



Course Syllabus
Gyanmanjari Science College
Semester-3 (M.Sc.)

Subject: Bio-Informatics-MSCMB13515

Type of course: Major

Prerequisite: Student must have basic knowledge of Computer and genome sequencing.

Rationale: Bridges the gap between the data deluge in biology and our ability to understand it. It allows researchers to make sense of complex biological processes and use that knowledge for various applications, like drug discovery, personalized medicine, and engineering new biomaterials.

Teaching and Examination Scheme:

Teaching Scheme			Credits	Examination Marks					Total Marks
CI	T	P		Theory Marks		Practical Marks		CA	
			ESE	MSE	V	P	ALA		
4	0	0	4	60	30	10	00	50	150

Legends: CI-Class Room Instructions; T – Tutorial; P - Practical; C – Credit; ESE - End Semester Examination; MSE- Mid Semester Examination; V – Viva; CA - Continuous Assessment; ALA- Active Learning Activities.



Course Content:

Unit No	Course content	Hrs	% Weightage
1	<p>Chapter:1 Introduction of Omics technology</p> <ul style="list-style-type: none"> • Introduction to genomics and proteomics, codon bias, gene expression, Genome size, DNA sequencing: Maxam-Gilbert, Sanger, pyrosequencing, automated DNA sequencing. • Other features of nucleic acid sequencing. Analysis and Annotation - ORF, Exon-intron boundaries. • DNA Microarray technology • Transcriptomics: Comparative transcriptomics, Differential • Gene expression; Genotyping/SNP detection • Genome editing: Role of CRISPR and Cas9 for advanced DNA and RNA editing and their applications. 	15	25%
2	<p>Chapter: 2 Database and sequencing</p> <ul style="list-style-type: none"> • Local alignment • Global alignment • Sequence Alignment • Multiple Sequence Alignment • DOT MATRIX SEQUENCE COMPARISON, BLAST, NCBI,DNA Sequence Analysis • Gene Structure Analysis and Prediction, Sequence Composition 	15	25%
	<ul style="list-style-type: none"> • Genome databases and search protocol: Genome databases at NCBI, SANGER, etc. • Secondary database search protocol, Use of Boolean operators 		
3	<p>Chapter: 3 Introduction to computational biology basics and biological databases</p> <ul style="list-style-type: none"> • History of Bioinformatics, Scope of Bioinformatics Introduction to Biological databases, Nucleic acid databases: Introduction to biological databases in general • Classification- Primary, Secondary, Composite databases, various file formats, FASTA, GENBANK, Nucleic acid sequence databases- GENBANK, EMBL, DDBJ etc. • Heuristic approach: BLAST, FASTA • Building Profiles and Profile based functional identification 	15	25%



4	<p>Chapter:4 Protein prediction and Proteomics</p> <ul style="list-style-type: none"> ➤ Protein databases ➤ Protein databases analysis. • Introduction to Mass spectrometers; MALDI-TOF and LC-MS analyses. • Protein- Protein interactions: Solid phase ELISA, Pull-down assay (using GST-tagged protein), Far Western analysis, Surface Plasmon Resonance techniques. • Protein arrays: definition, applications, diagnostics, expression, profiling. • Uses of automated technologies to generate protein arrays and chips. 	15	25%
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Continuous Assessment:

Sr. No	Active Learning Activities	Marks
1	<p>Phylogene preparation Faculty will provide the accession no. and student have to prepare phylogenetic tree on Blast Tool and upload it to GMIU web portal.</p>	10
2	<p>3D model Faculty will provide the knowledge about CRISPER. Prepare 3D model of CRISPER- CAS 9 and upload it to GMIU web portal.</p>	10
3	<p>Library Preparation Faculty will provide some species name and data students have to prepare FASTA Sequence library based on similarity and upload it to GMIU web portal.</p>	10
4	<p>Alignment chart Faculty will provide the Sequences and students have to prepare gap penalty chart by Global and Local alignment and upload it to GMIU web portal.</p>	10
5	<p>Protein structure analysis Faculty will provide protein structure and students will analyze the structure of protein and upload it to the GMIU web portal.</p>	10
Total		50



Suggested Specification table with Marks (Theory):60

Distribution of Theory Marks (Revised Bloom's Taxonomy)						
Level	Remembrance (R)	Understanding (U)	Application (A)	Analyze (N)	Evaluate (E)	Create (C)
Weightage	20%	40%	30%	10%	-	-

Note: This specification table shall be treated as a general guideline for students and teachers. The actual distribution of marks in the question paper may vary slightly from above table.

Course Outcome:

After learning the course the students should be able to:	
CO1	Pertain the principles and study the basic concept of bioinformatics.
CO2	Understand the principles and operation sequence analysis on different tools
CO3	Apply the principles of genomics on different methods.
CO4	Analyze the protein and predict the protein structure.

Instructional Method:

The course delivery method will depend upon the requirement of content and need of students. The teacher in addition to conventional teaching method by black board, may also use any of tools such as demonstration, role play, Quiz, brainstorming, MOOCs etc.

From the content 10% topics are suggested for flipped mode instruction.

Students will use supplementary resources such as online videos, NPTEL/SWAYAM videos, e-courses, Virtual Laboratory

The internal evaluation will be done on the basis of Active Learning Assignment

Practical/Viva examination will be conducted at the end of semester for evaluation of performance of students in laboratory.



Reference Books:

- [1] David W. Mount, Bioinformatics sequence and genomic analysis.
- [2] Andreas D. Baxevanis, B. F. Francis Ouellette, BIOINFORMATICS A Practical Guide to the Analysis of Genes and Proteins SECOND EDITION
- [3] Rui Jiang • Xuegong Zhang • Michael Q. Zhang Editors, Basics of Bioinformatics
- [4] Supratim Choudhuri, BIOINFORMATICS FOR BEGINNERS Genes, Genomes, Molecular Evolution, Databases and Analytical Tools.

