3
CLO5	3	3	3	3	2	3	2	1	3
Weightage	14	13	15	13	8	14	10	5	15
Weighted percentage of course contribution to PSOs	2.8	2.6	3	2.6	1.6	2.8	2	1	3

Methods of assessment:

Recall (K1) - Simple definitions, MCQ, Recall steps, Concept definitions.

Understand/ Comprehend (K2) - MCQ, True/False, Short essays, Concept explanations, short summary or overview.

Application (K3) - Suggest idea/concept with examples, Solve problems, Observe, Explain.

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Evaluate (K5) - Longer essay/ Evaluation essay, Critique or justify with pros and cons

Create (K6) – Check knowledge in specific or offbeat situations, group discussions.

COURSE	TITLE	CREDITS	HOURS / WEEK	TOTAL TEACHING HOURS
Elective II DESC II	**Structural Bioinformatics**	**3**	**5**	**65**

OBJECTIVES OF THE COURSE

- To develop new ways for analysing biological macromolecular data in order to address biological problems and discover new information
- To understand the factors that influence and determine the function of biological macromolecules
- To create general-purpose methods for manipulating information about biological macromolecules and the application of these methods to solve problems in biology

COURSE LEARNING OUTCOMES

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

Cos	Description	CL
CO1	Recognize the fundamental structural and functional concepts of DNA and RNA molecules	K1
CO2	Demonstrate the relativity and mechanisms of DNA molecules with protein molecules	K2
CO3	Utilise the knowledge on the structure and properties of protein molecules and identify them computationally using variety of tools	K3
CO4	Infer the functions, similarity, structural properties and their interactions in complex with other biological molecules using bioinformatics tools and databases	K4
CO5	Measure the importance of peptides to proteins in the body functions and apply for solving biological problems	K5, K6

Unit	Contents	Hrs	CO1
1	**Introduction**	10	CO

	Introduction to Molecular structures including genes and gene products: protein, DNA, and RNA structure. structure representation, comparison of structures, visualisation, and modelling, DNA sequence and structures- complementarity, Chargaff's rule, other base pairs in sequence, reverse complementarity, palindromic sequences, RNA sequences, types and structures – mRNA, tRNA, rRNA, miRNA, siRNA, circRNA, lncRNA, sg RNAs		1-5
2	**Nucleic acids** DNA – chromosome structure and architecture, Intron-exon boundary, histones, euchromatin, heterochromatin, CpG islands, methylated DNA structures, Computational Structure prediction – RNA Structure determination methods, RNA structural refinement, predicting targets for inhibitory RNAs, Reading frames; Codon Usage analysis; Translational and transcriptional signals, Splice site identification, Gene prediction methods and RNA fold analysis	10	CO1-5
3	**Proteins** Protein sequences and structure fundamentals, Amino acids – types, single letter codes, essential and non-essential amino acids, Protein sequence analysis-Compositional analysis, Hydrophobicity profiles, Amphiphilicity detection, Moment analysis, Transmembrane prediction methods, Protein function prediction, motifs and domains, predicting binding site geometry and evolution. Patterns and fingerprints. Point based and surface based binding site matching, Pattern based search using MeMe and PRATT); Motif-based search using ScanProsite and eMOTIF; Profile-based database searches using PSI-BLAST and HMMer.	15	CO1-5
4	**Structural Properties of Proteins** Protein structure determination - Secondary structure prediction methods – Chou fasman and GOR, tertiary structure prediction - ab initio modelling, threading, fold recognition, Protein-protein and protein-nucleic acid interactions, Protein structure refinement, comparison of structures. Prediction of Coiled coils, Low complexity, non-globular, and disordered regions, Contact prediction, Alternative splicing and protein structure, Target selection for diseases, CATH and SCOP, identification of Extreme	15	CO1-5

	environments, Protein-protein interactions, Protein evolution, Structure-function relationships in proteins, Functionally important residues, Local sequence motifs, Exons and domains, Mutations and their effect on structures		
5	**Peptides and Proteogenomics** Peptide modelling - Signal peptides, natural peptides, Proteome - peptide repositories – PRIDE DB, peptide modelling, epitope and antibody structures, Peptide- protein docking, Databases and tools for identifying protein- peptide interactions, network analysis, Tools and softwares to predict protein-protein and protein-peptide interactions. Protein complex modelling approaches, Proteogenomics - Proteogenomics overview, Phenotype- Genotype, Gene expression, Proteogenomics approach to unravel proteoforms, Sequence centric proteogenomics, ProTIGY.	15	CO1-5
Self study	Concepts from CSIR NET (Lifesciences) and ASRB-NET Bioinformatics related to this course can be discussed and taught	5	

BOOKS FOR STUDY

Jenny Gu, Philip E. Bourne, Structural Bioinformatics, 2nd Ed., 2009. ISBN: 978-0-470-18105-8

BOOKS FOR REFERENCE

Zoltan Gaspari, Structural Bioinformatics, Methods and Protocols, Springer publication, 2020.

