Dr. Jayashree

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION- December 2017

B.Tech Dual Degree (Biotechnology) IX semester

COURSE CODE: 13M11BT112 MAX. MARKS:35

COURSE NAME: Advanced 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. How do you use scoring matrix values to determine the extent of amino acids similarity? (1)

2. If we do not have scoring matrix (PAM, BLOSUM etc.), then how do we carry out sequence alignment? (1)

3. Suppose you joined a genomics lab, how do you use different bioinformatics (BI) tools for enhancing your research outputs? (Answer should be specific with examples). (2.5)

4. How does dot matrix plot identify low complexity regions? Why does most software remove this region before alignment? (2.5)

5. Why is sequence collection important in bioinformatics? Suppose you use different MSA software for a given set of sequences, how do you determine accuracy of MSA? (1+2)

6. NJ method provides better inferred tree than UPGMA and NR method, why? Provide the limitations of maximum parsimony inferred trees. (2)

7. Provide the major applications of local patterns such as motif, evolutionary profile, Pfam domain, PROSITE patterns,etc. (2)

8. Discuss the pros and cons of culturing and metagenomic techniques for the study of gut microbiome. (3)

9. (a) Distinguish between alpha and beta diversity and various measures used to calculate it. (5)

   (b) Why is weighted UniFrac better than Bray-Curtis or Chi-square measures for studying beta diversity? (2)

10. Explain the various steps involved in homology modeling. (3)

11. Discuss any two methods used for protein fold recognition. (4)

12. Discuss HMM and ANN used for gene prediction. (4)