

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:
5' -ATGCATGCATGCATGCATGCATGC-3' | (4) |
| | 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
(ii) Positive and negative regulation of gene expression.
(iii) Start codon and stop codon | (4) |
| 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)
