

Dr.BABASAHEB AMBEDKAR MARATHWADA UNIVERSITY, AURANGABAD



CIRCULAR NO.SU/M.Sc./Bioinformatics/68/2023

It is hereby inform to all concerned that, the syllabus 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 IIIrd & IVth 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 2023-24 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/2023/ 465-69
Date:- 03.06.2023.

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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,**
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- 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 S.Y.
(III & IV Semester)**

Course Structure and Curriculum

Choice Based Credit System (CBCS)

(Effective from Academic Year 2023-24 onwards)

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

Umy
C. Jadhav M.A.

[Signature]
Dean
Faculty of Science & Technology
Dr. Babasaheb Ambedkar Marathwada
University, Aurangabad

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 S.Y.)							
Semester III							
Course Code	Course Title	Teaching time/week	Credits	Scheme of Examination			
				Max Marks	CIA	UA	Min Marks
MBI-301	Molecular Phylogenetics	4 hours	4	100	20	80	40
MBI-302	LINUX for Bioinformatics	4 hours	4	100	20	80	40
MBI-303	Genomics & Proteomics	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)							

(Jadhav M.A.)

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University, Aurangabad

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	Bio-python & R Programming	4 hours	4	100	20	80	40
MBI-402	Metabolomes & metabolic pathway engineering	4 hours	4	100	20	80	40
MBI-403	Comparative Genomics	4 hours	4	100	20	80	40
MBI-404	Advanced Techniques in Biological Data Analysis	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 (In silico)	4 hours	2	50	-	50	20
		32	24	600	80	520	240

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


(Jadhav M.A.)


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Curriculum for M.Sc. Bioinformatics S.Y. Semester III

MBI-301: Molecular Phylogenetics

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Molecular phylogenetics-Overview, Concepts in molecular evolution & Nature of data, Molecular Phylogeny- Concept & overview, Distance-based methods: UPGMA & NJ, Character-based methods: Maximum Parsimony.

Unit-II

Probabilistic models and associated algorithms-Probabilistic models of evolution & Maximum likelihood algorithm, Phylogenetic analysis algorithms-Distance-based: UPGMA, Transformed Distance, Neighbors-Relation, Neighbor Joining o Character optimization; delayed and accelerated transformation, Maximum Parsimony o Reliability of trees: Bootstrap, jackknife, decay, randomization tests.

Unit-III

Phylogenetic trees and their comparison-Definition and description, various types of trees; Consensus (strict, semi-strict, Adams, majority rule, Nelson). Data partitioning and combination. Tree to tree distances, similarity, Numerical taxonomy & bacterial identification.

Unit-IV

Assessment of MSA models-Need for benchmark datasets, Gene and genome based phylogeny, Substitution models & fitness tests, Modeling sequence evolution using Bayesian methods, Molecular clock hypothesis.

Unit-V

Phylogeography: methods & practices, Phylogeny programs: BEAUTI & BEAST, Alignment-free phylogeny, In-silico methods for viral and bacterial typing.

References

- Bromham Lindell. Reading the Story in DNA: A Beginner's Guide to Molecular Evolution. Publisher: USA, Oxford University Press. 2008. ISBN: 9780199290918.
 - Bernardi Giorgio. Structural and Evolutionary Genomics, Volume 37: Natural Selection in Genome Evolution (New Comprehensive Biochemistry). Publisher: Netherlands, Elsevier Science.2005. ISBN: 9780444521361.
 - Marco Salemi, Anne-Mieke Vandamme. The phylogenetic handbook: a practical approach to DNA and protein phylogeny. Publisher: Cambridge University Press, 2003. ISBN: 052180390X.
 - Patthy Laszlo. Protein Evolution. Publisher: London, Blackwell Science Ltd. 1999. ISBN: 0632047747.
 - Pevzner ,Pavel, Bioinformatics for Biologists. Publisher: Cambridge University Press. 2011. ISBN: 9781107648876
 - Graur Dan, Wen-Hsiung Li. Fundamentals of molecular evolution Publisher: Sinauer Associates, 1991. ISBN: 0878932666.
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MBI-302: LINUX for Bioinformatics

