

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATIONS- 2023

B.Tech-III Semester (BI)

COURSE CODE (CREDITS): 18B11BI313

MAX. MARKS: 25

COURSE NAME: Biological computation

COURSE INSTRUCTORS: Dr. Shikha Mittal

MAX. TIME: 1 Hour 30 Minutes

Note: (a) All questions are compulsory.

(b) Marks are indicated against each question in square brackets.

(c) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems

Q1. Calculate score for the following alignment according to the given scoring criteria – [CO-1 & CO-2] (2 marks)

ATTCGGCATTTCAGAGCTAGA
ATTCGACATT - - - GCTAGT

Match =1, Mismatch/Gap opening =0.5, Gap extension = 0.2

Q2. Proteins are large complex molecules that play many critical roles in the body. Elaborate protein structure and also mention the bonds which help in stabilization of the structure. [CO-4] (3 marks)

Q3. List the assumptions used for phylogenetic analysis construction. What are the steps used for generation of phylogenetic tree in brief. [CO-3 & CO-4] (4 marks)

Q4. In a phylogenetic tree, the number of topologies varies with the number of taxa. If I have 4 taxa, then what will be the number of rooted and unrooted topologies? [CO-4] (2 marks)

Q5. For the construction of Ramachandran's plot values of Phi and Psi are plotted. What are the angles and bonds involved in construction of Ramachandran plot? [CO-5] (3 marks)

Q6. Explain the following – [CO-3, CO-4 & CO-5] (6 marks)

- A. Difference between cladogram and phylogram
- B. Applications of MSA
- C. Difference between UPGMA and NJ method

Q7. Calculate BLOSUM substitution matrix for the given sequences – [CO-1 & CO-2] (5 marks)

Sequence	Position			
Seq1	B	A	B	A
Seq2	A	A	A	C
Seq3	A	A	C	C
Seq4	A	A	B	A
Seq5	A	A	C	C
Seq6	A	A	B	C

JWT TEST 2 EXAMINATION, OCT-2023