

DR. BABASAHEB AMBEDKAR MARATHWADA UNIVERSITY



CIRCULAR NO.SU/M.Sc./Bioinformatics/27/2022

It is hereby inform to all concerned that, the syllabi prepared by the Ad-hoc Board and recommended by the Dean, Faculty of Science & Technology, the Hon'ble Vice-Chancellor has accepted **the syllabus of M.Sc. Bioinformatics Ist & IInd semester under the scheme of Choice Based Credit & Grading System** in his emergency powers under section 12(7) of the Maharashtra Public Universities Act, 2016 on behalf of the Academic Council as appended herewith.

This is effective from the Academic Year 2022-23 and onwards.

All concerned are requested to note the contents of this circular and bring the notice to the students, teachers and staff for their information and necessary action.

University Campus,
Aurangabad-431 004.
REF.NO.SU/2022/ 12800-09
Date:- 18.10.2022.

★
★
★
★

[Signature]
**Deputy Registrar,
Academic Section**

Copy forwarded with compliments to :-

- 1] **The Principal of all concerned Colleges,**
Dr. Babasaheb Ambedkar Marathwada University,
- 2] **The Director, University Network & Information Centre, UNIC, with a request to upload this Circular on University Website.**

Copy to :-

- 1] **The Director, Board of Examinations & Evaluation,**
Dr.BAMU,A'bad.
- 2] The Section Officer,[M.Sc.Unit] Examination Branch,Dr.BAMU,A'bad.
- 3] The Programmer [Computer Unit-1] Examinations, Dr.BAMU,A'bad.
- 4] The Programmer [Computer Unit-2] Examinations, Dr.BAMU,A'bad.
- 5] The In-charge,[E-Suvidha Kendra], Rajarshi Shahu Maharaj Pariksha Bhavan, Dr.BAMU,A'bad.
- 6] The Public Relation Officer, Dr.BAMU,A'bad.
- 7] The Record Keeper, Dr.BAMU,A'bad.

Dr. Babasaheb Ambedkar Marathwada University
Aurangabad - 431004 (MS) India



**Post-Graduate Master
Degree Program
in**

M.Sc. Bioinformatics

Course Structure and Curriculum

Choice Based Credit System (CBCS)

(Effective from Academic Year 2022-23 onward & progressively)

Dr. Babasaheb Ambedkar Marathwada University
Aurangabad – 431004 (MS) India

*Chairman,
Ad-hoc in Bioinformatics*
*Dean,
Faculty of Sci. & Tech.*
Page 1 of 34

INDEX

Sr. No.	Contents	Pg. No.
1	Preamble	
2	Course Structure	
3	Vision	
4	Mission	
5	Program Educational Objectives	
6	Program Outcome and Programme Specific Outcomes	
7	Eligibility	
8	Duration	
9	Medium of Instructions	
10	Choice Based Credit System, Credit- to -Contact Hour mapping ...	
11	Attendance	
12	Evaluation Methods / Scheme of Examination, Earning Credits, Grading System	
13	Curriculum: Semester – I	
14	Curriculum: Semester – II	

1. Preamble

Bio informatics is a rapidly maturing field at the confluence of biology, mathematics and computer science. It strives to better understand the molecules essential for life, by harnessing the power and speed of computers. Mathematical models and software are developed by computational biologists, who must have good skills in math and computer science. However, the working (experimental) biologist is generally a user of "black box" bio informatics software and databases, with little knowledge of the underlying algorithms. While there's no need for the working biologist to be able to develop sophisticated mathematical models or design and implement novel algorithms, there is a need to understand the broad ideas of algorithms underlying the tools the biologist uses. As a working professional in the medical and life sciences, this knowledge is important to understand the scope, applicability, and limitations of certain tools -- and, who knows, you may become turned on by the idea of ferreting out biological insights by applying mathematics and computer science, and so choose to pursue further courses to become a computational biologist.

Master of Science in Bioinformatics i.e. M.Sc. (Bioinformatics) is a 2-years (4-Semesters) Post Graduate Programme of professional nature. It is primarily aimed to enable biological science graduates with bioinformatics skills for a career in the Post-Genomics era. Though, its courses cater well specifically for biological science graduates but also suited to especially inspired aspirants from other backgrounds. It is now firmly accepted that computing and information technologies applies equally well to furtherance of research on proteins, genes etc. And that the new age biological research highly driven by high-end computing and computational modeling is inevitable. The Programme includes training in the major areas of Bioinformatics. In particular, the rigorous exposure in interdisciplinary areas is aimed additionally at equipping the students with strong analytical and technical skills to work competently in diverse areas including teaching, research and developments.

Bioinformatics refers to the creation and development of databases, software, computational and statistical techniques and theory to solve problems generated from the management and analysis of biological data. On the other hand, computational biology refers to the hypothesis based investigation of a specific

biological problem using computers, carried out with experimental or simulated data, with the primary goal of discovery and the advancement of biological knowledge.

In the recent years in this age of Internet and sequenced genome we have more information at our fingertips than ever before. Organizing this entire data and combating information overload is becoming more and more important. The advent of genetic engineering vastly increased size of the information. It is thus necessary for institutes like university evolve a system, which is most accurate and more student friendly. After completion of course, there are multiple job opportunities available for bioinformatics post graduate students in national & multinational companies in the field of life sciences, information technology, software development, database administration, pharmaceutical, agricultural, health & clinical research.

