

Reg No.: \_\_\_\_\_

Name: \_\_\_\_\_

**APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY**

Seventh semester B.Tech examinations (S), September 2020

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

Max. Marks: 100

Duration: 3 Hours

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

Marks

- |    |   |     |
|----|---|-----|
| 1  | What are the applications of Bioinformatics?  | (4) |
| 2  | Explain the concept of base pairing. If the amount of thymine in genome is 30%, calculate the percentage of cytosine? | (4) |
| 3  | What are the features of Biological databases?  | (4) |
| 4  | Explain the significance of sequence alignment.   | (4) |
| 5  | Explain the importance of scoring matrix in sequence alignment.   | (4) |
| 6  | Write note on Forward algorithm in HMM.   | (4) |
| 7  | Explain algorithms for protein folding?   | (4) |
| 8  | What are the purposes of regulation of Gene expressions?  | (4) |
| 9  | With the help of a diagram explain the structure of an amino acid.  | (4) |
| 10 | Write note on RNA polymerase in eukaryotes.   | (4) |

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

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|----|--|-----|
| 11 | a) Explain the bio-sequences associated with central dogma of molecular biology. | (6) |
|    | b) List the roles of mRNA, tRNA and rRNA.  | (3) |
| 12 | Write short note on primary biological databases.                                | (9) |
| 13 | a) Write short note on Entrez.   | (5) |
|    | b) What do you mean by Genomics? Mention some of its applications.               | (4) |

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

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|----|---|-----|
| 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: +5, mismatch score: -1, gap penalty: -2. | (9) |
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Write down the optimal global alignment between these sequences along with optimal score.

- 15 a) Differentiate PAM and BLOSUM series. (6)  
b) Explain the significance of Hidden Markov Model in bioinformatics. (3)
- 16 What is a phylogenetic tree? Explain the steps of UPGMA method for phylogenetic tree construction with an example. (9)

**PART D**

*Answer any two full questions, each carries 12 marks.*

- 17 Explain Prokaryotic Gene structure with neat diagrams. (12)
- 18 Explain any two methods for Protein Secondary Structure Prediction. (12)
- 19 a) What do you mean by Gene prediction? Explain the different strategies for Gene Predictions. (6)  
b) Explain Nussinov algorithm for RNA structure prediction. (6)

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