QP Code: R252G035 | Reg. No | | | | | | | | | | | AY 24

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

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

24MBIPC12003– 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. Write the URL of EMBL database	CO1	K1
b. What is the difference between Entrez and SRS	CO1	K1
c. How to estimate the secondary structures of protein based on GOR value	CO2	K1
d. What is the Hamming distance between the sequence HLIKLAAIWL and HLWKLAAIWA	CO3	K1
e. Convert the given molecular marker into MSA TCYGIFVL TCGIFVL SCYGIFVLSG ACGIFVLSG	CO4	K1

PART – B **(10 x 5 = 50 Marks)**

Answer ***ALL*** the questions	Marks	CO #	Blooms Level
2. a. Explain the layer of PIR database	5	CO1	K1
b. Write retrieving method and submission tools of PDB database	5	CO1	K1
(OR)			
c. Write short note of CATH and SCOP database	5	CO1	K1
d. Explain the option of BLAST and FASTA	5	CO1	K1
3.a. Find the optimal alignment and alignment score between two sequence GCATGCA and GATTACA by using Needleman-Wunch algorithm (Assume Match= 1, Mismatch = -1 and Gap= -1)	5	CO2	K2
b. Define PAM. Find the PAM value of all amino acid of the given MSA ACGCTAFKI GCGCTAFKI ACGCTAFKL GCGCTGFKI GCGCTLFKI ASGCTAFKL ACACTAFKL	5	CO2	K2
(OR)			
c. 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

d.	Which two sequence are very closed to each other justify it by using Hamming distance method ADIKLAAIKL ADSKLAAIKA KILASDPQWE	5	CO2	K2
4.a.	Design a HMM of the given MSA VGA- -H V - - - -N VEA- - D VKG - - - VYS - -T FNA - - N IAGADN	5	CO3	K2
b.	Suppose there are 20,000aminoacid in the database of which 2000 are serin and there are 5000 amino acids in helical conformation of which 500 are serin. calculate the type of information	5	CO3	K2
	(OR)			
c.	Explain FASTA3 program. Write its use	5	CO3	K1
d.	Design a phylogenetic tree	5	CO3	K2
5.a.	Explain different windows of Cn 3D	5	CO4	K1
b.	Find the fitch and transversion parsimony value of each of the phylogenetic tree constructed of the given MSA. How many rooted and unrooted phylogenetic tree is possible to construct. ACAGGAT ACACGCT GTAAGGT GCACGAC	5	CO4	K2
	(OR)			
c.	Explain molecular Dynamic Simulation. Write the process of study the dynamic behaviour of protein by AMBER package.	5	CO4	K1
d.	Explain type of motif. Draw the flow chart of motif discovery	5	CO4	K1
6.a.	Explain the steps involve in Homology modelling	5	CO5	K1
b.	Find the no. of valid shift of the given Test sequence- 31415926535 and patten sequence 26 using Rabin Krap algorithm	5	CO5	K2
	(OR)			
c.	What is protein Folding? Explain few methods to estimate the protein stability.	5	CO5	K1
d.	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	CO5	K2

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

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