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Why LINUX for bioinformatics? Introduction to Linux and Linux Utilities: A brief history of LINUX, architecture of LINUX, features of LINUX, introduction to vi editor. Linux commands- PATH, man, echo, printf, script, passwd, uname, who, date, stty, pwd, cd, mkdir, rmdir, ls, cp, mv, rm, cat, more, wc, lp, od, tar, gzip, file handling utilities, security by file permissions, process utilities, disk utilities, networking commands, unlink, du, df, mount, umount, find, unmask, ulimit, ps, w, finger, arp, ftp, telnet, rlogin. Text Processing utilities and backup utilities , tail, head , sort, nl, uniq, grep, egrep, fgrep, cut, paste, join, tee, pg, comm, cmp, diff, tr, awk, cpio.

Unit-II

Introduction to Shells: Linux Session, Standard Streams, Redirection, Pipes, Tee Command, Command Execution, Command-Line Editing, Quotes, Command Substitution, Job Control, Aliases, Variables, Predefined Variables, Options, Shell/Environment Customization. Filters: Filters and Pipes, Concatenating files, Display Beginning and End of files, Cut and Paste, Sorting, Translating Characters, Files with Duplicate Lines, Count Characters, Words or Lines, Comparing Files.

Unit-III

Grep: Operation, grep Family, Searching for File Content. Sed :Scripts, Operation, Addresses, commands, Applications, grep and sed. UNIX FILE STRUCTURE: Introduction to UNIX file system, inode (Index Node), file descriptors, system calls and device drivers. File Management :File Structures, System Calls for File Management – create, open, close, read, write, lseek, link, symlink, unlink, stat, fstat, lstat, chmod, chown, Directory API – opendir, readdir, closedir, mkdir, rmdir, umask.

Unit-IV

Process and Signals: Process, process identifiers, process structure: process table, viewing processes, system processes, process scheduling, starting new processes: waiting for a process, zombie processes, orphan process, fork, vfork, exit, wait, waitpid, exec, signals functions, unreliable signals, interrupted system calls, kill, raise, alarm, pause, abort, system, sleep functions, signal sets. File locking: creating lock files, locking regions, use of read and write with locking, competing locks, other lock commands, deadlocks.

Unit-V

Inter Process Communication: Pipe, process pipes, the pipe call, parent and child processes, and named pipes: fifos, semaphores: semget, semop, semctl, message queues: msgget, msgsnd, msgrcv, msgctl, shared memory: shmget, shmat, shmdt, shmctl, ipc status commands. Introduction To Sockets: Socket, socket connections - socket attributes, socket addresses, socket, connect, bind, listen, accept, socket communications.

References

- W. Richard. Stevens, Advanced Programming in the UNIX Environment, 3rd edition, Pearson Education, New Delhi, India.
- Unix and shell Programming Behrouz A. Forouzan, Richard F. Gilberg. Thomson.
- Linux System Programming, Robert Love, O'Reilly, SPD.
- Advanced Programming in the UNIX environment, 2nd Edition, W. R. Stevens, Pearson Education.
- UNIX Network Programming, W.R. Stevens, PHI. UNIX for Programmers and Users, 3rd Edition, Graham Glass, King Ables, Pearson Education

MBI-303: Genomics & Proteomics

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Genome projects – importance, objectives and strategies, Genome markers and mapping: STS, EST, RFLP, SNP, Genome sequencing – First, Second and Next generation sequencing platforms, Genome sequence assembly, Genome Annotation-Basic Aspects of Genome Annotation, Prediction of ORFs, Algorithms for gene prediction & gene modeling, Prediction of Promoters, splice sites, UTRs etc.

Unit-II

Structural Genomics, Functional Genomics, Gene Ontology-Basic concepts, GO terms and relationships (DAGs), Tools for GO data: (AmiGO, BioConductor), GO Browsers and editors o GO visualization tools o Microarray-related tools, Protein interaction related tools, Statistical analysis , Term enrichment tools.

