Shiromani Gurdwara Parbandhak Committee's

Guru Nanak Khalsa College of Arts, Science and Commerce (Autonomous)
Matunga, Mumbai – 400 019, Maharashtra

Syllabus for M.Sc. Bioinformatics
Program: Masters of Science
Course: M.Sc. Bioinformatics

(As per Choice Based Semester and Grading System with effect from Academic Year 2021 – 2022)

BIOINFORMATICS

Last two decades have witnessed the emergence of Bioinformatics as a major thrust area in the global scientific scenario. It is the interface between the two most rapidly advancing fields of biological and computational sciences. Bioinformatics is a scientific discipline and asset of skills that has now become one of the most important information gathering, data mining, and knowledge building tools in recent research and clinical applications.

Bioinformatics came out as one of the essential tools to analyze viral data as it provides vital information about the genetic makeup of the virus and also assists directly in the development of drugs or vaccines against the deadly disease.

Bioinformatics is used in personalized medicine to analyze data from genome sequencing or microarray gene expression analysis in search of mutations or gene variants that could affect a patient's response to a particular drug or modify the disease prognosis.

It also utilizes modern computer science that includes cloud computing, statistics, mathematics and even pattern recognition, reconstruction, machine learning, simulation and iterative approaches, and molecular modelling /algorithms.

OBJECTIVES OF THE COURSE

- Develop trained manpower in the field of Bioinformatics with special emphasis on understanding the origins of biological data, as well as how to manipulate them and determine their quality.
- Bridging the gap between data science and biomedicines with the help of bioinformatics to meet the demands and changing trends in bioinformatics Industry.
- Training in Instrumentation, NGS, Sequence analysis, Structural bioinformatics, Drug designing, Docking, MD Simulations, Machine learning, R, Biopython, Artificial Intelligence as a requirements of industry as well as research institute.
- Amalgamate conventional biological sciences with modern genomic and proteomic technologies under branch of NGS and whole genome sequencing.
- Publications in International/National Journals.
- Dissertation Research Projects are completed in collaboration with NIRRH, BARC, IITB, BDG Life Sciences, ACTREC, etc.
- Trained students to participate in Avishkar Competition, conferences & workshops.

M.Sc. Bioinformatics: SYLLABUS IN BRIEF Distribution of Credits

SEMESTER I

Paper	Code	Lectures (h)	Credits earned	Code	Practical (h)	Credits earned
Paper 1: Fundamentals of Biology	GNKPSBI101	60	4	GNKPSBIP101	60	2
Paper 2: Bioinformatics and Sequence Analysis	GNKPSBI102	60	4	GNKPSBIP102	60	2
Paper 3: Biostatistics	GNKPSBI103	60	4	GNKPSBIP103	60	2
Paper 4: Introduction to Programming Languages and Databases	GNKPSBI104	60	4	GNKPSBIP104	60	2
TOTAL		240	16		240	8
TOTAL CREDITS		24				

Paper	Code	Lectures (h)	Credits earned	Code	Practical (h)	Credits earned
Paper 1: Advance Biology	GNKPSBI201	60	4	GNKPSBIP201	60	2
Paper 2: Structural Biology & Bioinformatics	GNKPSBI202	60	4	GNKPSBIP202	60	2
Paper 3: Genomics and Proteomics in Bioinformatics	GNKPSBI203	60	4	GNKPSBIP203	60	2
Paper 4: Basic and Advances Java, Introduction to Linux	GNKPSBI204	60	4	GNKPSBIP204	60	2
TOTAL		240	16		240	8
TOTAL CREDITS		24				

SEMESTER III

Paper	Code	Lectures (h)	Credits earned	Code	Practical (h)	Credits earned
Paper 1: Separation techniques	GNKPSBI301	60	4	GNKPSBIP301	60	2
Paper 2: Cheminformatics & Drug Designing	GNKPSBI302	60	4	GNKPSBIP302	60	2
Paper 3: Immunology and Immunoinformatics	GNKPSBI303	60	4	GNKPSBIP303	60	2
Paper 4: Introduction to Perl and Mongodb	GNKPSBI304	60	4	GNKPSBIP304	60	2
TOTAL		240	16		240	8
TOTAL CREDITS		24				

SEMESTER IV

Paper	Code	Lectures (h)	Credits earned	Code	Practical (h)	Credits earned
Paper 1: Mass Spectroscopy, Research Methodology and Scientific Writing	GNKPSBI401	60	4	GNKPSBIP401	60	2
Paper 2: Molecular Modeling and Simulations	GNKPSBI402	60	4	GNKPSBIP402	60	2
Paper 3: Clinical Research and Clinical Data Management	GNKPSBI403	60	4	GNKPSBIP403	60	2
Paper 4: Python	GNKPSBI404	60	4	GNKPSBIP404	60	2
TOTAL		240	16		240	8
TOTAL CREDITS		24				

SYLLABUS FOR M. Sc. BIOINFORMATICS
DISTRIBUTION OF TOPICS

SEMESTER I	SEMESTER II
GNKPSBI101: Fundamentals of Biology • Cell Biology • Structure of Biomolecules and their Metabolism • Cell – Cell communication and Signal transduction • Enzyme Kinetics	**GNKPSBI201: Advance Biology** • Concept of Central Dogma • Recombinant DNA Technology • Genomics • Molecular Biology Techniques
GNKPSBI102: Bioinformatics and Sequence Analysis • Introduction to Bioinformatics • Biomolecular Databases • Sequence alignment and Algorithms • Molecular Phylogenetics	**GNKPSBI202: Structural Biology & Bioinformatics** • Introduction to Macromolecule Structures and Protein Chemistry • Protein Structure Prediction & Validation • Application of Bioinformatics in Biomolecular Diseases • Introduction to Proteomics and its applications
GNKPSBI103: Biostatistics • Basics of Mathematics • Statistical Measures • Random Variables and Bivariate Distribution • An Introduction to statistical inference	**GNKPSBI203: Genomics and Proteomics in Bioinformatics** • Genome and Genome Sequencing • Functional Genomics • Proteomics and Sequencing • Comparative Genomics and Proteomics
GNKPSBI104: Introduction to Programming Languages and Databases • Fundamentals of Computing and introduction to Database systems • Introduction to C++ • Advanced C++ • SQL	**GNKPSBI204: Basic and Advances Java, Introduction to Linux** • Introduction to OOPs concept and JAVA • Core Java and Advanced Java • JDBC and BioJava • Introduction to Linux and Basic Linux commands

SYLLABUS FOR M. Sc. BIOINFORMATICS
DISTRIBUTION OF TOPICS

SEMESTER III	SEMESTER IV
GNKPSBI301: Separation techniques • Biophysical Techniques • Spectroscopy • Spectroscopy techniques • Techniques for separation	**GNKPSBI401: Mass Spectroscopy, Research Methodology and Scientific Writing** • Introduction to Mass spectrometry basic • Hyphenated systems • Research Methodology • Scientific writing
GNKPSBI302: Cheminformatics & Drug Designing • Introductions to Chemoinformatic • Introduction to Molecular descriptors • Methods to understand molecular similarities • Introduction to Combinatorial Chemistry and library design	**GNKPSBI402: Molecular Modeling and Simulations** • Introduction to Structure-based drug Design • Introductions to QSAR and Machine Learning • Types of QSAR • Molecular Modeling and Drug Designing Software
GNKPSBIP303: Immunology and Immunoinformatic • Introduction to Immune systems • Antibodies, Receptors and MHC • Immunoinformatics and Vaccinology • Patinformatics	**GNKPSBI403: Clinical Research and Clinical Data Management** • Introduction to Clinical Research • Drug Discovery and Development • Regulation in Clinical Research • Clinical Trials & Data Management
GNKPSBI304: Introduction to Perl and Mongodb • Introduction to Perl • Regular Expression in perl • Database connectivity and Object-oriented Perl, File handling in perl • Introduction to Mongodb	**GNKPSBI404: Python** • Introduction to Python and OOPs Concept • Regular Expression and Pattern Matching • Biopython • Database Interaction with Mongo dB using python

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Syllabus for M.Sc. Semester I

Program: Masters of Science

Course: Bioinformatics

Paper: I

(As per Choice Based Semester and

Grading System with effect from

Academic Year 2021-2022)

Bioinformatics (2021-2022)
Paper I
Course Title: Fundamentals of Biology
Paper Code: GNKPSBI101
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- To study basis of cell biology.
- This course will enable students to understand structure of Biomolecules and their Metabolism.
- To lay a foundation of Enzyme Kinetics.

Learning Outcome:

- Gain an overview of cells - their origin and evolution. Students will understand the structures and purposes of basic components of prokaryotic and eukaryotic cells, especially macromolecules, membranes, and organelles. They will apply their knowledge of cell biology to selected examples of changes or losses in cell function.
- Students will be able explain/describe the synthesis of proteins, lipids, nucleic acids, and carbohydratesandtheirroleinmetabolicpathwaysalongwiththeirregulation. Students will be able to use current biochemical techniques to plan and carry out experiments.
- Students will understand the importance of Cell – Cell communication and Signal transduction in Biological systems.

