JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT TEST -3 EXAMINATIONS-2022

M.Sc.-II Semester (BT)

MAX. MARKS: 35 COURSE CODE (CREDITS): 20MS1BT213 (2) COURSE NAME: Bioinformatics MAX. TIME: 2 Hours COURSE INSTRUCTORS: Dr. Raj Kumar, Dr. Tiratha Raj Singh Note: All questions are compulsory. Marks are indicated against each question in square brackets. Q1. Realize the SOP method for MSA using a set of 5 sequences of length (7 characters or less) each. Use scoring system as follows: Match = 1, Mismatch = 0, Gap Penalty = 1. [4] [4*1.5=6] Q2. Differentiate between the following: (b) Pairwise and Multiple sequence alignments (a) Hamming vs Edit distance (d) BLAST and FASTA (c) Exact and Heuristic algorithms Q3.Interpret various types of phylogenetic reconstruction methods. Describe UPGMA method [3] for the sequences taken in Q1. Q4. Asses STAR alignment for the generation of MSA with an example data set. Use same [4] scoring system as provided in Q1. Q5. Give brief account on the following questions in context to protein conformation: 1) Amino acids may exhibit different structural conformation in peptides. What will be the effect of a cis-conformation on energetics of a dipeptide containing arginine and [2] phenylalanine residues? 2) Proline is a special amino acid found in proteins. Briefly discuss its effects on the conformation of protein structure. 3) Dihedral angle describes the rotation of the chain around the middle bond. Describe the properties and role of Omega (a) dihedral in protein structure and how it's different from [3] Ramachandran angles Phi (ϕ) and Psi (ψ) . Q6. Considering an emergency situation such as COVID-19 for which no FDA approved drugs are available, how virtual screening approaches can prove to be useful for identifying potential [3] drugs?

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Q8. Find out residues forming alpha-helix in the given sequence considering the below statistical propensities for alpha helices. [5]

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