MANIPAL INSTITUTE OF TECHNOLOGY MANIPAL (A constituent unit of MAHE, Manipal)

## IV SEMESTER B.TECH. END SEMESTER EXAMINATION MAY 2022 SUBJECT: INTRODUCTION TO BIOINFORMATICS

[BIO 4303]

Date of Exam: 20-06-2022 Time of Exam: 2:00 to 5:00 PM M

Max. Marks: 50

Q. No.	Questions									Marks	СО	BLT	
<b>1A</b>	With the help of an example, explain the significance of primary databases in Bioinformatics.										4	1	2
1B	'The concept of protein modularity has a huge impact on evolution.' Justify the statement.										3	1	2
1C	A scientific study use point mutation change would the polypeptide			es the gene seque es the gene to rea product of this gene c		ence: ATGCGTT ad ATGCGTTAT ene change? Expla		ATCGGGAGTAG. A GGGGGAGTAG. How ain.					
	т	TTT TTC TTA TTG	Phe Phe Leu Leu	TCT TCC TCA TCG	Ser Ser Ser Ser	TAT TAC TAA TAG	Tyr Tyr STOP STOP	TGT TGC TGA TGG	Cys Cys STOP Trp	T C A G			
	с	CTT CTC CTA CTG	Leu Leu Leu Leu	CCT CCC CCA CCG	Pro Pro Pro Pro	CAT CAC CAA CAG	His His Gln Gln	CGT CGC CGA CGG	Arg Arg Arg Arg	T C ⊂ G	3	1	4
	A	ATT ATC ATA ATG	lle Ile Ile Met*	ACT ACC ACA ACG	Thr Thr Thr Thr	AAT AAC AAA AAG	Asn Asn Iys Lys	AGT AGC AGA AGG	Ser Ser Arg Arg	T C A G			
	G	GTT GTC GTA GTC	Val Val Val Val	GCT GCC GCA GCG	Ala Ala Ala Ala	GAT GAC GAA GAG	Asp Asp Glu Glu	GGT GGC GGA GGG	Gly Gly Gly Gly	T C A G			
2A	Outline the BLAST algorithm with the help of an example.									4	2	3	
2B	A study is being carried out for a novel DNA sequence "TCAGTTGCC" from a new strain of bacteria. The study aims at finding areas of conservation by carrying out pairwise sequence alignment. One such alignment is being carried out with the sequence: "AGGTTGAACG", using the following criteria with +1 for a match, -2 for a mismatch, and -2 for a gap. Determine the best alignment.								om a rying with for a	3	2	5	

2C	Chou-Fasman Parameters Provember 2017 Other 151 Met 151 Met 151 Met 151 Met 152 Law 152 Met 163 Fro 133 Met 135 Met 105 Met 005 Met 00	3	2	6			
3A	For the following four sequences, construct a phylogenetic tree using the distance method (UPGMA): A: ACGCGTTGGGCGATGGCAAC B: ACGCGTTGGGCGACGGTAAT C: ACGCATTGAATGATGATGATAAT D: ACACATTGAGTGATAATAAT	5	3	6			
3B	With the help of suitable example, explain the concept of maximum parsimony in phylogenetic tree building.	3	3	1			
3C	Convert the following Newick notation into a phylogenetic tree: (D:5,(A:1,(C:1,B:6):1):3). Comment on the uniqueness of the Newick standard of tree representation.	2	3	3			
<b>4</b> A	With the help of an example, analyze the naïve bit and dictionary-based approach of genome compression. Comment on the necessity of these approaches.	5	4	1			
<b>4</b> B	From the point of view of a researcher assessing the genome databases, analyze the significance of genome annotation approaches.	3	4	4			
4C	Outline the methods that can be employed for comparing the genome of different species.	2	4	1			
5A	Discuss the application of sequence alignment approaches in assessing evolutionary relationships.	3	1	3			
5B	Analyze the parameters that are used in result analysis of a BLAST output.	4	2	4			
5C	Butgroup gorilla	3	3	5			
CO: Course Outcome; BLT: BLOOM TAXONOMY LEVEL: 1-Remember, 2-Understand, 3-Application, 4-Analysis, 5-Evaluation, 6-Creation							