DR. BABASAHEB AMBEDKAR MARATHWADA UNIVERSITY,
CHHATRAPATI SAMBHAJINAGAR.

CIRCULAR NO.SU/B.Sc./Bioinformatics/CBC&GS/91/2024

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, **Academic Council at its meeting held on 08 April 2024 has accepted the Syllabus of B.Sc. Bioinformatics (Degree) Vth & VIth semester (Third Year)** under the Faculty of Science & Technology as per Norms of Choiced Based Credit Grading System run at the Affiliated Colleges, Dr.Babasaheb Ambedkar Marathwada University as appended herewith.

This is effective from the Academic Year 2024-25 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/2024/26037-45
Date:- 09.05.2024.

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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, Dr.Babasaheb Ambedkar Marathwada University, Chhatrapati Sambhajinagar.
2] The Section Officer,[B.Sc.Unit] Examination Branch, Dr.Babasaheb Ambedkar Marathwada University, Chhatrapati Sambhajinagar.
3] The Programmer [Computer Unit-1] Examinations, Dr.Babasaheb Ambedkar Marathwada University, Chhatrapati Sambhajinagar.
4] The Programmer [Computer Unit-2] Examinations, Dr.Babasaheb Ambedkar Marathwada University, Chhatrapati Sambhajinagar.
5] The In-charge,[E-Suvidha Kendra], Rajarshi Shahu Maharaj Pariksha Bhavan, Dr.Babasaheb Ambedkar Marathwada University, Chhatrapati Sambhajinagar.
6] The Public Relation Officer, Dr.Babasaheb Ambedkar Marathwada University, Chhatrapati Sambhajinagar.
7] The Record Keeper, Dr.Babasaheb Ambedkar Marathwada University, Chhatrapati Sambhajinagar.

DR. BABASAHEB AMBEDKAR MARATHWADA UNIVERSITY, CHHATRAPATI SAMBHAJINAGAR

B.Sc. Bioinformatics (Degree)

Vth and VIth semester

(Third Year)

Course Structure and Curriculum

Choice Based Credit & Grading System.

From the Academic Year 2024-25 & Onwards/-

Dr. Babasaheb Ambedkar Marathwada University,

Chhatrapati Sambhajinagar – 431004 (MS) India.

Structure and Curriculum for

B.Sc. Bioinformatics (Degree)

(Choice Based Credit & Grading System)

Dr. Babasaheb Ambedkar Marathwada University, Aurangabad

Choice Based Credit System (CBC&GS) Curriculum
For
Faculty of Science and Technology
Course Structure and Scheme of Examination

(B.Sc. Bioinformatics T.Y.)

Semester V

	Course Code	Course Title	Teaching time/week	Credits	Scheme of Examination			
					Max Marks	CIA	UA	Min Marks
Discipline Specific core courses	BBI-511	**Select any one paper from** A1: Biodiversity Informatics B1: Medical Informatics	3 hours	3	50	10	40	20
	BBI-512	**Select any one paper from** A2: Introduction to PERL B2: Introduction to Julia	3 hours	3	50	10	40	20
	BBI-513	R Programming	3 hours	3	50	10	40	20
	BBI-514	Introduction to LINUX	3 hours	3	50	10	40	20
	BBI-515	Metabolism	3 hours	3	50	10	40	20
	BBI-516	Recombinant DNA Technology	3 hours	3	50	10	40	20
	BBI-521	LC13: Practical based on BBI-511 & BBI-512	4 hours	1.5	50	10	40	20
	BBI-522	LC14: Practical based on BBI-513 & BBI-514	4 hours	1.5	50	10	40	20
	BBI-523	LC15: Minor Project based on Wet Lab Techniques	4 hours	1.5	50	10	40	20
			30	22.5	450	90	360	180

Total Credits for Semester V : 22.5 (Theory : 18 ; Laboratory : 4.5)

Semester VI								
	Course Code	Course Title	Teaching time/week	Credits	Scheme of Examination			
					Max Marks	CIA	UA	Min Marks
Discipline Specific core courses	BBI-611	**Select any one paper from** A1: Machine Learning for Bioinformatics B1: Research Methodology & Personality Development	3 hours	3	50	10	40	20
	BBI-612	**Select any one paper from** A2: Data Science for Bioinformatics B2: Immunoinformatics	3 hours	3	50	10	40	20
	BBI-613	Molecular Phylogeny & Evolution	3 hours	3	50	10	40	20
	BBI-614	Programming in Python & Biopython	3 hours	3	50	10	40	20
	BBI-615	System Biology	3 hours	3	50	10	40	20
	BBI-616	Genomics & Proteomics	3 hours	3	50	10	40	20
	BBI-621	LC16: Practical based on BBI-611 & BBI-612	4 hours	1.5	50	10	40	20
	BBI-622	LC17: Practical based on BBI-613 & BBI-614	4 hours	1.5	50	10	40	20
	BBI-623	LC18: Major Project (In silico)	4 hours	1.5	50	10	40	20
			30	22.5	450	90	360	180
Total Credits for Semester VI : 22.5 (Theory : 18 ; Laboratory : 4.5)								
Total Credits for three years (06 semester) : 22.5 each semester X 06 (Semester) = 135 credits								

(Semester V)

(Select any one paper from following elective group)

BBI-511: A1: Biodiversity Informatics

Total Credit: 03 Contact Hours: 30 (Clock Hours)

Marks: 50 Periods: 45 (50 Min. each)

Learning Objectives

- To understand the concept of biodiversity informatics
- To understand the tools and techniques for biodiversity mapping
- To understand the strategies for biodiversity conservation and management

Learning outcomes:

After successful completion of course, students will be able to:

- Demonstrate knowledge and understanding of the biodiversity databases
- Demonstrate knowledge and understanding of the species identification tools
- Build on their knowledge and understanding in tackling more advanced and specialized techniques for biodiversity conservation and management.

Unit-I **(10 Periods)**

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 , taxonomic databases and biodiversity databases & resources-Map of Life (MOL), Biodiversity Maps, GBIF, Species 2000, Catalogue of Life, ITIS. Taxonomic Database Working Group (TDWG) standards, compatibility and interoperability, taxonomically intelligent systems.

Unit-II **(15 Periods)**

Identification of plants and animals: Floral and faunal survey techniques, inventorying and monitoring of species and the use of diversity indices to assess habitats. Biodiversity analytical tools:-Fundamental concepts of remote sensing, Introductory Geographical Information systems (GIS), bioclimatic and genetic algorithms for rule set production modeling, Biodiversity hotspot analyses; Taxonomic names, classification, character data: nature and use of names and classification in biodiversity informatics, significant global projects on taxonomic names; taxonomic character data, descriptions and keys, online keys and digital keys.

