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

Total No. of Questions : 18

B.Tech (BT)   (Sem.–5)

BIOINFORMATICS

Subject Code : BTBT-503-18

M.Code : 78237

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 have to attempt any FOUR questions.
3. SECTION-C contains THREE questions carrying TEN marks each and students have to attempt any TWO questions.

SECTION-A

Answer briefly :

1) What is flat file format?

2) What are secondary databases?

3) Give brief account on GenBank.

4) What is Global Alignment?

5) What is CATH?

6) What is E-Value?

7) Name any two MSA tools.

8) What is FASTA?

9) Give significance of Phylogenetic analysis.

10) Define Block based alignment.

SECTION-B

11) Differentiate between primary and secondary databases.

12) What is the difference between local and global alignment?

13) Explain Dot matrix method.

14) What is Needleman-Wunsch algorithm?

15) Explain clustering based methods of phylogenetic tree construction.

SECTION-C

16) Explain different types of substitution matrices.

17) Explain Blast word algorithm in detail.

18) What is phylogenetic analysis? Explain various tree terminologies.

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.