

Reg No.: _____

Name: _____

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

Seventh Semester B.Tech Degree Supplementary Examination June 2022 (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 list out any two of its applications	(4)
2	Differentiate coding and noncoding RNA	(4)
3	Compare primary and secondary biological database	(4)
4	Illustrate all possible rooted and unrooted trees for three species A,B,C	(4)
5	Describe various scoring matrices for nucleic acid sequence	(4)
6	Differentiate between similarity and distance matrix	(4)
7	Define transposition with its classification	(4)
8	Explain the significance of GC content and how it can be calculated?	(4)
9	Describe the structure of an amino acid and its classification	(4)
10	What is meant by protein folding? Explain the levels of protein folding.	(4)

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

11	a) Describe the structure of nucleic acids with a neat diagram	(7)
	b) A strand of DNA has the following sequence: 5'-GACGTTACGATG-3'. What is the mRNA complement that will be generated from this DNA template through transcription?	(2)
12	a) Describe the file format of DDBJ and EMBL database	(4)
	b) Define protein sequence database with an example	(5)
13	a) Explain central dogma of molecular biology and biological sequences associated with it with a neat diagram	(5)
	b) Write short notes on the data retrieval tool Entrez	(4)

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

14	Using Needleman and Wunsch dynamic programming method, construct the	(9)
----	--	-----

partial alignment score table for the following two sequences, using the following scoring parameters: match score: +1, mismatch score: -1, gap penalty: -1

Sequence 1: GCATGCA

Sequence 2: GATTACA

Obtain the optimal score of alignment.

- 15 Construct a phylogenetic tree for the given distance matrix using UPGMA method (9)

	A	B	C	D	E
A	0				
B	20	0			
C	15	18	0		
D	10	22	28	0	
E	14	26	20	24	0

- 16 a) Explain the construction of PAM matrix with an example. (6)
 b) Describe the character-based approach for phylogenetic tree analysis (3)

PART D

Answer any two full questions, each carries 12 marks.

- 17 Explain the gene structure of a prokaryotic and Eukaryotic genome with a neat diagram (12)
- 18 a) Explain various secondary structure elements of RNA (5)
 b) Predict the secondary structure of given RNA sequence using Nussinov algorithm (7)
 AAAGCCUU
- 19 a) Define Gene prediction. Explain various gene prediction methods (6)
 b) Explain any two methods of protein secondary structure prediction (6)
