GIET UNIVERSITY, GUNUPUR – 765022

M. Sc. (Second Semester) Examinations, September – 2021

20BTPC203 –Bio-Informatics

(Biotechnology)

Time: 2 hrs   Maximum: 50 Marks

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

PART – A

Q.1. Answer *ALL* questions   **(2 x 10 = 20 Marks)**

a. Write the retrieval methods of NCBI data base.

b. What are the data submission tools of DDBJ data base?

c. When BLASTN is used and how it differs from BLASTP?

d. What is MSA? Write the algorithms of MSA.

e. What is occupancy in protein 3D structures?

f. What is the hamming distance between the sequence HLIKLAAIWL and HLWKLAAIWA using amino acid composition?

g. What is genetic distance? write the formula of for genetic distance

h. Expand blosum. Write the formula to calculate odd matrix

i. What is the difference between similarity and homology?

j. Write the flowchart of predicted secondary structures of a protein by using neural network.

PART – B   (6 x 5 = 30 Marks)

Answer *ANY FIVE* the questions   Marks

2. Explain different layers of PIR database. Also explain Genbank database   (6)

3. Find the optimal alignment and alignment score of two sequences AATTCGCGTA and TATCGCTACA by using dot matrix algorithm.   (6)

4. Discuss three heuristics used by CLUSTALW   (6)

5. What is secondary structure of protein? Find the types of secondary structure information if a protein containing a total of 1800 residue and 810 of them are in helix, considering the residue Ala among 300 residue and 210 are in helix.   (6)

6. What is homology modelling? Write its flowchart. Execute the KMP algorithm to find the number of valid shift of String BACBABABABACAAB and Pattern ABABACA   1+1+4

7. Constructed a phylogenetic tree using UPGAM method of the given distance matrix.   (6)

	A	B	C	D
A	0			
B	5	0		
C	7	4	0	
D	10	7	5	0

8. Describe computational approaches for docking and scoring for ligand search   (6)

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