PAPER ID-310678

Subject Code: KBT503

Roll No: | | | | | | | | | | | | | |

B. TECH
(SEM-V) THEORY EXAMINATION 2020-21
BIOINFORMATICS I

Time: 3 Hours *Total Marks: 100*

Note: 1. Attempt all Sections. If require any missing data; then choose suitably.

SECTION A

1. Attempt *all* questions in brief. **2 x 10 = 20**

Q no.	Question	Marks	CO
a.	Enlist four (each) DNA, protein and specialized databases.	2	CO1
b.	What are the steps of laboratory database submission process?	2	CO1
c.	What are the different types of artifacts?	2	CO2
d.	What are the applications of pairwise sequence alignment?	2	CO2
e.	What are the tools for detection of functional sites in DNA?	2	CO3
f.	What kind of proteins were analyzed to develop PAM matrix?	2	CO3
g.	Define monophyletic, paraphyletic, and polyphyletic groups.	2	CO4
h.	Differentiate between cladogram and phylogram.	2	CO4
i.	Define motif and pattern.	2	CO5
j.	Which factors affect the choice of template selection during homology modelling?	2	CO5

SECTION B

2. Attempt any *three* of the following:

Q no.	Question	Marks	CO
a.	What are the key features of TrEMBL database? Explain the composition of TrEMBL database with the help of a diagram.	10	CO1
b.	What are the various multiple sequence alignment tools at EBI? How would you perform pairwise comparison of DNA using BLASTN?	10	CO2
c.	With the help of a flowchart, enumerate the steps taken to perform BLASTP. What are the various sub-types of BLASTP?	10	CO3
d.	What is a phylogenetic tree? Discuss the concept of mutation with reference to phylogenetic studies. Also draw a decision tree for phylogenetic tree construction.	10	CO4
e.	Which is the best protein secondary structure prediction method according to you? Justify your answer with comparing it with other methods.	10	CO5

SECTION C

3. Attempt any *one* part of the following:

Q no.	Question	Marks	CO
a.	Can sequence information be employed to understand evolution? Explain some tools for such an analysis?	10	CO1
b.	Define bioinformatics. Describe the importance of literature database in bioinformatics. What are the uses of organism specific databases?	10	CO1

4. Attempt any *one* part of the following:

Q no.	Question	Marks	CO
a.	Explain the relationship between alignment and similarity with examples.	10	CO2
b.	What is dot plot? Discuss its advantages and disadvantages.	10	CO2

5. Attempt any *one* part of the following:

Q no.	Question	Marks	CO
a.	Find the best alignment of these two sequences: ACTGATTCA ACGCATCA Using -2 as a gap penalty, -3 as a mismatch penalty, and 2 as the score for a Match.	10	CO3
b.	What matrix is used for alignment of DNA sequence? Comment on the features of the matrix associated with DNA sequence.	10	CO3

6. Attempt any *one* part of the following:

Q no.	Question	Marks	CO
a.	Name three methods to draw a phylogenetic tree. What is the difference between a distance-based method (NJ) and maximum parsimony (MP) methods?	10	CO4
b.	Explain: i. CLUSTAL W ii. Tree building Method	10	CO4

7. Attempt any *one* part of the following:

Q no.	Question	Marks	CO
a.	Write in detail the retrieval of high molecular weight molecules such as protein structure and visualization procedure in spd6 viewer.	10	CO5
b.	Draw a decision-making chart for protein structure prediction.	10	CO5