2. Structure and Curriculum for

M.Sc. Bioinformatics

(Choice Based Credit System)

Dr. Babasaheb Ambedkar Marathwada University, Aurangabad Choice Based Credit System (CBCS) Curriculum For Faculty of Science and Technology Course Structure and Scheme of Examination (M.Sc. Bioinformatics)							
Semester I							
Course Code	Course Title	Teaching time/week	Credits	Scheme of Examination			
				Max Marks	CIA	UA	Min Marks
MBI-101	Basic Biology and Biomathematics&Biostatistics	4 hours	4	100	20	80	40
MBI-102	Basic Concept in Computing & Database Management System	4 hours	4	100	20	80	40
MBI-103	Biochemistry & Central Dogma	4 hours	4	100	20	80	40
MBI-104	Biological Databases & Data Analysis	4 hours	4	100	20	80	40
Compulsory	Constitution of India	2 hours	2	50	10	40	-
MBI-111	Practical based on MBI-101	4 hours	2	50	-	50	20
MBI-112	Practical based on MBI-102	4 hours	2	50	-	50	20
MBI-113	Practical based on MBI-103	4 hours	2	50	-	50	20
MBI-114	Practical based on MBI-104	4 hours	2	50	-	50	20
		34	26	650	90	560	240
Total Credits for Semester I : 26 (Theory : 18 ; Laboratory : 08)							

Dr. Babasaheb Ambedkar Marathwada University, Aurangabad**Choice Based Credit System (CBCS) Curriculum****For****Faculty of Science and Technology****Course Structure and Scheme of Examination****(M.Sc. Bioinformatics)****Semester II**

Course Code	Course Title	Teaching time/week	Credits	Scheme of Examination			
				Max Marks	CIA	UA	Min Marks
MBI-201	Structural Bioinformatics	4 hours	4	100	20	80	40
MBI-202	Programming in C	4 hours	4	100	20	80	40
MBI-203	Object-Oriented Programming in JAVA & BIOJAVA	4 hours	4	100	20	80	40
MBI-204	Chemoinformatics & Biodiversity Informatics	4 hours	4	100	20	80	40
MBI-211	Practical based on MBI-201	4 hours	2	50	-	50	20
MBI-212	Practical based on MBI-202	4 hours	2	50	-	50	20
MBI-213	Practical based on MBI-203	4 hours	2	50	-	50	20
MBI-214	Practical based on MBI-204	4 hours	2	50	-	50	20
		32	24	600	80	520	240

Total Credits for Semester II : 24 (Theory : 16 ; Laboratory : 08)

Dr. Babasaheb Ambedkar Marathwada University, Aurangabad**Choice Based Credit System (CBCS) Curriculum****For****Faculty of Science and Technology****Course Structure and Scheme of Examination****(M.Sc. Bioinformatics)****Semester III**

Course Code	Course Title	Teaching time/week	Credits	Scheme of Examination			
				Max Marks	CIA	UA	Min Marks
MBI-301	Taxonomy &Phylogeny	4 hours	4	100	20	80	40
MBI-302	Introduction to LINUX	4 hours	4	100	20	80	40
MBI-303	Genomics, Proteomics & Genome to Drug & Vaccine	4 hours	4	100	20	80	40
MBI-304	Programing in PERL & Bio-PERL	4 hours	4	100	20	80	40
MBI-311	Practical based on MBI-301	4 hours	2	50	-	50	20
MBI-312	Practical based on MBI-302	4 hours	2	50	-	50	20
MBI-313	Practical based on MBI-303	4 hours	2	50	-	50	20
MBI-314	Practical based on MBI-304	4 hours	2	50	-	50	20
		32	24	600	80	520	240
Total Credits for Semester III : 24 (Theory : 16 ; Laboratory : 08)							

Dr. Babasaheb Ambedkar Marathwada University, Aurangabad Choice Based Credit System (CBCS) Curriculum For Faculty of Science and Technology Course Structure and Scheme of Examination (M.Sc. Bioinformatics)							
Semester IV							
Course Code	Course Title	Teaching time/week	Credits	Scheme of Examination			
				Max Marks	CIA	UA	Min Marks
MBI-401	Programming in Bio-python & R	4 hours	4	100	20	80	40
MBI-402	Advanced Techniques in Biological Data Analysis	4 hours	4	100	20	80	40
MBI-403	System Biology	4 hours	4	100	20	80	40
MBI-404	Emerging Areas in Bioinformatics	4 hours	4	100	20	80	40
MBI-411	Practical based on MBI-401	4 hours	2	50	-	50	20
MBI-412	Practical based on MBI-402	4 hours	2	50	-	50	20
MBI-413	Practical based on MBI-403	4 hours	2	50	-	50	20
MBI-414	Major Project	4 hours	2	50	-	50	20
		32	24	600	80	520	240
Total Credits for Semester IV: 24 (Theory : 16 ; Laboratory : 08)							

3. **Vision**

To empower students through the development of computational skills & analytical skills required to excel in the field of "life sciences"

4. **Mission**

- To make students globally competent by training them on advanced techniques through state-of-the-art facilities.
- Facilitating skill based training in computational and statistical techniques for biological data analysis.
- Enable students to efficiently involve themselves in data ware housing and data mining.
- To familiarize and train students on all biological databases along with on-line and many advanced off-line bio molecular data analysis software.

