BIRLA INSTITUTE OF TECHNOLOGY, MESRA, RANCHI
(END SEMESTER EXAMINATION MO/SP20**)

CLASS: BTECH   SEMESTER : V
BRANCH: BIOTECHNOLOGY   SESSION : MO/2022

SUBJECT: BE316 BIOINFORMATICS ALGORITHM
TIME: 03 Hours   FULL MARKS: 50

INSTRUCTIONS:
1. The question paper contains 5 questions each of 10 marks and total 50 marks.
2. Attempt all questions.
3. The missing data, if any, may be assumed suitably.
4. Tables/Data handbook/Graph paper etc., if applicable, will be supplied to the candidates

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Q.1(a)	What is proteomics?	[2]
Q.1(b)	What is structure database? Describe with example.	[3]
Q.1(c)	State DBMS architecture with diagram.	[5]
Q.2(a)	What is Theta notation?	[2]
Q.2(b)	State binary search and its importance.	[3]
Q.2(c)	Describe merge sort with following array of information: {4,1,87,54,37,66,78}	**[5]**
Q.3(a)	What is sequence motif?	[2]
Q.3(b)	State the probabilistic model of motif representation with example.	[3]
Q.3(c)	Draw the flowchart and describe DNA motif.	[5]
Q.4(a)	What is identity?	[2]
Q.4(b)	Compare BLAST and FASTA alignment.	[3]
Q.4(c)	Do global alignment for the following two sequences, TTAGGC and TAAGGT where match=1, mismatch=0 and gap=-1.	[5]
Q.5(a)	What is True negative and False positive?	[2]
Q.5(b)	Write the steps of GA and its application.	[3]
Q.5(c)	Compare supervised and unsupervised learning model.	[5]

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