Semester I

Unit		Title	No. of lectures
Unit 1		**Cell Biology**	
	1.1	Structure and Function of cells and intracellular organelles (of both prokaryotes and eukaryotes)	
	1.2	Cell Membranes- fluid mosaic model andits functions. Membrane transport, Na-KPump	**15**
	1.3	Structure, various models, its function. Cellular transport - simple diffusion, facilitated diffusion, active transport, nuclear transport, osmosis exocytosis and endocytosis	

	1.4	Cytoskeleton- Introduction to microfilaments, microtubules, and intermediate filaments, Nucleation	
	1.5	Mechanism of cell division including (mitosis and meiosis) and concept of motors. Programmed cell death	
	1.6	Characteristics of cancerous cells; Agents promoting carcinogenesis; molecular basis of cancer therapy, Tumor markers - AFP, CEA, hCG; Telomere replication; Telomerase and its role in cancer and aging.	
Unit 2		**Structure of Biomolecules and their Metabolism**	
	2.1	Carbohydrates: Structure and Classification, Glycosaminoglycans, Proteoglycans and Glycoproteins	
	2.2	Lipids: Structure and Classification, Acylglycerols; Phospholipids, Sphingolipids, Cholesterol and Membranes; Isopienoids, Icosanoids and their biological importance	
	2.3	Nucleic Acids: RNA and DNA; Different Structural Forms of DNA; Different Types of RNA.	**15**
	2.4	Glycolysis, Feeder Pathways for Glycolysis, its regulatory mechanisms, Citric acid cycle and its regulations.	
	2.5	Oxidative phosphorylation and electron transport chain.	
	2.6	Oxidation of Fatty Acids, Ketone Bodies Biosynthesis of Fatty Acids, Membrane Phospholipids	
	2.7	Overview of Nitrogen Metabolism, biosynthesis and Degradation of Amino Acids	
	2.8	Overview of Nitrogen Metabolism, biosynthesis and Degradation of Amino Acids	
Unit 3		**Cell – Cell communication and Signal transduction**	
	3.1	Signaling Pathways differentiation and programmed cell death (apoptosis)	
	3.2	Cell Junctions, Cell Adhesion, Extracellular Matrix and integrins	**15**
	3.3	Cell–Cell interaction and signal transduction, signaling by hormones and	
	3.4	Neurotransmitters	

Unit 4		Enzyme Kinetics	
	4.1	Introduction to Enzymes	
	4.2	Units of activity, coenzymes and metal cofactors.	
	4.3	Temperature and PH effects	15
	4.4	Michaelis – Menten Kinetics	
	4.5	Feedback inhibition and activation	
	4.6	Ribozyme and abzymes	

Semester I Evaluation Pattern
- **Internal: 25marks**
- **External: 75marks**

M.Sc. Bioinformatics (2021-2022)
Paper I
Course Title: Fundamentals of Biology
Paper Code: GNKPSBIP101
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. Biochemical estimation ofDNA
2. Biochemical estimation ofRNA
3. Estimation of vitamin C using UV- Visspectrophotometer.
4. 2D separation of amino acids, plant pigments using paperchromatography
5. Thin layer chromatography analysis of moderndrug.

References:
- Voet, Donald, Voe Judith, Pratt, Charlotte W. Fundamentals of Biochemistry: Life at the molecular Level 2nd Edition. Publisher: Asia, John Wiley & Sons.2006.
- Nelson David L., Cox Michale. Lehninger Principles of Biochemistry 5th Edition.Publisher: New York. W. H. Freeman.2008.
- R C Rastogi, Biochemistry 2nd edition,2003.
- Kleinsmith and Harden, The World of the cell, Becker, Academic Internet Publishers; 5th edition(2006)

- Geoffrey M. Cooper and Robert E. Hausman. The Cell: A Molecular Approach, Fourth Edition
- Harvey Lodish. Molecular cell Biology. W. H. Freeman; Sol edition(2007)

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Syllabus for M.Sc. Semester I

Program: Masters of Science

Course: Bioinformatics

Paper: II

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics (2021-2022)
Paper II
Course Title: Bioinformatics and Sequence Analysis
Paper Code: GNKPSBI102
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- To learn about the bioinformatics databases, databanks, data format and data retrieval from the online sources.
- To make students understand the essential features of the interdisciplinary field of science for better understanding biological data.
- To provide the student with a strong foundation for performing further research in bioinformatics.
- To understand and explore the sequence comparison tools for nucleotide and protein sequences.
- To interpret the results of sequence alignments (Pairwise-local and global alignments as wellas multiple sequence alignments).
- To understand the processing of macromolecular sequences using sequence comparison tools and how the derived data can be generated.
- To understand and explore the derived databases and their applications to biological systems.
- To explore various computational tools for analysis of biomolecular sequences.

Learning Outcome:

- Provide an introduction to what bioinformatics is and why it is important.
- Provide an overview of the application are as of bioinformatics, with a focus on the topics thatwill be taught.
- Explain what type of knowledge will be gained.
- Locate and use the main databases at the NCBI and EB I resources.
- Know the difference between databases, tools, repositories and be able to use each one to extract specific information.
- Extract data from specific databases using accessions numbers, gene names, etc.

Semester I

Unit		Title	No. of lectures
Unit 1		**Introduction to Bioinformatics**	
	1.1	Introduction to the Bioinformatics and its application in Basic Biology	
	1.2	Importance of Bioinformatics	
	1.3	Goals of Bioinformatics	
	1.4	Biological Sequence versus Structure Deficit	**15**
	1.5	Its Scope and opportunities	
	1.6	Limitation of Bioinformatics	
	1.7	New avenues of Bioinformatics /Use of Bioinformatics in Research	
	1.8	New Themes	
Unit 2		**Biomolecular Databases**	
	2.1	What are Database, Types of Databases and various types of Biological Databases	
	2.2	Major Bioinformatics resources NCBI & EBI	
	2.3	Literature database e.g. PUBMED & PMC	
	2.4	Nucleic acid: GENBANK, EMBL, DDBJ	**15**
	2.5	Protein sequence databases: PIR, Uniprot, SWISSPROT, TrEMBL	
	2.6	Protein structure databases: NDB, PDB, CCSD, PROSITE, Pfam, INTERPRO, PRINTS	
	2.7	Exploring tools on ExPASY server	
	2.8	Genome Databases at NCBI, EBI, TIGR, SANGER	
	2.9	Specialized Databases **(Any Two)**	
	2.10	Viral genome database: ICTVdb , Bacterial Genomesdatabase: Genomes OnLine Database (GOLD) Microbial Genome Database (MBGD)	
Unit 3		**Sequence alignment andAlgorithms**	
	3.1	Various file formats for bio- molecular sequences	**15**
	3.2	Basic Concepts of sequences similarity, Identity and homology, orthologues, Paralogues	

	3.3	Concepts of sequence alignments, Dot Matrix, Dynamic Programming, Heuristic Programming	
	3.4	Algorithms: Needleman &Wunch, Smith & Waterman	
	3.5	Scoring matrices: Basic concepts of scoring matrix, PAM and BLOSUM series and principles based on which these matrices are derived	
	3.6	Introduction to Multiple sequence alignment (MSA) and its various algorithm. Introduction to PSSM matrices and Profile Designing. Applications of MSA.	
	3.7	Tools for Sequence Alignment: BLAST and its types, FASTA and its types, PSI BLAST, PHI BLAST, CLUSTAL OMEGA/T-Coffee/MUSCLE	
Unit 4		**Molecular Phylogenetics**	
	4.1	Definition and description of Phylogenetic trees, Basic concepts in Taxonomy and Phylogeny.	
	4.2	Nature of data used in Taxonomy and Phylogeny	
	4.3	Concept of evolutionary trees – Dendogram and Phylogram and its various representations.	
	4.4	Procedure for Phylogenetic tree construction	**15**
	4.5	Methods for Tree construction: a) Distance based method: Clustering based method (NJ & UPGMA), Optimality based method (FM andME) b) Character based method: Maximum Parsimonyand Maximum likelihoodmethod	
	4.6	Phylogenetic Tree Evaluation Methods	
	4.7	Phylogenetic Analysis Program: PHYLIP, PAUP, MEGA4 (Introduction only)	

Semester I Evaluation Pattern
Internal: 25marks
External: 75marks

M.Sc. Bioinformatics (2021-2022)
Paper II
Course Title: Bioinformatics and Sequence Analysis
Paper Code: GNKPSBIP102
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. Exploring the integrated database system viz. Basic, Advanced and LIMITS w.r.t NCBI, EBI, SwissProt, PDB etc.
2. Biological Databases: Study of different Biological databases (esp. the ones givenbelow), Format, their distinguishing features, Uses and Applications
3. Exploring the PUBMED and PMC database using the ENTREZ search engine.
4. Sequence databases: EMBL, DDBJ, GenBank, UniProt, PIR,TrEMBL
5. Domain database: Prosite, PRINT, Pfam, BLOCK
6. Structure database: PDB
7. Specialized database: KEGG, PUBMED,OMIM
8. Exploring tools on ExPASY
9. Retrieving genomic information using NCBI/GOLD database.
10. Pair-wise global alignments of protein/ DNA sequences using Needleman-Wunsch algorithm
11. Pair-wise local alignments of protein and DNA sequences using Smith-Waterman algorithm
12. Use of BLAST and its variants (specially PSI and PHI Blast) for the identificationof very similar and divergent sequences
13. Use of FASTA and its comparison with BLAST
14. Multiple sequence alignment using Clustal/ T-Coffee/MUSCLE and preparation of simple phylogenetic trees using Tree View etc.

References:
- Bioinformatics: Sequence and Genome Analysis by Mount D., Cold Spring Harbor Laboratory Press, New York.2004
- Bioinformatics-aPracticalGuidetotheAnalysisofGenesandProteinsbyBaxevanis,A.D. and Francis Ouellellette, B.F., Wiley India Pvt Ltd.2009
- Introduction to Bioinformatics by Teresa K. Attwood, David J. Parry-Smith. Pearson Education.1999
- Introduction to Bioinformatics Algorithms, Neil C. Jones,PavelPevzner

- Introduction to Bioinformatics - S.Sundararajan andBalaji
- Instant notes – Bioinformatics – Westhead, Howard parish and Twyman. Viva books Pvt. Limited.Chennai
- Bioinformatics basic methods and applications – S.C.Rastogi
- Essential Bioinformatics by Jin Xiong,2006
- ORENGO, C., JONES, D. & THORNTON, J.: Bioinformatics: genes, proteins and computers. 2003. Bios Scientific Publishers, Ltd.Oxford
- Ingvar Eidhammer, IngeJonassen, William R. Taylor: Protein Bioinformatics. 2003 John Wiley And Sons Ltd (UK) 2. HIGGINS, D. & TAYLOR, W.: Bioinformatics : sequence, structure, and databank. 2000. Oxford University Press, Oxford,UK
- M. Lesk. (2002) Introduction to Bioinformatics Oxford University Press 68. G.B Fogel D.W Corne (2002) Evolutionary Computation inBioinformatics

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Syllabus for M.Sc. Semester I

Program: Masters of Science

Course: Bioinformatics

Paper: III

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics- Semester I (2021-2022)

Paper III
Course Title: Biostatistics
Paper Code: GNKPSBI103
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- Be able to restate an investigative question in terms of a statistical model or algorithm
- Successfully relate theoretical concepts to a real-world problem in a written report.
- Provide reproducible statistical analyses using accepted practices of their search community
- Demonstrate the ability to find appropriate research literature appropriate to theinvestigative task.

