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Reg No.:________________ Name:________________

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

Seventh Semester B.Tech Degree Regular and Supplementary Examination December 2021 (2015 Scheme)

Course Code: CS465

Course Name: BIOINFORMATICS

Max. Marks: 100 Duration: 3 Hours

PART A

Answer all questions, each carries 4 marks.

	Question	Marks
1	Define bioinformatics and computation biology.	(4)
2	Explain the structural difference between DNA and RNA.	(4)
3	Explain any two protein sequence databases.	(4)
4	Differentiate between distance and similarity matrix.	(4)
5	Illustrate the various scoring matrices for nucleic acid.	(4)
6	Explain the character based methods for phylogenetic tree analysis.	(4)
7	What are the significances of GC content? How do you find the GC content of a DNA sequence?	(4)
8	Explain various gene prediction methods.	(4)
9	What is meant by RNA folding? Explain the different secondary structure elements of RNA.	(4)
10	Explain the structure of amino acid and its classification.	(4)

PART B

Answer any two full questions, each carries 9 marks.

		Question	Marks
11	a)	Explain central dogma of molecular biology and biological sequence associated with it.	(6)
	b)	If a double stranded DNA has 20 percentage Adenine, calculate the percentage of Cytosine in the DNA.	(3)
12	a)	Explain the following protein sequence databases i)Genepept ii)Uniprot	(6)
	b)	Explain composite sequence databases,	(3)
13	a)	Classify different types of RNA and its functions.	(4)
	b)	Explain the features of data retrieval tool Entrez	(5)

PART C

Answer any two full questions,each carries 9 marks.

14 a) Using Needleman and Wunsch dynamic programming method, construct the partial alignment score table for the following two sequences, using the following scoring parameters: match score: +1, mismatch score: -1, gap penalty: -2. (9)

Seq1- ACGTCATCA

Seq2- TAGTGTCA

Write down the optimal global alignment between these sequences along with optimal score.

15 a) Use UPGMA method to reconstruct a phylogenetic tree using the following distance matrix. (9)

Species	A	B	C	D	E	F
A	0					
B	1	0				
C	3	3	0			
D	6	6	5	0		
E	7	7	6	1	0	
F	10	10	9	7	8	0

16 a) Explain various steps involved in the construction of PAM matrix with an example. (5)

b) Explain the applications of HMM in bioinformatics (4)

PART D

Answer any two full questions, each carries 12 marks.

17 Differentiate prokaryotic and eukaryotic gene structure with a neat diagram. (12)

18 a) Explain the Chou-Fasman and GOR method for protein secondary structure prediction (12)

19 a) Predict the secondary structure of given RNA sequence using Nussinov Algorithm (6)

GGGAAAUCC.

b) Define transposition. Compare Retrotransposons and DNA transposons. (6)

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