

**Rajarshi Shahu Mahavidyalaya, Latur (Autonomous College)**

**B.Sc. Biotechnology (Semester Pattern) VI Semester**

**Course Title: Computational Biology**

**Course Code: U-COB-705**

**Teaching plan for 2021-2022 (summer)**

**Name of Teacher: Dr. Sachin S. Kulkarni**

<b>Sr. No.</b>	<b>Subject Computational Biology</b>	<b>Unit/Chapter</b>	<b>Dates</b>	<b>No. of lectures</b>	<b>activities</b>	<b>test</b>
1	Unit I	Introduction to bioinformatics and data generation	16-12-2021 to 14-01-2022	01	Classroom	Unit – I 12/2/2021
		What is bioinformatics and its relation with molecular biology.		01	Group Discussion	Unit – II 16/03/2021
		Examples of related tools (FASTA, BLAST, RASMOL),		02		Unit –III 26/04/21
		databases (GENBANK, Pubmed, PDB ) and software (RASMOL)				
		Data generation; Generation of large scale molecular biology data (Through Genome sequencing, Protein sequencing, Gel electrophoresis, Applications of Bioinformatics.		04		
				01		
				01		

	Unit II	<p>Biological Database and its Types Introduction to data types and Source.</p> <p>Population and sample, Classification and Presentation of Data.</p> <p>Quality of data, private and public data sources.</p> <p>General Introduction of Biological Databases; Nucleic acid databases (NCBI, DDBJ, and EMBL).</p> <p>Protein databases (Primary, Composite, and Secondary).</p>	<p>15-01-2022 to 18-02-2022</p>	<p>03</p> <p>02</p> <p>02</p> <p>03</p> <p>02</p>	<p>Classroom</p> <p>Group Discussion</p>	
	Unit III	<p>Sequence Alignments and Visualization</p> <p>Introduction to Sequences, alignments, Local alignment and Global alignment (algorithm and example),</p> <p>Pairwise alignment (BLAST and FASTA Algorithm) and multiple sequence alignment (Clustal W algorithm).</p> <p>Methods for presenting large quantities of biological data: sequence viewers, 3D structure viewers (Rasmol, SPDBv, Chime, Cn3D, PyMol).</p>	<p>19-02-2022 to 20-03-2022</p>	<p>02</p> <p>02</p> <p>04</p> <p>04</p>	<p>Classroom</p> <p>Group Discussion</p>	

	Unit IV	General introduction to Gene expression in prokaryotes and eukaryote,  transcription factors binding sites. SNP, EST, STS.  General introduction to protein structure, prediction of secondary structure of protein,  computational protein modelling	21-02-2022 to 20-03-2022	02  02  03  02	Classroom  Group Discussion	
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### Practicals

Sr. No.	Subject	Practicals	Date	No. of Practicals
1	<b>Computational Biology</b>	A guided tour of NCBI/EBI : Data access – standard search engines : data retrievals tools – Entrez, DBGET and SRS (sequence retrieval systems); software for data building. submission of new revised data	11/2/2021 to 24/04/2021  Batch A,B,C,D	04
2		Sequence homology as product of molecular evolution, sequence similarity searches, sequence alignment-global, local, end free-space; measurement of sequence similarity, similarity and homology.		04
3		Multiple sequence alignment		04
4		Phylogeny reconstruction, PHYLIP package		04
5		Getting an amino acid sequence, nucleotide sequence by blasting		04
6		Multiple sequence alignment		04
7		Homology modeling		04
8		Protein identification & characterization with peptide mass fingerprinting data.		04

9		Primary structure analysis of proteins.		04
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