DR. BABASAHEB AMBEDKAR MARATHWADA UNIVERSITY,
CHHATRAPATI SAMBHAJINAGAR.

CIRCULAR NO.SU/M.Sc/College./NEP/95/2024

It is hereby inform to all concerned that, the Revised syllabi prepared by the Board of Studies/ Ad-hoc Boards & recommended by the Dean, Faculty of Science & Technology, **Academic Council at its meeting held on 08 April 2024 has accepted** the following Syllabi under the Faculty of Science & Technology **as per Norms of National Education Policy -2020** run at the Affiliated Colleges, Dr.Babasaheb Ambedkar Marathwada University as appended herewith.

Sr.No.	Courses	Semester
1.	**M.Sc.Zoology**	**IIIrd & IVth semester**
2.	**M.Sc. Biotechnology**	**IIIrd & IVth semester**
3.	**M.Sc.Bioinformatics**	**IIIrd & IVth semester**
4.	**M.A./M.Sc.Mathematics**	**IIIrd & IVth semester**

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/2024/26472-80
Date:- 20.05.2024

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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,[M.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.

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BABASAHEB AMBEDKAR MARATHWADA UNIVERSITY,

CHHATRAPATI SAMBHAJINAGAR

FACULTY OF SCIENCE & TECHNOLOGY

2 Years P.G. Programme in Science

(M.Sc.)

As per National Education Policy-2020

Course Structure and Curriculum

(Outcome Based Credit System)

M.Sc. Bioinformatics S.Y. (III & IV Sem)

[For Affiliated Colleges]

Subject: Bioinformatics

(Effective from 2024-25)

Dr. M.S. Patil

(Jadhav M.A)

AS PER NEP 2020

Illustrative Credit distribution structure M.Sc. Bioinformatics S.Y.

Class: M.Sc. Second Year **Semester: III**

Course type	Course Code	Course Name	Teaching Scheme (Hrs./ week)		Credits Assigned		Total Credits
			Theory	Pract.	Theory	Pract	
Major Mandatory DSC	BIOIN/MJ/600	Molecular Phylogenetics	2	-	2	-	14
	BIOIN/MJ/601	Genomics & Proteomics	2	-	2	-	
	BIOIN/MJ/602	Immunology & Immunoinformatics	2	-	2	-	
	BIOIN/MJ/603	Practical based on BIOIN/MJ/600	-	4	-	2	
	BIOIN/MJ/604	Practical based on BIOIN/MJ/601	-	4	-	2	
	BIOIN/MJ/605	Practical based on BIOIN/MJ/602	-	4	-	2	
	BIOIN/MJ/606	Skills in Python & Bio-Python	-	4	-	2	
DSE (Choose any one from pool of courses)	BIOIN/DSE/607	A. LINUX for Bioinformatics B. Glycoinformatics C. Advanced Julia D. Advanced Topics in Computational Biology	2	-	2	-	04
	BIOIN/DSE/608	Practical based on BIOIN/DSE/607	-	4	-	2	
RP	BIOIN/RP-1/649	Research Project-1		8	-	4	04
			16	12	16	06	22

(Jadhav M.A.)

