22	<b>P339</b> (Pages: 2)	Name:	
		Reg.No:	
THIRD SEMESTER M.Sc. DEGREE EXAMINATION, NOVEMBER 2023			
	(CBCSS - PG)		
	(Regular/Supplementary/Improvement)		
CC19P CSS3 E01D - BIOINFORMATICS			
	(Computer Science)		
	(2019 Admission onwards)		
Tim	ne: 3 Hours	Maximum: 30 Weightage	
	Part-A		
	Answer any four questions. Each question carries 2 weightage.		
1.	Explain Eukaryotic Cells and its charateristics.		
2.	Represent taxonomy Tree of Homo sapience and explain taxonomy tree.		
3.	. Provide a detailed note on PAM and BLOSUM in detail and also write the use of these matrix.		
4.	Review the use of multiple sequence alignment.		
5.	Discus Muscle tool for MSA.		
6.	Generalize protein sequence databases.		
7.	Summarize TrEMBL.		
		$(4 \times 2 = 8 \text{ Weightage})$	
	Part-B		
	Answer any four questions. Each question carries 3 weig	ghtage.	
8.	Review the uses of Bioinformatics branch.		
9.	Distinguish 1. Naıve string matching 2. Rabin-Karp algorithm.		
10.	Make a note on pair-wise sequence alignment and multiple sequence alignment	nent.	
11.	Describe phylogenetic algorithms.		
12.	Describe NCBI and EBI database.		

13. Compare FASTA and GENBANK databases.

14. Analyze the EMBL and DDBJ databases.

 $(4 \times 3 = 12 \text{ Weightage})$ 

## Part-C

Answer any two questions. Each question carries 5 weightage.

- 15. Describe what is central dogma.
- 16. Compare motif and tandem repeat in detail.
- 17. Make a detailed Smith-Waterman algorithm in detail.
- 18. Provide note on Local paire-wise algorithm. How Smith-waterman alogorithm works?

 $(2 \times 5 = 10 \text{ Weightage})$ 

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