Unit-III **(10 Periods)**

Cladistic method, parsimony and Bayesian approaches of data analysis. Software used to discover phylogenies, use and status of specimen data, species distribution, example software projects for compiling data. Current priorities in biodiversity informatics, challenges and future prospect.

Unit-IV **(05 Periods)**

Introduction to sustainable development: Valuation of biodiversity: Integrated and adaptive management. Ecosystem and species approach: Ex-situ conservation: Protected Area Network of India, Assessing the status of species, Threats from invasive alien species.

Unit-V IV **(05 Periods)**

Basic economic principles related to management of biodiversity:- National legislation, International conventions and treaties related to biodiversity conservation, Problems of law enforcement

References:

- Taxonomy and Biodiversity Informatics by R.C. Arora
- Multimedia Tools and Applications for Environmental & Biodiversity Informatics By Alexis Joly et al.
- Biodiversity informatics by P. Bryan Heidorn

BBI-511: B1: Medical Informatics

Total Credit: 03 Contact Hours: 30 (Clock Hours)

Marks: 50 Periods: 45 (50 Min. each)

Learning Objectives

- Facilitate understanding of current issues and developments in the medical field, provide basic skills for managing information
- To identify opportunities for the application of informatics principles to medical health research and practice
- Distinguish the various types of health care information including data, source, knowledge and importance of technology and standards.

Learning outcomes:

After successful completion of course, students will be able to:

- Interpret network systems and their application in medical laboratories
- Identify the issues surrounding the security of digital information especially as it relates to patient healthcare information
- Examine the application of image analysis software and expert systems/decision support systems in the healthcare and medical research environment
- Perform basic software functions using word processing, spread sheet, database, presentation and image analysis programs
- Demonstrate the need for standards in the formatting, distribution and storage of medical information.

Unit-I **(05 Periods)**

Overview of Medical Informatics: The Goals of Medical Informatics, Why computers in healthcare? Systems Design Considerations for the Clinical User.

Unit-II **(10 Periods)**

Electronic Health Records: Integrated Practice Management Systems, The Paper-based Medical Record, Current Use of HER in Healthcare Settings, Vist A (VA EHR System), Clinical support Systems: Hospital Information Systems,

Clinical Information Systems, Laboratory Information Systems, Pharmacy Information Systems.

Unit-III **(10 Periods)**

Introduction to Medical Networks: Introduction to Medical Network Design & Development and its applications, Emergence of Medical Informatics: Medical informatics as a Discipline, Predominant Architectures and Practices.

Unit-IV **(10 Periods)**

Informatics Issues in Virtual Healthcare, Telemedicine: e-Health, Virtual Healthcare Delivery System, Issues in Telemedicine: Real-time, Store and-forward, Contemporary issues: Industry expert lectures on contemporary issues

Unit-V **(10 Periods)**

Medical Informatics: Clinical Decision Making and recent technologies: Measuring Quality and Outcomes, Standards and Quality Improvement and Evidence-Based Medicine. Integrating the personal health record with mobile technology, implantable chips, personalized medicine, genome based medical care.

References:

- Bemmel, J.van; Musen, M.A. Handbook of Medical Informatics 1st ed.
- Computers In Medicine, Tata McGraw Hill
- Davidson, P., Best Practice Series: Healthcare Information Systems, Auerbach Publications
- Medical Informatics. A Primer: Mohan Bansal, Tata McGraw Hill
- Slack, Cyber medicine: How Computing Empowers Doctors and Patients for Better Health Care, Jossey-Bass, Revised
- Ellis, Technology and the Future of Health Care, Preparing for the Next 30 Years, Jossey Bass.

(Select any one paper from following elective group)

BBI-512: A2: Introduction to PERL

Total Credit: 03 Contact Hours: 30 (Clock Hours)

Marks: 50 Periods: 45 (50 Min. each)

Learning Objectives:

- To introduce the fundamentals of Perl programming language to the student.
- To familiarize with Perl modules and to write scripts for manipulating/processing genomic and proteomic data

Learning outcomes:

After successful completion of course, students will be able to:

- Able to write Perl scripts for processing biological data
- Able to use toolkit of Perl modules for various bioinformatics applications

Unit-I **(10 Periods)**

Perl Basic Data types: Scalar Variables, Scalar Operations and Functions, Array Variables, Literal Representation of an Array, Array Operations and Functions, Scalar and List Context, Hash Variables, Literal Representation of a Hash, Hash Functions, Using Hashes for the Genetic Code, Gene Expression Data Using Hashes.

Unit-II **(10 Periods)**

Perl Regular Expression: Concepts on Regular Expressions, Uses of Regular Expressions in biological data handling, metacharacters, quantifiers, Pattern-matching, Substitutions, Transliteration, split and join functions.

Unit-III **(10 Periods)**

Modular Programming: Subroutines, Advantage of Subroutines, Scoping and Subroutines, Arguments, Passing Data to Subroutines, Modules and Libraries of Subroutines, Concept on File handle, Opening and Closing a File, Opening and Closing a Directory, Reading a Directory, File and Directory Manipulation.

Unit-IV **(05 Periods)**

Common Gateway Interface (CGI): The CGI.pm Module, CGI program in Context, Simple CGI programs, Passing Parameters via CGI, Perl and the Web.

Unit-V **(10 Periods)**

Bioperl: Introduction to Bioperl, Installing Procedures, Architectures, General Bioperl Classes, Sequences -Bio::Seq Class, Sequence Manipulation, Features and Location ClassesExtracting CDS, Alignments -AlignIO, Analysis -Blast, Databases- Database Classes, Accessing a Local Database.

References:

- Mastering Perl for Bioinformatics (1st Ed.), J. Tisdall, O'Reilly
- Mastering Perl: Creating Professional Programs with Perl (2nd Ed.), Brian d foy, O'Reilly
- Programming Perl (3rd Ed), L.Wall, T. Christiansen and J. Orwant, O'Reilly
- Beginning Perl for Bioinformatics (1st Ed.), J. Tisdall, O'Reilly, 2004

BBI-512: B2: Introduction to Julia

Total Credit: 03 Contact Hours: 30 (Clock Hours)

Marks: 50 Periods: 45 (50 Min. each)

Learning Objectives

- To understand the concepts of Julia Programming.
- To learn about the control structures, class with attributes and methods used in Julia.

