GIET UNIVERSITY, GUNUPUR – 765022

M. Sc (Second Semester) Examinations, July – 2023

22BTPC203 – 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.	What are the submission tools of Gen Bank? Explain its use.	CO1	K1
b.	Write the flowchart of the retrieve method of the EMBL database	CO1	K1
c.	Explain the option of BLAST.	CO1	K1
d.	Convert the given molecular marker into MSA TCYGIFVL TCGIFVL SCYGIFVLSG ACGIFVLSG	CO2	K3
e.	How many rooted and un rooted phylogenetic trees can be obtained by using 3 sequence	CO2	K2
f.	Write flow chart of homology model	CO1	K2
g.	What is propensity of an amino acid. Write the procedure to calculate propensity value	CO1	K1
h.	How many windows are opened in Swiss pdb viewer? Name them.	CO3	K2
i.	Write the name of database for portion stability	CO1	K1
j.	What is pattern? Name the pattern matching algorithm.	CO3	K3

PART – B   **(10 x 5 = 50 Marks)**

Answer *ANY FIVE* questions

		Marks	CO #	Blooms Level
2. a.	Write the storing and retrieving method of NCBI database?	5	CO1	K1
b.	Explain PDB Database	5	CO1	K1
3.a.	Find the optimal alignment and alignment score of two sequences AATTCGCGTA and TATCGCTACA by using dot matrix algorithm.	7	CO3	K2
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?	3	CO1	K2
4. a.	Design a phylogenetic tree by using NJ Method	7	CO2	K3

	A	B	C	D	E
A	0	22	39	39	41
B		0	41	41	43
C			0	18	20
D				0	10
E					0

b.	Write short note on HMM.	3	CO1	K2
5.a.	Find the no. of valid shift of the given Test sequence- 31415926535 and patten sequence 26 using Rabin Krap algorithm ?	5	CO2	K2
b.	Write the flowchart of the homology modelling	5	CO3	K2
6. a.	Calculate PAM-I of the given MSA ACGCTAFKI GCGCTAFKI SCGCTAFKL GCGCTGFKI GCGCTLFKI ASGCTAFKL ACACTAFKL	7	CO2	K3
b.	What is PSA? Write the algorithms of PSA	3	CO1	K1
7.a.	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?	5	CO3	K2
b.	Design a HMM of the given MSA VGA- -H V - - - -N VEA- - D VKG - - - VYS - -T FNA - - N IAGADN	5	CO3	K2
8. a.	What is protein Folding? Explain few methods to estimate the protein stability.	7	CO3	K3
b.	Write the steps involve in Threading modelling.	3	CO2	K2

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