

Gandhi Institute of Engineering and Technology University, Odisha, Gunupur (GIET University)

M.Tech. (Second Semester - Regular) Examinations, May – 2026

24MBTPE12001 – Bioinformatics

Biotechnology

Time: 3 hrs

Maximum: 60 Marks

Answer ALL questions

(The figures in the right hand margin indicate marks)

PART – A

(2 x 5 = 10 Marks)

Q.1. Answer **ALL** questions

- | | CO # | Blooms Level |
|---|------|--------------|
| a. What is Entrez .Write its process | CO1 | K1 |
| b. Write layers of KEGG | CO1 | K1 |
| c. What is the difference between Needleman-Wunch and Smith –Waterman algorithm | CO2 | K1 |
| d. How many rooted and unrooted trees can be obtained using 7 OUT | CO3 | K1 |
| e. Write the flowchart of QSAR | CO5 | K1 |

PART – B

(10 x 5 = 50 Marks)

Answer **ALL** the questions

- | | Marks | CO # | Blooms Level |
|--|-------|------|--------------|
| 2. a. Discuss the storing and retrieving method of EMBL database | 5 | CO1 | K1 |
| b. Explain Cn3d software | 5 | CO1 | K1 |
| (OR) | | | |
| c. Discuss the storing and retrieving method of PDB database | 5 | CO1 | K1 |
| d. Discuss the label of SCOP and CATH | 5 | CO1 | K1 |
| 3.a. Find the Hamming distance of two DNA sequence A C G T A C and A G G T T C | 5 | CO3 | K2 |

b.

A	B	C	D	E
0	22	39	39	41
	0	41	41	43
		0	18	20
			0	10
				0

5 CO2 K2

Design a Phylogenetic tree by NJ method

(OR)

- | | | | |
|--|---|-----|----|
| c. Suppose there are 20,000 amino acid in the database of which 2000 are Serin and there are 5000 amino acids in helical conformation of which 500 are serine. Calculate the type of information | 5 | CO3 | K2 |
| d. Find the optimal alignment and alignment score between two sequence GGATCGA and GAATTCAGTTA (Assuming match =5, Mismatch = -3 and gap = -4) by using Smith -Waterman algorithm | 5 | CO2 | K2 |
| 4.a. Make a PAM matrix of all amino acid of the given MSA
GGGTCGGTAT
ACTCCGGAAC
TTCACGTTAC
TTCTACAAGG
ATTCCGTCAT | 5 | CO3 | K3 |

- b. Explain the Rabin Krap Algorithm race the execution of the Rabin Krap matching algorithm for Text: 31415926535 and Pattern: 26
(OR)
- c. Define Block and print. Find the blosum value of all amino acid of the given block.
PPT
QPL
RPL
RPW
PPL
- d. Explain the Naive String Matching Algorithm race the execution of the naive string matching algorithm for Text: 1011101110 and Pattern: 111
- 5.a. Find type of information of Ala and Val of the given sequence
- | |
|---|
| T | E | A | E | K | E | A | S | E | D | | L | K | K | H | G | V | T | V | T | A |
| S | H | H | H | H | H | H | | H | H | H | H | H | H | H | H | H | H | | H | H |
- b. Find the no of valid shift of the text sequence 1011101110 and pattern 111
(OR)
- c. Explain MEME and RSAT
- d. Explain P fam and Profile
- 6.a. Explain Threading model
- b. Explain computational method of conventional method drug design
(OR)
- c. Write the process of study the dynamic behaviour of protein by AMBER package
- d. Explain method to estimate the protein stability

5 CO4 K3

5 CO4 K3

5 CO4 K2

5 CO5 K2

5 CO5 K2

5 CO5 K1

5 CO5 K1

5 CO6 K1

5 CO6 K1

5 CO6 K1

5 CO6 K1

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