Dr. Jayashree Ramana.

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST 3 EXAMINATIONS - DECEMBER 2018
BTDD IX Semester (BT)

COURSE CODE: 13M11BT112 MAX. MARKS: 35
COURSE NAME: Advanced 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.*

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1. Which method will you use for protein structure prediction- homology modeling, threading or ab initio and why? Explain. (3)
2. Explain one method for protein structure prediction based on threading. How efficient is the method? (5)
3. Explain the differences between perceptron and multi-layer perceptron. (4)
4. How has metagenomics revolutionized the microbiome research? (4)
5. Describe two ways of naming elements in a vector in R? (2)
6. How would you create a vector containing the values 0, 0.25, 0.5, 0.75 and 1? (2)
7. Describe how GWAS is important to crop improvement. (4)
8. Explain the various steps and software used for RNA-seq analysis. (5)
9. Illustrate the application of Multi-layer perceptron on the OR GATE. You may assume any weights to start with. (3)
10. Which diversity measures are used to describe the microbiome diversity? (3)