Learning outcomes:

After successful completion of course, students will be able to:

- Knowledge of the structure and model of the Julia programming language.
- Understand the basic principles of creating Julia applications with meta programming and parallel computing.
- Demonstrate the use of Julia in data visualization

Unit-I **(10 Periods)**

Basic Concepts in Julia programming language, Introduction to Julia language, History of Julia language, Why to Learn Julia Programming Language?, Datatypes in Julia language, Operators in Julia language, Introduction to loops, Introduction to Conditions, Mathematical Operators in Julia, Arithmetic Operators, Bitwise operators, Numeric Comparisons, Operator Precedence, Numeric Conversions, Strings in Julia, String basics, Interpolation, Triple quoted String literals, Non Standard String Literals, Regular Expressions, Raw String Literals

Unit-II **(10 Periods)**

Intermediate Concepts of Julia Programming Language , Introduction to Arrays, Basic Functions, Indexing and Assignment, SubArrays, Concatenating Arrays, Multidimensional Arrays in Julia, Dictionaries in Julia, Introduction to Matrices, Date and Time in Julia, Scopes of variables in Julia, Global Scope, Local Scope, Constants, Introduction to Sparse matrix :

Input/Output Operations using Julia, Constructors in Julia, Outer Constructor, Inner Constructor, Parametric Constructor

Unit-III **(10 Periods)**

Advance Concepts in Julia Programming Language, Functions in Julia, Argument Passing Behavior, The return keyword, Anonymous Functions, Multiple Returned Values, Optional Arguments, Modules in Julia, Interfaces in Julia, Iteration, Indexing, Abstract Arrays, Working with Packages in Julia, Various operations on different datatypes using Julia, Reading and Writing files using Julia, Introduction to DataFrames in Julia, Dealing with missing values, Recursion in Julia, Closure in Julia, Currying in Julia, MapReduce in Julia

Unit-IV **(07 Periods)**

Higher Level Programming Concepts with Julia, Meta Programming, Expression and Evaluation, Macros, Expression and Evaluation, Parallel Computing, Channels, Data Movement, Shared Arrays, Parallel Map and Loops, Running External Programs, Interpolation, Quoting, Pipelines, Workflow Tips

Unit-V **(08 Periods)**

Data Visualization using Julia, Scatter Plot in Julia, Multidimensional Scatter Plot in Julia, Histogram in Julia, Bar Graphs in Julia, Boxplot in Julia, Trigonometric Plots in Julia, Customizing the graphs with Julia, Whiskers graph in Julia, Line Graphs in Julia, Pie Chart using Julia, Sub Graph Plotting in Julia, Funnel Chart with Julia, Relative Frequency Histogram, Segmented Bar Graph

References:

- Julia 1.0 Programming Cookbook by Prezemyl
- The Little Book of Julia Algorithms - A workbook to develop fluency in Julia programming by Ahan Sengupta
- Think Julia: How to Think Like a Computer Scientist by Ben Lauwens
- JULIA Programming for beginner by Deeraj Mehrotra

BBI-513: R Programming

Total Credit: 03 | Contact Hours: 30 (Clock Hours)

Marks: 50 | Periods: 45 (50 Min. each)

Learning Objectives

- To understand the concept of R Prog.
- To understand the architecture of R Prog.
- To understand the concept of data manipulation and visualization in R

Learning outcomes:

After successful completion of course, students will be able to:

- Install and handle R programming interface
- Use various data types and packages
- Study string manipulation operations

Unit-I **(10 Periods)**

What is R? – Why R? – Advantages of R over Other Programming Languages - R Studio: R command Prompt, R script file, comments – Handling Packages in R: Installing a R Package, Few commands to get started: installed.packages(), package.Description(), help(), find.package(), library() - Input and Output – Entering Data from keyboard – Printing fewer digits or more digits – Special Values functions : NA, Inf and –inf.

Unit-II **(10 Periods)**

R Data Types: Vectors, Lists, Matrices, Arrays, Factors, Data Frame – R - Variables: Variable assignment, Data types of Variable, Finding Variable ls(), Deleting Variables - R Operators: Arithmetic Operators, Relational Operators, Logical Operator, Assignment Operators, Miscellaneous Operators - R Decision Making: if statement, if – else statement, if – else if statement, switch statement – R Loops: repeat loop, while loop, for loop - Loop control statement: break statement, next statement. Solving problems from Assignment sheet.

Unit-III **(10 Periods)**

R-Function : function definition, Built in functions: mean(), paste(), sum(), min(), max(), seq(), user-defined function, calling a function, calling a function without an argument, calling a function with argument values - R-Strings – Manipulating - R Vectors – Sequence vector, rep function, vector access, vector names, vector math, vector recycling, vector element sorting - R List - Creating a List, List Tags and Values, Add/Delete Element to or from a List, Size of List, Merging Lists, Converting List to Vector - R Matrices – Accessing Elements of a Matrix, Matrix Computations: Addition, subtraction, Multiplication and Division- R Arrays: Naming Columns and Rows, Accessing Array Elements, Manipulating Array Elements, Calculation Across Array Elements - R Factors –creating factors, generating factor levels gl().

Unit-IV **(07 Periods)**

String Manipulation in R language: String fnctions : grep(), nchar() , paste(), sprintf(), substr(), strsplit(), regex() gregexpr(), toupper(), tolower(), paste(),Creating Data Frames and visualization of Data: Data Frames –Create Data Frame, Data Frame Access, Understanding Data in Data Frames: dim(), nrow(), ncol(), str(), Summary(), names(), head(), tail(), edit() functions - Extract Data from Data Frame, Expand Data Frame: Add Column, Add Row - Joining columns and rows in a Data frame rbind() and cbind() – Merging Data frames merge() – Melting and Casting data melt(), cast(). Installing RMySQL Package, Creating Database, table under MYSQL, Inserting data in a table , Update and alter table, Display content of table.,

Unit-V **(08 Periods)**

Tools for R programming in bioinformatics- Bioconductor, ggplot2, Shiny, dplyr, Applications of R Programming in bioinformatics.

References:

- "The Book of R" by Tilman M. Davies, no starch press (San Francisco)
- "The Art of R programming" by Norman Matloff, no starch press(San Francisco)

BBI-514: Introduction to Linux

Total Credit: 03 Contact Hours: 30 (Clock Hours)

Marks: 50 Periods: 45 (50 Min. each)

Learning Objectives:

- Describe the History of Linux
- Execute General purpose commands.
- Explain the file types.
- Create and modify files using the vi editor.
- Execute Linux filters.

Learning outcomes:

After successful completion of course, students will be able to:

- Describe the overview of Linux
- Execute general purpose commands.
- File management
- Create and modify files using the vi editor.
- Execute Linux filters.

Unit-I **(07 Periods)**

Introduction to Linux Operating System: Introduction to Operating System and Linux. History, Overview of Linux, Shell: Bourne, Korn, Cshell. Linux releases, Linux File Systems (ext) and versions.

