

BACHELOR OF COMPUTER SCIENCE AND ENGINEERING
FOURTH YEAR
FIRST SEMESTER EXAM 2025
Bioinformatics

Time : Three hours

Full Marks : 100

Answer any five questions. 5 X 20 = 100

1. What is splicing? Discuss the process of translation with diagram. 5+15=20 [CO1]
2. Write mathematical formulation of Smith-Waterman algorithm. Apply the algorithm to align the following two sequences, using match score=+2 and mismatch/gap score=-1,
Sequence 1 = ACGTATCGCGTATA
Sequence 2 = GATGCTCTCGGAAA. 10+10=20 [CO1]
3. Briefly discuss Physical/Chemical properties of protein. Use UPAGMA to reconstruct a phylogenetic tree using the following distance matrix:

Species	A	B	C	D
B	9	-	-	-
C	8	11	-	-
D	12	15	10	-
E	15	18	13	5

10+10=20 [CO2]

4. Write short notes on any TWO of the following: 2x10=20 [CO1]
 - a) PSSM
 - b) Ram Chandran Plot
 - c) Reverse Transcription
 - d) Alpha-sheet and Beta-helix
5. Discuss the basic steps for secondary structure prediction of protein? What are the differences between PAM and BLOSSUM. Explain diagrammatically Phy and Pshy angles. 10+5+5=20 [CO4]
6. What are regulatory genes? Discuss role of promoter in formation of GRN? What are the properties of a scale-free network? 5+10+5=20 [CO3]
7. Describe Blast algorithm. Explain FASTA method with respect to the following example (word length as 1) :

Query Sequence: FAMLGFIKYLPGCM

Target Sequence : TGFIKYLPGACT.

10+10=20 [CO1]

8. Why local similarity is preferred over global similarity between any two protein strings? Explain how dot plot is useful for finding global and local similarities. 5+15=20 [CO4]