1. **Major Mandatory (DSC)**:-

BIOIN/MJ/600: Molecular Phylogenetics

BIOIN/MJ/601: Genomics & Proteomics

BIOIN/MJ/602: Immunology & Immunoinformatics

BIOIN/MJ/603: Practical based on BIOIN/MJ/550

BIOIN/MJ/604: Practical based on BIOIN/MJ/551

BIOIN/MJ/605: Practical based on BIOIN/MJ/552

BIOIN/MJ/606: Skills in Python & Bio-Python

2. Discipline Specific Elective (DSE): (Choose any one from Pool /Basket)

BIOIN/DSE/607:- A. LINUX for Bioinformatics

B. Glycoinformatics

C. Advanced Julia

D. Advanced Topics in Computational Biology

BIOIN/DSE/508:- Practical based on BIOIN/DSE/607

3. RP: BIOIN/RP-1/649: Research Project-1

Class: M.Sc. Second Year **Semester: IV**

Course type	Course Code	Course Name	Teaching Scheme (Hrs./ week)		Credits Assigned		Total Credits
			Theory	Pract.	Theory	Pract	
Major Mandatory DSC	BIOIN/MJ/650	Metabolomes & Metabolic Pathway Engineering	2	-	2	-	12
	BIOIN/MJ/651	Advanced Techniques in Biological Data Analysis	2	-	2	-	
	BIOIN/MJ/652	R Programming	2	-	2	-	
	BIOIN/MJ/653	Practical based on BIOIN/MJ/650	-	4	-	2	
	BIOIN/MJ/654	Practical based on BIOIN/MJ/651	-	4	-	2	
	BIOIN/MJ/655	Practical based on BIOIN/MJ/652	-	4	-	2	
DSE (Choose any one from pool of courses)	BIOIN/DSE/656	A. Programming in PERL & Bio-PERL B. Translational Bioinformatics C. Neuroinformatics D. Data Science for Bioinformatics	2	-	2	-	04
	BIOIN/DSE/657	Practical based on BIOIN/DSE/656	-	4	-	2	
RP	BIOIN/RP-2/699	Research Project-2		12	-	6	06
			16	12	16	06	22

(Jadhav M'A)

1. **Major Mandatory (DSC)**:-

BIOIN/MJ/650: Metabolomes & Metabolic Pathway Engineering

BIOIN/MJ/651: Advanced Techniques in Biological Data Analysis

BIOIN/MJ/652: R Programming

BIOIN/MJ/653: Practical based on BIOIN/MJ/650

BIOIN/MJ/654: Practical based on BIOIN/MJ/651

BIOIN/MJ/655: Practical based on BIOIN/MJ/652

2. Discipline Specific Elective (DSE): (Choose any one from Pool /Basket)

BIOIN/DSE/656:- A. Programming in PERL & Bio-PERL

B. Translational Bioinformatics

C. Neuroinformatics

D. Data Science for Bioinformatics

BIOIN/DSE/508:- Practical based on BIOIN/DSE/607

3. RP: BIOIN/RP-1/699: Research Project-2

Semester-III

Name of Course: Molecular Phylogenetics

Course Code: BIOIN/MJ/600 **Course Type:** Major (DSC)

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

- To understand the concept of molecular phylogenetics
- To understand the methods of phylogenetic tree construction
- To understand the working of phylogenetic software programs

Course Outcomes:

Upon successful completion of this course, students will be able to:

- Know the mechanism of evolution and its impact on phylogenetic relationships.
- Know the algorithmic approach of phylogenetic tree construction
- Handle phylogenetic software.

Unit-1- 10

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

Unit-2. 10

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-3. 10

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.

Name of Course: Genomics & Proteomics

Course Code: BIOIN/MJ/601 **Course Type:** Major (DSC)

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

- Principles of basic methods of genomic, transcriptomic and proteomic analysis.
- Extensive knowledge of various methodologies of next generation sequencing and Mass spectroscopic, and microarray technologies
- Crucial concepts and techniques applied in genomics, transcriptomics and proteomics.

Course Outcomes:

Upon successful completion of this course, students will be able to:

- Inferring the basic concepts of genomics, transcriptomics and proteomics
- Suggesting and outlining solution to theoretical and experimental problems in Genomics, Transcriptomics and Proteomics fields.
- Comprehend and solve diverse problems of genomics. transcriptomics and proteomics in human welfare, health and disease.

Unit-1- 10

Genomics & its importance, Genome sequencing method-NGS and its platforms, Genome assembly and annotation, structural and functional genomics, comparative genomics. Bioinformatics tools in genomics.

Unit-2. 10

Organization of proteome: Basic concept of proteome; history, types of proteomics and applications of proteomics, Conventional and advanced techniques in proteomics.

Unit-3. 10

Genomics tools: VarScan2, NovoAlign, FastQC, Proteomics tools: PROTPARAM, SOPMA, PSORT, MASCOT.

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.

