JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST 2 EXAMINATION - OCTOBER 2018

B.Tech Semester (III)

COURSE CODE: 10B11BI311

COURSE NAME: Biological Computation

COURSE CREDITS: 04

MAX. MARKS: 25

MAX. TIME: 1.5 HRS

Note: *All questions are compulsory. Carrying of mobile phone during examinations will be treated as case of unfair means. Marks are indicated against each question in square brackets.*

Q1. Discuss the algorithm employed by the NCBI Blast program to search for similarity in the sequences. List and explain all important parameters that affect the search results of Blast.
(CO-1, 4 marks)

Q2. You have a query sequence Q of length L that matches to a sequence in a database with an E-value of E1. How would the E-value change if only the first half of Q were searched against the database? Explain your answer with the help of formula. (CO-2, 3 marks)

Q3. Find the traceback path for the following matrix (NW) and write the aligned sequence. (CO-2, 3 marks)

Q4. Explain the following with an example. (CO-2, 6 marks)
   a) Needleman-Wunch Algorithm
   b) Smith-Waterman Algorithm

Q5. What is multiple sequence alignment (MSA). What additional information do we obtain from MSA compared to pairwise alignment. Discuss the applications of MSA. (CO-3, 3 marks)

Q6. Discuss the advantage and disadvantages of dynamic programming method for multiple sequence alignment. (CO-3, 3 marks)

Q7. What alignment strategy is used by the popular MSA program ClustalW? Explain the steps. (CO-3, 3 marks)