Reg No.:_____   Name:_____

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

Seventh Semester B.Tech Degree (S, FE) Examination May 2024 (2015 Scheme)

Course Code: CS465

Course Name: BIOINFORMATICS

Max. Marks: 100   Duration: 3 Hours

PART A

Answer all questions, each carries 4 marks.   Marks

1	Differentiate between mRNA and tRNA. If the sequence of the coding strand in a transcription unit is written as follows: 5' -ATGCATGCATGCATGCATGCATGCATGC-3' Write down the sequence of its mRNA.	(4)
2	What is the scope of bioinformatics? Why is it an interdisciplinary field?	(4)
3	What is pairwise sequence alignment? Differentiate local and global sequence alignment.	(4)
4	Explain any two protein sequence databases.	(4)
5	Illustrate the various scoring matrices for nucleic acid.	(4)
6	Explain how Viterbi algorithm is used in Hidden Markov Model.	(4)
7	What are the significance of GC content? How do you find the GC content of a DNA sequence?	(4)
8	Explain various gene prediction methods.	(4)
9	Explain the two principal approaches used for RNA structure prediction.	(4)
10	What is meant by RNA folding? Explain the different secondary structure elements of RNA.	(4)

PART B

Answer any two full questions, each carries 9 marks.

11	a)	With the help of a diagram explain the concept of central dogma of molecular biology	(6)
	b)	List the roles of mRNA, tRNA and rRNA.	(3)
12	a)	What are biological databases? Why are they so important?	(5)
	b)	Describe the file format of DDBJ and EMBL database	(4)
13	a)	What is the significance of data retrieval tools? Explain the features of Entrez?	(6)
	b)	Write a short note on protein data bank.	(3)

PART C

Answer any two full questions, each carries 9 marks.

14   Using Needleman and Wunsch dynamic programming method, construct the   (9)
partial alignment score table and find the optimal alignment for the following two
sequences, using the following scoring parameters:

match score: +5, mismatch score: -1, gap penalty: -2.

Sequence 1: TCCTA

Sequence 2: TCATA.

15   Construct a phylogenetic tree for the given distance matrix using UPGMA   (9)
method

Species	A	B	C	D
B	9	-	-	-
C	8	11	-	-
D	12	15	10	-
E	15	18	13	5

16 a) Differentiate between PAM and Blossum matrix   (4)

    b) What is phylogenetic analysis? Explain character based method of phylogenetic   (5)
analysis

PART D

Answer any two full questions, each carries 12 marks.

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

18 a) Write a note on the gene structure of a eukaryotic genome.   (6)

    b) Explain the purpose of gene prediction in bioinformatics.   (6)

19   Explain Nussinov algorithm for RNA secondary structure prediction with an   (12)
example.

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