Learning Outcome:

- They have the versatility to work effectively in a broad range of analytic, scientific, government, financial, health, technical and other positions.
- They have a broad background in Mathematics and Statistics, an appreciation of how its various sub-disciplines are related, the ability to use techniques from different areas, and an in-depth knowledge about topics chosen from those offered through the department.
- They recognize and appreciate the connections between theory and applications

Semester I

Unit		Title	No. of lectures
Unit 1		**Basics of Mathematics**	
	1.1	SET THEORY: Introduction, Examples of Sets, Representation of a set (Roaster form and Set builder form), Notation, Different types of sets- null set, singleton set, finite set, infinite set, sub set, proper and improper subsets, equal sets, equivalent sets, universal set, disjoint set, Set operations- Union, properties of union of sets, Intersection of sets, properties of insertion operation, De Morgan's Law, Complement of a set, Set Difference, Venn diagram, problem based on sets	15

	1.2	Calculus: Limits: Right hand and left-hand limits, working rule for finding out the limit, problems based on limits. o Differentiation and Integration Introduction, Basic concepts and problems related to differentiation and integration.	
	1.3	Vectors & Matrices: Additions and Subtraction, Dot product and cross product of vectors, Scalar triple product, Matrix algebra and Eigen Vectors – Addition, Subtraction, Multiplication, transpose inverse and conjugate of matrix.	
Unit 2		**Statistical Measures**	
	2.1	Mean, mode, median, Variance, standard deviation, coefficient of variation, Raw and Central Moments upto fourth order, measures of skewness and kurtosis	
	2.2	Probability: Introduction, Events and types of events, Probability of events, Mutually exclusive events, favorable events, exhaustive events, independent events, addition theorem on probability, conditional probability, Multiplication theorem, Problem based on probability theorem, Baye's theorem, Problem based on Baye's theorem.	**15**
Unit 3		**Random Variables and Bivariate Distribution**	
	3.1	Random variable, Distributions of random variables: Uniform, Bernoulli, Binomial, Poisson, Geometric, Normal distribution, Exponential. Central Limit Theorem. Normal approximation to Binomial and Poisson distributions	**15**
	3.2	Correlation and regression analysis, curve fitting (linear, non-linear, multilinear).	
Unit 4		**An Introduction to statistical inference**	
	4.1	Hypothesis testing: Simple and composite hypotheses, Null and alternative hypotheses critical region Type I and Type II errors Level of significance p- value, power of a test	
	4.2	Test of significance viz. Z test, t test, pair t test, chi2 test of goodness of fit	**15**
	4.3	Non-parametric tests: median test, sign test, Kruscal-Wallis test	

Semester I Evaluation Pattern
Internal: 25marks
External: 75marks

M.Sc. Bioinformatics- Semester I (2021-2022)
Paper III
Course Title: Biostatistics
Paper Code: GNKPSBIP103
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. The Basics of R
2. Types of Data Objects in R
3. Probability Distributions using R
4. Statistical Problems using R tool

References:
1. BIOSTATISTICS by P.N. Arora & P.K.Malhan
2. Biostatistics, BANNADURAI
3. Intuitive Biostatistics: A NonmathematicalGuide

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Syllabus for M.Sc. Semester I

Program: Masters of Science

Course: Bioinformatics

Paper: IV

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics- Semester I (2021-2022)
Paper IV
Course Title: Introduction to Programming Languages and Databases
Paper Code: GNKPSBI104
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- Explore various programming paradigms as well as principles of building object-oriented software
- Solidify your understanding of Computer Science in theory and practice related to biological data.
- Learn the essential elements of computing theory including logic, proof techniques, combinatorics, algorithm analysis, discrete data models (sets, relations, trees), and finite automata.

Learning Outcome:

- Understand dynamic memory management techniques using pointers, constructors,destructors, etc.
- Classify inheritance with the understanding of early and late binding, usage of exception handling, generic programming.
- Understand generic programming, templates, file handling.

Semester I

Unit		Title	No. of lectures
Unit 1		**Fundamentals of Computing and introduction to Database systems**	
	1.1	Overview and functions of a Computer System	
	1.2	Memory: Register, buffer, RAM, PROM, EPROM, EEPROM	
	1.3	Overview of various computer threats viz. Trojan horses, viruses etc.	**15**
	1.4	Operating systems concepts(Windows , Unix, Linux)	
	1.5	Software Development Life cycle (SDLC)	
	1.6	Concepts of various types of Databases and Data models	
	1.7	Instances, Schemes and E – R Model	

Unit 2		Introduction to C++	
	2.1	Input and Output	15
	2.2	Data types and Functions	
	2.3	Derived data types	
	2.4	Structure in C++ and string manipulations	
	2.5	Basic Input output and File handling	
Unit 3		Advanced C++	
	3.1	Basics of object oriented programming	15
	3.2	Concept of Object, class, Constructor and Destructors	
	3.3	Data encapsulation	
	3.4	Inheritance	
	3.5	Polymorphism	
	3.6	Virtual function and friend function	
Unit 4		SQL	
	4.1	Data definition statement; Data Manipulation Statements	15
	4.2	Select statement	
	4.3	Data Control Statement	
	4.4	Other Database Objects (Views, Sequences, Synonyms etc)	
	4.5	Security, Grants, Roles, Privileges	

Semester I Evaluation Pattern
Internal: 25marks
External: 75marks

M.Sc. Bioinformatics- Semester I (2021-2022)
Paper IV
Course Title: Introduction to Programming Languages and Databases
Paper Code: GNKPSBIP104
Credits: 02
No. of Lectures: 04/per week (04 hours each)
Marks: 50

1. Programs on C++
2. Programs on Advanced C++ with respect to syllabus
3. Practical on SQL commands

References:
1. C++: The Complete Reference, 4thEdition
2. Advanced C++ byBpb
3. SQL The Complete Reference, 3rd Edition

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Syllabus for M.Sc. SemesterII

Program: Masters of Science

Course: Bioinformatics

Paper:I

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics (2021-2022)
Paper I
Course Title: Advance Biology
Paper Code: GNKPSBI201
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- To teach concept of Central Dogma. Describe the general principles of gene organizationand expression in both prokaryotic and eukaryotic organisms.
- To give a grounding in the Recombinant DNA technology and recent advancement in field of Molecular Biology.
- To describe advance molecular biology techniques to disease diagnosis and researchinvestigation.

Learning Outcome:

- Students will analyze structural-functional relationships of genes and proteins from bacteria to eukaryotes using genomic methods based on evolutionary relationships.
- Students will be able to explain the synthesis of proteins and nucleic acids with their regulation at the epigenetic, transcriptional, translational, and post-translational levels
- Studentswillbetrainedtousecurrentbiochemicalandmoleculartechniquestoplanand carry out experiments. Interpret the outcome of experiments that involve the use of recombinant DNA technology and other common gene analysis techniques.

Semester II

Unit			Title	No. of lectures
Unit 1			**Concept of Central Dogma**	
	1.1		DNA Replication, various enzymes involved, DNA topology, super coiling of DNA, origin of replication	
	1.2		Transcription – enzymes involved, sigma factor, DNA binding sites, initiation, elongation and termination	15
	1.3		Translation or protein synthesis – enzymes or factors involved polyribosome	
	1.4		Operon model in prokaryotes and eukaryotes, lac operon, trp operon	
	1.5		Gene splicing, Post translation modifications	

Unit 2		**Recombinant DNA Technology**	
	2.1	History of rDNA Technology, enzymes involved – restriction endonucleases, ligases etc.	
	2.2	Cloning vectors – plasmids, bacteriophage vectors for eukaryotes- YAC.	
	2.3	DNA manipulation–cutting and joining DNA using nucleases and ligases, linkers and adapters	15
	2.4	Cloning strategies, construction of libraries	
	2.5	Transformation of DNA into host cells, Screening for recombinants, blue white screening	
	2.6	DNA fingerprinting techniques	
	2.7	Application of recombinant DNA technology	
Unit 3		**Genomics**	
	3.1	Prokaryotic and Eukaryotic genome & their expression	
	3.2	Comparative eukaryotic genomics: chloroplast, mitochondrial and nuclear genomes	15
	3.3	Gene organization and control of gene expression; manipulation and exploitation in biotechnology	
	3.4	Major techniques in gene manipulation of plants, Genetic manipulation of chloroplasts	
	3.5	Genetically modified organism and their applications	
	3.6	Epigenetics	
Unit 4		**Molecular Biology Techniques**	
	4.1	Protein/DNA/RNA probes, southern and western blotting, In situ hybridization	
	4.2	DNA Sequencing	
	4.3	Microarray	
	4.4	Flow cytometry	15
	4.5	Capillary Electrophoresis	
	4.6	PCR and Real time PCR	
	4.7	Next Generation Sequencing	

Semester II Evaluation Pattern
Internal: 25marks
External: 75marks

M.Sc. Bioinformatics- Semester I (2021-2022)
Paper I
Course Title: Advance Biology
Paper Code: GNKPSBIP201
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. Isolation of plasmid DNA and chromosomal DNA
2. Restriction digestion of DNA
3. Ligation
4. PAGE separation of human serum proteins
5. To perform Polymerase Chain Reaction of gene of interest
6. Demonstration of DNA Sequencer
7. Demonstration of Flow cytometer
8. Demonstration of Real time PCR

References:
- Primrose, S.B. and Twyman, R.M. (2006) Principles of Genetic Manipulation and Genomics. Seventh Edition. Blackwell Publishing,USA.
- Winnacker, E-L.(1987) From Genes to Clones. VCH Publishers,USA.
- SambrookJ.andRussellD.2001.MolecularCloning:ALaboratoryManual,3rdedition.Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NewYork.
- B. M. Turner, Chromatin and Gene Regulation: Molecular Mechanisms inEpigenetics
- Russell Peter J. iGenetics: A Molecular Approach 3rd edt.: Pearson International Edition. Publisher: New York, Pearson ISBN:9780321610225.

