QP Code: R262G011 | Reg. No | | | | | | | | | | | AY 25

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

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

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 some basic commands of Unix and Linus system	CO1	K1
b. Write submitting tools of DNA sequences to database	CO2	K1
c. Explain difference between Global and Local Alignment	CO3	K1
d. Design a Distance matrix of the given MSA ACGCGTTGGGCGATGGCAAC ACGCGTTGGGCGACGGTAAI ACGCATTGAATGATGATAAI ACACATTGAGTGATAATAAI	CO4	K1
e. What is PHD? Write its flow chart	CO5	K1

PART – B **(10 x 5 = 50 Marks)**

Answer ***ALL*** the questions	Marks	CO #	Blooms Level
2. a. Explain Genbank database	5	CO1	K1
b. Discuss the storing and retrieving method of EMBL database	5	CO1	K1
(OR)			
c. Discuss the windows of Swiss PDB Viewer	5	CO1	K1
d. Explain the layers of PIR database	5	CO1	K1
3.a. Explain Rabin Krap Algorithm .Find the number possible pattern of 26 present in the text sequence 31415926535	5	CO2	K2
b. Clustal the MSA and show the root of the MSA NYLS NKYLS NFS NFLS	5	CO2	K2
(OR)			
c. What is Motif? How motif are discovery by MEME algorithm	5	CO2	K1
d. Explain methods of structural variation of DNA	5	CO2	K1
4.a. Find the optimal alignment and alignment score of two sequence MGREAKQ and MRIGKDALE by using Dot matrix.	5	CO3	K2
b. Design a phylogenetic tree of the given MSA by NJ method GTCGAGGTCA GGTCGCTGTC ATCGAAGGCG	5	CO3	K3

TCTTCCACCT
GCTGCTGGAG

(OR)

c. Find Hamming distance and significant among the sequences
GCCAAGAAAG
AACACAGCAA
AGACCGCTAC — 5 CO3 K2

d. Identify Invariant site, Informative site and Singleton site of the given MSA. Design the number of possible phylogenetic tree by using Parsimony method
TCAGATCTAG
TTAGAACTAG
TTCGATCGAG
TTCTAAGGAC — 5 CO3 K3

5.a. Suppose there are 21000 aminoacid in the database of which 2100 are Ala and there are 5100 aminoacid in helical conformation of which 600 are Ala .Calculate the type of information — 5 CO4 K2

b. Define Block and print. Find the blosum value of all amino acid of the given block.
PPT
QPL
RPL
RPW
PPL — 5 CO4 K3

(OR)

c. Based on Propensity value find type of information of Ala and Val of the given sequence — 5 CO4 K2

V	L	S	E	G	E	W	Q	L	V		L	H	V	W	A	K	V	E	A	D
H	H	H	H	H	H	H		H	H	H	H	H	H	H	H	H	H		H	H

d. Design a HMM of the given MSA
VGA- -H
V- - - - N
VEA - - D
VKG - - -
VYS - - T
FNA - - N
IAGADN — 5 CO4 K3

6.a. Explain briefly the homology modelling. Write the computational procedure for homology modelling by swiss model. — 5 CO5 K2

b. Explain molecular Dynamic Simulation. Write the process of study the dynamic behaviour of protein by AMBER package — 5 CO5 K2

(OR)

c. What is protein Folding? Explain few method to estimate the protein stability — 5 CO6 K2

d. Explain the steps involve in Threading model — 5 CO6 K2

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