VII SEMESTER B.TECH. END EXAMINATIONS DECEMBER 2021 SUBJECT: COMPUTATIONAL BIOLOGY [BIO 4064]

Date: 20/12/2021 Max. Marks: 20

PART - B

1a.	Give any Three SQL commands and explain them with their outputs.	(3)
1b.	You forgot your mobile phone at home. When you returned back home, you started searching the phone, which was in silent mode. You planned to search it based on the information of places where you usually keep the phone. Which algorithm method will you use? Justify.	(2)
1c.	You were asked to group the data points in to three clusters. Which clustering algorithm will you use? Describe the algorithm.	(5)
2a.	What is the difference between edit distance and tree distance? What are degenerate triples?	(3)
21	Explain any two methods available for protein secondary structure prediction.	(3)
2b.	Explain any two methods available for protein secondary structure prediction.	
2 D.	Derive a profile HMM for the given multiple sequence alignment.	(3)
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20.	Derive a profile HMM for the given multiple sequence alignment.	
20.	Derive a profile HMM for the given multiple sequence alignment. Scarites CTTAGATCGTACCAAA	
20. 2c.	Derive a profile HMM for the given multiple sequence alignment. Scarites CTTAGATCGTACCAAA Carenum CTTAGATCGTACCACA-TA	
	Derive a profile HMM for the given multiple sequence alignment. Scarites CTTAGATCGTACCAAA Carenum CTTAGATCGTACCACA-TA Pasimachus ATTAGATCGTACCACTATA	(4)
	Derive a profile HMM for the given multiple sequence alignment. Scarites C T T A G A T C G T A C C A A A Carenum Pasimachus A T T A G A T C G T A C C A C T A T A Pheropsophus C T T A G A T C G T T C C A C A	
	Derive a profile HMM for the given multiple sequence alignment. Scarites CTTAGATCGTACCAAA Carenum CTTAGATCGTACCACA-TA Pasimachus ATTAGATCGTACCACTATA Pheropsophus CTTAGATCGTACCACA Brachinus armiger ATTAGATCGTACCACA	