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Syllabus for M.Sc. SemesterII

Program: Masters of Science

Course: Bioinformatics

Paper:II

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics (2021-2022)
Paper II
Course Title: Structural Biology & Bioinformatics
Paper Code: GNKPSBI202
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- To study introduction of structural bioinformatics, conformational analysis of proteins and nucleic acids.
- To understand the protein structure prediction, and molecular interactions.
- This course will enable the students to: understand the levels of structural organization. of macromolecules and experimental methods of structure determination.
- Helps to understand the approaches for structure analysis and acquire knowledge of various algorithms & methods of structure prediction.
- Understand the genomic information.
- Describe the genome annotation pipeline, including manual and automated annotation.
- To understand the principles of macromolecular interactions.
- Understand Protein-Protein Interaction analysis and Protein Chips.

Learning Outcome:

- Acquire skills to use different approaches for prediction of protein structure.
- To understand the structural organization, structural properties and various techniques employed in the structure determination of Biological macromolecules – DNA, Protein.
- Advances understanding about primary and secondary structures of proteins
- Expansions understanding about tertiary and quaternary structures of proteins
- Designate about protein folding and its significance and helps to gain knowledge for the same.
- Use the UCSC genome browser to explore the available annotation tracks for a gene of interest.
- Helps in interpretation of   the structure for a protein sequence based on an identified template.
- Determine if the correct fold has been assigned to a model.
- Distinguish between good, medium, and poor-quality structures.

Semester II

Unit		Title	No. of lectures
Unit 1		**Introduction to Macromolecule Structures and Protein Chemistry**	
	1.1	Overview of structural bioinformatics – understanding structural basis for biological phenomena– challenges in structural bioinformatics – integration of structural data with other data.	**15**
	1.2	Macromolecular Structure : Protein - Primary, Secondary, Super secondary, Tertiary and Quaternary structure, Potential energy maps, Ramachandran map, Nucleic acid – DNA and RNA, Carbohydrates, Co-ordinate systems	
	1.3	Macromolecular interactions: Protein – Protein (Proteomic analysis of Post-translational Modification- Phosphorylation, ubiquitination, and glycosylation) , Protein – Nucleic acids , Protein – carbohydrates, etc. Yeast two Hybrid Technique,Tools to study protein interaction: STRING, MIPS (other equivalent methods)	
	1.4	Principles of protein folding and methods to study protein folding.	
	1.5	Anfinsen experiment	
	1.6	Overview of experimental techniques to study macromolecular structures, Methods to study 3D structure: X-ray, NMR, Cryo-electron microscopy, Validation using Procheck/PROSA, etc.	
	1.7	Wet Lab protein data pull-out in *in-silico* databases and its interpretation along with comparison study: PDB, PDBSUM and Comparison tool	
	1.8	Visualization of secondary structures and topologies of proteins using molecular visualization software's such as RasMol, Cn3D, Chime, Mol4D, PyMOL (other equivalent methods)	
Unit 2		**Protein Structure Prediction & Validation**	
	2.1	Prediction of protein structure: secondary structure prediction methods: First, second and third generation methods.	
	2.2	Tool for Secondary protein structure prediction: GOR/SOPMA/ExPASY	

	2.3	Prediction of protein Tertiary structure prediction: Homology modeling, fold recognition and ab initio methods	15
	2.4	Tool for Tertiary protein structure prediction: MODELLER/SWISSMODEL/PHYRE2(or other equivalent methods)	
	2.5	Validation of protein tertiary structure: Ramachandran Plot/RAMPAGE/SAVES (or other equivalent methods)	
	2.6	Protein Classification studies: CATH and SCOP	
	2.7	Visualization of tertiary structures, quaternary structures, architectures and topologies of proteins and DNA using molecular visualization softwares such as RasMol, Cn3D, SPDBV, Chime, Mol4D, PyMOLetc	
Unit 3		**Application of Bioinformatics in Biomolecular Diseases**	15
	3.1	Genome and its databases, Gene: Introns, Exons and its identification tools, Open Reading Frame (ORFs),	
	3.2	Predictions of genes, promoters, splice sites, regulatory regions: basic principles, application of methods to prokaryotic and eukaryotic genomes and interpretation of results. (Synteny and gene order) Mutations and diseases	
	3.3	Basic concepts on identification of disease genes; role of bioinformatics –OMIM database, reference genome sequence, integrated genomic maps, gene expression profiling	
	3.4	Tools for analysis: SOFTBERRY server, KEGG, UCSC browser	
	3.5	Case study of biomolecular disease w.r.t. to GPCR	
	3.6	Orphan GPCRs, Identification of Orphan GPCRs, Reverse Pharmacology, Reverse Pharmacology for Orphan GPCRs, Deorphanisation	
	3.7	Analysis of diseases gene using microarray studies OR Protein Microarray in Drug Discovery	
Unit 4		**Introduction to Proteomics and its applications**	
	4.1	Proteomics- Introduction, Need, scope and challenges of proteomics, how proteomics is applied in real-life scientific research	

	4.2	Protein Identification with antibodies, protein sequence determination by chemical degradation, Edman's degradation, Short-gun proteomics for proteome profile	
	4.3	Computational tools- advanced tools for data analysis at Expasy	15
	4.4	Protein arrays: bioinformatics-based tools for analysis of proteomics data (Tools available at ExPASy Proteomics server); databases (such as InterPro) and Protein Arrays, Protein Chips and their application	

Semester II Evaluation Pattern
Internal: 25marks
External: 75marks

M.Sc. Bioinformatics (2021-2022)
Paper II
Course Title: Structural Biology & Bioinformatics
Paper Code: GNKPSBIP202
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. Detection of general signals, regulatory regions and promoter prediction
2. Secondary structure prediction using various available tools
3. Tertiarystructureandfunctionpredictionusinghomologymodelingandabinitiomethod
4. Structural Blast – VAST &DALI
5. Binding pocket prediction – Castp; Glycosylation, phosphorylation sites prediction (other equivalent methods)
6. Validation of predicted structure by SAVS server or verify 3d (other equivalent methods)
7. Visualization of 3D protein structure using Rasmol, VMD, PyMol etc.
8. Protein Classification: CATH & SCOP
9. Genome Browser: UCSC
10. Ensembl @EBI
11. MapViewer @NCBI
12. Genome Annotation and assembly
13. Integrated Genome annotation server

References:

- CesareniGiovanni,GimonaMario,SudolMarius,YaffeMichael(Editors).ModularProtein Domains. Publisher: Weinheim Wiley-VCH. 2005. ISBN:352730813X.
- Höltje Hans-Dieter, Sippl Wolfgang, Rognan Didier, FolkersGerd. Molecular Modeling: Basic Principles and Applications. Publisher: New York, Wiley-VCH. 2003. ISBN: 3527305890.
- WebsterDavid(Editor).ProteinStructurePrediction:MethodsandProtocols(Methodsin Molecular Biology) Volume 143. Publisher: New Jersey Humana Press. 2000. ISBN: 0896036375.
- SternbergMichaelJ.E.ProteinStructurePrediction:APracticalApproach.Publisher:USA, Oxford University Press. 1997. ISBN:0199634953.
- R.M. Twyman, "Principles of Proteomics (Advanced Text Series)", Bios Scientific, 2004.2
- DanielC.Liebler,"IntroductiontoProteomics:ToolsfortheNewBiology",HumanaPress Inc.,2002
- Ian M. Rosenberg , "Protein Analysis and Purification: Benchtop Techniques "- , Springer, 2005 2. Philip L.R. Bonner, "Protein Purification", Taylor & Francis,2007
- David W Mount, "Bioinformatics- Sequence and genome analysis", Cold Spring Harbor Laboratory Press, second edition,2004
- .S.R.Pennington,M.J.Dunn,"Proteomics:fromProteinSequencetoFunction",Springer publications, first edition,2001.
- Timothy Palzkill,"Proteomics",Springer,2002.
- GibsonG.andMuseS.V.APrimerofGenomeScience,SecondEditionSinauerAssociates, Inc. Sunderland,MA
- Igor Jurisica, Dennis Wigle. Knowledge Discovery in Proteomics. 2006. Chapman & Hall / CRC Pennington SR (Ed), Dunn M. J. (Ed) Proteomics: from protein sequence to function. 2002 Viva Books Pvt.Ltd.
- Srivastava Sudhir (Ed). Informatics in Proteomics 2005 Taylor & Francis Group /CRC

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Syllabus for M.Sc. SemesterII

Program: Masters of Science

Course: Bioinformatics

Paper:III

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics (2021-2022)
Paper III
Course Title: Genomics and Proteomics in Bioinformatics
Paper Code: GNKPSBI203
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- To study prokaryotic and eukaryotic genomes, general methods of genome sequencing techniques, genome analysis and annotations, genome mapping techniques and applications of genomics.
- To understand the proteins enclosed by the genes with respect to structure, function, protein – protein interactions, techniques for separation and analysis, database and applications.
- Define whole genome sequencing.
- Appreciate and explore the comparative genomics databases.
- Recognize various algorithms used for comparisons of full genome and gene order.
- Know the concepts of SNPs and their significance.
- Realize and appreciate the proteomics concepts and technology.

Learning Outcome:

- Appreciate the importance of full genome comparisons and helps in further research studies.
- Genome mapping solves the complicated puzzle of genes with pieces of information coming from laboratories all over the world and helps to detect the functions of the genes.
- Helps of proteomics studies may lead to better treatments in future.

