QP Code: RM23MTECH123 Reg. No | | | | | | | | | | | AY 23

GIET UNIVERSITY, GUNUPUR – 765022

M. Tech (Second Semester) Examinations, May – 2024

MPEBT2032 - Applied Bioinformatics

(Biotechnology)

Time: 3 Hrs Maximum: 70 Marks

(The figures in the right hand margin indicate marks.)

PART – A **(2 x 10 = 20 Marks)**

Q.1. Answer all questions		CO#	Blooms Level
a.	Convert the given molecular marker into MSA TCYGIFVL TCGIFVL SCYGIFVLSG ACGIFVLSG	CO2	K 2
b.	What is phylogenetic? How many rooted and unrooted trees can be obtained using five sequences?	CO2	K 2
c.	Write the difference between the Needleman-Wunch algorithm and the Smith-Waterman algorithm.	CO1	K 1
d.	Find the Hamming distance between two sequence HLIKLAAIWL and HLWKLAAIWA	CO2	K 2
e.	How many windows are opened in Cn3D? Name them.	CO1	K 1
f.	Write the tools for plotting protein-ligand interaction.	CO1	K 2
g.	What is propensity of an amino acid? Write the procedure to calculate propensity value.	CO3	K 2
h.	Define a profile. What important information does a profile contain?	CO3	K 1
i.	Draw the flow chart of molecular docking.	CO3	K 1
j.	What is propensity? Write its signification.	CO3	K 1

PART – B **(10 x 5=50 Marks)**

Answer ***ANY FIVE*** questions		Marks	CO#	Blooms Level
2. a.	Write the storing and retrieving method of EMBL database.	5	CO1	K1
b.	Expand PDB database discuss some menu and sub menu on PDB site with their signification and explain some data deposition tools of PDB database.	5	CO1	K1
3.a.	Explain different layer of PIR database.	5	CO1	K1
b.	Explain the division of KEGG database.	5	CO1	K1
4. a.	Find the BLOSUM value of the given block AAI SAL TAL TAV AAL	5	CO2	K2

b. Find the optimal alignment and alignment score of two sequences AATTCGCGTA and TATCGCTACA by using dot matrix algorithm. 5 CO2 K2

5.a. Design a phylogenetic tree by using UPGMA method. 5 CO2 K2

	A	B	C	D
A	0			
B	8	0		
C	7	9	0	
D	12	14	11	0

b. Suppose there are 20,000aminoacid in the database of which 2000 are serin and there are 5000 amino acid in helical conformation of which 500 are serin .calculate the type of information. 5 CO2 K2

6. a. Design a HMM of the given MSA 5 CO2 K2

VGA- -H
V - - - -N
VEA- - D
VKG - - -
VYS - -T
FNA - - N
IAGADN

b. Explain windows of Swiss PDB viewer. 5 CO2 K1

7.a. Explain Molecular Dynamic Simulation. Discuss 3 bioinformatic packages for MDS 5 CO3 K1

b. What is protein stability? How the protein stability are estimated? 5 CO3 K1

8. a. Explain the computational method of Drug design. 5 CO3 K1

b. Explain the steps involve in Homology modelling. 5 CO3 K1

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