Unit-III

Organization of proteome: Basic concept of proteome; history, types of proteomics and applications of proteomics, Experimental techniques in Proteomics: (Conventional techniques: Cell disruption methods, chromatography (GF, IEC, AC, HPLC, RP-HPLC, Mud-LC), dialysis, ELISA and Western blotting. Advance techniques: Gel based techniques (1DE, 2DE, 2-D DIGE), In-gel digestion, Protein sequencing methods, Mass spectrometry (LC-MS, ESI-Q-MS, MALDI-TOF-MS, SELDI-TOF-MS, ESI-MS/MS, etc.), yeast two hybrids, Protein microarrays. Quantitative techniques: ICAT, SILAC, iTRAQ. o High throughput techniques: X-ray crystallography, NMR, AFM, FRET, etc

Unit-IV

Computational methods in Proteomics: Proteomics databases- PRIDE, SWISS-2DPAGE, PIR, Human Protein Atlas., MS data analysis tools- ProFound,

MASCOT, SEQUEST, prospector, FindPept, InsPect, MALDI PepQuant, PepFrag, etc. o Protein identification tools- PeptideMass, AACompldent, Taglent, HAMAP.

Unit-V

Protein characterization tools- PeptideCutter, PredictProtein, PROPSEARCH, PSORT, TargetP, SMART, ELM, ProtParam, GPMW lite, etc. o PTM analysis tools- FindMod, GPS, NetAcet, NetPhos, NetNGlyc, SUMOsp CSSPalm, etc, Protein-protein interaction databases-STRING, DIP, BIND, BioGRID, MINT, MIPS-MPact, MIPS-MPPI; Meta-databases (APID, MPID8, PINA); PPIs prediction databases (PIPs, I2D, UniHI).

References

- Brown, T.A. Genomes 2 Publisher: New York, BIOS Scientific Publishers Ltd. 2002, ISBN: 1859960294.
- Old R.W. and Primrose S.B. Principles of Gene Manipulation: An Introduction to Genetic Engineering Publisher: University of California Press, 1980
- Benjamin Lewin, Jocelyn E. Krebs, Elliott S. Goldstein, Stephen T. Genes XIth Edition. Publisher: Kilpatrick Jones & Bartlett Publishers, 2014.
- Introduction to Proteomics: Principles and Applications by Nawin Mishra, John Wiley & Sons.
- Principles of Proteomics Second edition by Richard Twyman, Garland Science, 2013.
- Introduction to Proteomics: Tools for the New Biology by Daniel C. Liebler, Springer Science & Business Media, 2002.
- Integrative Proteomics by Hon-Chiu Eastwood Leung, Janeza Trdine 9, 51000 Rijeka, Croatia.
- Proteomics: Biomedical and Pharmaceutical Applications by Hubert Hondermarck, Kluwer Academic Publishers, 2004.
- Bioinformatics for Comparative Proteomics by Cathy H. Wu, Humana Press, 2011

MBI-304: Programming in PERL & Bio-PERL

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Concepts of flowcharting, algorithm development, pseudo codes etc.
Introduction: Use of Perl in Bioinformatics, history of Perl, Availability, Support, Basic Concepts, Running Perl program, editors, Scalar Data: What is Scalar Data? Numbers, Strings, Scalar Operators, Scalar Variables, Scalar Operators and Functions.

Unit-II

Basic I/O, Array operators and Functions, Scalar and List Context, Control Structures: Statement Blocks, Hash Functions, Hash Slices, Regular Expressions, Subroutines, Miscellaneous Control Structures.

Unit-III

File handles and File Tests, Directory Handles, File and Directory Manipulation, Process Management: Using system and exec, Using Backquotes, Working with biological data, extraction from various sources.

Unit-IV

Database Manipulation: DBM Databases and DBM Hashes, Opening and Closing DBM Hashes, Fixed-Length Random-Access Databases, Variable-Length (Text), Databases, Win32 Database Interfaces, CGI Programming: The CGI.pm Module, CGI Program in Context, Simple CGI Programs, Passing Parameters via CGI, Perl and the Web.

Unit-V

Object oriented perl: Introduction to modules, Creating Objects, Bioperl: Introduction, Installation procedures, Architecture, Uses of bioperl, programs using various modules and functions of Bioperl.

