

Reg No.: _____

Name: _____

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

Seventh Semester B.Tech Degree (Hons.) Examination December 2021 (2015 Scheme) (2018 admn.)

**Course Code: CS465****Course Name: BIOINFORMATICS**

Max. Marks: 100

Duration: 3 Hours

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

Marks

- | | | |
|----|--|-----|
| 1 | Differentiate DNA and RNA. | (4) |
| 2 | Write notes on secondary biological databases with an example. | (4) |
| 3 | List out four features of biological databases. | (4) |
| 4 | Differentiate pairwise sequence alignment and multiple sequence alignment. | (4) |
| 5 | Explain the purpose of phylogenetic analysis and mention any two methods used for this analysis. | (4) |
| 6 | Explain how Viterbi algorithm is used in Hidden Markov Model. | (4) |
| 7 | Mention any two purposes of the regulation of gene expression. | (4) |
| 8 | Differentiate prokaryotic and eukaryotic genomes. | (4) |
| 9 | Explain the two principal approaches used for RNA structure prediction. | (4) |
| 10 | Explain protein folding with its four stages. | (4) |

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

- | | | |
|----|--|-----|
| 11 | a) A strand of DNA has the following sequence: 5'-TACGTTACG-3'. What is the mRNA complement that will be generated from this DNA template through transcription? | (2) |
| | b) If a species contains 40% guanine in its DNA, what is the percentage of cytosine that it would contain? | (2) |
| | c) Define and compare bioinformatics and computational biology. | (5) |
| 12 | a) Explain the biological database GenBank. | (4) |
| | b) Explain Entrez. | (5) |
| 13 | a) Describe DNA structure with a neat diagram. | (5) |
| | b) Describe nucleic acid sequence database and mention an example. | (4) |

PART C

Answer any two full questions, each carries 9 marks.

- 14 Using Needleman and Wunsch dynamic programming method, construct the partial alignment score table for the following two sequences, using the following scoring parameters: match score: +1, mismatch score: -1, gap penalty: -2. (9)

Sequence 1: TGGTG

Sequence 2: ATCGT

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

| | A | B | C | D | E |
|---|---|----|---|---|---|
| A | | | | | |
| B | 1 | | | | |
| C | 8 | 8 | | | |
| D | 8 | 10 | 3 | | |
| E | 9 | 9 | 3 | 2 | 0 |

- 16 a) Explain the significance of sequence alignment. Compare local alignment and global alignment. (5)
- b) Describe any two applications of HMM in the field of bioinformatics. (4)

PART D

Answer any two full questions, each carries 12 marks.

- 17 a) Write a note on the gene structure of a eukaryotic genome. (6)
- b) Explain the purpose of gene prediction in bioinformatics. (6)
- 18 a) Explain the Nussinov algorithm for RNA structure prediction. (6)
- b) Draw the basic structure of amino acids and explain the formation of peptide bond. (6)
- 19 a) Explain the significance of gene prediction. (6)
- b) Distinguish the four levels of a protein structure. (6)