Unit-II **(10 Periods)**

General Purpose Utilities: cal: The calendar, date: Displaying the system date, echo: Displaying message, printf: An alternative to echo, bc: The calculator, script: Recording your session, Email basics, mailx: The universal mailer, passwd: Changing your password, who: Who are the users? uname: Knowing your machine charactristics, tty: Knowing your terminal, stty: Displayig and setting terminal characteristics

Unit-III **(10 Periods)**

File Management in Linux : The file: Ordinary file, Directory file, Device file, File name, The parent-child relationship, UNIX file system tree, The Unix file system, The home directory, pwd: Checking your current directory, cd:

Changing the current directory, mkdir: Making directories, rmdir: Removing directories, ls: Listing directory contents, Absolute pathnames, Relative pathnames, Handling ordinary files, cat: Displaying and creating files, cp: Copying file, rm: Deleting files, mv: Renaming files, more: Paging output, The lp subsystem: printing a file, file: knowing the file types, wc: Counting lines, words and characters, od: Displaying data in octal, cmp: Comparing two files.

Unit-IV **(10 Periods)**

The vi Editor and Shell: The vi Editor: vi Command, Input, and Line Editing Modes. Creating, Saving and Quitting a File in vi, Managing Editing Modes in vi., vi Editing Commands: Common Operations. Navigation: Movement in the four direction (h, j, k and l), Word navigation (b, e and w), Moving to Line extremes (0, | and $), Scrolling ([Ctrl-f], [Ctrl-b], [Ctrl-d] and [Ctrl-u], Absolute Movement (G), Searching for a pattern(/ and ?), Repeating the last pattern search (n and N), The Shell: The Shell's interpretive cycle, Shell offerings, Pattern matching: The wild-cards, Escaping and quoting, Redirection: The three standard files, /dev/null and /dev/tty: Two special files

Unit-V **(08 Periods)**

Filters, Regular Expressions and Shell Programming-Simple Filters: The sample database, pr: Paginating files, head: Displaying the beginning of a file, tail: Displaying the end of a file, cut: Splitting a file vertically, paste: Pasting files, sort: Ordering file, uniq: Locate repeated and nonrepeated lines, tr: Translating characters, Filters using regular expressions, grep: Searching for a pattern, Basic regular expression (BRE)- An introduction, Extended regular expressions (ERE) and egrep, sed: The stream editor, Essential Shell programming, Shell scripts, read: Making scripts interactive, Using command line arguments, exit and Exit status of command, The logical operators && and ||- Conditional executions, The if conditional, Using test and [ ] to evaluate expressions, the case conditional, expr: Computation and string handling, $0: Calling a script by different names, while: Looping, for: Looping with a list

References:

- Richard Petersen Linux The Complete Reference McGraw Hill, 6th edition ISBN Number 978- 0071492478
- Richard Blum Linux command line and shell scripting Wiley India ISBN Number 978-1118983843
- Prof. Dayanand Ambawade Linux Lab: Hands on Linux Dreamtech Press ISBN Number 9789350040003

BBI-515: Metabolism

(Treat it as base of Metabolomics and not as Biochemistry)

Total Credit: 03 Contact Hours: 30 (Clock Hours)

Marks: 50 Periods: 45 (50 Min. each)

Learning Objectives:

- To understand basic concept of metabolism
- To understand carbohydrate and lipid metabolism
- To understand the nature and contents of metabolomics databases

Learning outcomes:

After successful completion of course, students will be able to:

- Study anabolic, catabolic and other pathways
- Study enzyme-metabolites interaction in pathways
- Study nature and contents of metabolomics databases

Unit-I **(10 Periods)**

Basic concept: Definition, Anabolism, Catabolism, Amphibolism, Intermediary metabolism, metabolic pathways, Anapleurotic pathways, Regulation of metabolic pathways, Bioenergetics.

Unit-II **(08 Periods)**

Carbohydrate metabolism, Glycolysis, Gluconeogenesis, Glycogen synthesis, Glycogenolysis, TCA cycle, Glyoxylate bypass

Unit-III **(07 Periods)**

Calvin cycle, ETC, oxidative phosphorylation, substrate level phosphorylation.

Unit-IV **(10 Periods)**

Lipid metabolism: Activation of fatty acid and transport in mitochondria, Oxidation of fatty acids (Even, odd, α, β, Ø)

Unit-V **(10 Periods)**

Metabolomics Databases: KEGG, BRENDA, ENZYME, ECOCYC and METACYC databases.

References:

- Biochemistry by Stryer 5th Edition WH Freeman
- Cohn & Stump, Outline of Biochemistry Wiley Eastern Ltd.
- Harpers Review of biochemistry Prentice Hall
- Cregnton Protein Structure & Molecular Properties
- A.L. Lchninger, D. L. Nelson & M M Cox Principles of Biochemistry.
- Lippincott's Biochemistry 4th edition
- Basic Medical Biochemistry: A Clinical Approach, PI edition,by Lieberman and Marks

BBI-516: Recombinant DNA Technology

Total Credit: 03 Contact Hours: 30 (Clock Hours)

Marks: 50 Periods: 45 (50 Min. each)

Learning Objectives:

- To familiarize the student with emerging field of biotechnology i.e. Recombinant DNA Technology
- To create understanding and expertise in techniques in genetic engineering.

Learning outcomes:

After successful completion of course, students will be able to:

- Obtain the fundamental principle of genetic engineering procedure.
- Attain competency to undertake genetic engineering by cloning any DNA/gene using tools of rDNA technology in an appropriate expression vector for recombinant protein production.
- Design molecular techniques for diagnosis of various diseases.
- Assess the risk versus benefits of rDNA technology and practice, safety and other regulations for rDNA work

Unit-I **(10 Periods)**

Landmarks in Molecular biology and Biotechnology, What is genetic engineering and recombinant DNA technology? Advantages of using microorganisms in Genetic Engineering Genetic engineering in E. coli and other prokaryotes, yeast, fungi and mammalian cells.

Unit-II **(10 Periods)**

Tools in genetic engineering: Enzymes: DNA polymerases, ligases, reverse transcriptases, nucleases restriction endonucleases (Restriction modification system, Restriction mapping) and, terminal transferases, phosphatases, polynucleotide Kinase etc. Cloning vectors: plasmids, bacteriophage vectors, cosmids, phagemids BAC, YAC vectors, Shuttle vectors, expression vectors etc.

Unit-III **(10 Periods)**

Recombinant DNA techniques: Polymerase chain reaction (PCR) and its types Molecular Probes and Nucleic acid labeling Blotting Techniques (Northern, Southern and Western) Autoradiography, Hybridization, DNA foot printing, Electrophoretic mobility gel shift assay (EMSA) DNA sequencing, site directed mutagenesis and its applications DNA fingerprinting, RAPD, RFLP, AFLP. Different methods for analysis of gene expression

Unit-IV **(08 Periods)**

Gene cloning: Isolation and purification of DNA (genomic, plasmid) and RNA. Isolation of gene of interest- restriction digestion, electrophoresis, Cutting and joining of DNA, Methods of gene transfer in prokaryotic and eukaryotic cells. Methods for Recombinant selection and screening: genetic, immunochemical, South-western analysis, nucleic acid hybridization, HART, HRT Expression of cloned DNA molecules and maximization of gene expression Cloning strategies- genomic DNA libraries, cDNA libraries, subtractive hybridization, chromosome walking and jumping.