- To provide basic to core biological knowledge to relate biological information on gene function and protein structure/function with sequence and genome.
- To enable students to work on platforms like Drug designing, Molecular Docking, Chemoinformatics, NGS data analysis, Microarray data analysis etc.
- To deliver ICT enabled teaching and learning.

5. **Program Educational Objectives:**

1. Advance knowledge through quality research in important emerging areas in the discipline and to build strong relationship with industry, academia and society.
2. Able to analyze, design and implement optimized solutions for the real-world problems and become engineering professional, innovator, product developer or entrepreneur.
3. Develop an ability to adapt, work as a team to implement trans-disciplinary and multidisciplinary projects using the cutting edge tools and technologies.
4. Graduates will be ethical and socially responsible and be able to pursue higher education/research in reputed institutions

6. **Programme Outcomes (POs) and Programme Specific Outcomes:**

- Students will learn through applying the strategies and tools used in bioinformatics to topical problems drawn from ongoing research and applications in a variety of fields.
- A number of recent workforce studies have shown that there is a high current and unmet demand for people trained to various levels of expertise in bioinformatics.
- The emergence of new Internet technologies, new and more accurate algorithms and the development of High Performance Computing coupled with DNA sequencing, serial analysis of gene expression, microarrays, and new mass spectrometry has enabled bioinformatics to address the biological problems from several different angles. It is this change in paradigm that has led to the development of Bioinformatics as a separate skill oriented discipline.
- This course provides scope for employment opportunities in various industries in the applied aspects Biotechnology, Microbiology, Molecular biology, Drug discovery and Drug design and Information technology.
- The ability to formulate mathematical models and problem-solving skills through programming techniques for addressing real-time problems using appropriate data structures and algorithms.
- The ability to design hardware and software through system programming skills based on the knowledge acquired in the system software and hardware courses.
- The ability to interpret relationships among living things and analyze the biological problems, from molecular to ecosystem level, solving those using basic biological concepts, algorithms, and tools available in computer science and to facilitate the biological database system.

7. **Eligibility:** B. Sc. degree in Science (Bioinformatics, Biotechnology, Botany, Zoology, Microbiology, Physics, Chemistry, Computer Science & IT, and Agriculture) or B.E./B.Tech, B.Pharm, Medical Science, Veterinary Science.

8. **Duration:** The course will be of two years duration and shall be completed in four semesters.

9. **Medium of Instructions:** English

10. **Choice Based Credit System (CBCS) and Credit-to-contact hour mapping:**

One Credit would mean equivalent of 15 periods of 60 minutes each for theory lecture. For lab course/ workshops/internship/field work/project, the credit weightage for equivalent hours shall be 50% that for lectures /workshop

11. **Attendance:** A candidate is required to put in a minimum of 75% of attendance in both theory papers practical separately in each subject before admission to the examination. This relaxation in attendance includes for medical & any other reasons approved by the head of the Institution. A candidate lacking in the prescribed attendance and progress in any one of the subjects in theory and practical in the first appearance shall not be permitted for admission to the entire examination.

12. **Evaluation Methods/ Scheme of Examination, Earning Credits, Grading System:**

Theory

a. Each theory paper examination shall be of 3 hours duration and of maximum marks 80.

b. There will be three question papers (03 sets each) for each year and shall be in accordance with the different subjects/area covered during each of the M. Sc. Bioinformatics two year course.

c. The Paper setter shall set the questions within the prescribed course of study of the concerned paper. There will be a set pattern of question papers duly approved by Academic Council, Dr. Babasaheb Ambedkar Marathwada University, Aurangabad.

d. Internal Assessment – Internal assessment shall be of 20 marks for each theory paper.

e. Passing criteria - A candidate will have to obtain at least 40% marks in each Theory paper to pass.

f. To conduct 02 internal exams of each theory paper per semester, pattern of internal exam should be objectives.

Practical

- Practical examination will be conducted in presence of internal & external examiner as per university guidelines.

- Students shall be required to obtain a minimum of 40% marks in the each paper of practical examination. A candidate who fails to obtain 40% marks shall be declared failed.
- Practical exam should be conducted at the end of each semester

The Grading:

At the end of each semester, the teacher will assign grades to each student and will submit it to the department. The department will submit these grades to the university to give official results to students.

The grade will be as follows:

- **O (Outstanding)** will have 9.00-10 points
- **A++ (Excellent)** will have 8.00-8.99 points
- **A+ (Exceptional)** will have 7.00-7.99 points
- **A (Very good)** will have 6.00-6.99 points
- **B+ (Good)** will have 5.50-5.99 point
- **B (Fair)** will have 5.00-5.49 point
- **C+ (Average)** will have 4.50-4.99 point
- **C (Below average)** will have 4.01-4.49 point
- **D (Pass)** will have 4.00 point.
- **F (Fail)** will have 0 point.

Any student with F grade will be considered to be failed in the course. He has to repeat the course in the next semester or in some other semester as instructed by the Head of the department. There will not be any reevaluation or reexamination in the system.

The Grade Point Average (GPA):The student will have GPA between 4 to 10 computed as follows:

GPA= $\frac{\text{Sum (Course credit * number of points in the course by a student)}}{\text{Sum (Course Credit)}}$ The final grading which will be consistent with the UGC scheme will be awarded as per the GPA .

