

Reg No.: _____

Name: _____

0720MCA287112401

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

Third Semester MCA (Two Year) Degree (R,S) Examination December 2024

Course Code: 20MCA287

Course Name: BIOINFORMATICS

Max. Marks: 60

Duration: 3 Hours

PART A

Answer all questions, each carries 3 marks.

Marks

- | | | |
|----|---|-----|
| 1 | What is the scope of bioinformatics? | (3) |
| 2 | Given the DNA sequence as follows:
5'-GGATTATCGACGTAA-3'
Write down its complementary strand. | (3) |
| 3 | What is the importance of biological databases in bioinformatics? | (3) |
| 4 | Write a short note on SWISS-PROT database. | (3) |
| 5 | Determine the score of the following aligned sequence
ATGACCTGATATT
AT TTTTA
Match = +1, Mismatch = 0 and Gap penalty = -1 | (3) |
| 6 | Differentiate between PAM and BLOSUM matrices. | (3) |
| 7 | Write a short note on gene expression in eukaryotes. | (3) |
| 8 | What are microarrays? | (3) |
| 9 | Explain the significance of genetic algorithm in bioinformatics. | (3) |
| 10 | Explain structure visualization in bioinformatics. | (3) |

PART B

Answer any one question from each module. Each question carries 6 marks.

Module I

- | | | |
|----|---|-----|
| 11 | With the help of a diagram explain the concept of Central Dogma of Molecular Biology. | (6) |
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OR

- 12 Describe the functions of mRNA, tRNA and rRNA. (6)

Module II

- 13 Explain different types of primary sequence biological databases. (6)

OR

- 14 Describe structure classification databases in bioinformatics. (6)

Module III

- 15 Using Needleman and Wunsch dynamic programming method, construct the partial alignment score and trace back matrix for the sequences **ATGCT** and **AGCT** with match: +1, mismatch: -1, gap penalty: -2. Also write down the optimal global alignment between these sequences along with optimal score. (6)

OR

- 16 Using Smith Waterman method, Find the best local alignment between **AGCGA** and **ACGAA** with match: +1, mismatch: -1, gap penalty: -2. (6)

Module IV

- 17 Explain the gene structure of prokaryotic genome. (6)

OR

- 18 Describe the GC content of the eukaryotic genome. (6)

Module V

- 19 Explain how Neural Networks is used in bioinformatics to analyze the biological data. (6)

OR

- 20 Describe the pattern recognition and discovery process in bioinformatics. (6)
