JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2025

B.Tech-IV Semester (BT)

COURSE CODE (CREDITS): 18B11BT413 (4)   MAX. MARKS: 25

COURSE NAME: Introduction to Bioinformatics   MAX. TIME: 1 Hour 30 Min

COURSE INSTRUCTORS: Dr. Raj Kumar, Prof. Tiratha Raj Singh

Note: *(a) All questions are compulsory.*

   (b) The candidate is allowed to make Suitable numeric assumptions wherever required

    for solving problems

Q.No	Question	CO	Marks
Q1	Compute the sequence alignment through FASTA method for the given two sequences: Seq X = 'ARNDCHKL'; Seq Y = 'NDCHK'	2	3
Q2	Provide a comparative analysis of Central Dogma's of 'Molecular Biology' and 'Computational Biology'	1	1
Q3	Compare local and global alignments with an example of each. How Blast is working to solve the alignment problem? Explain in brief.	2	2
Q4	Implement dynamic programming for local alignment for the following sequences: Seq A = 'TAGCTGCACT', Seq B = 'GCTGCA'. Use scoring system as Match = 1, Mismatch = 0, Gap Penalty = -2.	3	5
Q5	Explain the internal working of BLAST. Provide a comparative analysis of various BLAST versions with a special emphasis on data types used in searching.	3	4
Q6	What search query would you use to find human genes annotated with "Type 2 Diabetes" in the NCBI Gene database?	1,2	2
Q7	Describe the structure of a GenBank file for nucleotide sequences. Compare and contrast FASTA and GenBank formats.	2,3	3
Q8	Explain the role of structural databases. Describe the type of data they may contain?	2,3	3
Q9	Justify the role of the DrugBank database. What are the various categories of chemical compound information stored in the DrugBank database?	2,3	2