13. Curriculum for Semester I

MBI-101: Basic Biology and Biomathematics & Biostatistics

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

The concept of origin of Life, Systematics: Species concept; kingdom to species; the five kingdoms; classical, phenetic and cladistics approaches, Prokaryotic & Eukaryotic Cells, Structural and functional capitalization of cell, Structure of bacterial cell; bacterial types; transformation, transfection, transduction and conjugation; nutrition and phylogeny, Biology of viruses; bacteriophages, plant and animal viruses; replication of viral genome, Corona Virus.

Unit-II

Protists: Endosymbiont theory of eukaryotic origin; protozoan, algae, slime and water molds Fungal World: Feeding, reproduction, diversity and relationships Plant Diversity: Broad classification and inter-relationships of non-vascular and vascular plants; tissue organization; reproductive patterns; transport mechanisms, growth, photosynthesis, hormones. Animal Life: Major animal phyla, characteristics and interrelationships; tissues, organs and organ/systems; principles of nutrition, digestion, thermoregulation, osmoregulation and excretion, muscle contraction, neural reflexes, circulation, respiration and endocrines.

Unit-III

Basic Mathematics, Vectors: Vector algebra, Dot and Cross products. Matrices: Algebra of Matrices, Transpose and inverse, Diagonalization of Matrices and Characteristic roots. Basic Differentiation and Integration Techniques.

Unit-IV

Basics of biostatistics: Population, Sample, Variable, Parameter, Primary and Secondary Data; Screening, Representation and Classification of Data; Frequency Distribution, Tabulation and Graphical Representations; Mean, Geometric Mean, Harmonic Mean, Median and Mode; Quartiles and Percentiles; Measures of Dispersion: Range, Variance, Standard Deviation, and Coefficient of Variation.

Unit-V

Probability and Distributions, Correlation & Regression: Methods of studying simple correlation: Scatter Diagram, Karl Pearson's Co-efficient of Correlation, Spearman's Rank Correlation. Regression Analysis: Meaning and Purpose of Regression. Simple and Multiple Linear Regressions, Concept of ANOVA. Tests of significance based on Chi-square, t and F distributions: Chi-square test for Population Variance, Goodness of fit & test for independence of attributes. T-test for single mean, difference of means, paired t-test, correlation coefficients. F-test for Population Variances.

References

- Goon A.M., Gupta M.K. and Dasgupta B. (2002): Fundamentals of Statistics, Vol. I & II, 8th Edn. The World Press, Kolkata.
- Miller, Irwin and Miller, Marylees (2006): John E. Freund's Mathematical Statistics with Applications, (7th Edn.), Pearson Education, Asia.
- Campbell R.C.- Statistics for Biologists, Cambridge University Press, Cambridge.
- Ward Law A.C. (1985)- Practical statistics for Experimental Biologists.
- Baily N.T.J- Statistical Methods in Biology, English University Press.
- P.S.S. Sunderrao and J. Richards-An introduction to Biostatistics, Prentice Hall Pvt. Ltd. India.
- B.S. Verma Discrete Mathematics, Vishwa Prakashan.
- Adam Purcell Basic Biology: an Introduction

MBI-102: Basic Concept in Computing & Database Management System

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Introduction to Computer, Characteristics & features of Computers. Components of Computers. Organization of Computer. Generation of Computers, Classification of Computers. Computer Languages: Types of Programming Languages, Machine Languages, Assembly Languages, High Level Languages, Interpreter & Compiler. Input Devices, Output Devices, Computer Memory, Types of computer Memory (Primary and Secondary), Computer Software and Types.

Unit-II

Operating system Concepts: Functions of Operating System, Types of Operating System, Comparison of Windows, Linux, Unix etc. Computer Networking, Network Topologies, FTP, TCP/IP Protocols, Local Area Network (LAN), Wide Area Network (WAN), Metropolitan Area Network (MAN).

Unit-III

Introduction to DBMS: Applications, Purpose of Database Management System, Database Architecture: 3-Level architecture, Database Users & Administrators Functional Components of Database system: Storage & Query Processor, Transaction Management. Type of Data Model: Relation Data Model, E-R Data Model, Object Based Data Model Semi-Structured Data Model, Hierarchical Data Model and Network Data Model E-R. Data Model: Entity, Entity set, Entity types, Attributes, Types of Attributes, E-R diagram. Mapping Cardinalities, Data Association, Specialization, Aggregations and Integrity constraints

Unit-VI

Functional Dependencies and Normalization: First Normal Form (1NF), Second Normal Form (2NF), Third Normal Form (3NF), and Boyce-Codd Normal Form (BCNF). Relational Algebra Operations – Select, Project, Rename, Union, Intersection, Set Difference, Join, and Division Operations

Unit-V

SQL: Introduction to SQL, Data Types, DDL: create, alter, drop, DML: insert, select, update, delete, DML Queries with where clause, TCL: commit, rollback, savepoint, DCL: grant, revoke, Key Constraint: not null, Primary Key, Foreign

Key, Renaming Attributes, Aggregate Functions, Join Operations. Logical Operator.

References:

- Fundamentals of Computers By V.Rajaraman, PHI Publication, IVth Edition.
- Computer Organisation by Hamacher,
- Fundamentals of Information Technology By Chetan Srivastava
- Database System concepts: Korth, Siberschatz,
- An Introduction to Database Systems by Date, C.J., Addison Wesley Publishers.
- Fundamentals of Database Systems by Elmasri and Navathe, Addison Wesley Publishers.