Unit-V **(07 Periods)**

Applications of Recombinant DNA technology: Gene therapy, medicine, crop improvement, disease resistance: In vivo approach, ex-vivo approach of gene therapy, Antisense therapy, Interference technology (siRNA, shRNA, miRNA) CRISPAR Cas 9 mediated gene therapy, Transgenics

References:

- Principles of Gene Manipulation and Genomics by Sandy B. Primrose and Richard Twyman, eighth edition, John Wiley and Sons Ltd.
- Analysis of gene and Genome by Richard J Reece, Wiley.
- Gene Cloning and DNA Analysis: An Introduction by T. A. Brown, Sixth edition Wiley-Blackwell.
- Molecular Cloning A Laboratory Manual (Vol 1,2,3) Michael R. Green, Joseph Sambrook, Fourth edition, Cold Spring Harbor Laboratory Press.

BBI-521: LC13-Based on BBT-511 & BBT-512

Total Credit: 1.5 | Contact Hours: 30 (Clock Hours)

Marks: 50 (40 + 10) | Periods: 45 (50 Min. each)

Practical based on BBT-511 (A1)-Biodiversity Informatics

- To access map of life resource for retrieval of biodiversity data.
- To retrieve biodiversity map resource
- To study geographic information system
- To study LINNAEUS species name recognition and normalization software.
- To study AInsectID - a free to use species identification, image analysis and colour mapping software
- To study MEGA 6.0 software to discover phylogenies

Practical based on BBT-511 (B1)-Medical Informatics

- To study ICU DataMart
- To study SoHP: Health Informatics Resources
- To study VistA
- Downloading and handling of Open Hospital v1.14.1 software
- To study pharmacy information system
- To study healthcare network design
- To study e-hospital resource

Practical based on BBT-512 (A2)-Introduction to PERL

- Basic PERL programs on arithmetic operations
- Uses of Scalar and Array Variables to manipulate DNA/RNA/Protein sequence data
- Concatenation DNA fragments, Transcribing DNA into RNA
- Calculating the Reverse complement of a DNA strand
- Uses of common Array Operators
- Uses of Do-Until Loops
- Uses of 'substr' function to look into the string
- Reading a sequence data from a file and writing the results to a file
- Opening and closing a Directory Handle, Reading a Directory and other directory manipulation functions.
- Uses of Subroutines
- Uses of Hashes for the genetic code: translating codons into amino acids
- Uses of subroutine to read FASTA files
- Translate a DNA sequence in all six reading frames
- Uses of Regular Expressions
- Extract annotation and sequence from GenBank file
- Parsing GenBank annotation using arrays
- Extract sequence chains from PDB file
- Uses of CGI.pm Module and Passing Parameters via CGI, Debugging CGI programs
- Installing Bioperl, Uses of Bioperl modules for sequence manipulation, accessing local database

Practical based on BBT-512 (B2)-Introduction to JULIA

- Installation of JULIA and its packages
- Basic programs on Julia
- Programs on simple Julia functions
- Programs on basic string operations
- Programs on string conversion and formatting
- Programs on string manipulations
- Programs on array
- Programs on loop and map
- Programs on conditional evaluation
- Programs on plotting (To draw plots using suitable package in Julia)

BBI-522: LC-14: Practical based on BBI-513 & BBI-514

Total Credit: 1.5 | Contact Hours: 30 (Clock Hours)

Marks: 50 (40 + 10) | Periods: 45 (50 Min. each)

Practical based on BBT-513 (A2: R Programming)

- Write a program to check whether a year (integer) entered by the user is a leap year or not?
- Write an R program to find the sum of natural numbers without formula using the if–else statement and the while loop.
- Write an R program to make a simple calculator that can add, subtract, multiply and divide using switch cases and functions
- Write a program to perform searching within a list (1 to 50). If the number is found in the list, print that the search is successful otherwise print that the number is not in the list.
- Create a list and data frame that stores the marks of any three subjects for 10 students. Find out the total marks, average, maximum marks and minimum marks of every subject
- To study bioconductor repository and assignments on it
- To study CRAN repository and assignments on it

Practical based on BBT-514 (B2: Introduction to LINUX)

- Installation of LINUX
- Study of Basic commands of Linux.
- Study of Advanced commands of Linux.
- Study of current directory according to the following arguments:
  a. Suffix to be replaced
  b. Replacement suffix
- Shell scripting using general-purpose utilities.
- Shell programming using filters (including grep, egrep, fgrep).
- Write a shell script to validate the entered date. (eg. Date format is : dd-mm-yyyy)
- Write a shell script to check entered string is palindrome or not.
- Basic LINUX commands useful in bioinformatics analysis

BBI-523: LC-15: Minor Project based on Wet Lab Techniques

Project will be based on any one of the techniques mentioned below

- Microbial
- Biotechnological
- Molecular
- Cell Biology
- Genomics
- Any discipline in life sciences

(Semester VI)

(Select any one paper from following elective group)

BBI-611: A1: Machine Learning for Bioinformatics

Total Credit: 03 Contact Hours: 30 (Clock Hours)

Marks: 50 Periods: 45 (50 Min. each)

Learning Objectives:

- Learn what is machine learning
- Learn algorithms used in machine learning.
- Learn how to implement machine learning for biological problems.

. Learning outcomes:

After successful completion of course, students will be able to:

- Different types of machine learning and its utility in bioinformatics
- Application of Hidden Markov Model and Artificial neural networks to different types of bioinformatics data
- Determination of Bayesian Network (BN) from expression data
- Application of stochastic context-free grammar (SCFG) to predict RNA secondary structure

Unit-I **(10 Periods)**

Introduction: Overview of intelligent systems and machine learning, Hidden Markov Model (HMM): Viterbi algorithm, Forward algorithm, Backward algorithm, Profile-HMM, Baum-Welch algorithm to optimize HMMprofile, Multiple alignment and database searching using profile- HMM.

Unit-II **(07 Periods)**

Symbolic Machine Learning: Nearest neighbour approach to predict secondary structure, Decision tree methods, Identification tree methods.

