JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT **TEST-1 EXAMINATIONS-2022**

B.Tech-III Semester (BI)

COURSE CODE (CREDITS): 18B11BI313 (4)

MAX. MARKS: 15

COURSE NAME: Biological Computation

COURSE INSTRUCTORS: Dr. Shikha Mittal

MAX. TIME: 1

Hour

Note: All questions are compulsory. Marks are indicated against each question in square brackets.

- Q1. Consider the DNA strings AGATGGCCCCATCG and CGGTCCCCCGATGG. Compute the best global alignment of the two strings assuming match score of 1, and mismatch/indel penalty of -1. Compute the best local alignment, and the best global alignment. Are the two different? [CO-1] (3 marks)
- Q2. What is sequence alignment? Describe the methods used for sequence alignment [CO-1] (3 marks)
- Q3. What is difference between PAM and BLOSUM matrices? [CO-1 & CO-2] (2 marks)
- Q4. Define BLAST. Describe BLAST algorithm in details. What are BLAST variants? [CO-2] (4 marks)
- Q5. Explain the following [CO-1 & CO-2] (3 marks)
- (a) Difference between sequence similarity and sequence identity with an example
- (b) Orthologous
- (c) Difference between Tandem and segmental duplication