MBI-103: Basic Biochemistry & Central Dogma

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Cellular and chemical foundations of life, Water: Unique properties, weak interactions in aqueous systems, ionization of water, buffers, water as a reactant and fitness of the aqueous environment. Nucleic Acid: Nucleotides - structure and properties. Nucleic acid structure – Watson - Crick Model of DNA. Structure of major species of RNA - mRNA, tRNA and rRNA. Nucleic acid chemistry.

Unit-II

Amino acids: Definition, classification & structures. Physico-chemical properties of amino acids, Peptide bond: Definition, structure and geometry of peptide bond, example of biologically important peptide and its functions. Proteins: Definition of structure, primary, secondary, tertiary and quaternary structure (definition and example), Globular, Membrane & Fibrous proteins (definition and example), forces that stabilize structure of proteins. Enzyme: Nomenclature, Classification and their kinetics.

Unit-III

Carbohydrate: Monosaccharides - structure of aldoses and ketoses, ring structure of sugars, conformations of sugars, mutarotation, anomers, epimers and enantiomers, structure of biologically important sugar derivatives, oxidation of sugars. Formation of disaccharides, reducing and non- reducing disaccharides. Polysaccharides– homo- and heteropolysaccharides, structural and storage polysaccharides. Structure and role of proteoglycans, glycoproteins and glycolipids. Lipids: Building blocks of lipids - fatty acids, glycerol, ceramide. Storage lipids - triacyl glycerol and waxes. Structural lipids in membranes – glycerophospholipids, galactolipids and sulpholipids, sphingolipids and sterols, structure, distribution and role of membrane lipids. Lipids as signals, cofactors and pigments (preliminary ideas only)

Unit-IV

Bacterial, eukaryotic & extrachromosomal replicons, Replication in prokaryotes--Escherichia coli replication as role model, DNA polymerases –with reference to their functional properties, formation of replication fork, primer formation, replication on leading and lagging strand, termination of replication. Eukaryotic DNA replication: Origin Recognition Complex, Licensing factor, components of replicase and other polymerases. Replication fork – experimental proof for multiple replication forks in eukaryotes. Process of replication, initiation, elongation and termination& their regulation. Extrachromosomal DNA replication.

Unit-V

Prokaryotic transcription- Transcription in Escherichia coli a role model for prokaryotes –RNA polymerase, structural components and assembly of core and holoenzyme, process of initiation, elongation & termination, antiterminators from bacteria & bacteriophages, Eukaryotic Transcription-RNA polymerase, mechanism and elements involved in initiation, elongation & termination. Mechanism of prokaryotic & eukaryotic translation, post translational modification & protein transport.

References

- Lehninger: Principles of Biochemistry (2013) 6th ed., Nelson, D.L. and Cox, M.M., W.H. Freeman and Company (New York), ISBN: 13: 978-1-4641-0962-1 / ISBN: 10:1-4292- 3414-8.
- Fundamental of Biochemistry, Voet and Voet- provide necessary details on latest edition Edited by Prof. Hiren K Das (JNU)
- Molecular Biology –David Frifelder
- Genes IX –Benjamin Lewin
- Molecular biology of the gene J. D. Watson and et. al.,
- Molecular Biology of the Cell –Bruce Alberts and et. al.,

MBI-104: Biological Databases & Data Analysis

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Introduction of Bioinformatics, scope & applications, Role of internet and WWW in bioinformatics. Basic biomolecular concepts: Protein and amino acid, DNA & RNA, Sequence, structure and function. Forms of biological information, Types of Nucleotide Sequence: Genomic DNA, Complementary DNA (cDNA), Recombinant DNA (rDNA), Expressed sequence tags (ESTs), Genomic survey sequences (GSSs). DNA sequencing methods: Basic and Automated DNA sequencing.

Unit-II

Bioinformatics Resources – NCBI, EBI, SIB, The knowledge of databases and bioinformatics tools available at these resources, organization of databases: data contents, purpose and utility. Biological Database: Definition and types, Sequence databases – Nucleic acid sequence databases: GenBank, EMBL, DDBJ; Protein sequence databases: Uniprot: UniParc, Uniref, UniprotKB: SWISS-PROT, TrEMBL, Derived Databases: Prosite, PFam, Structure Databases: PDB, NDB. Sequence file formats: Various file formats for biomolecular sequences: GenBank, FASTA, GCG, MSF etc., READSEQ tool.

Unit-III

Genome Databases: EnsEMBL, UCSC Genome Browser, Metabolic Pathway databases-KEGG, EcoCyc and MetaCyc, Enzymes, Compounds and Reaction databases- LIGAND -Biochemical Compounds and Reactions, BRENDA - Comprehensive Enzyme Information System, Entrez: Concept & application.

Unit-IV

Overview of concepts in sequence analysis, pairwise and multiple sequence alignment and their significance, Local and global sequence alignment and its algorithm, Sequence similarity search tools- BLAST-Concept, algorithm and working procedure, FASTA, Multiple sequence alignment, Clustal Omega,

Unit-V

Protein structures; Primary, Secondary, Tertiary and Quaternary. Protein folding, Secondary structure prediction methods-Chou-Fasman, GOR, Jpred, Three-dimensional structure prediction Methods; Comparative modeling (Homology modeling), Fold recognition or Threading method, Ab-Initio methods, Molecular Visualization using Rasmol, Cn3D, Comparative Genomics and Proteomics.

