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 30 minutes

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

Q1. Calculate BLOSUM substitution matrix for the given sequences – (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

Q2. BLAST is a heuristic approach for sequence alignment. Explain in detail different variants of BLAST and BLAST algorithm. (4 marks)

Q3. How do you describe multiple sequence alignment? What are the applications of multiple sequence alignment as in comparison to pair wise sequence alignment? (3 marks)

Q4. 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? (3 marks)

Q5. To predict the structure of an unknown protein from its amino acid sequence, what will be criteria for template modeling? And also explain the method of comparative modeling in detail. (4 marks)

Q6. Explain the following – (6 marks)

   a) Difference between paralogs and orthologs

   b) P-value and Bit score in BLAST

   c) Dynammic programming algorithm