

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- MARCH-2023

COURSE CODE (CREDITS): 20MS1BT213 (2)

MAX. MARKS: 15

COURSE NAME: Bioinformatics

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 TCGCA and TCCA. Compute the best global alignment of the two strings assuming match score of 1, and mismatch/indel penalty of -1 ? [CO-1] (3 marks)

Q2. What is sequence alignment? Describe the methods used for sequence alignment [CO-1] (4 marks)

Q3. Describe the various databases that deal with DNA and protein structure. [CO-2] (3 marks)

Q4. Explain genome-specific databases with examples. [CO-2] (2 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