B.Tech (Biotechnology) V Semester

Course Code: 10B11BT511                              MAX. MARKS: 25

Course Name: Introduction to Bioinformatics          Course Credits:4

MAX. TIME: 1.5 Hours

*Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means. Marks are indicated in square brackets against each question.*

1. Discuss the shortcomings of UPGMA method and get the tree for the following data based on UPGMA method.    (2+6) **[CO-V]**

|   | A | B | C | D | E |
|---|---|---|---|---|---|
| B | 2 |   |   |   |   |
| C | 4 | 4 |   |   |   |
| D | 6 | 6 | 6 |   |   |
| E | 6 | 6 | 6 | 4 |   |
| F | 8 | 8 | 8 | 8 | 8 |

2. Why are rRNA molecules preferred for performing phylogenetic analysis?  (4) **[CO-V]**

3. Discuss the different types of dotplots along with the pros and cons of each. (3) **[CO-II]**

4. How is the iterative method of multiple sequence alignment better than the progressive method? (4) **[CO-III]**

5. Distinguish between the following: (6) **[CO-II]**

(a) PSI-BLAST and PHI-BLAST

(b) Raw score and bit score in the BLAST program

(c) BLASTX and TBLASTX