

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT  
TEST - 2 EXAMINATIONS-2022

M.Sc. -II Semester (Biotechnology/Microbiology)

COURSE CODE (CREDITS): 20MS1BT213 (2)

MAX. MARKS: 25

COURSE NAME: Bioinformatics

COURSE INSTRUCTORS: Dr. Raj Kumar, Dr. Tiratha Raj Singh MAX. TIME: 1 Hour 30 Min

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

Q1. Answer the following questions:

- An operating system has several components. Which component acts as an interface between hardware and all applications? [1 Mark]
- Suppose you are working in 'Documents' directory of your Linux system. Which command will you use to know the path of the working directory? What is the possible output of the command you will use? [2 Marks]
- Suppose you are working in 'Desktop' directory. How will you create a text file in the 'Documents' directory without moving out of the 'Desktop' directory? [2 Marks]

Q2. Answer the following questions:

- Homology modelling of protein structures normally proceeds along a series of distinct steps. Explain various steps involved in copying the 3D coordinates from the template. [2 Marks]
- Structure prediction programs generally include energy minimization and model optimization steps. How will you validate the final model? [2 Marks]
- What is the importance of a thermodynamically stable state? [1 Mark]

Q3. There are different methods for tertiary structure prediction of protein. List criteria to choose the most reliable among these methods? [3 Marks]

Q4. Align the following two sequences X and Y using FASTA method: X= PTNCDQ, Y = TNCDE [4 Marks]

Q5. For any two nucleotide sequences of similar length ( $l=10$ ) which method will be appropriate to measure the distance? If 2 characters deleted from the first sequence, then what method will be applicable? Prove your answer with an example set of sequences for both the cases. Scoring system can be taken arbitrarily. [4 Marks]

Q6. If "Pair-wise alignment whispers, MSA shouts out loud". Can you prove this statement with a profile (PSSM) and consensus sequence generation. [4 Marks]