Reg No.:_____   Name:_____

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY
SEVENTH SEMESTER B.TECH DEGREE EXAMINATION, DECEMBER 2018

Course Code: CS465

Course Name: BIOINFORMATICS

Max. Marks: 100   Duration: 3 Hours

PART A
Answer all questions, each carries 4 marks.
Marks

1. What is translation? List two essential roles of ribosome during translation. (4)

2. Write short notes on SWISS PROT (4)

3. a) Group the following as nitrogenous bases and nucleosides: (4)
   Adenine, Cytidine, Thymine, Guanosine, Uracil and Cytosine.
   b) If a double stranded DNA has 20 percent of cytosine, calculate the percent of adenine in the DNA.

4. Distinguish between PAM & BLOSUM matrices. (4)

5. Differentiate between rooted and unrooted phylogenetic trees. How many (4)
   rooted and unrooted trees are possible for n species?

6. Discuss the advantages and disadvantages of using HMMs (4)

7. What is genomics and how does structural genomics differ from functional (4)
   genomics?

8. Describe the secondary structure of RNA (4)

9. Write short note on Prokaryotic Gene Structure with diagram? (4)

10. Explain the significance of protein folding. (4)

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

11. a) With a neat diagram describe the structural and functional differences between (6)
    DNA and RNA?

    b) If the sequence of one strand of DNA is written as follows: (3)
    5'-ATGCATGCATGCATGCATGCATGCATGC-3'
    Write down the sequence of complementary strand.

12. Briefly describe the importance of biological databases in bioinformatics. (9)
    Explain protein sequence databases.

13. a) Compare and contrast DDBJ, Genbank. (6)

    b) Is bioinformatics an interdisciplinary subject? Justify your answer. (3)

PART C

Answer any two full questions, each carries 9 marks.

14 Using Smith Waterman method construct the partial alignment scoring table   (9)
and obtain the optimal local alignment of the following two sequences:

ACGTATCGCGTATA

GATGCTCTCGGAAA

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

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

16 a) What are scoring matrices? How PAM is derived?   (6)

b) State advantages and disadvantages of parsimony methods   (3)

PART D

Answer any two full questions, each carries 12 marks.

17 Explain The Chou-Fasman and GOR Methods for Protein Secondary Structure   (12)
Prediction

18 a) How do the RNA polymerases of prokaryotes and eukaryotes differ?   (6)

b) Why GC content is important? How do you calculate GC percentage? Give   (6)
notes on the GC content of human genome.

19 a) What are micro arrays? How is it constructed?   (6)

b) Draw the basic structure of amino acids and explain the formation of peptide   (6)
bond.

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