Forbes J. Burkowski, Structural Bioinformatics An algorithmic approach, 2009. Taylor and Francis Publication.

JOURNALS

Journal of Structural Biology
BMC Structural Biology
Computational and Structural Biotechnology Journal
Journal of Molecular Biology

WEBSITES

https://ball-project.org/ballaxy/
https://bio.tools/bioinfo3d
https://computomics.com/services/megan6.html

	POs						PSOs		
	1	2	3	4	5	6	1	2	3
CLO1	1	2	1	2	2	3	2	1	3
CLO2	2	2	1	1	1	3	1	1	3
CLO3	3	2	3	3	2	3	3	1	3
CLO4	3	3	3	3	3	3	3	1	3
CLO5	3	3	3	3	3	3	3	1	3
Weightage	12	12	11	12	11	15	12	5	15
Weighted percentage of course contribution to PSOs	2.4	2.4	2.2	2.4	2.2	3	2.4	1	3

Method of Evaluation

Internal Assessment			End semester exams	Total
Test 1	**Test 2**	**Other components (Seminars/quiz/assignments)**		
10	10	5	75	100

Methods of assessment:

Recall (K1) - Simple definitions, MCQ, Recall steps, Concept definitions.
Understand/ Comprehend (K2) - MCQ, True/False, Short essays, Concept explanations, short summary or overview.
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COURSE	TITLE	CREDITS	HOURS / WEEK	TOTAL TEACHING HOURS
Elective DESCII	**Network biology and visualisation**	**3**	**5**	**65**

OBJECTIVES OF THE COURSE

- To describe and express the role and importance of networks in biology
- To facilitate the inclusion of graph theory and networks in disease diagnosis
- To understand the analytical methods available for Network prediction and visualisation

COURSE LEARNING OUTCOMES

On successful completion of the course, students will be able to

COs	Description	CL
CO1	Understand of the basic concepts of graph theory	K1
CO2	Learn available algorithm for creating networks	K2
CO3	Create biological networks from clinical data	K3
CO4	Infer functional association networks	K4
CO5	Justify the use of genome scale networks in clinical settings	K5, K6

Unit	Contents	Hrs	COs
1	Introduction to graph theory, Probabilistic graphical model representation of molecular networks. Bayesian networks. Graphical Gaussian models. Network-based data integration and interpretation. Random walk on the graph. Diffusion on graphs. Graph kernels. Clustering and supervised classification	10	CO 1-5
2	Network theory and algorithms. Network versus matrix representations. Weighted and directed networks. Edges based on "co-citation" and correlation Bipartite networks and hypergraphs. Degree and cluster coefficient. Protein interaction graphs- Spatial interaction analysis (APEX) Residue contact maps. Domain-domain and protein structural interactions	10	CO 1-5
3	Introduction: why biological networks? Molecular networks bridge genotype to phenotype. Networks as the next phase of the Genome	10	CO 1-5

	Project. Types of biological networks Network databases and the NDEx cloud.		
4	Genetic interaction networks. Epistasis versus epistacy; Statistical genetic interactions. Dependency maps and Mutual exclusivity. Epistatic miniarrays Combinatorial CRISPR. Functional association networks (FANs)	10	CO 1-5
5	Genome-scale modelling and network integration. Evolution of molecular networks. Software- cytoscape. Networks as guiding tools. Types of graph alignment problems. Network layout and visualisation. Properties of good visualisations. Force-directed graph layout Eades algorithm. Kamada & Kawaii algorithm. Hyperbolic & spherical layout. Other layouts	15	CO 1-5

BOOKS FOR REFERENCE:

Edited by Narsis A. Kiani, Karolinska Institutet, Stockholm, David Gomez-Cabrero, King's College London, Ginestra Bianconi, Networks of Networks in Biology, 2021,ISBN: 9781108553711, https://doi.org/10.1017/9781108553711, Cambridge University Press

Alpan Raval, Animesh Ray, Introduction to Biological Networks, 2016, ISBN: 9781420010367, Chapman and Hall/CR

JOURNALS

Journal of network biology

Journal of health informatics and network biology

	POs						**PSOs**		
	1	2	3	4	5	6	1	2	3
CLO1	2	1	1	2	2	3	1	3	2
CLO2	2	1	2	1	1	3	1	3	2
CLO3	2	3	2	2	3	2	2	3	3
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CLO5	3	3	3	3	3	3	2	3	3
Weightage	12	11	11	11	12	13	8	14	13
Weighted percentage of Course Contribution to PSOs	2.4	2.2	2.2	2.2	2.4	2.6	1.6	2.8	2.6

Method of Evaluation

Internal Assessment			End semester exams	Total
Test 1	**Test 2**	**Other components (Seminars/quiz/assignments)**		
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