COURSE CODE: 10B11BT511   MAX. MARKS:35

COURSE NAME: Introduction to Bioinformatics

COURSE CREDITS: 4   MAX. TIME: 2 Hrs

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

1. Distinguish between: (16)

   (a) Direct and indirect approaches for gene prediction
   (b) Nussinov and Zuker algorithms for RNA secondary structure prediction
   (c) Chou-Fasman and GOR methods of secondary structure prediction
   (d) Coincidental and parallel substitutions

2. What is codon adaptation index? Explain with the mathematical expression. Explain its correlation with gene expression? (4)

3. Calculate the number of rooted and unrooted trees for six sequences. (2)

4. Discuss the following for phylogenetic reconstruction: (6)

   (a) Jukes Cantor and Kimura 2- and 3-parameter model
   (b) Parsimony and maximum likelihood methods
   (c) Cladogram and phylogram

5. Explain how two-hit method is an improvement over the older version of BLAST program. Discuss. (2)

6. How can we detect transmembrane proteins in a protein using bioinformatics tools? (2)

7. Why are rRNAs suitable for studying molecular phylogeny? Explain. (3)