Name of Course: Immunology & Immunoinformatics

Course Code: BIOIN/MJ/602 **Course Type:** Major (DSC)

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

- To understand the role of B and T cell in immunity
- To study immunological techniques used for diagnosis of disease
- To understand the role of computational technology to study immunology

Course Outcomes:

Upon successful completion of this course, students will be able to:

- Study antibody and antigen and their interactions
- Know the principle and working of different assay in immunology
- Know the epitope prediction methods and software tools

Unit-1- 10

Basic concept of Immunology, Structure and function-- Monoclonal antibodies. B Cell generation and differentiation: BCR--Antibody diversity: Genetic basis—T- dependent activation of B cells-B lymphocyte signal transduction. Cytokines. Complement system. Antigen- antibody interaction: antibody affinity and activity- Isolation of lymphoid cells from blood and lymphoid organs--precipitation reaction.

Unit-2. 10

Agglutination reaction --Radioimmunoassay, ELISA, Western Blot, Immunoprecipitation, Immun-fluoresence, flow cytometry. Cell cultures and Experimental animal models. Analysis of gene expressions. Prediction of Cytotoxic T Cell (MHC Class I) Epitopes- Antigen Processing in the MHC Class I Pathway. MHC-II PREDICTION: Prediction of Helper T Cell (MHC Class II) Epitopes- Processing of MHC Class II Epitopes

Unit-3. **10**

Recognition of Antigen by B Cells vaccine design - Web-Based Tools for Vaccine Design. The IMGT® Immunoinformatics page. Databases associated with Immunoglobulins (or Antibodies) (IG), T cell receptors (TR), Major histocompatibility (MH), Antigens, Allergens, Peptides binding to MH etc., Vaccine development and Immunoinformatics: Recombinant vaccines, combined vaccines, polyvalent vaccines. Immunoinformatics, databases in immunology, DNA, Plant and protein based recombinant antigens as vaccines.

References:

- Immunological Bioinformatics‖ Ole Lund Darren Flower, MIT press, Springer.
- Immunoinformatics: Predicting Immunogenicity in Silico‖ Darren R Flower Humana Press
- Mmunoinformatics Bioinformatics Strategies for Better Understanding of Immune Function‖ Rammensee Wiley
- Computational Immunology: Basics Shyamasree Ghosh CRC Press
- Kuby Immunology Thomas J. Kindt , Richard A. Goldsby, Barbara A borne W. H. Freeman & Company

Name of Course: Practical based on BIOIN/MJ/600

Course Code: BIOIN/MJ/603 **Course Type:** Major (DSC)

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- 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 dendogram & phylogenetic tree
- Reconstruction of phylogenetic tress 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 tress & species tree
- Numerical taxonomy & Bacterial identification using matrices

Name of Course: Practical based on BIOIN/MJ/601

Course Code: BIOIN/MJ/604 **Course Type:** Major (DSC)

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- 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.

Name of Course: Practical based on BIOIN/MJ/602

Course Code: BIOIN/MJ/605 **Course Type:** Major (DSC)

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- To retrieve of antigen related data from AntigenDB
- Kolaskar-Toongoankar antigenicity prediction
- Protective antigen prediction using VaxiJen 2.0
- Classification of protein as a vaccine or non-vaccine candidates using Vaxi-DL
- 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

Name of Course: Skills in Python & Bio-python

Course Code: BIOIN/MJ/606 **Course Type:** Major (DSC)

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- Write a Python program that asks the user for two DNA sequences, and prints the reverse complement of their concatenation.
- Write a Python program that asks the user for a DNA sequence, and prints both the corresponding mRNA sequence and protein sequence, including stop codons (according to the standard translation table).
- Write a Python program that asks the user for a DNA sequence, and prints both the corresponding mRNA sequence and protein sequence, including stop codons (according to the Yeast Mitochondrial Code translation table).
- Write a Python program that takes the sequence of the 1AI4 PDB protein (download the FASTA file manually), and writes a corresponding UniProt file.
- Write a Python program that takes the sequences.fasta file and writes N single-sequence FASTA files, called sequence{number}.fasta, each one containing a single sequence of the original file.
- Do the same, but create N GenBank files instead.
- Write a Python program that takes the sequences.fasta file and writes a revcomp.fasta file with the reverse complements of the original sequences.

