C. Rout

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -1 EXAMINATION- Sept. 2017
B.Tech VII Semester (BTDD)

COURSE CODE: 13M11BT112 MAX. MARKS: 15
COURSE NAME: ADVANCED BIOINFORMATICS
COURSE CREDITS: 03 MAX. TIME: 1Hour

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

Q1. Each question carries 2 marks. Answer any three (2x3=6)

i. How do you infer function of a new sequence using pairwise sequence alignment? If two sequences match partially, how do you identify structural and functional equivalences? (1+1) (Use also diagram in your answer)

ii. How amino acids classification is performed (Provide examples)? How do you use scoring matrix values to determine amino acid similarity quantitatively? (1+1)

iii. Most of the alignment softwares use affine gap penalty, why? How do you verify that the alignment is correct, and if it is incorrect then how is curation performed?

iv. Compare three steps (initialization, fill and traceback) of local and global pairwise alignment methods? In two sequences, when do you get same alignment using both the methods? (1.5+0.5)

Q2. Each question carries 3 marks. (3x3=9)

i. Discuss the steps involved in progressive multiple sequence alignment (MSA) and justify the significance of each steps? Discuss the scoring method used in Clustalw software? What is the significance of W in ClustalW software? (1.5+1+0.5)

ii. What are outputs in BLAST database search method and discuss their significances? Discuss about the different modules of BLAST and their applications? (2+1)

iii. What is a low complexity region in a sequence and how this region is determined using dot matrix plot? In database search or pairwise alignment, why this region should be removed before alignment? Is there any other method available for the same? (1.5+1+0.5)