

End Semester Examinations - 2015-16 Even Semester - May 2016

14BT3005 Computational Biology

Set B

Time : 3 hrs
Total Marks: 100

1. a. Briefly describe the concept and technology involved in SAGE(15)
b. Give a detailed note on the importance of protein-protein interaction in biology.(5)
OR
2. a. Define microarray.(2)
b. Application of protein micro array(3)
c. Explain the preparation of microarray plate and the procedure involved in the microarray analysis(15)
3. a. Why do we use dynamic programming algorithms for pairwise sequence?(5)
b. Alignment problems but not for multiple pairwise alignment? (10)
c. Compare the use of the affine gap penalty with the constant gap penalty. (5)
OR
4. a. Why do we use dynamic programming algorithms for sequence alignment Problems (10)
b. Describe what needs to be taken into account for gaps in DNA sequence alignment. (10)
5. a. What are the most important differences between PatternHunter, BLAST?(10)
b. Smith-Waterman and Needleman-Wunsch algorithms? (10)
OR
6. Compare the heuristic used by Clustal with a dynamic programming
a. Algorithm for multiple alignment. (10)
b. Give a brief account on comparative genomics.(10)
7. a. Explain various types of compositional measures.(10)
b. Discuss the computational views of transposable elements. (10)
OR
8. a. Enumerate the structure and function of proteasomes and predicted proteome. (10)
b. Give an elaborate account on the role of assigning a gene function to elaborate functional proteins. (10)
9. Discuss the various Databases used for protein interaction and identification and characterization. (20)

Wishing you All the Best