QP Code: RM21BTECH447 Reg. No ☐☐☐☐☐☐☐☐☐☐ AY 21

GIET UNIVERSITY, GUNUPUR – 765022

B. Tech (Sixth Semester Regular) Examinations, May – 2024

21BBTPC36002 – Bioinformatics

(Biotechnology)

Time: 3 hrs Maximum: 70 Marks

(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 different between Genbank , EMBL and DDBJ	CO1	K 1
b. Explain the term // and XX on a flat file.	CO2	K 2
c. What are the data not accepted by Gen Bank	CO2	K 2
d. Explain QSAR and pharmacophore model	CO3	K 1
e. Write the flowchart of phylogeny	CO3	K 2

PART – B **(15 x 4 = 60 Marks)**

Answer ***ALL*** questions	Marks	CO #	Blooms Level
2. a. Explain NCBI data model. How to download all the bacterial protein data from NCBI?	7	CO1	K 1
b. Explain the window of Rasmol .	8	CO1	K 1
(OR)			
c. Write short note (Any two) (i) Genbank (ii) PIR (iii) EMBL	7	CO1	K 1
d. Expand PDB database discuss some menu and sub menu on PDB site with their signification and explain some data deposition tools of PDB database	8	CO1	K 1
3.a. Differentiate between BLAST and FASTA. Write its option.	7	CO2	K 2
b. Design a phylogenetic tree by using UPGMA method	8	CO2	K 2

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

(OR)			
c. Find the optimal alignment and alignment score of two sequences AATTCGCGTA and TATCGCTACA by using dot matrix algorithm.	7	CO2	K 2
d. Calculate PAM-I of the given MSA	8	CO2	K 2

ACGCTAFKI
GCGCTAFKI

	SCGCTAFKL GCGCTGFKI GCGCTLFKI ASGCTAFKL ACACTAFKL			
4.a.	Suppose there are 20,000 aminoacid 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 .	7	CO3	K 2
b.	Find the BLOSUM value of the given block PPQ SPR TPR TPV PPR	8	CO3	K 2
	(OR)			
c.	If a protein contains a total of 1800 residues and 810 of them are in helix, considering the residue Ala among 300 residues 210 are in helix. What is the information content of Ala in helix	7	CO3	K 2
d.	Design a HMM of the given MSA VGA- -H V - - - -N VEA- - D VKG - - - VYS - -T FNA - - N IAGADN	8	CO3	K 2
5.a.	Explain the computational method of Drug design.	7	CO3	K 1
b.	Explain Molecular Dynamic Simulation. Discuss 3 bioinformatics packages for MDS.	8	CO3	K 1
	(OR)			
c.	What is protein –Ligand interaction? Explain different type of protein ligand interaction.	7	CO3	K 1
d.	Explain briefly the homology modeling. Write the computational procedure for homology modelling by swiss model. How it is differ from threading modelling?	8	CO3	K 1

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