

F

10000CS465122001

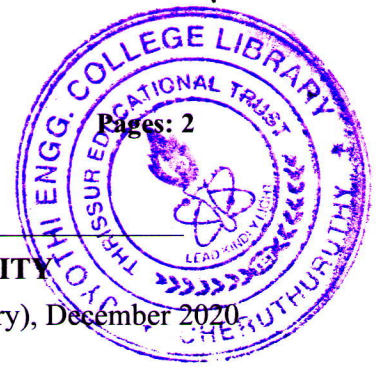
Pages: 2

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

- 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.

- 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.

- 14 Using Needleman-Wunsch algorithm, obtain the optimal global alignment of the sequences TGGTG and ATCGT and find the optimal score. (9)
(match score : +1, mismatch score : -2, gap penalty : -2)

- 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)
