KONERU LAKSHMAIAH EDUCATION FOUNDATION
(Deemed to be University, Estd. u/s. 3 of UGC Act 1956)

B.Tech - Odd Sem : End Semester Exam
Academic Year:2020-2021

18BT3110 - Bioinformatics

Set No: 2

Time:		**Max.Marks: 100**					
S.NO	Answer All Questions	Choice	Options	Marks	CO	CO BTL	COI BTL
1.	Outline the Knowledge Discovery from Databases used in bioinformatics.	choice Q-2		10Marks	CO1	3	3
2.	Explain the information in molecular biology and express about bioinformatics approach.			10Marks	CO1	3	1
3.	Answer both A and B	choice Q-4		15Marks	CO1	3	2
3.A.	Classify the databases that are widely used in bioinformatics research based on the sources of information.			8Marks	CO1	3	2
3.B.	Summarize the applications of bioinformatics.			7Marks	CO1	3	2
4.	Answer both A and B			15Marks	CO1	3	3
4.A.	Illustrate the methodology implemented for the human genome project			8Marks	CO1	3	3
4.B.	Explain any three sequence file formats used for nucleic acid and proteins with examples.			7Marks	CO1	3	3
5.	Relate Homology, Similarity, and Identity in connection to protein or gene sequence comparisons.	choice Q-6		10Marks	CO2	3	1
6.	Compare and contrast BLAST and FASTA algorithms.			10Marks	CO2	3	3
7.	Answer both A and B	choice Q-8		15Marks	CO2	3	3
7.A.	“DNA and proteins can be regarded as molecular fossils”. Interpret this statement.			7Marks	CO2	3	1
7.B.	Use the Dot plot method for sequence alignment of two DNA fragments “AGCTGC” and “ACTTGC”. Discuss any 3 applications of Dot matrices			8Marks	CO2	3	2
8.	Answer both A and B			15Marks	CO2	3	3
8.A.	Differentiate between PAM and BLOSUM matrices.			7Marks	CO2	3	3
8.B.	Use the Needleman-Wunsch algorithm to determine the optimal alignment for the following nucleotide sequences Sequence1: “UCTCA” , Sequence2: “UCCA” Apply the alignment scores for (a) Match = 1, (b) Mismatch = 0, and (c) Gap penalty = -1 respectively.			8Marks	CO2	3	2
9.	Demonstrate the sum of pairs method with an illustration	choice Q-10		10Marks	CO3	3	1
10.	Differentiate between UPGMA and Maximum Prasimony methods with illustrations.			10Marks	CO3	3	3
11.	Answer both A and B	choice Q-12		15Marks	CO3	3	3

11.A.	Define profile and protein patterns and Discuss the database for the profile and pattern.			7Marks	CO3	3	2
11.B.	Outline the concept of Multiple Sequence Alignment and discuss its applications.			8Marks	CO3	3	2
12.	Answer both A and B			15Marks	CO3	3	3
12.A.	Elaborate the transitions and transversions used in phylogenetic tree construction.			7Marks	CO3	3	3
12.B.	Apply progressive methods of multiple sequence alignment to compare four sequences (GGCGTGT, GGAGTGT, GACGTCT, and GAAATCT).			8Marks	CO3	3	2
13.	Summarize various data types in Perl programming language and give relevant examples.	choice Q-14		10Marks	CO4	3	3
14.	“The Ramachandran plot is a fundamental tool in the analysis of protein structures”. Interpret the statement using an illustration.			10Marks	CO4	3	2
15.	Answer both A and B	choice Q-16		15Marks	CO4	3	3
15.A.	Point out the forces stabilizing protein structure.			7Marks	CO4	3	3
15.B.	Outline the methods for protein secondary structure prediction.			8Marks	CO4	3	2
16.	Answer both A and B			15Marks	CO4	3	3
16.A.	Explain various approaches involved in predicting the three-dimensional structure of a protein from its primary sequences			8Marks	CO4	3	2
16.B.	Categorize and illustrate various secondary and super-secondary structures of proteins.			7Marks	CO4	3	2

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