References

- Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins - By: Andreas D. Baxevanis (Ed), B. F. Francis Ouellette (Ed) Publisher: Wiley, John & Sons, Incorporated ISBN: 0471478784
- Introduction to Bioinformatics- By: Arthur M. Lesk Publisher: Oxford University Press, ISBN: 0199251967
- Bioinformatics and Functional Genomics-By Jonathan Pevsner Publisher: WileyBlackwell, ISBN: 0470085851
- Protein- Protein Interaction-By C. Frieden & L.W. Nichol. Publisher: John Wiley & Sons, Chichester, UK.
- Introduction to Bioinformatics, (Atwood, T. K. and Parry-Smith, D. J).
- An introduction to Computational Biochemistry. (C. Stain Tsai, A. John Wiley and Sons, Inc., publications).
- Bioinformatics: Methods and applications; Genomics, Proteomics and Drug Discovery; (Rastogi, S. C. and Mendiratta and Rastogi, P.

MBI-111: Practical based on MBI-101

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

1. Representation of statistical data by histogram ogive curves and pie diagram.
2. Measure of Central tendencies: Arithmetic Mean, median and mode
3. Calculation of Measure of Dispersion: Mean deviation, Standard deviation and coefficient of variation, Quartile deviation .
4. Test of Significance: Chi-square test, t- test, Standard error
5. Problems on correlation & regression
6. Problems on one way & two way ANOVA.
7. Problems on MATRIX.

MBI-112: Practical based on MBI-102

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Handling of Windows LINUX & Mac operating system
- Handling of MS Word
- Handling of MS Excel
- Handling of MS Access
- Handling of MS PowerPoint
- Design a Database and create required tables. For e.g. Bank, College Database
- Apply the constraints like Primary Key, Foreign key, NOT NULL to the tables.
- Write a sql statement for implementing ALTER, UPDATE and DELETE
- Write the queries to implement the joins
- Write the query for implementing the following functions: MAX (), MIN (), AVG (), COUNT ()
- Write the query to implement the concept of Integrity constraints
- Write the query to create the views
- Perform the queries for triggers
- Perform the following operation for demonstrating the insertion, updation and deletion using the referential integrity constraints with reference to biological database.
- Write the query for creating the users and their role.

MBI-113: Practical based on MBI-103

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Estimation of pKa values of amino acids
- Estimation of carbohydrates by qualitative methods
- Estimation of carbohydrates by quantitative method
- Estimation of proteins –(Folin Lowry / Biurets method)
- Estimation of DNA
- Estimation of RNA
- Isolation & Purification of genomic DNA from bacteria
- Isolation & Purification of plasmid DNA
- Agarose gel electrophoresis of chromosomal & plasmid DNA
- Restriction Digestion of chromosomal & plasmid DNA Isolation of DNA fragment from agarose gel
- Protein separation using SDS-PAGE

MBI-114: Practical based on MBI-104

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Exploring the integrated database system at NCBI server and querying the PUBMED and GenBank databases using the ENTREZ search engine
- Exploring the integrated database system at EBI server and searching the EMBL Nucleotide database Exploring and querying the SWISSPROT database
- Exploring and querying the PIR database
- Exploring and querying the EnsEMBL& UCSC Genome browser
- Database (homology) searches using different versions of BLAST and interpretation of the results to derive the biologically significant relationships of the query sequences (proteins/DNA) with the database sequences
- Database (homology) searches using different versions of FASTA and interpretation of the results to derive the biologically significant relationships of the query sequences (proteins/DNA) with the database sequences
- Pair-wise local alignments of protein and DNA sequences using Smith-Waterman algorithm and interpretation of results (EMBOSS_WATER).
- Pair-wise global alignments of protein and DNA sequences using Needleman-Wunsch algorithm and interpretation of results to deduce homology between the sequences (EMBOSS_NEEDLE).
- Multiple sequence alignments of sets of sequences using web-based and stand-alone version of CLUSTAL program & interpretation of results to identify conserved and variable regions and correlate them with physico-chemical and structural properties
- Exploring & querying the derived databases: PROSITE, PRINTS, BLOCKS, Pfam and Prodom for pattern searching, domain searches etc.

14. Curriculum for Semester II

MBI-201: Structural Bioinformatics

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Nucleic acid structures DNA & their types, RNA folding, RNA loops, conformational study, various ribose ring conformations, ribose-ring puckering. Structure and chemistry of amino acids Basic structural features of polypeptides Primary structure, Secondary structure, Tertiary and quaternary Structure Protein main-chain conformation and Ramachandran plots Side chain conformation and rotamer libraries.

Unit-II

Protein folding patterns and structural classification and structural superposition, Protein folding Classes, protein folding problem, protein-protein interactions, protein ligand interactions, DNA-binding proteins, RNA-binding proteins, SCOP & CATH database.

Unit-III

Structural databases: - Protein Data bank (PDB), Nucleic Acid Data Bank (NDB), Molecular modeling Data Bank (MMDB), Protein Secondary structure prediction method: GOR & Chau-Fasman and related biotools available on web, Protein 3D Structure Prediction methods:- Homology modeling, Threading (fold recognition) and Ab Initio, online & offline tools for protein 3D structure prediction, protein identification and characterization tools:- AACompIdent, and PROTPARAM, PepSea, FindPept, Predicting transmembrane helices, motifs, profiles, patterns and fingerprints search.

