JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT
TEST -1 EXAMINATION
B.Tech. (Biotechnology) ; Vth Semester

Course Code: 10B11BT511

Course Name: Introduction to Bioinformatics

Course Credits: 03

MAX. MARKS: 15

MAX. TIME: 1 Hr

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

1. Explain the advantages/significance of Gotoh's algorithm with respect to Needleman-Wunsch and Smith-Waterman algorithm. (2)

2. Discuss the cases in which you will prefer semi-global alignment over global alignment. (2)

3. Discuss the role of sequence filters in the BLAST program. (3)

4. Why and how do we normalize the raw scores in the BLAST program? (3)

5. Is the BLAST program based on dynamic programming? Justify your answer with arguments. (2)

6. Explain the different types of databases with respect to data type in bioinformatics. (3)