Semester II

Unit		Title	No. of lectures
Unit 1		**Genome and Genome Sequencing**	
	1.1	Genome structure and organization, Eukaryotic genome, Genomics of Microbes Genome, sequencing technologies- Next generation sequencing (Introduction only), Genome assembly and finishing methods	**15**

	1.2	Genome Sequencing: Goals of the Human Genome Project, cloning vectors, concept of maps, physical maps, shotgun libraries, DNA polymorphism, nucleotides, DNA sequences and analysis in sequence databases such as GenBank/ EMBL/ DDBJ, Recombinant DNA technology, restriction enzymes, resource for restriction enzyme (REBASE)	
	1.3	GENOMICS: GENE IDENTIFICATION: Genome information and special features, coding sequences (CDS), untranslated regions (UTR's), cDNA library, expressed sequence tags (EST), detecting functional sites in the DNA. Internet resources for gene identification, detection of functional sites, gene expression.	
Unit 2		**Functional Genomics**	
	2.1	Functional genomics - Large scale gene expression analysis –Experimental methods - Computational tools for expression analysis-Hierarchical clustering – Gene expression analysis– STS-EST-GSS-Assessing levels of gene expression using ESTs - cDNA databases – Transcriptome analysis and applications	**15**
	2.2	The Transcriptome Strategies for generating ESTs and full-length inserts	
	2.3	EST clustering and assembly, EST databases (DBEST, UNIGene, TGI, STACK, EGI) SAGE	
Unit 3		**Proteomics and Sequencing**	
	3.1	Proteomics: Protein arrays: basic principles. Computational methods for identification of polypeptides from mass spectrometry.	
	3.2	Protein arrays: bioinformatics-based tools for analysis of proteomics data (Tools available at ExPASy Proteomics server); databases (such as InterPro) and analysis tools.	**15**
	3.3	Protein-protein interactions: databases such as DIP, PPI server and tools for analysis of protein-protein interactions	
Unit 4		**Comparative Genomics and Proteomics**	
	4.1	Objective and Overview of Genome Comparisons	

	4.2	Genome Alignments by BLAST2Go/ MUMmer/ PipMaker/ VISTA (other equivalent methods)	15
	4.3	Comparison of Gene Order	
	4.4	Comparative Genomics Databases- COG/ VirGen/ CORG (other equivalent methods)	
	4.5	Single Nucleotide Polymorphism (dbSNP) and its analysis in diagnosis	

Semester II Evaluation Pattern
Internal: 25marks
External: 75marks

M.Sc. Bioinformatics (2021-2022)
Paper III
Course Title: Structural Biology & Bioinformatics
Paper Code: GNKPSBIP203
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

Report on Industrial Visit-Any 1 OR Report on research paper.

References:

1. SándorSuhai, Genomics and Proteomics: Functional and Computational Aspects, Kluwer Academic Publishers,2002
2. Azuaje F &Dopazo J. 2005. Data Analysis and Visualization in Genomics and Proteomics. John Wiley &Sons.
3. Akay M. (Ed) Genomics and Proteomics Engineering in Medicine and Biology 2007 WileyInterscience John Wiley & sons, Inc. Publication,USA
4. "Microbial Genomics And Proteomics" by NiyazAhmed
5. Christendat D, et al. Structural proteomics of an archeon.Nat. Struct. Biol. 2000;7(10):903–909. [PubMed]
6. Discovering Genomics, Proteomics and Bioinformatics 2nd edition - by A. Malcolm Campbell and Laurie J. Heyer. by Cold Spring Harbor Laboratory Press2006.

7. Principles of Genome Analysis and Genomics (3rd Ed.) by Primrose, S.B. and Twyman, R.M., Blackwell Publishing Company, Oxford, UK.2003

8. IntroductiontoProteomics–Toolsforthenewbiology(1stEd.)byLiebler,D.C.,Humana Press Inc., New Jersey, USA.2002

9. BioinformaticsandFunctionalGenomicsbyPevsner,J.,JohnWileyandSons,NewJersey, USA. 2003

10. Bioinformatics: Sequence and Genome Analysis by Mount, D., Cold Spring Harbor Laboratory Press, New York.2004

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Syllabus for M.Sc. SemesterII

Program: Masters of Science

Course: Bioinformatics

Paper:IV

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics- Semester II (2021-2022)
Paper IV
Course Title: Basic and Advances Java, Introduction to Linux
Paper Code: GNKPSBI204
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- Gain knowledge about basic Java language syntax and semantics to write Java programsand use concepts such as variables, conditional and iterative execution methods etc.
- Understand the fundamentals of object-oriented programming in Java, including defining classes, objects, invoking methods etc and exception handling mechanisms.
- Understand the principles of inheritance, packages and interfaces.

Learning Outcome:

- Identify classes, objects, members of a class and relationships among them needed fora specific problem.
- Application of Biological data using Biojava.

Semester II

Unit		Title	No. of lectures
Unit 1		**Introduction to OOPs concept and JAVA**	
	1.1	An introduction to Object-Oriented Programming	
	1.2	Object-oriented programming and Java	**15**
	1.3	Introduction to Java basics	
Unit 2		**Core Java and Advanced Java**	
	2.1	Objects, Arrays, Conditionals and Loops	
	2.2	Creating Classes and Applications in Java, methods	
	2.3	Java Applets Basics, Graphics, Fonts and Color	
	2.4	Managing Simple Events and Interactivity	**15**
	2.5	Creating User Interfaces with AWT	
	2.6	Packages and Interfaces	
	2.7	Exception, Multithreading, Streams and I/O	

Unit 3		JDBC and BioJava	
	3.1	Introduction to JDBC	
	3.2	Client Server Application	15
	3.3	Java Drivers	
	3.4	Executing SQL Statements	
	3.5	Installing BioJava	
	3.6	Symbols, reading sequences	
	3.7	Basic Sequence Manipulation (DNA to RNA, Reverse Complement, motif as regular expression)	
	3.8	Translation (DNA to Protein, Codon to amino acid)	
	3.9	Sequence I/O	
	3.10	Locations and Features (Point Location, Range Location, Feature modifications)	
Unit 4		Introduction to Linux and Basic Linux commands	
	4.1	History and design	
	4.2	Principles of Linux	
	4.3	Functions of Linux OS	15
	4.4	Basic shell commands	
	4.5	Understanding Linux file permissions	
	4.6	Basic script building and File creation in Linux	

Semester II Evaluation Pattern

Internal: 25marks

External: 75marks

M.Sc. Bioinformatics (2021-2022)

Paper IV

Course Title: Basic and Advances Java, Introduction to Linux

Paper Code: GNKPSBIP204

Credits: 02

No. of Practical's: 04/per week (04 hours each)

Marks: 50

1. Programs on Core Java and Advanced Java.
2. Programs on JDBC and Basic programs on Biojava
3. Basic commands on LINUX

References:

1. Java: The Complete Reference (English, SchildtHerbert).
2. Core and Advanced Java, Black Book, Recommended by CDAC, Revised and Upgraded KindleEdition
3. Fundamentals of Linux: Explore the essentials of the Linux command line KindleEdition
4. Practical Guide to Linux Commands Editor, by Mark G.Sobell.

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Syllabus for M.Sc. Semester III

Program: Masters of Science

Course: Bioinformatics

Paper: I

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics (2021-2022)
Paper I
Course Title: Separation techniques
Paper Code: GNKPSBI301
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- Acquire knowledge about the widely used analytical Instruments.
- Know the instruments used in hospital for routine clinical analysis, drug and pharmaceutical laboratories, biopharmaceutical industries, oil refineries and above allfor environmental pollution monitoring.
- Learn Biophysical technique.

Learning Outcome:

- Students will have a thorough theoretical and practical understanding of advanced analytical instruments.
- Students will be able to select Instrument for a particular analysis with come idea of its merits, demerits and limitations.
- Students will be able to develop methods for sample analysis and its interpretation.

Semester III

Unit		Title	No. of lectures
Unit 1		**Biophysical Techniques**	
	1.1	Microscopic techniques	
	1.2	Centrifugation techniques: Principal, type of centrifuge and application.	15
	1.3	Electrophoresis: AGE and PAGE	
	1.4	2-D electrophoresis	
	1.5	Isoelectric focusing	
Unit 2		**Spectroscopy**	
	2.1	Properties of electromagnetic radiation	
	2.2	Wavelength and Energy	15
	2.3	The Interaction of Light with Matter	
	2.4	The Beer-Lambert Law	
	2.5	Types of Spectroscopy	

Unit 3		Spectroscopy techniques	
	3.1	UV-vis Spectrophotometer	
	3.2	Turbidimetry and Nephelometry	
	3.3	X-ray spectroscopy	15
	3.4	Infrared and Raman Spectroscopy	
	3.5	Nuclear Magnetic Resonance Spectroscopy	
	3.6	Spectrofluorimetry	
	3.7	Circular dichroism spectroscopy	
Unit 4		Techniques for separation	
	4.1	Liquid chromatography	
	4.2	Thin layer chromatography and HPTLC	
	4.3	High Performance Liquid Chromatography	
	4.4	Adsorption chromatography	15
	4.5	Partition chromatography	
	4.6	Affinity chromatography	
	4.7	Ion-exchange chromatography	
	4.8	Gas chromatography	

Semester III EvaluationPattern
Internal: 25marks
External: 75marks

M.Sc. Bioinformatics (2021-2022)
Paper I
Course Title: Separation techniques
Paper Code: GNKPSBIP301
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. HPTLC separation of modern drug from its formulation (e.g. Diclofenac sodium)
2. HPLC separation of modern drug from its formulation (e.g. Diclofenac sodium)
3. Gas Chromatographic separation of volatile sample.
4. IR analysis of a modern drug (e.g. Diclofenac Sodium)

- **References:**
- Robert D.Braun, Introduction to Instrumental Analysis, McGraw-Hill, Singapore,1987
- L.R.Snyder, J.J.Kirkland, Introduction to Modern Liquid Chromatography 2nd ed., John Wiley &Sons
- Douglas A.Skoog ,Principles of Instrumental Analysis,Saunders CollegePublihsing
- William David Cooper,AlbertD.Helfrick ,Electronic Instrumentation andMeasurement Technique ,Prentice Hall of IndiaPvt.Ltd

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Syllabus for M.Sc. Semester III

Program: Masters of Science

Course: Bioinformatics

Paper: II

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics (2021-2022)
Paper II
Course Title: Cheminformatics & Drug Designing
Paper Code: GNKPSBI302
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- Study the basic concepts of molecular modeling.
- Study the representation of structures and descriptors.
- Predict the biological activities through QSAR analysis.
- Emphasize the significance of chemical libraries.
- Comprehend the fundamentals of chemoinformatic.
- Practice chemical databases and storage systems.
- Salvage and analyze data using physicochemical properties.
- Realize the model structure-activity relationship.