References

- Moorhouse Michael, Barry Paul. Bioinformatics, Biocomputing and Perl: an introduction to bioinformatics computing skills and practice. Publisher: John Wiley and Sons. ISBN: 047085331X.
- Bal, H.P. Perl programming for Bioinformatics. Publisher: Tata McGraw-Hill. ISBN: 0070474478.
- Curtis Jamison D. Perl programming for biologists. Publisher: John Wiley & sons. ISBN: 0471430595.
- Tisdall James D. Beginning Perl for bioinformatics. Publisher: Shroff Publishers and distributors O'Reilly Media. ISBN: 8173663955.
- Gibas Cynthia, Jambeck Per. Developing Bioinformatics Computer Skills. Publisher: Shroff Publishers and distributors O'Reilly Media. ISBN: 8173662428
- Schwartz Randal L., Phoenix Tom. Learning Perl. Publisher: Shroff Publishers and distributors O'Reilly Media, Inc. ISBN: 8173663718
- Tisdall James D. Mastering Perl for bioinformatics. Publisher: Shroff Publishers and distributors O'Reilly Media. ISBN: 8173666768.
- Scott Guelich, Gunther Birznieks, CGI Programming With Perl. Publisher: O'Reilly Media. • Michael Saltzman, Modern Perl Programming. Publisher: Prentice Hall. ISBN: 0130089656

MBI-311: Practical based on MBI-301

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Compilation & curation of dataset, format conversion
 - Survey of software programs available for phylogenetic analysis
Installation of at least 2 public domain packages for both Windows & Unix environment: Phylip, PAUP, MEGA.
 - MSA using MUSCLE-Informative and variable sites; Singleton sites etc.
 - Reconstruction of phylogenetic trees using distance-based methods (1 datasets)
 - Converting sequence data into distance data
 - UPGMA, Neighbor-joining, Neighbor-relations & Transformed distance
 - Difference between dendrogram & phylogenetic tree
 - Reconstruction of phylogenetic trees using character-based methods
Maximum Parsimony & Maximum likelihood
 - Plotting, visualizing & printing phylogenetic trees: TreeView and other tools, Various rendering o Formatting & labeling, Interpretation of trees
 - Comparison of trees drawn using RNA, Nucleotide & protein data, Gene trees & species tree
 - Numerical taxonomy & Bacterial identification using matrices
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MBI-312: Practical based on MBI-302

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Learning installation and upgradation of the Linux operating system.
 - Basic Linux commands: User and session management commands: useradd, groupadd, userdel, groupdel, passwd; General purpose utilities: echo, printf, bc, who, whoami, tty, uname, clear, ls.
 - Linux commands: cat-create a file, append a file and open a file. file, wc, cp, rm, mv, more, head, tail, gzip, gunzip. vi editor- commands, navigation commands and creating a vi editor file.
 - Finding a file containing a particular text string
 - Regular expressions in grep command.
 - Search multiple words / string pattern using grep command on bash shell
 - Write a shell script that accepts a file name, starting and ending line numbers as arguments and displays all the lines between the given line numbers
 - Write a shell script to find factorial of a given integer
 - Write a shell script to list all of the directory files in a directory.
 - Write a C program that makes a copy of a file using standard I/O and system calls
 - Downloading & installation of bioinformatics software on PC with Linux OS.
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MBI-313: Practical based on MBI-303

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Browsing & viewing genome data-Ensembl@EBI, MapViewer@NCBI, UCSC Genome Browser Visualization, Browsing and searching of Protein coding and non-coding Genes, ESTs, STSs, Retrotransposons, RFLPs, SNPs, regions exhibiting Synteny
- Genome Annotation o Using integrated genome annotation servers such as the server developed at IMTech, Chandigarh (<http://imtech.res.in/raghava/gp.html>)-Gene Prediction and Gene Modeling Prediction of genes and gene structures (gene modeling) using online (web) servers of different methods tailored for prokaryotic and eukaryotic organisms such as GLIMMER, GeneMark, Grail, GENSCAN etc. Interpretation of results and comparison with known gene models (where available).
- Prediction of promoters using methods such as Neural Network Promoter Prediction (NNPP) at Berkeley Drosophila Genome Project server, Genome inspector for combined analysis of multiple signals in genomes etc. Using Promoter databases.
- Prediction of alternate splice sites using methods such as Splice Site Prediction by Neural Network (at Berkeley Drosophila Genome Project server), GenScan, NetGene2, GeneSplicer etc. Prediction of PCR primers using Primer 3, ePCR etc.
- Identification of proteins with its molecular weight and pI from sequence using bioinformatics tools.
- MS data analysis using ProFound/MASCOT/prospector tools.
- Prediction of protein motifs and domain using online tools.
- Prediction of protein-protein interaction and protein-ligand interaction.
- Visit to virtual proteomic laboratory and ExPASy Bioinformatics Resource Portal.