Unit-III **(10 Periods)**

Bayesian Network (BN): Calculation of statistical significance by using Bayesian methods, Factorization and Markov blanket rule, d-separation,

Equivalence classes, Learning of Bayesian network, Learning of Gaussian network

Unit-IV **(10 Periods)**

Artificial Intelligence (AI): Search strategies, logic, deduction, and pathways comparison, Artificial Neural Network (ANN): Basics and introduction to terminologies, Supervised and non-supervised learning, Feed forward back propagation error method, Application of ANN methods: Protein sub-cellular localization and secondary structure prediction

Unit-V **(08 Periods)**

Stochastic Context Free Grammar (SCFG): Transformational grammar, Parsing, Chomsky hierarchy (regular, context-free, context-sensitive, and unrestricted grammar), Automata, Context-free grammar, Application of SCFG for prediction of secondary structure of RNA

References:

- R. Durbin, S. Eddy, A. Krogh, and G. Mitchison, Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids. Cambridge University Press
- Edward Keedwell and Ajit Narayanan, Intelligent Bioinformatics: The Application of Artificial Intelligence Techniques to Bioinformatics Problems, Wiley
- P Baldiand S Brunak, BIOINFORMATICS: The Machine Learning Approach.

BBI-611: B1: Research Methodology & Personality Development

Total Credit: 03 | Contact Hours: 30 (Clock Hours)

Marks: 50 | Periods: 45 (50 Min. each)

Learning Objectives:

- To provide overview of how to identify research problem and conduct research.

Learning outcomes:
After successful completion of course, students will be able to:

- Students can understand the basics of how to design, conduct research, analyze and communicate the results to research community.
- Also team work ethos and stress management strategies would help to cope-up with their day-to-day life in a competitive world

Unit-I **(10 Periods)**

Research Methodology: Objectives of research and motivation; Problem Identification & Formulation – Research Question - Hypothesis and Hypothesis Testing; Types of research - Qualitative vs Quantitative Research - Applied vs. Fundamental Research; Features of good research design; Data Collection - Data Analysis - Interpretation of results and Report writing.

Unit-II **(10 Periods)**

Scientific writing: Introduction - Types of scientific writings - Thesis or dissertation writing – Research paper writing; Types of publications - Open access and subscription based resources; Scientific paper writing - Choosing a journal- Instructions to authors - Structure and Style Authorships –figures tables with legends - References and citations – Acknowledgements Conflict of interest; Peer review mechanism and publication process; Scientometric Analyses of a paper/journal; Ethics in publishing and Plagiarism issues. Use of software for Reference Management – (Mendeley/endnote) and detection of Plagiarism (turnitin).

Unit-III **(10 Periods)**

Oral Presentation: Planning the oral presentations and visuals- In-class discussion (Students in small groups or individually will take up the assignments or select a research project/ topic and prepare oral presentations followed by a Q&A sessions).

Unit-IV **(07 Periods)**

Poster Presentation: Elements and Significance of poster presentations- Planning and designing a poster- Individual Poster presentation (Students select a research project/topic and prepare posters followed by a Q & A sessions).

Unit-V **(08 Periods)**

Personality development & team building: Recruitment process and interview techniques, Team work - Personality development - Interpersonal skills, Time and human resources management - Goal setting - planning and scheduling work, stress at work - work-life balance, Culture and cultural ethos - cultural diversity - diversity in organizations.

References:

- Experimental design for the life sciences, 4th edition, by Ruxton, G.D. and Colegrave, N. Oxford University Press, Oxford.
- Successful Scientific Writing: A Step-by-Step Guide for the Biological and Medical Sciences (4th Ed.) by J.R. Matthews and R.W. Matthews, Cambridge University Press.
- Scientific Writing 2.0: A Reader and Writer's Guide, by Jean Luc-Lebrun, World Scientific Publishing Company; 2nd Revised ed.
- Writing and Presenting Scientific Papers, 2nd Edition by Birgitta Malmfors, Phil Garnsworthy and Michel Grossman, Nottingham University Press. Viva Books Pvt. Ltd.

(Select any one paper from following elective group)

BBI-612: A2: Data Science for Bioinformatics

Total Credit: 03 Contact Hours: 30 (Clock Hours)

Marks: 50 Periods: 45 (50 Min. each)

Learning Objectives:

- To understand the life cycle of data science
- To understand the nature of genomic data
- To understand data analysis strategies

Learning outcomes:
After successful completion of course, students will be able to:

- Aware with the life cycle of data science
- Capture, maintain and analyze genomic data
- Understand methods and techniques for data analysis to draw predictions

Unit-I **(10 Periods)**

Brief history of data science, data science as conjunction of computer science statistics and domain knowledge. Definition of data science, data science life cycle - capture, maintain, process, analyze, communicate and its applications in bioinformatics.

Unit-II **(10 Periods)**

Genomics, genome structure, genome sequencing technology-NGS: Concept and applications, genome assembly and annotation, data types in genomics-DNA, RNA and protein sequences, biological databases and tools in genome data analysis.

Unit-III **(07 Periods)**

Genomic data analysis: data preprocessing and quality control-quality assessment of raw sequencing data, Data preprocessing-trimming, filtering and adaptor removal, Genome variant analysis-variant calling: SNV's, small

indels and structural variants, annotation of genetic variants and its functional impact on disease etiology.

Unit-IV **(10 Periods)**

Transcriptomic Analysis: RNA sequencing data analysis: alignment, quantification and differential expression. Alternative splicing analysis and gene co-expression network analysis, Epigenomics & DNA methylation analysis.

Unit-V **(08 Periods)**

Genomic data visualization: Visualization techniques for different types of genomic data, Interactive tools for exploring and interpreting large scale genomic data, **Genomic data integration**: Multiomics data integration approach, Integrative analysis of genomics, transcriptomics and epigenomic data.

References:

- Bioinformatics algorithms: An active learning approach by Phillip Compeau & Pavel Pevzner
- Genomics: A Data Science Approach by Atul J Butte
- Practical Computing for Biologist by Steven H.D. Haddock & Casey W. Dunn

BBI-612: B2: Immunoinformatics

Total Credit: 03 | Contact Hours: 30 (Clock Hours)

Marks: 50 | Periods: 45 (50 Min. each)

Learning Objectives:

- To understand the concept of immunoinformatics
- To understand the nature and contents of immunological databases
- To understand the types of vaccine & reverse vaccinology approach

Learning outcomes:
After successful completion of course, students will be able to:

- Study various components of immunoinformatics
- Retrieve contents of immunological databases
- Study of vaccines and reverse vaccinology

Unit-I **(10 Periods)**

Overview of immunoinformatics-Scope & importance, Types of immunity, Cells involved in immunity, Introduction to antigen-antibody interaction, Antibody databases: AntigenDB, ExactAntigen, IMGT/3Dstructure-DB.

Unit-II **(10 Periods)**

Major histocompatibility (MH) databases: HLA database, IMGT/MH-DB, B cell epitope database-Bcipep, IEDB resource, Ag-Ab: Sequential and conformational epitopes.

Unit-III **(07 Periods)**

Principles of B-cell and T-cell epitope prediction, T-cell epitope prediction tools: Tepitool, MHC-NP, TCR Analysis-TCRmatch, Structure tools-LYRA, SCEptRe, Docktope. B-cell epitope prediction tools: Discotope, Ellipro.