Learning Outcome:

- Aids to know how to organize, analyze and solve other new problems and to understand scientific data in the development of novel compounds.
- Grasp the knowledge on the basic concepts of QSAR.
- Discuss the detail about the QSAR.
- Ability to apply mathematical methods to solving science problems.
- Capability to create effective visual representations of models and datasets.
- Escalate complementary aspects of Chemoinformatics and bioinformatics for design ofbioactive molecules.
- Understand the details on the impact of SAR/QSAR studies to the 3Dmodeler.

Semester III

Unit		Title	No. of lectures
Unit 1		**Introductions to Chemoinformatics**	15
	1.1	Representation and manipulation of Molecular structures (2D and 3D)	
	1.2	Substructure searching	
	1.3	Conformational Search and analysis	
	1.4	3D Pharmacophore generation	
Unit 2		**Introduction to Molecular descriptors**	15
	2.1	2D atomic descriptors	
	2.2	3D Molecular descriptor	
Unit 3		**Methods to understand molecular similarities**	15
	3.1	Similarities based on 2D fingerprints	
	3.2	Similarities based on 3D structure	
Unit 4		**Introduction to Combinatorial Chemistry and library design**	15
	4.1	Diverse and focused libraries	
	4.2	Library enumeration	
	4.3	Library design strategies	
	4.4	Product-based library design	

Semester III EvaluationPattern

Internal: 25marks

External: 75marks

M.Sc. Bioinformatics (2021-2022)
Paper II
Course Title: Cheminformatics & Drug Designing
Paper Code: GNKPSBIP302
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. Drawing, edit and manipulating 2D and 3D structures and understanding various file formats to represent molecular structures (To be restricted to small molecules). / Practicalsessionforchemicalstructurerepresentationandstorageinspecialfileformats (SMILES, WLN, sd and mol).
2. Generating and analyzing conformations using different methods.
3. Generation and validation of 3D Pharmacophore and selective best Pharmacophore map (Various different methods to be used and comparedwith)
4. Generating and understanding various molecular descriptors and their significance with the chemical properties
5. Importance of 3D structures and method of generation from 1D & 2Drepresentations.
6. A brief introduction to building molecular databases with special emphasis on retrieval using structure input.
7. Substructure/Exact/similar structure-based searching
8. Property based search of molecular databases
9. Quantitative Structure Activity/Property/Toxicity Relationship Studies.

References:
- Bunin Barry A. SieselBrian,MoralesGuillermo,Bajorath Jürgen. Chemoinformatics: Theory, Practice, & Products Publisher:New York, Springer. 2006. ISBN:1402050003.
- Gasteiger Johann, Engel Thomas. Chemoinformatics: A Textbook. Publisher: WileyVCH; 1st edition. 2003. ISBN:3527306811.
- Leach Andrew R., Valerie J. Gillet. An introduction to chemoinformatics.Publisher: Kluwer academic , 2003. ISBN:1402013477.
- Gasteiger Johann, Handbook of Chemoinformatics: From Data to Knowledge(4 Volumes), 2003. Publisher: Wiley-VCH.ISBN:3527306803.
- Bunin BA. 2006. Chemoinformatics: Theory, Practice and Products. Springer Gasteiger J & Engel T. 2003. Chemoinformatics: A Textbook. Wiley-VCH. HinchliffeA.2003.

Molecular Modelling for Beginners. John Wiley & Sons. Leach AR. 1996. Molecular Modelling: Principles and Applications. Longman.

- F.K. Brown (1998). "Chapter 35. Chemoinformatics: What is it and How does itImpact Drug Discovery". Annual Reports in Med. Chem. 33: 375.doi:10.1016/S0065-7743(08)61100-8.
- Satya Prakash Gupta, QSAR and Molecular Modeling, Springer, Anamaya Publishers, 2008.

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Syllabus for M.Sc. Semester III

Program: Masters of Science

Course: Bioinformatics

Paper: III

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics (2021-2022)
Paper III
Course Title: Immunology and Immunoinformatic
Paper Code: GNKPSBI303
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- Know the immune system, its components and their functions.
- Learninginformatics-basedapproachesforpredictionofepitopes,design of vaccines and immuno-diagnostic tools
- Comprehend and explore sequence and structural databases relevant in the area of immunology.
- Explore sequence and structural features of antibodies using computational tools.
- Characterize and understand principles of antigen-antibody interactions.
- To know algorithms and methods for prediction of epitopes.
- Discover and use approaches for vaccine design.

Learning Outcome:

- Helps to understand the concepts and underlying various aspects of *in silico* vaccine development
- Understand the functioning of various databases and tools.
- Interpretation of patents is understood

Semester III

Unit		Title	No. of lectures
Unit 1		**Introduction to Immune systems**	
	1.1	Innate and adaptive immunity in vertebrates Infectious diseases o Categories of vaccines	
	1.2	Antigen processing and presentation	
	1.3	Contemporary challenges to the immune system	**15**
	1.4	Infectious diseases	
	1.5	Autoimmune diseases	
	1.6	Categories of vaccines	

Unit 2		Antibodies, Receptors and MHC	
	2.1	Immunoglobulin classes and subclasses	15
	2.2	CDR and LDR regions and sequence numbering	
	2.3	Immunogenetics & immunogenomics Hybridoma technology: applications	
	2.4	Humanization of antibodies by design	
	2.5	The B-cell surface receptor for antigen (BCR)	
	2.6	The T-cell surface receptor for antigen (TCR)	
	2.7	The major histocompatibility complex (MHC), MHC polymorphism , Causes of MHC polymorphism, MHC supertypes	
	2.8	Epitopes: Affinity Maturation , Recognition of Antigen by B cells, Neutralizing Antibody	
Unit 3		Immunoinformatics and Vaccinology	
	3.1	Overview of Immunoinformatics	15
	3.2	Reverse vaccinology	
	3.3	Rational Vaccine design	
	3.4	Databases & tools: IMGT & IEDB, BciPep, Epitome, CED, Ag-Ab.	
	3.5	Molecular interactions, Specificity and characterization	
	3.6	Ag-Ab: Sequential and conformational epitopes,	
	3.7	MHC- peptide designing tool	
	3.8	T cell, B cell epitope prediction tool	
Unit 4		Patinformatics	
	4.1	IPR: Patents and reading the patent	15
	4.2	Patinformatics	
	4.3	Patent prosecution	
	4.4	Copyrights	

Semester III Evaluation Pattern

Internal: 25marks

External: 75marks

M.Sc. Bioinformatics (2021-2022)
Paper III
Course Title: Immunology and Immunoinformatic
Paper Code: GNKPSBIP303
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. Browsing and searching sequence & structure databases to retrieve data on Immunoglobulin: Introduction to sequence and structure databases
2. Study of Antibody sequence and structure: Antibody numbering: Kabat, Chothia and other equivalent methods and its importance.
3. Visualization of structure & mapping CDRs on structure
4. Study of variable and constant domains via Topology diagram
5. Study of Ag-Ab interactions epitopes (Any Tool working/Demo)
6. Prediction of T cell & B cell epitopes : MHC Class I epitopes and MHC Class II epitopes
7. Web-based tools for vaccine design (Write Up / Case study)

References:
- OleLund,"ImmunologicalBioinformatics",MITpress, September2005. 2. DarrenFlower, "InSilicoImmunology",Springer,2006.
- Darren R Flower, "Immunoinformatics: Predicting Immunogenicity inSilico", HumanaPress,2007. 2. Rammensee, "Immunoinformatics- Bioinformatics Strategies for Better Understanding of Immune Function",Wiley,2003.
- Text book of Immunology by Kuby,2008
- Text book of Immunology by Riot,2006
- Essential of Immunology byRoit
- Immunology by NandiniShetty
- W. E. Paul; Fundamental Immunology, RavenPress
- Immunoinformatics: A Brief ReviewbyNamrata   Tomar   and   Rajat   K.   De
- Indian Patent Act as amended by Act No 15 April2015
- Brennan, M. Chem. Eng. News 2000, 78 (27),4–5
- Diamond v Chakrabarty, 447 U.S. 303(1980).

- Diamond v Diehr, 450 U.S. 175(1981).
- In re Lowry, 32 F.3d 1579 (Fed. Cir.1994).
- State Street Bank & Trust Co. v Signature Financial Group, Inc., 149 F.3d 1368 (Fed. Cir.1998).
- AT&T Corp. v Excel Communications Inc., 172 F.3d 1352 (Fed. Cir.1999).
- Law of Intellectual Property and Bioinformatics by Jagadish.A.T, Faculty of Law, JSS Law College, Autonomous, Kuvempunagar,Mysore.
- The IPR PatentAct,1970
- Handbook on Intellectual Property Rights In India by Rajkumar S.Adukia

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Syllabus for M.Sc. Semester III

Program: Masters of Science

Course: Bioinformatics

Paper: IV

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics- Semester III (2021-2022)
Paper IV
Course Title: Introduction to Perl and Mongodb
Paper Code: GNKPSBI304
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- Experience learning a programming language "on your own" as is commonly the casein industry.
- understand the syntax and semantics of the Perl language and their similarity and differences from Java
- understand how to develop and implement various types of programs in the Perl language
- understandvariousformsofdatarepresentationandstructuressupportedbythePerl language
- understand the appropriate applications of the Perl language
- Recognize similarities and common characteristics of programming languages.

