

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- 2026

B.Tech-III Semester (BI)

COURSE CODE (CREDITS): 25B11BI311

MAX. MARKS: 15

COURSE NAME: Biological Computation

COURSE INSTRUCTOR: Dr. Raj Kumar

MAX. TIME: 1 Hour

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

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

(c) Use of calculator is not allowed

| Q.No | Question                                                                                                                                                                    | CO | Marks        |
|------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----|--------------|
| Q1   | Explain the difference between similarity and homology.                                                                                                                     | 1  | 2            |
| Q2   | Calculate sequence identity score for given alignment:<br><div style="text-align: center;"> A C T T G T C T T A T G C<br/> A C T _ G _ _ T T A _ _ C </div>                 | 1  | 2            |
| Q3   | A major drawback of dot-plots is the noise. What is noise in dot plots, how can it be reduced?                                                                              | 2  | 2            |
| Q4   | Align the following sequences using Needleman-Wunsch global sequence alignment approach:<br>Scoring scheme: Match = 1, Mismatch = -1, Gap = -2<br>Seq1 = ATTGC, Seq2 = AGGC | 3  | 4            |
| Q5   | Short notes:<br>a) Stop codons<br>b) Orthologs<br>c) INSDC<br>d) FASTA format<br>e) Local vs Global sequence alignment                                                      | 2  | 5 × 1<br>= 5 |