MBI-314: Practical based on MBI-304

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Basic PERL programming on arithmetic operations, looping, decision making statements.
 - PERL programming for database connectivity
 - PERL programming for CGI
 - To align the sequence using Local Blast.
 - Write a script to search for genes from Genscan.
 - Protein Sequence Generation.
 - To count start and stop codons in a sequence.
 - To calculating the reverse complement of DNA Sequence.
 - To concatenating DNA Fragments Transcription: DNA to RNA.
 - Program to simulate DNA Mutation.
 - Write a code to check file extensions using Perl.
 - Write a code to search the given string in an entered sequence.
 - To compute total and average length of the proteins in these files.
 - Reading a protein sequence from a file.
 - Write a sequence in a file.
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Curriculum for M.Sc. Bioinformatics SY Semester IV

MBI-401: Bio-python & R Programming

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Introduction to python: What is Python and history of Python?, Unique features of Python, Python-2 and Python-3 differences, Install Python and Environment Setup, First Python Program, Python Identifiers, Keywords and Indentation, Comments and document interlude in Python, Command line arguments, Getting User Input, Python Data Types, What are variables?, Python Core objects and Functions. Control Statements - if-else, if-elif-else, while loop, for loop, break, continue, assert, pass, return.

Unit-II

List, Ranges & Tuples in Python, Python Dictionaries and Sets, Input and Output in Python -Reading and writing text files, writing Text Files, Appending to Files and Challenge, Writing Binary Files Manually, Using Pickle to Write Binary Files, Python built in function-Python user defined functions, Python packages functions, Defining and calling Function, The anonymous Functions, Loops and statement in Python, Python Modules & Packages, object oriented python, exception handling in python.

Unit-III

Python Regular Expressions, Python Multithreaded Programming, Python MySQL Database Access, Data Science Using Python- Numpy & Pandas, GUI in Python -Button Widget, Label Widget, Text Widget, Django Web Framework in Python-Introduction to MVC and MVT architecture in Web development, Django folder structure and flow of control.

Unit-IV

Bio python: Introduction, Installing Bio-Python, Working with sequence, connecting with biological database, Sequence annotation Object, Sequence

Input/Output, Multiple Sequence Alignment Object, Blast Running over internet, Blast and other sequence searching tools, Searching Enterez Database EMBL, Searching NCBI Database, Phylogenetic with Bio-Python, BioSQL connectivity.

Unit-V

What is R Programming, Advantages of R Programming in bioinformatics, Tools for R Programming in Bioinformatics-Bioconductor (Packages: GenomicRanges, DESeq2 & Biostrings), ggplot2, Shiny, dplyr, Applications of R Programming in Bioinformatics.

References

- Charles Dierbach, "Introduction to Computer Science Using Python", 1st Edition, Wiley India Pvt Ltd. ISBN-13: 978-8126556014.
- Wesley J Chun, "Core Python Applications Programming", 3rd Edition, Pearson Education India, 2015. ISBN-13: 978-9332555365.
- Ekmekci, B., McAnany, C. E., & Mura, C. (2016). An Introduction to Programming for Bioscientists: A Python-Based Primer. PLoS Computational Biology, 12(6). <https://doi.org/10.1371/journal.pcbi.1004867>
- Giorgi, F. M., Ceraolo, C., & Mercatelli, D. (2022). The R Language: An Engine for Bioinformatics and Data Science. Life, 12(5). <https://doi.org/10.3390/life12050648>
- Grunberg, R., Nilges, M., & Leckner, J. (2007). Biskit A software platform for structural bioinformatics. Bioinformatics, 23(6), 769–770.

