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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.