  Hint. The SeqIO.write() function can write an entire **list** of SeqIO records
- Write a program that, given a fasta file containing multiple protein sequences and a string specified by the user, prints to a new file only sequences that contain at least one occurrence of the string (regular expressions are allowed). Test your program with the file sequences.fasta, printing sequences containing a stretch of at least three glutamines.

- Ask the user for the path to a pdb file. Print the header of the PDB file on screen, including the name, author, resolution and release date of the PDB structure.
- Ask the user for the path to a pdb file, as well as the name of a chain. Print the number of atoms that each of its residues has.
- Ask the user for the path to a pdb file, and convert its sequence to a FASTA file.

  Note. You will need to convert from three-letter amino acid codes to one-letter codes. ***Hint.*** You can use the SeqIO module, but it is not mandatory.

(Choose any one from pool of courses)

Name of Course: A. LINUX for Bioinformatics

Course Code: BIOIN/DSE/607 **Course Type:** DSE

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

- Use basic fundamental utilities which are required again and again on daily basis to work on a modern operating system.
- To understand and make effective use of Linux utilities and shell scripting language to solve problems.
- To develop the skills the necessary for systems programming including file system programming, process.

Course Outcomes:

Upon successful completion of this course, students will be able to:

- Students will be able to understand the basic commands of Linux operating system.
- Students will be able to create file systems and directories and operate them

Unit-1- 10

What is Operating Systems, Types of Operating System, Linux Basics: Introduction to Linux: History, GNU, System Organization (Kernel and Shell), Difference between Linux and Windows, Difference between Linux and UNIX, Advantages and Disadvantages of Linux in Bioinformatics, Application of Linux in Bioinformatics, Importance of Linux Kernel, Files and Directories, Linux Architecture, Linux File System.

Unit-2. 10

Types of user-Root user (#) and normal user($), Multiple logins at same time(Ctrl + Alt + F1,F2..F6), Help: whatis, --help, man command, init and run levels. Linux Installation, touch, ls, mkdir, rm, cat. cat > file, cat >> file, cp, move, rename,

nm, who. Use of /, all directories under /, absolute path & relative path. Basic calculator, date utilities. Filter Commands: tr, head, tail, last, grep, sort, piping. Find Command with various options. Managing user accounts- Sudo.

Unit-3. 10

User Administration: useradd, usermod and userdel, passwd, chown, File Permissions: adding and removing permissions. Package installation through GUI/apt-get process. Shell Programming: Types of Shells, Shell Variables, and Shell Scripts. Debugging scripts, echo, read, operators, and keywords, Integer Arithmetic and String Manipulation, Decision Making: if-else-elif. Loop Control, while, for, until, break & continue Functions.

References:

- Operating System Concepts by Abraham Silberschatz, Peter B. Galvineg Gagne, Wiley Publications.
- Fundamentals of Linux, by Maidsani D, Firewall Media.
- Shell Scripting: Expert Recipes for Linux, Bash and more‖, Steve Parker, Wrox Publication.
- Linux Command Line and Shell Scripting Bible‖, Richard Blum, Christine Breshnahan, Wiley Publications.

Name of Course: B. Glycoinformatics

Course Code: BIOIN/DSE/607 **Course Type:** DSE

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

- To understand the concept of glycoinformatics
- To understand the nature of glycobiology computational resources
- To understand the nature of glycobiology computational tools

Course Outcomes:

Upon successful completion of this course, students will be able to:

- Know the glycobiology & glycoinformatics and its applications
- Study glycobiology computational resources
- Study glycobiology computational tools

Unit-1. 10

Introduction of Glycobiology & Glycoinformatics, Historical background and overview, Saccharide structure & nomenclature, Evolution of Glycan Diversity, Conformation of Oligosacchrides, N-linked glycosylation & O-linked glycosylation, Glycolipids and membrane protein glycosylation, Glycoinformatics and its resources-GlyTouCan, KEGG GLYCAN, CAZY database, GlyGen database.