Unit-IV **(10 Periods)**

Known epitope analysis tools: Population Coverage, Epitope Conservancy Analysis, RATE, ImmunomeBrowser, PepX, PepSySco.

Unit-V **(08 Periods)**

Vaccine, Types of vaccine, reverse vaccinology approach and applications, rational vaccine development pipeline.

References:

- Kuby Immunology by Jenni Punt et al.
- New generation vaccines by Levine
- Roitts's Essential Immunology by Martin
- Jadhav M.A., Pawar S.V., Deshmukh G.S. (2023). Reverse vaccinology approach towards the prevention of SARS COV-2 Infections, International Journal of Scientific Research, 12(6), 1-4.
- Jojare R.A., Jadhav M.A., Chavan D.P. (2024) Computational Efficacy of Artificial Intelligence Model for In silico Vaccine Development, Journal for Research in Applied Sciences and Biotechnology, 3(1), 139-146.

BBI-613: Molecular Phylogeny & Evolution

Total Credit: 03 | Contact Hours: 30 (Clock Hours)

Marks: 50 | Periods: 45 (50 Min. each)

Learning Objectives:

- To understand the concept of molecular evolution & phylogeny
- To understand various steps of phylogenetic analysis
- To understand the working principles of phylogenetic data analysis tools.

Learning outcomes:

After successful completion of course, students will be able to:

- Study molecular basis of evolution
- Study various methods of phylogenetic tree construction
- Perform phylogenetic data analysis

Unit-I **(10 Periods)**

Introduction to molecular evolution, goals of molecular phylogeny, Molecular Clock Hypothesis, Positive & Negative Selection, Neutral theory of evolution.

Unit-II **(10 Periods)**

Molecular phylogeny-Concept and applications, Properties of trees-Tree roots, Enumerating trees and selecting search strategies, Types of trees-species trees vs gene/protein trees, DNA, RNA or Protein based trees, Transitions & Transversions.

Unit-III **(07 Periods)**

Phylogenetic Analysis-Sequence Acquisition, Multiple sequence alignment, Models of DNA and Amino Acids Substitution: Jukes-Cantor one parameter model & Kimura two parameter model, Gamma Distribution Model.

Unit-IV **(10 Periods)**

Phylogenetic tree building methods-Character based methods: 1. Maximum Parsimony-Identification of informative sites, Transform Parsimony matrix,

Fitch Matrix, Construction of trees, and Selection of tree as per shortest path of evolutionary changes, 2. Maximum Likelihood Method-Concept and applications.

Unit-V **(08 Periods)**

Distance based tree building methods: Neighbor-Joining & UPGMA, Tree evaluation method-Bootstrap, Phylogenetic data analysis tools: PAUP, MEGA, PHYLIP, TREE-PUZZLE & MrBayes.

References:

- R.D.M. Page and E.C. Holmes, Molecular Evolution a Phylogenetic Approach, Blackwell Scientific. ISBN 0-86542-889-1
- L. Patthy, Protein Evolution, Blackwell Scientific. ISBN 0-63204-774-7
- Jonathan Pevsner Bioinformatics and Functional Genomics, pp. 215-274. Wiley-Blackwell Publication

BBI-614: Programming in Python & Biopython

Total Credit: 03 | Contact Hours: 30 (Clock Hours)

Marks: 50 | Periods: 45 (50 Min. each)

Learning Objectives:

- To aware the student with Python & biopython is the best-known Python library to process biological data.
- It will aware the students with sequences, NCBI queries, BLAST, trees, and 3D structures

Learning outcomes:

After successful completion of course, students will be able to:

- Understand what python & biopython is and what it can do.
- Learn how to get biopython running.
- Learn how to retrieve data records from NCBI.
- Learn how to read and write sequence files.

Unit-I **(07 Periods)**

Introduction, Python programming language, interpreter, Python's basic data types, literals constant, error handling, lists.

Unit-II **(10 Periods)**

Conditional Statements, if-then, looping, while-loops, for-loops, break, continue, functions, arguments, function parameter, local variables, global variables, return values, operators, passing arguments, reference argument.

Unit-III **(10 Periods)**

String processing, case changing method, string manipulation, string slices, string comparison, regular expression, non greedy matching, Module, make own module, import statement, loading, classes, creating instances.

Unit-IV **(10 Periods)**

Biopython introduction, bio sequence, sequence reading, sequence writing, bio Swissprot, Regular entries, bio genbank, reading entries, running blast, clustal W or Omega.

Unit-V **(08 Periods)**

Seq feature, slicing seq record, reading sequence file, writing sequence file, sequence alignment, single alignment, multiple alignment, ambiguous alignment

References:

- Brueck, D. and Tanner, S., Python 2.1 bible, hungry minds Inc.
- Schuerer, K. and Letondal, C., Python course in Bioinformatics, Pasteur Institute

BBI-615: System Biology

Total Credit: 03 Contact Hours: 30 (Clock Hours)

Marks: 50 Periods: 45 (50 Min. each)

Learning Objectives:

- The main goal of this course is to help students in learning the basic concepts and computational methods involved in the computational modelling of the biological systems

Learning outcomes:

After successful completion of course, students will be able to:

- The student will have a system-level understanding of the biological systems.
- Develop and analyze the properties of in silico models of gene-gene interactions and protein-protein interactions

Unit-I **(10 Periods)**

Introduction & Biological Networks: Systems Biology: Emergent property, Applications in health and diseases. Microarrays and its applications in systems biology. Connectivity maps (CMap) and Library of Integrated Network-based Cellular Signatures (LINCS) - definition and its uses. Biological Networks: Degree distribution, Clustering coefficient, Random networks, Scale-free networks, small-world effect.

Unit-II **(10 Periods)**

Simulation of pathways: Metabolic network, Metabolic reconstruction, Flux Balance Analysis (FBA): Translating biochemical networks into linear algebra, Stoichiometric matrix, Elementary mode, Extreme pathways, Objective function, Optimization using linear programming. Genome-scale cellular models: Virtual Erythrocytes, Global human metabolic model (Recon 3D).

Unit-III **(10 Periods)**

Signaling & Experimental methods in systems biology: Slow and auto–regulation The coherent FFL and incoherent FFL, single-input module (SIM): LIFO and FIFO, DOR, signaling networks and neuronal circuits. Robustness

and optimality in Biological complex systems: Biological Robustness: System control, modularity, decoupling. Optimal design of gene circuits I- cost and benefit: gene circuits II- selection of regulation. Stochasticity in gene expression.

Unit-IV **(07 Periods)**

Databases and softwares for Systems Biology: Introduction- databases: KEGG, EMP, MetaCyc. Expression databases and other databases related to systems biology. Cytoscape, visANT & CellDesigner.

