

**FOUR YEAR UNDERGRADUATE PROGRAM (2024 – 28)**  
**Department of Biochemistry**  
**Course Curriculum**

<b>PART- A: Introduction</b>			
<b>Program: Bachelor in Science</b> <i>(Honors / Honors with Research)</i>		<b>Semester - VIII</b>	<b>Session: 2024-2025</b>
1	<b>Course Code</b>	BCSE - 09 T	
2	<b>Course Title</b>	Bioinformatics	
3	<b>Course Type</b>	Discipline Specific Elective (Theory)	
4	<b>Pre-requisite (if, any)</b>	As per the Program	
5	<b>Course Learning Outcomes (CLO)</b>	<p><i>On successful completion of the course, the student shall be able to:</i></p> <ul style="list-style-type: none"> <li>➤ Understand various databases and GenBank used in storing biological data.</li> <li>➤ Analyze the basic concepts of sequence similarity by BLAST and FASTA algorithms.</li> <li>➤ Explain the phylogenetic analysis and various genome projects.</li> <li>➤ Apply the techniques for the protein structure prediction.chem.-informatics and medicinal biochemistry.</li> </ul>	
6	<b>Credit Value</b>	<b>3 Credits</b>	<i>Credit = 15 Hours - learning &amp; Observation</i>
7	<b>Total Marks</b>	<b>Max. Marks: 100</b>	<b>Min Passing Marks: 40</b>
<b>PART -B: Content of the Course</b>			
<b>Total No. of Teaching-learning Periods (01 Hr. per period) - 45 Periods (45 Hours)</b>			
Unit	Topics (Course contents)		No. of Period
I	<b>Introduction to bioinformatics and data generation:</b> Bioinformatics and its relation with molecular biology Examples of related tools (FASTA, BLAST, BLAT, RASMOL), databases (GENBANK, Pub med, PDB ) and software (RASMOL, Ligand Explorer). Data generation; Generation of large scale molecular biology data. (Through Genome sequencing, Protein sequencing, Gel electrophoresis, NMR Spectroscopy, X-Ray Diffraction, and microarray). Applications of Bioinformatics.		12
II	<b>Biological Database and its Types:</b> Introduction to data types and Source. Population and sample. Classification and Presentation of Data. Quality of data, private and public data sources. General Introduction of Biological Databases; Nucleic acid databases (NCBI, DDBJ, and EMBL). Protein databases (Primary, Composite, and Secondary). Specialized Genome databases: (SGD, TIGR, and ACeDB). Structure databases (CATH, SCOP, and PDB sum)		11
III	<b>Data storage and retrieval and Interoperability:</b> Flat files, relational, object oriented databases and controlled vocabularies. File Format (Genbank, DDBJ, FASTA, PDB, SwissProt). Introduction to Metadata and search; Indices, Boolean, Fuzzy, Neighboring search. Data exchange and integration. Ontologies, interchange languages and standardization efforts. General Introduction to XML, UMLS, CORBA, PYTHON and OMG/LIFESCIENCE.		11
IV	<b>Gene Expression and Representation of patterns and relationship</b> General introduction to Gene expression in prokaryotes and eukaryotes, transcription factors binding sites. SNP, EST, STS. Regular Expression, Hierarchies, and Graphical models (including Marcov chain and Bayes notes). Genetic variability and connections to clinical data.		11
<b>Keywords</b>		FASTA, BLAST, BLAT, RASMOL, NCBI, DDBJ, SNP, EST, STS	

Name and Signature of Convener & Members of CBoS:

**PART-C: Learning Resources****Text Books, Reference Books and Others****Text Books Recommended –**

- BAXEVANIS, AD & OUELLETTE, BFF : Bioinformatics: a practical guide to the analysis of genes and proteins. 2nd Ed.. 2002.
- BAXEVANIS, AD, DAVISON, DB, PAGE: Current protocols in bioinformatics. 2004.
- RDM & PETSKO, GA ORENGO, C, JONES, D & : Bioinformatics: genes, proteins and computers. 2003
- THORNTON, J Ingvar Eidhammer, IngeJonassen, : Protein Bioinformatics. 2003
- William R Taylor HIGGINS, D & TAYLOR, W : Bioinformatics: sequence, structure, and databank. 2000.
  - David Mount: Bioinformatics: sequence and genome analysis. 2004

