

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

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

**APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY**

Seventh Semester B.Tech Degree Examination (Regular and Supplementary), December 2020

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

Max. Marks: 100

Duration: 3 Hours

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

Marks

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|----|---|-----|
| 1  | What is the scope of bioinformatics? Why is it an interdisciplinary field?              | (4) |
| 2  | Explain genetic code. Mention the start codon and stop codon.                           | (4) |
| 3  | Compare primary databases and secondary databases.                                      | (4) |
| 4  | What is pairwise sequence alignment? Differentiate local and global sequence alignment. | (4) |
| 5  | Point out the significance of assigning gap penalties in sequence alignment.            | (4) |
| 6  | Describe the forward algorithm in HMM.  | (4) |
| 7  | Differentiate the genome of Prokaryotes and Eukaryotes.                                 | (4) |
| 8  | What is gene regulation? Explain its types.   | (4) |
| 9  | Explain the structure of amino acids with neat diagram.                                 | (4) |
| 10 | What do you mean by propensity value of amino acid? How is it calculated?               | (4) |

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

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|----|--|-----|
| 11 | a) Show the structure of nucleic acids and discuss its components.                   | (6) |
|    | b) Summarise the steps in translation.   | (3) |
| 12 | a) Differentiate coding and non-coding RNA. Explain its types.                       | (6) |
|    | b) Mention the relevance of biological databases.                                    | (3) |
| 13 | a) What is the significance of data retrieval tools? Explain the features of Entrez? | (6) |
|    | b) Write a short note on protein data bank.  | (3) |

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

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|----|--|-----|
| 14 | Using Needleman-Wunsch algorithm, obtain the optimal global alignment of the sequences TGGTG and ATCGT and find the optimal score.<br>( match score : +1, mismatch score : -2, gap penalty : -2) | (9) |
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- 15 Use UPGMA to reconstruct a phylogenetic tree using the following distance matrix. (9)

Species	A	B	C	D	E
A	0				
B	20	0			
C	60	50	0		
D	100	90	40	0	
E	90	80	50	30	0

- 16 a) Discuss the principle on which PAM and BLOSUM matrices are created. (5)  
b) Compare Markov Model and Hidden Markov Model. (4)

**PART D**

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

- 17 a) What is transposition? Explain different classes of transposable elements. (6)  
b) Describe different gene prediction methods. (6)
- 18 Illustrate Nussinov Algorithm for RNA structure prediction with an example. (12)
- 19 a) Explain the different stages in Gene expression. (6)  
b) Describe different levels of protein structure. (6)

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