Unit-V **(08 Periods)**

Synthetic Biology: Introduction, definition and Basics, Synthetic Oligonucleotide/DNAbased, RNA-based, Peptide-based Technologies and Applications, Technologies and Applications of Directed Evolution and Microbial Engineering, Potential Hazards of Synthetic Biology, iGEM.

References:

- Introduction to Systems Biology: Design Principles of Biological Circuits by Uri Alon, Chapman & Hall/CRC.
- Synthetic Biology: A Primer by P.S. Freemont & R.I. Kitney, Imperial College Press.
- Introduction to Systems Biology, S. Choi, Humana Press.
- Linked – The New Science of Networks, Albert-László Barabási, Perseus Publishing.
- Networks – an Introduction, Mark Newman, Oxford University Press.

BBI-616: Genomics & Proteomics

Total Credit: 03 | Contact Hours: 30 (Clock Hours)

Marks: 50 | Periods: 45 (50 Min. each)

Learning Objectives:

- To understand basic and applied aspects in genomics and proteomics
- Understand applications of genomics and pharmacogenomics in clinical settings
- Provide an example of pharmacogenomics
- Appreciate possible ethical and legal issues

Learning outcomes:

After successful completion of course, students will be able to:

- Describe the development of Omics technologies, with emphasis on genomics and proteomics.
- Synthesize information to discuss the key technological developments that enabled modern genomic and proteomic studies.
- Describe advanced genomics and proteomics technologies and the ways in which their data are stored.
- Use bioinformatics techniques to query examples of genomic and proteomic databases to analyze cell biology.

Unit-I **(07 Periods)**

What is genomics, Genetics to genomics, Whole genomes sequencing. Genome Sequence Acquisition and Analysis, Biomedical Genome Research: Genomic sequences to make new vaccines, new types of antibiotics.

Unit-II **(08 Periods)**

Next Generation Sequencing: Introduction, Types, Different platforms for NGS like Illumina, PacBio; SOLiD Applications of NGS in transcriptome analysis, genome sequencing, and exome sequencing.

Unit-III **(10 Periods)**

Genomic Variations: Variation in the human genome, known examples of SNPs that cause diseases, Pharmacogenomics, Ethical Consequences of Genomic Variation.

Unit-IV **(10 Periods)**

DNA/RNA Microarrays, the oligo microarray/chip technology, Affymetrix protocol and data generation, the spotted microarray technology, cDNA and oligo spotted arrays, Biomedical applications; Cancer and genomic microarrays.

Unit-V **(10 Periods)**

Introduction, Protein 3D Structures, Protein identifications (2-hybrid system, 2- D gel electrophoresis, mass spectrometry , Methods of ionization ,Mass analyser, MALDI- TOF, application of NMR , Mining of protein databases, applications to human disease studies.

References:

- Discovering Genomics, Proteomics, & Bioinformatics (2003). Campbell & Heyer Pearson Education
- Bioinformatics, Methods of Biochemical Analysis, Series Vol. 43, Baxevanis& Ouellette, John Wiley & Sons.
- Computational Molecular Biology .Pevzner, P.A. MIT Press.
- Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. Andreas D. Baxevanis & B. F. Francis Ouellette. 3rd Edition. Wiley & Sons.

BBI-621: LC16-Practical based on BBI-611 & BBI-612

Practical based on BBT-611 (A1: Machine Learning for Bioinformatics)

- Implementation of crisp KNN for a microarray file
- Implementation of fuzzy KNN for a microarray file
- Identification tree construction using See5 and Weka
- Implementation of perceptron on LOGIC GATES
- Calculation of AAC and DPC for SVM and ANN input files
- Calculation of pseudo amino acid composition
- Implementation of ANN using SNNS software
- Implementation of SVM using SVM-light, LIBSVM and Weka
- Implementation of HMM for prediction of CpG islands
- HMM using HMMER package
- Stochastic context free grammar

Practical based on BBT-611

(B1: Research Methodology & Personality Development)

- The student is expected to read and critically evaluate minimum of 05 research papers related to **applications of bioinformatics in various disciplines** and present the inference of any 01 paper in a clear and precise manner in **the form of a report and short seminar (PPT's)** at the end of semester.

Practical based on BBT-612 (A2: Data Science for Bioinformatics)

- To study open source bioinformatics tools & platforms
- Setting up the required software & data resources
- To assess the quality of raw sequencing reads using FastQC
- Genome alignment of NGS reads using BWA
- Visualization of aligned reads with Interactive Genomics Viewer (IGV)
- Annotation of variants using ANNOVAR
- Detection of structural variants using Delly 2.0 tool
- Building and analyzing protein-protein interaction network with STRING

Practical based on BBT-612 (B2: Immunoinformatics)

- To retrieve of antigen related data from AntigenDB
- To retrieve structural data of antigen by accessing IMGT/3DStructureDB
- To retrieve HLA related data from HLA Database
- To study IEDB resource
- To search B-cell epitopes by accessing BCIPEP database
- To predict B cell epitope by using Discotope
- To predict T cell epitope by using Tepitool

BBI-622: LC17-Practical based on BBI-613 & BBI-614

Practical based on BBI-613 (Molecular Phylogeny & Evolution)

- Phylogenetic data retrieval from OrthoDB & Pfam.
- Multiple sequence alignment of phylogenetic data using MUSCLE, Clustal Omega
- To analyzing and visualizing molecular evolution by using MEGA
- To visualize phylogenetic trees using TreeViewX2.0
- To analyze phylogenetic data by using different programs in PHYLIP
- To analyze phylogenetic data by using PAUP
- To analyze phylogenetic data by using MrBays

Practical based on BBI-614 (Programming in Python & Biopython)

- Downloading & Installation of Python on windows & Macintosh platform
- Programs on basic to advanced python covering general aspects of python programming
- Installation of Biopython Package
- Installation of application specific biopython libraries-Biskit, Scikit-learn, Numpy, MatPlotLib
- Python File handling-Read Write Fasta.
- Gene Expression Analysis with Python.
- Sequence analysis- Reading DNA/Protein sequences, sequence length, GC%, handle string search.
- Programs using string handling function substring search, count of nucleotides, check RNA/DNA, ORF finding, Transcription, Translation.
- Program with regular expression.
- Define RE for a set of sequences, search for subsequences/patterns, locations.
- Programs for processing FASTA files.
- Analyze Biological/Bioinformatics data: Epidemic Modeling of COVID dataset.

LC18: Major Project (In silico)

The course is designed to result in the satisfactory completion and defense of the Masters dissertation (Only bioinformatics in silico projets).

This process includes (Project Report in prescribed format and PPT's)

a) The conceptualization of the independent research that will comprise the dissertation

b) The preparation of and satisfactory defense of the dissertation proposal,

c) The collection, analysis, and interpretation of data,

d) Presentation of findings in the dissertation format, and

e) Oral defense of the dissertation.

Dissertation activity must be completed within prescribed time frame for the semester.

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