QP Code: R252B066 | Reg. No | | | | | | | | | | | AY 24

GANDHI INSTITUTE OF ENGINEERING AND TECHNOLOGY UNIVERSITY, ODISHA, GUNUPUR

(GIET UNIVERSITY)

M.Tech. (Second Semester) Regular Examinations, July – 2025

24MBTPE12001– Applied 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. Define Flat File, File and Field.	CO1	K1
b. Write the difference between global sequence alignment and local sequence alignment	CO1	K1
c. What are the menus of graphic window of Rasmol? Write its use	CO1	K2
d. Find the no of valid shift of the Text sequence 1011101110 and pattern 111.	CO1	K2
e. How protein folding is estimated?	CO1	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 the menu and submenu of PDB database.	5	CO1	K1
(OR)		CO1	K1
c. Write short note of CATH and SCOP database.	5	CO1	K1
d. Based on data type, Explain different layer of PIR database.	5	CO1	K1
3.a. Find the optimal alignment and alignment score between two sequence CCATACGA and CAGCTAGCG by using Dot matrix algorithm.	5	CO2	K2
b. Convert the given molecular marker to MSA and justify it. TCYGIFVL TCGIFVL SCYGIFVLSG TCFGIFVL ACGIFVLSG	5	CO2	K2
(OR)			
c. Find the optimal alignment and alignment score between two sequence GGATCGA and GAATTCAGTTA (Assumeing match = 5, Mismatch = -3 and gap = -4) bu using smith-Waterman algorithm.	5	CO2	K2
d. Make a PAM matrix of all amino acid of the given MSA. ACGCTAFKI GCGCTAFKI ACGCTAFKL GCGCTGFKI GCGCTLFKI ASGCTAFKL ACACTAFKL	5	CO2	K2

4.a.	Suppose there are 20,000 aminoacid 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
b.	Design a HMM of the given MSA. VGA- -H V - - - -N VEA- - D VKG - - - VYS - -T FNA - - N IAGADN	5	CO3	K1
	(OR)			
c.	Find the BLOSUM value of all amino acid of the given block. AAI SAL TAL TAV AAL	5	CO3	K2
d.	Design a phylogenetic tree.	5	CO3	K2

	A	B	C	D	E
A		94	111	180	206
B			115	194	218
C				188	218
D					217
E					

5.a.	Using Euclidean distance method, Justify the MSA. ADIKLAAIKL ADSKLAAIKA KILASDPQWE	5	CO4	K2
b.	Find the no. of valid shift of the given Test sequence- 31415926535 and patten sequence 26 using Rabin Krap algorithm	5	CO4	K2
	(OR)			
c.	What is pattern? Find the no. of valid shift of the given Test sequence 1011101110 and patten sequence 111 using Naïve string-matching algorithm.	5	CO4	K2
d.	Define Block and print. Find the blosum value of all amino acid of the given block. AAI SAL TAL TAV AAL	5	CO4	K2
6.a.	Explain AMBER process programs.	5	CO5	K1
b.	Explain the type of protein – ligand interaction.	5	CO5	K1
	(OR)			
c.	How do you predict the 3D structure of proteins by threading modelling.	5	CO5	K1
d.	Explain steps involve in the Drug design.	5	CO5	K1

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