

Reg No.: _____

Name: _____

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

Seventh Semester B.Tech Degree Regular and Supplementary Examination December 2021 (2015 Scheme)

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 and computation biology. | (4) |
| 2 | Explain the structural difference between DNA and RNA. | (4) |
| 3 | Explain any two protein sequence databases. | (4) |
| 4 | Differentiate between distance and similarity matrix. | (4) |
| 5 | Illustrate the various scoring matrices for nucleic acid. | (4) |
| 6 | Explain the character based methods for phylogenetic tree analysis. | (4) |
| 7 | What are the significances of GC content? How do you find the GC content of a DNA sequence? | (4) |
| 8 | Explain various gene prediction methods. | (4) |
| 9 | What is meant by RNA folding? Explain the different secondary structure elements of RNA. | (4) |
| 10 | Explain the structure of amino acid and its classification. | (4) |

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

- | | | |
|----|---|-----|
| 11 | a) Explain central dogma of molecular biology and biological sequence associated with it. | (6) |
| | b) If a double stranded DNA has 20 percentage Adenine, calculate the percentage of Cytosine in the DNA. | (3) |
| 12 | a) Explain the following protein sequence databases | (6) |
| | i) Genepept | |
| | ii) Uniprot | |
| | b) Explain composite sequence databases, | (3) |
| 13 | a) Classify different types of RNA and its functions. | (4) |
| | b) Explain the features of data retrieval tool Entrez | (5) |

PART C

Answer any two full questions, each carries 9 marks.

- 14 a) 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)
- Seq1- ACGTCATCA
Seq2- TAGTGTC A
- Write down the optimal global alignment between these sequences along with optimal score.
- 15 a) Use UPGMA method to reconstruct a phylogenetic tree using the following distance matrix. (9)

Species	A	B	C	D	E	F
A	0					
B	1	0				
C	3	3	0			
D	6	6	5	0		
E	7	7	6	1	0	
F	10	10	9	7	8	0

- 16 a) Explain various steps involved in the construction of PAM matrix with an example. (5)
- b) Explain the applications of HMM in bioinformatics (4)

PART D

Answer any two full questions, each carries 12 marks.

- 17 Differentiate prokaryotic and eukaryotic gene structure with a neat diagram. (12)
- 18 a) Explain the Chou-Fasman and GOR method for protein secondary structure prediction (12)
- 19 a) Predict the secondary structure of given RNA sequence using Nussinov Algorithm (6)
- GGGAAAUCC.
- b) Define transposition. Compare Retrotransposons and DNA transposons. (6)