Learning Outcome:

- The student will proficient programming in the Perl language and programming in general
- They design and revision of Perl scripts
- They can do debugging techniques appropriate for the Perl language

Semester III

Unit		Title	No. of lectures
Unit 1		**Introduction to Perl**	
	1.1	Introduction: What is Perl? Why use Perl in Bioinformatics? History of Perl, Availability, Support, Basic Concepts	15
	1.2	Scalar Data: What Is Scalar Data?, Numbers, Strings, Scalar Operators, Scalar Variables, Scalar Operators and Functions	

	1.3	Arrays and List Data: What Is a List or Array? Literal Representation, Variables, Array Operators and Functions, Scalar and List Context	
	1.4	Control Structures: Statement Blocks, basic I/O	
	1.5	Hashes, Hash Variables, Literal Representation of a Hash, using Hashes	
	1.6	Subroutines, System and User Functions, The local Operator	
Unit 2		**Regular Expression in perl**	
	2.1	Concepts of Regular Expressions, Simple Uses of Regular Expressions, metacharacters, quantifiers etc.	**15**
	2.2	Pattern matching, substitution	
	2.3	split and join Functions, Formatting Data, Sorting, Transliteration	
	2.4	Finding a Substring, Extracting and Replacing a Substring, Variable-length Parameter Lists, Notes on Lexical Variables	
Unit 3		**Database connectivity and Object-oriented Perl, File handling in perl**	
	3.1	Database Manipulation	
	3.2	Object oriented Perl: Introduction to modules, Creating Objects	**15**
	3.3	BioPerl: Introduction, Installation procedures, Architecture, Uses of BioPerl	
	3.4	File handles and File Tests, Opening and Closing a File handle, die, Using File handles	
Unit 4		**Introduction to Mongodb**	
	4.1	Introduction to MongoDB	
	4.2	Key Features of MongoDB, Organizations that use MongoDB	**15**
	4.3	MongoDBvs SQL Databases, Advantages of MongoDB	
	4.4	Commands of Mongodb	

Semester III Evaluation Pattern

Internal: 25marks

External: 75marks

M.Sc. Bioinformatics (2021-2022)
Paper III
Course Title: Introduction to Perl and Mongodb
Paper Code: GNKPSBIP304
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. Basic programs on perl.
2. Basic programs on Regular Expression.
3. Programs on Database, File handling and Bioperl.
4. Queries on Mongodb.

References:
1. "MongoDB Applied Design Patterns" by RickCopeland
2. The Little Mongo DB Schema DesignBook
3. Beginning Perl for Bioinformatics - O'ReillyMedia

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Syllabus for M.Sc. Semester IV

Program: Masters of Science

Course: Bioinformatics

Paper: I

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics (2021-2022)
Paper I
Course Title: Mass Spectroscopy, Research Methodology and Scientific Writing
Paper Code: GNKPSBI401
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- The learner will be able to define Fundamentals of Mass Spectrometry, Ionizationtechniques, Mass Analyzers and hyphenated technique used in pharma and biopharmaceutical industries.
- Students will read scientific articles and gain a critical understanding of their contents.
- Research Methodology and Scientific Writing will aid to select a particular area of interest for project work.

Learning Outcome:

- Student will gain insight into the most significant field of mass spectroscopy used today in biopharmaceutical.
- Studentswillgainskillsrequiredtoeffectivelydoscientificresearch.Morespecifically, students will learn to implement the scientific method by proposing hypotheses to explain biological phenomena, designing and conducting experiments to test these hypotheses, and critically interpreting the resulting data.
- Students will learn to effectively communicate their results, both orally and in writing. In addition, they will be able to critically evaluate scientific literature and the current state of research progress in their area of interest. They will learn to work in a team.

Semester IV

Unit		Title	No. of lectures
Unit 1		**Introduction to Mass spectrometry basic**	
	1.1	Mass spectrometry	
	1.2	Components: ion sources, analyzers, detectors, vacuum system	**15**
	1.3	Application of MS	
	1.4	Recent advances in field of MS	
Unit 2		**Hyphenated systems**	

	2.1	Gas chromatography – mass spectrometry (GC_MS)	**15**
	2.2	High performance liquid chromatography – mass spectrometry	
	2.3	Supercritical fluid chromatography – mass spectroscopy (SFC-MS)	
	2.4	Tandem mass spectrometry (MS-MS)	
	2.5	Inductively coupled plasma – mass spectrometry (ICP-MS)	
	2.6	MALDI-TOF	
Unit 3		**Research Methodology**	
	3.1	Definition and objective of Research	
	3.2	Types of research – Descriptive, Analytical, Applied, Fundamental, Quantitative, Qualitative, Conceptual, Empirical and Other Types of Research	
	3.3	Research Approaches, motivation in research, Criteria of Good Research	**15**
	3.4	Research Methods vs. Methodology; Research and Scientific Method	
	3.5	Research Process: Steps of research process;	
	3.6	Sampling, Sample size determination, Plan for data collection, Methods of data collection, Plan for data processing and analysis	
	3.7	Ethical considerations during research	
Unit 4		**Scientific writing**	
	4.1	Meaning of Scientific and non scientific writings	
	4.2	Structures of Research proposals	
	4.3	Synopsis, Dissertations, Thesis, Research paper writings (Abstract, Introduction, Review literature, methodology, Results, Discussions, Summary, Conclusion, Bibliography etc); Presentations: Graphical, Tabular, Animation, Power point etc	**15**

Semester IV Evaluation Pattern

Internal: 25marks

External: 75marks

M.Sc. Bioinformatics (2021-2022)
Paper I
Course Title: Mass Spectroscopy, Research Methodology and Scientific Writing
Paper Code: GNKPSBIP401
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

A Report to be submitted at the time of Examination-THESIS

Reference:

- W.M.A Niessen, Chromatography – LCMS 2nd and 3rdedition
- J Mendham, R C Denney, J D Barnes, M J K Thomas, Vogel's Textbook of Quantitative chemical Analysis 6thedition
- Misra R.P., 1989, Research Methodology: A Handbook, New Delhi, Concept Publishing Company
- Kumar, R., 2005, Research Methodology - A Step-by-Step Guide for Beginners,(2nd.ed.), Singapore, PearsonEducation.
- Bhattachraya, D.K., 2006, Research Methodology,(2nd.ed.),New Delhi, ExcelBooks.
- Panneerselvam R., 2012, Research Methodology, New Delhi, PHI Learning Pvt.Ltd.

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Syllabus for M.Sc. Semester IV

Program: Masters of Science

Course: Bioinformatics

Paper: II

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics (2021-2022)
Paper II
Course Title: Molecular Modeling and Simulations
Paper Code: GNKPSBI402
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- Comprehend the drug discovery and development process.
- To provide an understanding about the various mechanisms taking place in a biological environment with special emphasis to macromolecules, their structural and thermo-dynamical properties, a necessity for drug designing.
- To understand molecular dynamics concepts of temperature, ensemble, and periodic boundaries.
- Thoughtful the structural properties and energy minimization in folding process
- To set up free energy calculations.
- Appreciate the working and paraments for the software.
- To understand the modeling of molecules including hard potentials, soft potentials, torsion and bend potential.
- Toprovidebiophysicsknowledgetothestudentsthiswillpaveawayforfurtherexcellent application of the concepts.

Learning Outcome:

- To understand the basic concepts which determines the design and discovery of drugs.
- To absorb the Bioorganic, medicinal and physico-chemical principles behind the rational designing and mechanism of drugs.
- Helps to determine the drug stereochemistry in drug design and molecular modeling.

- Understand how quantum mechanical models can be used to describe chemical reactions and properties.
- Evaluate the accuracy of performed calculations
- Explain how quantum mechanics can contribute to the understanding of reaction mechanisms in organic chemistry and catalysis.
- Understand the theory, concepts and terminology of computational chemistry with anemphasis on electronic structure calculations using the molecular-orbital model.

Semester IV

Unit		Title	No. of lectures
Unit 1		**Introduction to Structure-based drug Design**	
	1.1	Introduction to Molecular docking, validation and Scoring	
	1.2	Various methods for conformation generations for docking.	
	1.3	Methods to incorporate receptor flexibility	**15**
	1.4	Scoring Functions	
	1.5	Structure-based virtual screening (special emphasis on enrichments)	
Unit 2		**Introductions to QSAR and Machine Learning**	
	2.1	QSAR- Historical aspects, Hansch analysis and Free-Wilson analysis	
	2.2	Deriving QSAR equations (Simple and Multiple linear regressions, Principle component regression, Partial Least squares, and Genetic algorithms) and selection of diverse sets (Clustering analysis, dissimilarity-based methods, etc)	**15**
	2.3	Introduction to Machine learning (Neural networks, random forest methods, Support vector machines and other deep learning methods such as PyTorch platform)	
	2.4	Various aspects of validating results from QSAR and machine learning methods. Special emphasis on applicability domains	
Unit 3		**Types of QSAR**	
	3.1	Introductions to various 3D QSAR (molecular field analysis) methods (CoMFA, CoMSIA, CoRIA, COMBINE, AFMoC, etc)	**15**
	3.2	Brief overview of Higher order QSAR methods (4D to 6D)	
Unit 4		**Molecular Modeling and Drug Designing Software**	
	4.1	GROMACS	**15**
	4.2	AUTODOCK	
	4.3	Discovery studio Visualizer	

Semester IV Evaluation Pattern
Internal: 25marks
External: 75marks

M.Sc. Bioinformatics (2021-2022)
Paper II
Course Title: Molecular Modeling and Simulations
Paper Code: GNKPSBIP402
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. PerformingMoleculardockingstudiesusingatleast2differentmethods(variousstepsto be emphasized) and validating molecular docking using experimental data
2. Performing QSAR studies on at least 3 sets (different molecular targets with at least 50 molecules) and validation of these models (at least 8-10 parameters). Demonstration on use of applicability domains using one of the aforementioned sets
3. Molecular Modeling Software: GROMACS, AUTODOCK, Discovery studio Visualizer

