JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -3 EXAMINATION- 2024

B. Tech-VIII Semester [All Except Bio]

COURSE CODE(CREDITS): 21B1WBT833 (3) MAX. MARKS: 35

COURSE NAME: Computational Biology for Engineers MAX. TIME: 2 Hours

COURSE INSTRUCTORS: Dr. Raj Kumar, Dr. Tiratha Raj Singh, Dr. Shikha Mittal.

***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

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Q1. Differentiate between the following: (CO:3-5) [2×4=8]

(a) Global and Local Alignments (b) Pairwise and Multiple Sequence Alignment

(c) Distance and Similarity (d) Progressive and Iterative Alignment Algorithms for MSA

Q2. What is Sum of Pairs (SoP) method? Explain its implementation with an example containing 5 nucleotide sequences. Scoring system is Match = +2, Mismatch = -1, Gap Penalty = -2. (CO: 5) [4]

Q3. Define BLAST. Describe the algorithm used by BLAST to perform sequence alignment. Highlight its key steps (CO: 5) [5]

Q4. Briefly explain (CO: 5) [3 × 2 = 6]

a) What are the different types of BLAST searches?
b) Homologs and Orthologs
c) E-value and Bit-score in BLAST

Q5. Discuss various stages in a drug development process. (CO: 5) [3]

Q6. What is molecular docking? Discuss main components of molecular docking. (CO: 5) [3]

Q7. What is a Quantitative Structure-Activity Relationship? Enlist some important molecular descriptors used in QSAR modeling. (CO: 5) [3]

Q7. Write short notes: (CO:3-5) [3 × 1 = 3]

a) Drug repurposing
b) Lead optimization
c) Lipinski's rule of five