Reg. No. : | | | | | | | | | | | | |

Question Paper Code: U6D02

B.E./B.Tech. DEGREE EXAMINATION, APRIL 2024

Sixth Semester

Biotechnology

21UBT602 - BIOINFORMATICS

(Regulations 2021)

Duration: Three hours | Maximum: 100 Marks

PART A - (10 x 2 = 20 Marks)

1.	What is DBMS? Mention the four main types of data organization	CO1- U	
2.	Define file format?	CO1- U	
3.	Write a short note on ExPaSy.	CO1-U	
4.	What are Next generation sequencing platforms?	CO1- U	
5.	What is cladogram and phylogram ?	CO1-U	
6.	What are protein visualization tools? Give examples.	CO1 - U	
7.	Give applications of peptide mass fingerprinting.	CO2- App	
8.	Write a note on Machine learning techniques?	CO1- U	
9.	Write a syntax note on simple constructs.	CO1- U	
10.	Write a note on local variables.	CO1- U	

PART – B (5 x 16= 80 Marks)

11.	(a)	Explain in detail about the different data file formats used in biological databases	CO1- U	(16)
		Or		
	(b)	Define operating system. Explain the architecture and organization of an operating system.	CO1- U	(16)
12.	(a)	Enumerate the various types of multiple sequence alignment. Give the programs under each category and mention the drawbacks of progressive alignment.	CO1- U	(16)
		Or		

	(b)	Explain PSIBLAST and PHIBLAST algorithm? Explain Needleman and Wunsch algorithm, Smith waterman algorithm in detail?	CO1- U	(16)
13.	(a)	Construct a Phylogenetic tree for the given sequences using UPGMA method. Seq A - ATCGATCG Seq B - GTAGACGA Seq C - ACCGTACG Seq D - TCAGTCAG Seq E - GCCTACAG	CO2- App	(16)
		Or		
	(b)	What is homology modeling and how does homology modeling differ from other protein structure prediction methods?	CO2- App	(16)
14.	(a)	Analyze how informatics techniques contribute to the analysis and interpretation of genomic and proteomic data?	CO3- Ana	(16)
		Or		
	(b)	How do researchers use DNA molecules as computational elements, and what advantages does DNA computing offer in terms of parallelism and massive data storage?	CO3- Ana	(16)
15.	(a)	Write a program to calculate the reverse compliment of strand of DNA.	CO2- App	(16)
		Or		
	(b)	Write a PERL program to display the DNA string and count the number of occurrences of A.	CO2- App	(16)