Unit-2. 10

Glycan Library – a list of approximately 830 lipid-linked sequence-defined glycan probes derived from diverse natural sources or chemically synthesized, Glyco3D – a portal of 3D structures of mono, di, oligo and polysaccharides and carbohydrate recognizing proteins, SugarBindDB: provides information on known carbohydrate sequences to which pathogenic organisms.

Unit-3. 10

Glycobiology data analysis tools- CASPER – a tool for calculating NMR chemical shifts of oligo- and polysaccharides, NetOGlyc - 4.0: O-GalNAc (mucin type) glycosylation sites in mammalian proteins, GlycoDomainViewer – an online resource to study site glycosylation with respect to protein context and conservation, SweetUnityMol – software to display 3-D structures of carbohydrates, polysaccharides and glycoconjugates, GlycoMod – an online tool to predict oligosaccharide structures on proteins from experimentally determined masses.

References:

- Introduction to Glycobiology, Taylor, Maureen, Oxford University Press
- Essentials of Glycobiology by Ajit Varki, Richard Cummings (Editor), Jeffrey Esko (Editor), Hudson Freeze (Editor), Gerald Hart (Editor) Cold Spring Harbor Laboratory Press NY.
- Essentials of Glycobilogy, Edited by Ajit Varki et al. Cold Spring Harbor Laboratory Press NY.

Name of Course: C. Advanced Julia

Course Code: BIOIN/DSE/607 **Course Type:** DSE

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

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

Course Outcomes:

Upon successful completion of this 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-1. 10

Advanced 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-2. 10

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-3.

10

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

Name of Course: D. Advanced Topics in Computational Biology

Course Code: BIOIN/DSE/607 **Course Type:** DSE

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

- To expose the students to emerging areas in the field of new biology from a computational perspective

Course Outcomes:

Upon successful completion of this course, students will be able to:

- To provide basic introduction to Systems Biology, properties of biological systems and approaches in systems biology to analyse and interpret data
- To give an overview of Synthetic Biology and analytical computational methods discussed with the help of tools and software
- To understand the recent trends in genomics like toxicogenomics, pharmacogenomics, NGS etc

Unit-1. 10

Systems biology: Self-organization, emergence, modularity and abstraction, feedback, control analysis, Enzyme Kinetics and Thermodynamics: The Law of Mass Action; Reaction Kinetics, Rate Equation, Michaelis-Menten Equation, Hill Equation, Interaction networks overview- Gene Regulatory Network, Protein – Protein Interaction Network, Signaling Pathways, Metabolic pathways; network motifs, Systems Biology tools and standards: Matlab -Systems Biology toolbox; SBML; SBGL (Systems Biology Graphical Language); KEGG; Tools for systems Biology- Cell designer; Cytoscape.

Unit-2. 10

Synthetic Biology: Engineering Biology; design and construction of novel biological systems; Abstraction hierarchy-Part, Device, Systems; BioBricks - a standard for (physical) DNA composition, Designing a biological system from Biobricks; iGEM; SBOL, Computational Synthetic biology: Codon optimization; AND gate and OR gate in biology; Operons; Switches and clocks; Repressilator;

Applications- Environment, Energy, Pharmaceutical needs, Ethical issues of Synthetic Biology

Unit-3. 10

Niche areas in Genomics: Toxicogenomics, Pharmacogenomics- Pharmacogenetics, SNP, Personalized medicine, Metagenomics, Comparative genomics, Functional genomics, structural genomics, QTL, HGP.

References:

- Alon, U. (2006). An introduction to systems biology: design principles of biological circuits. CRC press.
- Benson, G. (2003). Algorithms in Bioinformatics. Springer Berlin Heidelberg.
- Boogerd, F., Bruggeman, F. J., Hofmeyr, J. H. S., & Westerhoff, H. V. (Eds.). (2007). Systems biology: philosophical foundations. Elsevier.
- Choi, S. (Ed.). (2007). Introduction to systems biology. New Jersey:: Humana Press.
- Demin, O., & Goryanin, I. (2010). Kinetic modelling in systems biology. CRC Press.

