Roll No. ☐☐☐☐☐☐☐☐☐☐☐   Total No. of Pages : 02

Total No. of Questions : 09

B.Sc.(BT) (2013 to 2017)   (Sem.–6)
BIOINFORMATICS
Subject Code : BSBT-302
Paper ID : [F0227]

Time : 3 Hrs.   Max. Marks : 60

INSTRUCTION TO CANDIDATES :
1. **SECTION-A is COMPULSORY consisting of TEN questions carrying TWO marks each.**
2. **SECTION-B contains FIVE questions carrying FIVE marks each and students has to attempt any FOUR questions.**
3. **SECTION-C contains THREE questions carrying TEN marks each and students has to attempt any TWO questions.**

SECTION A

1. **Answer briefly :**

   a. Data abstraction.

   b. PubMed.

   c. What does the number 60 signify in BLOSUM60?

   d. Dynamic Programming.

   e. TrEMBL.

   f. Cladogram and Phylogram.

   g. Log Odd Score.

   h. tBlastx.

   i. Define PAM120.

   j. E value.

SECTION B

2. Differentiate between Primary and Secondary databases. Explain giving suitable examples.

3. Describe the salient features of PDB database.

4. Discuss briefly the *insilico* applications of Bioinformatics.

5. Describe the concept of PAM matrices as given by Margarett Dayhoff.

6. Explain BLAST algorithm. What are the applications of using BLAST?

SECTION C

7. Explain the Progressive Alignment method for Multiple Sequence Alignment. Name a few tools for performing MSA.

8. Explain the Maximum Parsimony method of Phylogenetic estimation.

9. What are Dotplots and add a note on their applications? Explain the concept of window size and stringency in dotplots.