**PART -D: Assessment and Evaluation****Suggested Continuous Evaluation Methods:****Maximum Marks: 100 Marks****Continuous Internal Assessment (CIA): 30 Marks****End Semester Exam (ESE): 70 Marks**

<b>Continuous Internal Assessment (CIA): (By Course Teacher)</b>	Internal Test / Quiz-(2): <b>20 +20</b>	Better marks out of the two Test / Quiz + obtained marks in Assignment shall be considered against <b>30</b> Marks
	Assignment / Seminar - <b>10</b>	
Total Marks - <b>30</b>		
<b>End Semester Exam (ESE):</b>	<b>Two section – A &amp; B</b>	
	Section A: Q1. Objective – 10 x1= 10 Mark; Q2. Short answer type- 5x4 =20 Marks	
	Section B: Descriptive answer type qts., 1out of 2 from each unit-4x10=40 Marks	

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1	<b>Course Code</b>	BCSE - 09 P	
2	<b>Course Title</b>	Bioinformatics	
3	<b>Course Type</b>	Discipline Specific Elective (Practical)	
4	<b>Pre-requisite (if, any)</b>	As per Program	
5	<b>Course Learning Outcomes (CLO)</b>	<i>On successful completion of the course, the student shall be able to:</i> <ul style="list-style-type: none"> <li>➤ Demonstrate the use of databases.</li> <li>➤ Demonstrate the gene and protein sequence retrieval techniques.</li> <li>➤ Produce novel DNA and protein structures to be used in therapeutics.</li> <li>➤ Perform phylogenetic studies to establish the relationship between two genomes.</li> </ul>	
6	<b>Credit Value</b>	1 Credits	<i>Credit =30 Hours Laboratory or Field learning/Training</i>
7	<b>Total Marks</b>	<b>Max. Marks: 50</b>	<b>Min Passing Marks: 20</b>
<b>PART -B: Content of the Course</b>			
<b>Total No. of learning-Training/performance Periods: 30 Periods (30 Hours)</b>			
<b>Module</b>	<b>Topics (Course contents)</b>		<b>No. of Period</b>
<b>Lab./Field Training/ Experiment Contents of Course</b>	<ul style="list-style-type: none"> <li>➤ Retrieval of sequences from NCBI, EBI and EMBL databases.</li> <li>➤ Retrieval of sequences from NBRF-PIR, SWISSPROT and P databases.</li> <li>➤ Transition and Translation of sequences.</li> <li>➤ Retrieval of genome from genome databases.</li> <li>➤ Exploring DIP and PPI.</li> <li>➤ Exploring BIND and PIM.</li> <li>➤ Exploring MINT and GRID.</li> <li>➤ Analysis of phylogenetic tree</li> <li>➤ Exploring PDB file.</li> <li>➤ Analysis of active site by pymol</li> </ul>		<b>30</b>
<b>Keywords</b>	DIP, MINT and GRID, PDB file		


  
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**PART-C: Learning Resources****Text Books, Reference Books and Others****Text Books Recommended –**

- DA Bender Nutritional Biochemistry of the Vitamins
- R.L. Pike and M.L. Brown Nutrition: An integrated approach -
- G.P. Talwar Text book of Biochemistry and Human Biology
- DWS Wong Mechanism and theory in food chemistry
- M.S. Banji N P. Rao & V. Reddy Text book of Human Nutrition
- Linten Nutritional Biochemistry and Metabolism

**PART -D: Assessment and Evaluation****Suggested Continuous Evaluation Methods:****Maximum Marks: 50 Marks****Continuous Internal Assessment (CIA): 15 Marks****End Semester Exam (ESE): 35 Marks**

<b>Continuous Internal Assessment (CIA):</b> (By Course Teacher)	Internal Test / Quiz-(2): <b>10 &amp; 10</b> Assignment/Seminar + Attendance - <b>05</b> Total Marks - <b>15</b>	Better marks out of the two Test / Quiz + obtained marks in Assignment shall be considered against <b>15 Marks</b>
<b>End Semester Exam (ESE):</b>	<b>Laboratory / Field Skill Performance: On spot Assessment</b> A. Performed the Task based on lab. work - <b>20 Marks</b> B. Spotting based on tools & technology (written) – <b>10 Marks</b> C. Viva-voce (based on principle/technology) - <b>05 Marks</b>	<b>Managed by</b> <b>Course teacher</b> as per lab. status

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