MBI-402: Metabolomes and metabolic pathway engineering

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Gene and Regulatory Networks: Types of molecular interactions – overview / revision, Types of biological networks- Gene regulatory network, gene co-expression network, metabolic networks. Properties of metabolic Networks, Representation of biological networks: Graphs, Types of networks: Linear, Boolean, Bayesian.

Unit-II

Organization of metabolic systems: Components of pathways; Modes of enzymes- enzyme chains, multi-enzyme complexes, multifunctional enzymes: Modes of pathways- linear, branched and cyclic pathways; Types of pathways-anabolic, catabolic, amphibolic, anaplerotic, cataplerotic, shuttle pathways, secretory pathways and signal transduction; Regulation of pathways- reversible and irreversible regulation, feedback and feedforward regulation; regulatory enzymes, pacemaker enzymes and linker enzymes

Unit-III

Major Metabolic Pathways and metabolic diseases: Glycolysis, Citric acid cycle, Oxidative phosphorylation, Gluconeogenesis, Pentose phosphate pathway, Glycogen synthesis and degradation, Fatty acid oxidation and synthesis, Amino acid catabolism, Purine and pyrimidine nucleotide synthesis.

Unit-IV

Metabolic Pathway databases KEGG, EMP, EcoCyc and MetaCyc, LIGAND - Biochemical Compounds and Reactions, BRENDA -Comprehensive Enzyme Information System. BiGG database.

Unit-V

Metabolic disease database- HMDB, MPMP, Comparison of Metabolic Pathways
Engineering of Metabolic Pathways Representation of Metabolic Pathway.

References

- Nelson David L., Cox Michale. Lehninger Principles of Biochemistry 5th Edition. Publisher: New York. W. H. Freeman.. ISBN 978 0716771081.
- Berg, Jeremy M, Tymoczko, John L. Stryer, Lubert. Biochemistry 6th Edition. Publisher: New York: W.H. Freeman. ISBN: 071676766X.
- Collado-Vides Julio, Hofstadt Ralf. Gene Regulation and Metabolism: Post-Genomic Computational Approaches. Publisher: England, The MIT Press. ISBN: 026203297X.
- Computing for Biologists- A. Fielding, Addison Wesley Pub., UK
- Microcomputers in Biochemical Education- E. J. Wood (Ed), Taylor and Francis Ltd., UK.
- Computer Games and Simulation for Biochemical Engineering- H. R. Bungay, John Wiley and Sons Ltd., New York.
- Microcomputers in Biology- A practical approach- C. R. Ireland and S.P. Lang, IRL Press Ltd.

MBI-403: Comparative Genomics

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Objectives and Overview of Genome Comparisons -Genome Alignments, Genomic and Pairwise BLAST, MUMmer, PipMaker, LAST, Mauve.

Unit-II

Comparison of Gene Order & Synteny analysis - Recombination methods and analysis, RDP, Analysis of Population structure- Prokaryotic & Eukaryotic.

Unit-III

Population diversification: dN/dS ratio and selection pressure analysis, Single Nucleotide Polymorphism, dbSNP and other SNP-related databases

Unit-IV

GWAS resources and analysis of polymorphism in populations

Unit-V

Comparative Genomics-Viruses, Microbes, Pathogens, Eukaryotes

References

- Xia, Xuhua, Comparative Genomics, 2013, Springer-Verlag Berlin Heidelberg, 978-3-642- 37146-2
- Mount, David. Bioinformatics: sequence and genome analysis. Publisher: Cold Spring Harbor Laboratory Press, 2004. ISBN: 087967121
- Arcady R. Mushegian, Foundations of Comparative Genomics, 2007Publisher: Academic Press, ISBN-10: 0120887940

MBI-404: Advanced Techniques in Biological Data Analysis

Total Credit: 04

Contact Hours: 04 hrs/week

Marks: 100

Unit-I

Advanced Techniques for Sequence Analysis- next-generation sequencing and high-throughput screening data and their analysis and related Bio-tools, Principles of Sequence Similarity Searches- Substitution scores and substitution matrices, The alignment concepts and principal algorithms, Sequence database search algorithms, Gapped BLAST, PSI-BLAST, PHI-BLAST, WU-BLAST.

