

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -1 EXAMINATION, September-2016
B.Tech IIIrd Semester (BI)

COURSE CODE: 10B11BI311

MAX. MARKS: 15

COURSE NAME: BIOLOGICAL COMPUTATION

COURSE CREDITS: 04

MAX. TIME: 1 HR

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

Q1. Each question carries 1 mark. Answer any four.

(1x3=3)

- i. How do you use the sequence analysis techniques to predict function of a protein from sequences (explain with examples)?
- ii. How do you use the Smith-Waterman algorithm for database searching?
- iii. What are the functional aspects of BI and how is it being explored for better understanding of biological system?
- iv. How (exactly) is seeding performed in the BLAST method (Explain with example)?

Q2. Each question carries 2 marks.

(2x3=6)

- i. How does scoring scheme of multiple sequence alignment (MSA) differ from pairwise alignment and give their justification? What are the important features that were included in ClustalW method to provide efficient MSA and how were these features satisfy the structural constraints of a protein? (0.5+1.5)
- ii. How do you calculate gap penalty using affine gap penalty system (explain with example) and provide justification of employing this scoring scheme? When do you employ double- and triple affine gap penalty schemes? (1.5+0.5)
- iii. How does local alignment scoring scheme differ from that of global alignment? Take any two extreme cases to show alignment depends on scoring scheme, even Smith-Waterman algorithm may provide global alignment?

Q3. Each question carries 3 marks.

(3x2=6)

- i. Progressive MSA is basically an iterative pairwise alignment. Suppose you will be given five sequences. How do you calculate distances among sequences and guide tree from these distances? How do you use the guide tree in aligning sequences by implementing dynamic programming sequentially (explain with suitable example)?
- ii. Blosom 62 matrix will be provided and gap penalty is -6. Two sequences are given below. Use Smith-Waterman local alignment algorithm to determine the alignment?

Seq1: GINHY

Seq2: AIQKF