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Reg No.:_______________ Name:_______________

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

Seventh Semester B.Tech Degree (S, FE) Examination January 2023 (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 Differentiate between bioinformatics and computational biology. (4)

2 Define genetic codes. Also explain start and stop codons. (4)

3 Compare primary sequence database and composite sequence database. (4)

4 Explain the various scoring matrices for nucleic acid sequence. (4)

5 Describe the application of HMM in bioinformatics. (4)

6 Compare various phylogenetic tree topologies. (4)

7 Differentiate between prokaryotic and eukaryotic cell (4)

8 Define gene expression. (4)

9 Explain the major RNA secondary structure elements (4)

10 Describe the structure of amino acids (4)

PART B

Answer any two full questions, each carries 9 marks.

11 a) Explain central dogma of molecular biology with a neat sketch. (6)

b) Illustrate the structure of DNA (3)

12 a) Describe any two nucleic acid sequence database. (5)

b) Describe any two protein sequence database (4)

13 a) Compare the structural and functional difference between DNA and RNA (6)

b) Define the data retrieval tool entrez. (3)

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 and find the optimal alignment for the following (9)

two sequences, using the following scoring parameters:

match score: +5, mismatch score: -1, gap penalty: -2.

Sequence 1: TCCTA

Sequence 2: TCATA.

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

	A	B	C	D	E	F
A						
B	1					
C	3	2				
D	7	6	4			
E	17	16	14	10		
F	19	18	16	12	2	

16 a) Differentiate between PAM and Blossum matrix (4)

b) Explain Viterbi Algorithm with an example (5)

PART D

Answer any two full questions, each carries 12 marks.

17 a) Explain prokaryotic and eukaryotic gene structure with appropriate diagrams (9)

b) Explain the significance of GC content in DNA (3)

18 a) Explain Nussinov algorithm with an example to predict the secondary structure of RNA (9)

b) Explain different classification of Amino acid (3)

19 a) Explain Chou- Fasman and GOR methods of protein secondary structure prediction (6)

b) Define Micro array. Explain the applications of Micro array. (6)

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