COURSE CODE: 10B11BT511   MAX. MARKS: 35

COURSE NAME: Introduction to Bioinformatics

COURSE CREDITS: 04   MAX. TIME: 2 HRS

Note: All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means.

1. Explain the maximum likelihood and maximum parsimony methods for phylogenetic reconstruction along with example. (5)

2. Explain the significance of bootstrapping in phylogenetic inference. (2)

3. Explain the direct and indirect approaches used for gene prediction. (5)

4. Describe the various steps used in BLAST program. (3)

5. Why do we use 16S rRNA sequences for phylogenetic reconstruction? (4)

6. Explain why DNA sequences are more informative than protein sequences for phylogenetic reconstruction. (3)

7. Explain the differences between UPGMA and NJ methods. (3)

8. Explain the two different types of dotplots. (3)

9. (a) Explain the meaning of dynamic programming. (1)

(b) How is dynamic programming implemented in the case of Smith-Waterman method? (3)

(c) How is Smith-Waterman method different from Needleman-Wunsch method though both are based on dynamic programming? (3)