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Reg No.:_______________ Name:______________________________

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY
SEVENTH SEMESTER B.TECH DEGREE EXAMINATION(R&S), DECEMBER 2019

Course Code: CS465

Course Name: BIOINFORMATICS

Max. Marks: 100 Duration: 3 Hours

PART A
Answer all questions, each carries 4 marks.

			Marks
1		Differentiate Bioinformatics and Computational biology.	4
2		Differentiate nucleotides and nucleosides.	4
3		Write a short note on Composite databases with suitable examples.	4
4		How can we evaluate alignment of long multiple sequences?	4
5		What is phylogenetic analysis? Explain distance matrix method for phylogenetic analysis.	4
6		How Viterbi algorithm solve HMM problems?	4
7		Explain how Microarrays can be used for gene analysis?	4
8		Write down the functions of RNA polymerases in prokaryotes and eukaryotes ?	4
9		Define reverse protein folding.	4
10		Write the features of the regular protein secondary structures of alpha helix and beta pleated sheet.	4

PART B
Answer any two full questions, each carries 9 marks.

11	a)	If a double stranded DNA has 40% of cytosine, calculate % of adenine in DNA.	2
	b)	If the sequence of the coding strand in a transcription unit is written as follows: 5′GCATGCATGCATGCATGCATGCAT3′. Write down the sequence of its mRNA.	1
	c)	With the help of a diagram explain the concept of central dogma of molecular biology	6
12	a)	Describe a)OWL b)CATH	5
	b)	What are biological databases? Why are they so important?	4
13	a)	With a neat sketch describe DNA structure.	4
	b)	Explain Entrez in detail	5

PART C

Answer any two full questions, each carries 9 marks.

14 Using the Needleman and Wunsch dynamic programming method, construct the partial alignment score matrix and trace back matrix for the following two sequences, using the following scoring parameters match score=+1,mismatch score=0,gap penalty =-1. 9

ACAGTCGAACG

ACCGTCCG

What is the optimal global alignment and score between sequences?

15 Use UPGMA to reconstruct a phylogenetic tree using the following distance matrix: 9

Species	A	B	C	D
B	3	-	-	-
C	6	5	-	-
D	9	9	10	-
E	12	11	13	9

16 a) Draw the phylogenetic tree that corresponds to standard Newick format as ((A,B)C)(D,E)). 3

b) Draw all possible unrooted trees for the species having taxa A,B,C and D. 2

c) What is the importance of BLOSUM matrix? 4

PART D

Answer any two full questions, each carries 12 marks.

17 a) What is GC content? How it differ in eukaryotic and prokaryotic genomes. 6

b) How protein folding is done? 6

18 a) Elaborate Chou-Fasman and GOR methods for predicting secondary structure. 6

b) Explain the gene structure of eukaryotic and prokaryotic genome. 6

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

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