Name of Course: Practical based on BIOIN/DSE/607: A

Course Code: BIOIN/DSE/608 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- Write a shell script to create files with the names passed on command line.
- Write a shell script to input number from user and display its factorial.
- Write a shell script to input file name and create multiple directories individually for the name in the file given.
- Write a shell script that receives any number of file names as arguments checks if every argument supplied is a file or a directory.
- Use Linux commands for efficient organization and manipulation of bioinformatics data. Leverage find and grep to search and filter datasets.
- Write Bash scripts to automate repetitive tasks and create bioinformatics workflows. Utilize the command-line interface for batch processing.
- Use Git and GitHub to manage and version bioinformatics code and analyses.
- Use Linux commands to pre-process genomic data, align sequences, and perform variant calling.

Name of Course: Practical based on BIOIN/DSE/607: B

Course Code: BIOIN/DSE/608 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- To retrieve biological information of carbohydrates by accessing GluTouCan Database.
- To derive a list of lipid linked glycans by accessing Glycan library
- To retrieve 3D structures of carbohydrates by accessing Glyco3D database
- To retrieve carbohydrates associated with pathogenic organism by accessing SugarBindDB
- To calculate NMR chemical shift of carbohydrates by CASPER
- To predict glycosylation site of mammalian protein sequence using NetOGlyc tool
- To predict oligosacchrids structure by using GlycoMod
- To display 3D structures of carbohydrates by using SeetUnityMol

Name of Course: Practical based on BIOIN/DSE/607: C

Course Code: BIOIN/DSE/608 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- 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)

Name of Course: Practical based on BIOIN/DSE/607: D

Course Code: BIOIN/DSE/608 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- To analyse enzyme kinetics data using RENZ R package
- To perform spectrum analysis by using MATLAB's System Biology Toolkit
- Install & Handle CellDesigner tool to analyse biological network
- To study SBGN Cytoscape plugin
- To retrieve pathway specific information by accessing KEGG database
- Study of Biobricks resource
- To analyse biological networks using Cytoscape

Name of Course: Research Project-1

Course Code: BIOIN/RP-1/649 **Course Type:** RP

Credit: 04 **Contact Hours:** 60 **Hours/Week:** 08

Total Marks: 100

(Project will based on applied disciplines in the field of bioinformatics)

Semester-IV

Name of Course: Metabolomes & Metabolic Pathway Engineering

Course Code: BIOIN/MJ/650 **Course Type:** Major (DSC)

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

- To understand the nature of biological network and their structure
- To understand biochemical basis of major metabolic pathways
- To understand the contents & computational organization of metabolic pathways

Course Outcomes:

Upon successful completion of this course, students will be able to:

- Study properties and representation of biological pathways
- Study biochemical reactions occurs in major metabolic pathways
- Access metabolic pathway databases

Unit-1. 10

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-2. 10

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-3. 10

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

Name of Course: Advanced Techniques in Biological Data Analysis

Course Code: BIOIN/MJ/651 **Course Type:** Major (DSC)

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

- To understand the algorithmic approach of gene identification
- To understand the algorithmic approach of motif detection
- To understand the algorithmic approach of structure analysis

Course Outcomes:

Upon successful completion of this course, students will be able to:

- Handle gene prediction software tools
- Handle motif prediction software tools
- Handle structure analysis software tools

Unit-1. 10

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-2. 10

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-3. 10

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

Name of Course: R Programming

Course Code: BIOIN/MJ/652 **Course Type:** Major (DSC)

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course 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

Course Outcomes:

Upon successful completion of this course, students will be able to:

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

Unit-1. 10

Introduction to R Programming: What is R? Installing R and RStudio, Working in the Console, Arithmetic Operators, Logical Operations, Built-in Functions, Getting Help in R and RStudio, Creating Variables, Numeric, Character and Logical Data, Vectors, Data Frames, Factors, Sorting Numeric, Character, and Special Values. Data structures, variables, data types. Iteration: while loops, for loops. Conditional statements: If / else, Boolean logical operators. Writing functions Reporting: Creating functions, calling of functions.