Unit-II

Identification of Genes in a Genomic DNA Sequence- Prediction of protein-coding genes, Algorithms and software tools for gene identification- GeneMark, Glimmer, Grail, GenScan, GeneBuilder, Splice site prediction-HSPL, NNSPLICE, GENESPLICER, SNP data analysis & related bio-tools.

Unit-III

Protein sequence motifs and methods for motif detection, Protein domains, PSSMs, and advanced methods for database search, Prediction of subcellular localization of the protein.

Unit-IV

Reverse vaccinology analysis-Epitope Prediction Methods, DNA & protein microarray data analysis and advanced phylogenetic data analysis and related softwares.

Unit-V

Advanced Techniques for Structure Analysis- Molecular replacement method, direct method & Fiber diffraction, .Methods for Comparison of 3D structures, Electrostatics of biomolecules .Molecular Dynamics Simulations & Monte Carlo Methods, Docking and Scoring.

References

- Preparation and analysis of protein crystal; Alexander McPherson
 - DNA Sequencing: From Experimental Methods to Bioinformatics
Author(s): Luke Alphey.
 - Systems Bioinformatics: An Engineering Case-Based Approach *Author(s): Gil Alterovitz and Marco R. Ramoni*
 - Text Mining for Biology and Biomedicine *Editor(s): Sophia Ananiadou and John McNaught*
 - Introduction to Bioinformatics *Author(s): Teresa Attwood, David Parry-Smith*
 - Ontologies for Bioinformatics *Author(s): Kenneth Baclawski and Tianhua Niu*
 - Bioinformatics: The Machine Learning Approach *Author(s): P. Baldi and S. Brunak*
 - DNA Microarrays and Gene Expression: From Experiments to Data Analysis and Modeling *Author(s): Pierre Baldi, G. Wesley Hatfield*
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MBI-411: Practical based on MBI-401

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Write python program to print Hello World
 - Write python program to Hello World using string variable
 - Write python program to store data in list and then try to print them.
 - Write python program to do basic trim and slice on string.
 - Write python program to print list of numbers using range and for loop
 - Write python program to store strings in list and then print them.
 - Write python program to let user enter some data in string and then verify data and print welcome to user.
 - Write python program in which an function is defined and calling that function prints Hello World
 - Write python program in which an function (with single string parameter) is defined and calling that function prints the string parameters given to function.
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- Write python program in which an class is define, then create object of that class and call simple print function define in class.
 - Use of R packages for biological data visualization and analysis
 - Programs based on bio python package installation and its applications in bioinformatics data generation & analysis.
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MBI-412: Practical based on MBI-402

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 100

- Browse & search following metabolic pathway databases-KEGG, BioCyc, MetaCyc, EcoCyc, Reactome, BiGG
 - Browse & search following metabolic disease databases-HMDB, MPMP
 - Browse & search following Enzymes, Compounds and Reactions databases-BRENDA, ExplorEnz, IntEnz, ExPASy Enzyme database, LIGAND.
 - Visualization and reconstruction of gene regulatory networks using Cytoscape.
 - Building of co-expression network.
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MBI-413: Practical based on MBI-403

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50

- Comparative genomics resources and NCBI and EBI
 - Comparison of full / partial genomic sequences using following methods to identify conserved genes and map/compare the annotations of the two sequences BLAST2, MegaBLAST and Discontiguous MegaBLAST, MUMmer, PipMaker, LAST, Mauve & Artemis
 - Gene order comparison & Synteny analysis
 - RDP
 - Structure using case studies of – virus, microbes, model organisms
 - Calculating dN/dS ratio and selection pressure analysis
 - Explore and query SNP and SNP-related databases
 - GWAS resources and analysis of polymorphism
 - Workout any one comparative genomics case study based on publication & reproduce the output.
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MBI-414: Major Project (In silico)

Total Credit: 02

Contact Hours: 04 hrs/week

Marks: 50
