Reg No.:_____ Name:_____

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

SEVENTH SEMESTER B.TECH DEGREE EXAMINATION(S), MAY 2019

Course Code: CS465

Course Name: BIOINFORMATICS

Max. Marks: 100 Duration: 3 Hours

PART A

Answer all questions, each carries 4 marks. Marks

1 Define Bioinformatics. Enumerate the applications of Bioinformatics? (4)

2 Differentiate between mRNA and tRNA. If the sequence of the coding strand in a transcription unit is written as follows: (4)

5' -ATGCATGCATGCATGCATGCATGCATGC-3'

Write down the sequence of its mRNA.

3 Write short notes on nucleic acid sequence databases. (4)

4 What is sequence alignment in bioinformatics? State the difference between global alignment& local alignment. (4)

5 BLAST and FASTA are two widely used tools for sequence alignment. What are the similarities and differences in their approach? (4)

6 Differentiate between a Markov model and Hidden Markov Model (HMM). What are the various applications of HMMs in bioinformatics? (4)

7 What does GC content mean? How do you find the GC content of a DNA? (4)

8 Distinguish between (4)

(ii) Positive and negative regulation of gene expression.

(iii) Start codon and stop codon

9 What is protein threading and how does it work? (4)

10 What are the four levels of protein structure? How do they differ? (4)

PART B

Answer any two full questions, each carries 9 marks.

11 a) What is the central dogma of molecular biology? Explain. (6)

b) What is DNA fingerprinting? Mention its applications. (3)

12 a) Mention a highly annotated protein sequence database and describe its features. (5)

b) Write short notes on (4)

I. EMBL

II. DDBJ

13 a) What are nucleotides? Explain the structure of nucleic acids. (3)

b) Briefly describe the different levels of CATH databases. (6)

PART C

Answer any two full questions, each carries 9 marks.

14 Consider the sequences S1 = ACTCG and S2 = ACAGTAG. Assume that the match score is +1, mismatch score is 0 and gap penalty is -1. Construct the dynamic programming alignment grid for a global alignment between sequences, S1 and S2. What is the score of the optimal global alignment and what alignment does this score correspond to? (9)

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

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

16 a) Compare PAM & BLOSUM matrices. (4)

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

PART D

Answer any two full questions, each carries 12 marks.

17 With neat diagrams compare the secondary structure of a typical prokaryotic gene and eukaryotic gene. (12)

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

19 a) What do you mean by gene prediction? What are the different approaches for gene prediction? (6)

b) Explain the process for comparative modelling of protein structure. (6)

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