Unit-IV

Molecular modeling:-Introduction, force field, quantum chemistry, Schrödinger equation, potential energy functions, energy minimization, local and global minima, saddle point, grid search, various approximations; LCAO, HF, semi-empirical calculations; single point calculations, full-geometry optimization methods, ZDO, MNDO, CNDO, NDDO, AM1, PM3, RM1, conformational search, Z-matrix, docking, molecular modeling packages, Molecular mechanics:- Definition, balls and springs, force fields, bond-stretching, bond-bending, dihedral motions, out of plane angle potential, non-bonded interaction, coulomb interactions, conformational search, united atoms and cut-offs.

Unit-V

Molecular dynamics:-Introduction, Newton's equation of motion, equilibrium point, radial distribution function, pair correlation functions, MD methodology, periodic box, algorithm for time dependence; leapfrog algorithm, Verlet algorithm, Boltzman velocity, time steps, duration of the MD run. Starting structure, analysis of MD job, uses in drug designing, ligand protein interactions.

References

- Creighton, T. E. Ed.: Protein Structure: A Practical Approach.
- Creighton, T.E.: Proteins: Structure And Molecular Properties. Second Edition. New York. W. H. Freeman and Company
- Creighton, T.: Protein Folding, 1992.
- Sternberg, M.I.E.: Protein structure prediction: a practical approach
- Pain, R.G.: Mechanisms of protein folding
- Leach.A.R: Molecular modeling: principles and applications

MBI-202: Programming in C

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Introduction of C, Basic structure of C program, creating a simple C program, Executing a C program, Data types, Operators and Expressions: Character set, keywords and identifiers, constants and variables, Data Types, declaration of variables, defining symbolic constants. Operators: Relational Operators, Logical Operators, Assignment Operators, Increment And Decrement Operators, Conditional Operator, Library Functions.

Unit-II

Data Input Output, Branching and Loops: Reading a character, writing a character, formatted input and formatted output. Decision making and if... else statement, nesting of if... else statement, the switch statement, the? : Operator, the goto statement, the while statement, the do statement, the for statement. Arrays and Functions: One dimensional arrays, two dimensional arrays. String manipulation functions.

Unit-III

Functions: Introduction, types of functions. Defining functions, Arguments, Function prototype, actual parameters and formal parameters, Calling function, Returning function results, Call by value, Recursion. Structure: Introduction, Declaration and initializing structure, Accessing structure members, Nested structures, Arrays of structure, typedef statement.

Unit-IV

Introduction, Memory organization. Declaration and initialization of pointers. The pointer operator * and &, De-referencing, Pointer expression and pointer arithmetic, Pointer to pointer.

Unit-V

File handling: Introduction, Opening & closing a file, Input/Output operations on files, text and binary files, getc(), putc() function. Graphics in C: Introduction: initgraph() and detectgraph() function, Drawing object in C, Line, Circle, Rectangle, Ellipse, Changing foreground & background colors, Filling object by color.

References:

- Programming in C: E. Balagurusamy, Tata macgraw hill.
- Complete reference with C Tata McGraw Hill
- The C programming language : Kerninghan and Ritchie
- Graphics Under C : Y. Kanetkar

MBI-203: Object-Oriented Programming in JAVA & BIOJAVA

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Basic concepts of Object oriented programming: class & object, data abstraction and encapsulation, inheritance, polymorphism, dynamic binding, message communication. Benefits and applications of OOP. History and features of Java. Structure of java program, symbolic constants. Variables and Data types, Operators and Its Types.

Unit-II

Decision Making and Branching: Decision Making with If statement - Simple If Statement, If else Statement, Nesting If Else Statement, else if Ladder, The switch Statement, conditional operator (? and :). Looping: for, while, do while statement. Arrays: creating an Array, One-dimensional Arrays, Two dimensional Arrays.

Unit-III

Class Objects and Methods: Defining a Class - Fields Declaration, Methods Declaration, Creating Objects, Accessing class members, Constructors. Methods Overloading, Methods Overriding, Inheritance: Super and sub class, defining a subclass. Single inheritance, multilevel inheritance and hierarchical inheritance.

Unit-IV

Interface: Defining interfaces, implementing interfaces, extending interfaces, accessing interface variables. String class and its methods. Exception handling: syntax of exception handling code, multiple catch statements, throw: throwing own exceptions, throws and finally.

Unit-V

Packages: Java API Packages - Using system Packages, Creating Packages, Accessing a Package, Using a Package, Adding a Class to a Package. BioJava – Installing BioJava, Symbols and Symbolists, Sequences and Features, Sequence IO Basics, Alphabets: Cononical, SubSequence, Transcribe, Reverse, Edit, ReadGES, List and Filter.

Reference

- Programming with Java A Primer, E. Balaguruswamy Tata McGrawHill Companies
- The complete reference JAVA2, Hervert schildt.
- BioJava Cookbbok
- A BioJava: Programming Guide by Kaladhar DSVGK.

MBI-204: Chemoinformatics & Biodiversity Informatics

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Introduction to chemoinformatics, Evolution of chemoinformatics, History of chemical information science, Use of chemoinformatics, Prospectus of chemoinformatics, History of medicinal chemistry, Basic Stereochemistry, Amino acids and Proteins and Properties; pKa, pH and ionization of acids and bases; Protein structure & stability, Introduction to drug action, pro drug design and applications.