Unit-2. 10

Input and Output in R: Basic file handling, Viewing files, File manipulation, Working with R's binary format. File input and output: Reading rectangular data, Writing data, Debian Control Format (DCF), FASTA Format. Built-in capabilities: Modifying text, Sorting and comparing, Matching a set of alternatives, Formatting text and numbers, Special characters and escaping, Parsing and deparsing, Plotting with text and Manipulating and analyzing data with dplyr.

Unit-3. 10

Regular expressions: Regular expression basics, Matching, Using regular expressions, Globbing and regular expressions, Prefixes, suffixes and substrings, Biological sequences, Matching patterns: Matching single query sequences, Matching many query sequences, Palindromes and paired matches, Alignments. R Packages: Package basics, The search path, Package information, Data and demos, Vignettes, Package management: biocViews, Managing libraries, Package authoring.

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)

Name of Course: Practical based on BIOIN/MJ/650

Course Code: BIOIN/MJ/653 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- Browse & search following metabolic pathway database-KEGG
- Browse & search following metabolic pathway database- BioCyc
- Browse & search following metabolic pathway database-MetaCyc
- Browse & search following metabolic pathway database-EcoCyc
- Browse & search following metabolic pathway database-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.

Name of Course: Practical based on BIOIN/MJ/651

Course Code: BIOIN/MJ/654 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- Browse & search following metabolic pathway database-KEGG
- Browse & search following metabolic pathway database- BioCyc
- Browse & search following metabolic pathway database-MetaCyc
- Browse & search following metabolic pathway database-EcoCyc
- Browse & search following metabolic pathway database-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.

Name of Course: Practical based on BIOIN/MJ/652

Course Code: BIOIN/MJ/655 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- Exploring the basic programming concepts using R or RStudio.
- Sequence Concatenation.
- ATGC and It's pair Counting
- Transcriptions and Translation of Sequences.
- Slicing the Sequence.
- Matching the Sequence Pattern.
- Explore your data using visualizations using scatter plots.
- Explore your data using visualizations using heatmaps.
- Explore your data using visualizations using boxplots.

(Choose any one from pool of courses)

Name of Course: A. Programming in PERL & Bio-PERL

Course Code: BIOIN/DSE/656 **Course Type:** DSE

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

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

Course Outcomes:

Upon successful completion of this course, students will be able to:

- Write Perl scripts for processing biological data
- Use toolkit of Perl modules for various bioinformatics applications

Unit-1. 12

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, 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-2. 12

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

Unit-3. 06

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.

Name of Course: B. Translational Bioinformatics

Course Code: BIOIN/DSE/656 **Course Type:** DSE

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

- To understand the concept of translational bioinformatics
- To study variation and their impact on disease etiology
- To study microbiome genome at molecular level

Course Outcomes:

- Upon successful completion of this course, students will be able to:
- Study network biology approach to complex diseases
- Understand single nucleotide and other types of variations and disease ontology.

Unit-1. 10

Introduction to translational bioinformatics, biomedical knowledge integration, data driven view of disease biology, small molecules and disease, protein interactions and disease, network biology approach to complex disease.

Unit-2. 10

Structural variations and medical genomics, Pharmacogenomics, Biological knowledge assembly and interpretation, Analysis using disease ontologies, Mining genome wide genetic markers, Genome-Wide Association Studies.

Unit-3. 10

Human Microbiome Analysis, Mining electronic health records in the genomic era, Cancer Genome Analysis, Disease gene prioritization, Text mining for translational bioinformatics, Bioimage informatics for systems pharmacology.

References:

- Translational Bioinformatics by Xiangdong Wang Springer.
- Computational Biology, Translational Bioinformatics Collections, PLOS.
- Methodologies of Multi-Omics Data Integration and Data Mining Techniques and Applications by Kang Ning

Name of Course: C. Neuroinformatics

Course Code: BIOIN/DSE/656 **Course Type:** DSE

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

- To understand the challenges & opportunities in neuroinformatics
- To understand the electrophysiology & biophysics behind the neurology
- To understand the contents of neuroscience knowledge bases

Course Outcomes:

Upon successful completion of this course, students will be able to:

- Analyse neuroscience data
- Study various components of electrophysiology & biophysics involved in neuroscience
- Access neurological data from neuroscience knowledge bases

Unit-1. 10

Overview of neuroinformatics challenges and opportunities, Neuronal morphology: NeuroMorpho.Org functionality and pipeline, Neuronal reconstructions: from image stacks to digital vector traces. Reconstruction, analysis, visualization, modeling. ImageJ, Neuron_Morpho plug-in, Neuromantic, Vaa3D, Neuronland, CVAPP, L-Measure, neuroConstruct, Py3DN.