References:
- Bunin BA. 2006. Chemoinformatics: Theory, Practice and Products. Springer Gasteiger J & Engel T. 2003. Chemoinformatics: A Textbook. Wiley-VCH. HinchliffeA.2003.
- Molecular Modelling for Beginners. John Wiley & Sons. Leach AR. 1996.Molecular Modelling: Principles and Applications.Longman.
- Bioinformatics : Databases, Tools & Algorithms – OrpitaBosu and Simminder Kaur Thukral (Oxford HigherEducation)
- A Text Book of Bio-informatics - Singhal and Singhal (PragatiPrakashan) Molecular Modelling and drug Design (Leech) Textbook of Drug Design and Discovery (Editedby
- PovlKrogsgaard – Larsen, Tommy Liljefors and Ulf Madsen) Taylor FrancisPublication.
- Molecular Modeling for Beginners: AlanHincliffe
- Text Book of Drug Design and Discovery (Edited by PovlKrogsgaard – Larsen, Tommy Liljefors and Ulf Madsen) Taylor and FrancisPublication.
- Bioinformatics basic methods and applications – S.C.Rastogi

- Molecular Modelling for Beginners, (2nd Edition) by Alan Hinchliffe, JohnWiley & Sons Ltd. 20082.
- Molecular Modeling and Simulation – An interdisciplinary Guide by TamarSchlick, Springerverlag.2000
- Textbook of Drug Design and Discovery (Edited by PovlKrogsgaard – Larsen, Tommy Liljefors and Ulf Madsen) Taylor FrancisPublication.
- Text Book of Drug Design and Discovery (Edited by PovlKrogsgaard – Larsen, Tommy Liljefors and Ulf Madsen) Taylor and FrancisPublication
- Höltje Hans-Dieter, Sippl Wolfgang, Rognan Didier, FolkersGerd. MolecularModeling: Basic Principles and Applications. Publisher: New York, Wiley-VCH. 2003. ISBN: 3527305890
- Computational Chemistry and Molecular Modeling-Principles and Applications by Ramachandran
- Molecular Modeling and Simulation – An interdisciplinary Guide by TamarSchlick, Springerverlag.2000

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Syllabus for M.Sc. Semester IV

Program: Masters of Science

Course: Bioinformatics

Paper: III

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics (2021-2022)
Paper III
Course Title: Clinical Research and Clinical Data Management
Paper Code: GNKPSBI403
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- That the trial database is complete, accurate and a true representation of what tookplace in the trial
- That the trial database is sufficiently clean to support the statistical analysis and its interpretation
- To manage the clinical data within a research study.
- Helps to gather concepts and processes involved in CDM.
- Train on various aspects of CDM like CRF Designing, Data entry, Data Collection, AEManagement, Report Creation etc.
- Students will learn regulations impacting clinical data management, describe the framework for clinical data management operations, and processes involved in thesetup of clinical data management.

Learning Outcome:

- Aids to understand data security.
- Understand the theoretical knowledge on various essential CR topics: Drug Discovery, Regulatory, GCP, Ethics etc.
- Roles and Responsibilities CR and CDM personnel along with its application required toexecute at various levels.

Semester IV

Unit		Title	No. of lectures
Unit 1		**Introduction to Clinical Research**	**15**
	1.1	Introduction to Clinical Research and Preclinical testing	
	1.2	Terminologies and definition in Clinical Research	
	1.3	Origin and History of Clinical Research	
	1.4	Pharmaceutical Industry – Global and Indian Perspective	
	1.5	Preclinical testing and Investigational New Drug Application	

1.6	Post marketing surveillance and Pharmacovigilance	
1.7	Investigation of New Drug Application, Its Approvaland Clinical Trials	
1.8	Careers in Clinical research	

		Drug Discovery and Development	
Unit 2	**2.1**	Introduction to Pharmacology and concept of drugs and various sources of drugs	**15**
	2.2	Routes of Drug Administration and Formulations	
	2.3	Introduction to Pharmacokinetics and Pharmacodynamics: Concept of Absorption, Distribution, Metabolism, Excretion and Toxicity	
	2.4	Introduction to CYP-450 class of enzymes and drug metabolism.	
	2.5	Concept of metabolic stability of drugs	
	2.6	Various Pharmacological models for evaluation of drug efficacy and potency (in vitro, in vivo and ex vivo models)	
	2.7	Evolutionary Classification of the strategies for Drug Discovery	
	2.8	Basics of Drug Discovery & Development	
	2.9	Approaches to Drug Discovery	
	2.10	Introduction to Drug Discovery and Development: Target identification and validation, Hit identification, Hit-to-lead and lead optimization	
	2.11	Emerging technologies in Drug Discovery: High throughput and High-content screening	
	2.12	Introduction to concept of Prodrugs and Biosteres	
	2.13	Hurdles in Drug Development &Preclinical Testing	

		Regulation in Clinical Research	
Unit 3	**3.1**	Introduction of Clinical Trial Regulation	**15**
	3.2	European Medicine Agency	
	3.3	Food and Drug Administration (US FDA)	
	3.4	Drug and cosmetics act: Schedule Y	
	3.5	ICMR Guideline	

		Clinical Trials & Data Management	
Unit 4	**4.1**	Project Management, Protocol in Clinical Research, Informed Consent	
	4.2	Case Report Form : Investigator's Brochure (IB), Selection of an Investigator and Site , Clinical Trial Stakeholders, Contract Research Organization (CRO) , Site management organizations (SMO)	**15**

	4.3	Introduction to CDM: CRF Design, Clinical Data Entry, Electronic Data Capture , Data Validation, Discrepancy Management, Clinical Data Coding, SAE Reconciliation, Quality Assurance & clinicalData Management and Guideline & Regulation in Clinical trial data	

Semester IV Evaluation Pattern
Internal: 25marks
External: 75marks

M.Sc. Bioinformatics (2021-2022)
Paper III
Course Title: Clinical Research and Clinical Data Management
Paper Code: GNKPSBIP403
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. Demonstration and interpretation of LC/MS/MS quantitation of a modern drug (e.g.Diclofenac Sodium).
2. Demonstration and interpretation of MALDI-TOF.
3. Case study on Clinical Data Management

References:
1. SusanneProkscha(2011),PracticalGuidetoClinicalDataManagement,ThirdEdition,CRC Press; 3 edition (18 November 2011), ISBN-13:978-1439848296.
2. Richard K Rondel (2000) Clinical Data Management, Second Edition. Wiley Publishing House. ISBN:978-0-470-85335-1.
3. Data management in clinical research: An overview by BinnyKrishnankutty, Shantala Bellary,NaveenB.R.Kumar,andLathaS.Moodahadu,IndianJPharmacol.2012Mar-Apr; 44(2): 168–172. doi:10.4103/0253-7613.93842
4. A tiered quality assurance review process for clinical data management standard

operating procedures in an academic health center by Ittenbach RF1, Baker CL, Corsmo JJ., Acad Med. 2014 May;89(5):745-8. doi:10.1097/ACM.000000000000022

5. InfrastructureandcontentsofclinicaldatamanagementplanByShenT,XuLD,FuHJ,Liu Y, He J, Chen PY, Song YF. , Yao XueXueBao. 2015Nov;50(11):1388-92.

6. ClinicalDataAcquisitionStandardsHarmonizationimportanceandbenefitsinclinicaldata management by Gaddale JR1.,PerspectClin Res. 2015 Oct-Dec;6(4):179-83. doi: 10.4103/2229-3485.167101.

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Syllabus for M.Sc. Semester IV

Program: Masters of Science

Course: Bioinformatics

Paper: IV

(As per Choice Based Semester and Grading System with effect from Academic Year 2021-2022)

M.Sc. Bioinformatics- Semester IV (2021-2022)
Paper IV
Course Title: Python
Paper Code: GNKPSBI404
Credits: 04
No. of Lectures: 60
Marks: 100

Learning Objectives:

- To understand why Python is a useful scripting language for developers.
- To learn how to design and program Python applications.
- To learn how to use lists, tuples, and dictionaries in Python programs.
- To learn how to identify Python object types.
- TolearnhowtouseindexingandslicingtoaccessdatainPythonprogramsforbiological data.

Learning Outcome:

- Problem solving and programming capability.
- Students can use command line tools to write and edit code.
- Students can write code in Python to perform mathematical calculations and scientific simulations.
- Students can produce publication-ready graphics from a dataset.

Semester IV

Unit		Title	No. of lectures
Unit 1		**Introduction to Python and OOPs Concept**	
	1.1	Basic of python commands,	
	1.2	Numbers and other data types, Expressions and Operators	**15**
	1.3	Decisions and Loops, List	
	1.4	String Functions	
	1.5	Functions	
	1.6	Object-Oriented Programming	
Unit 2		**Regular Expression and Pattern Matching**	
	2.1	Introduction to Regular expressions	**15**
	2.2	RegEx Module, RegEx Functions	

	2.3	Metacharacters	
	2.4	Special Sequences	
	2.5	Spilt and Join function	
Unit 3		**Biopython**	
	3.1	Introduction	
	3.2	Working with sequences	
	3.3	Sequence objects	**15**
	3.4	Sequence annotation objects	
	3.5	Sequence Input/ Output	
	3.6	BLAST and other sequence search tools	
Unit 4		**Database Interaction with Mongo dB using python**	
	4.1	Installation	
	4.2	Establishing a Connection, Accessing Databases, Inserting, Retrieving data	**15**
	4.3	Simple Queries using python	

Semester IV Evaluation Pattern
Internal: 25marks
External: 75marks

M.Sc. Bioinformatics- Semester IV (2021-2022)
Paper IV
Course Title: Python
Paper Code:GNKPSBIP404
Credits: 02
No. of Practical's: 04/per week (04 hours each)
Marks: 50

1. Basic programs on Python.
2. Programs on Regular expression and Pattern Matching.
3. Programs on Biopython.
4. Programs on connectivity with python and Mongodb

References:

1. Python - The Complete Reference (English, Brown MartinC.)
2. Python Cookbook, Thirdedition
3. Python Programming: A modular approach byPearson
4. MongoDB: The Definitive Guide" by KristinaChodorow