Unit-II

History of scientific information communication-chemical literature-chemical information, chemical information search, chemical information sources-chemical name and formula searching, Chemical Structure: Databases: Pubchem, ChEMBL, ChEMSpider, ChEMBI, DrugBank, CSD etc., File Formats & Notations, Drawing and Structure Visualization Tools.

Unit-III

Genetic basis of disease; personalized medicine and gene-based diagnostics, drug targets, Drug discovery pipeline, Pharmacokinetics & Pharmacodynamics, Introduction to drugs, natural sources of drug molecules, physical & chemical properties of drug molecules, biological concept about drug metabolism & elimination.

Unit-IV

Drug discovery methods: structure based & ligand based, 3D database searching and virtual screening, Sources of data, molecular similarity and similarity searching, prediction of binding energy of ligand-receptor complex-Free energies and salvation-electrostatic and non-electrostatic contribution & various molecular docking approaches.

Unit-V

Introducing biodiversity informatics: - Global patterns of distribution of biodiversity, biomes, Composition and distribution of biodiversity in India, Causes and consequences of biodiversity loss, Species extinctions, Concept and the rapid development, introduction to taxonomic databases and biodiversity databases.

References

- Medicinal Chemistry; Wilson Gisvold
- Principles of Medical Chemistry; William O Foye
- Organic and Medical Chemistry; Kadam Mahadik Bothara
- Textbook of Pharmacognasy; T.E Walis
- Pharmacology and Pharmacothearupetics; Satoskar and Bhandarker
- Pankhurst, R.I.: Practical taxonomic computing.
- Biodiversity, Conservation Environment pollution, Ecology; B.N. Pandey
- Protein Evolution; Laszlo Pathy

MBI-211: Practical based on MBI-201

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Model building of nucleic acid, protein and organic molecules using the MoluCAD.
- Querying& Retrieval structural information from PDB
- Querying & Retrieval structural information from NDB
- Hands on molecular visualization tools-Rasmol, Cn3D, SPDBViewer
- Proteinprimary structure analysis using PROTPARAM
- Protein secondary structure prediction by using SOMPA & GOR
- Three dimensional structure prediction by using the homology modeling technique using SPDBV.
- Energy calculation of the biomolecules using molecular mechanics and quantum mechanics using ArgusLab.
- Molecular Docking of protein and ligand by using Autodock.
- Energy Minimization, Molecular dynamics (MD) simulation using AMBER

MBI-212: Practical based on MBI-202

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Create, compile, debug, run and test simple C programs
- Using different data types available in C, perform arithmetic operations in C, perform formatted input/output operations, and perform character input/output operations.
- Using relational operator, logical operator, assignment operator, ternary operator, and other operators. Evaluation of Expression to check operator precedence and associativity.
- Create decision making programs using control statements like; if, if..else, if..else ladder, nested if, and switch cases.
- Create programs using loops (for, while, do while, nested loops) and realize the differences between entry controlled and exit controlled loops.
- Create, manipulate arrays and matrices (single and multi-dimensional), work with pointers, dynamically allocate/de-allocate storage space during runtime, manipulate strings (character arrays) using various string handling functions.
- Create user-defined functions with/without parameters or return type, create recursive functions, use function call by value and call by address, work with automatic, global and static variables.
- Create and use simple structures, array of structures, nested structure. Passing structure and array of structure to function, concept of pointer to structure
- Create programs that addresses pointer arithmetic, pointers and arrays, pointer and character strings, pointers and functions, pointer and structure, and dynamic memory allocation.
- Create files that address random access and input/output operations in file, create files to keep records and manipulation of records etc.
- Determining the base composition in a nucleic acid sequence and amino acid composition in a protein sequence using C program
- Generating the complimentary sequence of a DNA sequence
- Locate palindromic sequence stretches in a DNA sequence.
- Translate a DNA sequence into protein sequence in the forward and reverse frames.

MBI-213: Practical based on MBI-203

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Develop a program to declare a class 'student' having data members name, roll_no and percentage. Accept and display this data for one object.
- Write a program to insert an element (specific position) into an array.
- Write a program that creates box Object and use constructor and method overloading and return result to calling method.
- Write a program that extends box class and add color information in extended class and display color information with volume of the box.
- Write a Program to handle Arithmetic exception using try - catch statement.
- Write a Program to create multiple threads.
- Write a Program to make a simple moving banner applet.
- Write a program for creating, opening, closing, reading and writing a file.
- Write a Program to make a package.
- Write a class called MyCalculator which implements the interface. divisorSum function just takes an integer as input and return the sum of all its divisors. For example divisors of 6 are 1, 2, 3 and 6, so divisor_sum should return 12.
- Installation of BioJava and their packages
- Using BioJava package, perform sequence similarity searching

MBI-214: Practical based on MBI-204

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- To access small molecules 3D structure by accessing PUBCHEM.
- To access small molecules 3D structure by accessing DRUGBANK
- Model building of organic molecules (Drug Like) using the ChemSketch.
- Similarity searching of small drug like molecules using ChemMine Tool
- Virtual screening analysis of small drug like molecules using DrugMint
- Evaluation of pharmacokinetics and drug likeliness of small molecules using SwissADME.
- Drug target prediction using SwissTargetPrediction.
- 3D structure prediction of drug target using online servers.
- To perform interaction between ligand & receptor using molecular docking tools available on web.
- To generate 3D ligand & receptor interaction diagrams using LigPlot+.