Unit-2. 10

Electrophysiology and biophysics: Compartmental simulations: a brief historical overview on the theory, illustrative results and applications. NEURON and ModelDB, Hippocampus, hippocampal circuitry , neuron types, the Hippocampome and functional hippocampal models. System neuroanatomy, contours, surfaces, and volumes: Cytoarchitecture and Hippocampus3D.

Unit-3. 10

Neuroscience knowledge bases: NIF and NeuroLex; INCF, Neuron Registry and NeuronID; Senselab, Whole Brain Catalog, BrainInfo, and BAMS, Neuroscience bioinformatics:=

NCBI resources (e.g. BLAST, Swissprot, in-situ hybridization, microarrays, GEO, etc.), NeuroMab, GENSAT, Allen Brain Expression Maps. Non-invasive human brain imaging. NeuroVault, LONI resources (ICBM, BIRN, CCP, ADNI, HCP, MAP, etc.), BraVa, NITRC. Whole-brain network simulations and human connectome project.

References:

- Theoretical Neuroscience- Computational and Mathematical Modelling of Neural System by Dayan and Abbot
- Dynamical Systems in Neuroscience by Eugene Izikevich
- Tutorial on Neurobiology: Single neuron to brain chaos by Walter Freeman

Name of Course: D. Data Science for Bioinformatics

Course Code: BIOIN/DSE/656 **Course Type:** DSE

Credit: 02 **Contact Hours:** 30 **Hours/Week:** 02

Total Marks: 50

Course Objectives:

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

Course Outcomes:

Upon successful completion of this 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-1. 10

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, analyse, communicate and its applications in bioinformatics, **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-2. 10

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. **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-3. 10

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

Name of Course: Practical based on BIOIN/DSE/656 A

Course Code: BIOIN/DSE/657 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- 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

Name of Course: Practical based on BIOIN/DSE/656 B

Course Code: BIOIN/DSE/657 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- To study integrative Biomedical Knowledge Hub with reference to Alzheimer disease.
- To access data related to genes & variants associated with human diseases from DisGeNET database
- To access data related to genes associated with human diseases from DISEASES database
- Study of eDGAR: a database of Disease-Gene Associations with annotated Relationships among genes
- GWAS analysis using GWASTool (Bioconductor)
- Study of disease ontology knowledgebase
- Study of Mining of electronic health records (EHRs)
- Study of Cancer Imaging Archive to analyse cancer data
- To study the cancer proteome atlas portal
- Bioimage analysis using ImageJ2 software

Name of Course: Practical based on BIOIN/DSE/656 C

Course Code: BIOIN/DSE/657 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- To access neuronal reconstruction data from NeuroMorpho.org resource
- To analyse & visualize neuronal data using VAA3D Software
- To study, installation & handling of software maintained by Neuronland
- To retrieve neuroscience models by accessing ModelDB.
- To demonstrate BrainSuite
- To study NeuroVault
- Introduction to LONI resources

Name of Course: Practical based on BIOIN/DSE/656 D

Course Code: BIOIN/DSE/657 **Course Type:** DSE

Credit: 02 **Contact Hours:** 60 **Hours/Week:** 04

Total Marks: 50

Practical:

- 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 analysing protein-protein interaction network with STRING

Name of Course: Research Project-2

Course Code: BIOIN/RP-2/699 **Course Type:** RP

Credit: 06 **Contact Hours:** 120 **Hours/Week:** 12

Total Marks: 150

The course is designed to result in the satisfactory completion and defence 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 defence of the dissertation.

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

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