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

Total No. of Questions : 09

B.Sc.(BT) (2014 to 2017) (Sem.–6)

BIOINFORMATICS

Subject Code : BSBT-302

M.Code : 47064

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) Homology

   b) Pairwise sequence alignment

   c) Global alignment

   d) BLASTN

   e) Bit Score

   f) CLUSTAL X

   g) Cladogram

   h) PUBMED

   i) Gap penalty

   j) Dynamic programming

SECTION-B

2. Write a note on Hidden Markov Model.

3. Differentiate between PAM and BLOSUM matrices.

4. Explain the algorithm of BLAST.

5. Write an overview of Bioinformatics.

6. Describe the Unrooted tree formation.

SECTION-C

7. Write a note on Database Management System.

8. Discuss the different methods used for multiple sequence alignment.

9. What is the importance of E-journals and describe their features?

NOTE : Disclosure of Identity by writing Mobile No. or Making of passing request on any page of Answer Sheet will lead to UMC against the Student.