JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- 2025

B.Tech-III Semester (BI)

COURSE CODE (CREDITS): 25B11BI311 **MAX. MARKS: 15**

COURSE NAME: Biological Computation

COURSE INSTRUCTORS:Dr. Shikha Mittal **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

Q.No	**Question**	**CO**	**Marks**
Q1	Align the following two sequences using the Needleman-Wunsch algorithm (match: +1, mismatch: -1, gap:-2): **Sequence A:** ACTG **Sequence B:** ACG a) Construct the scoring matrix b) Perform traceback to find the optimal alignment c) Provide the final alignment and score	CO-I	(04)
Q2	Define Biological databases. Distinguish between primary, secondary and derived databases. Mention any two nucleotide sequence databases and two protein sequence databases.	CO-II	(03)
Q3.	Given the following observed substitutions in a protein family, calculate the **log-odds score** for a substitution matrix. **Pair** — **Observed Frequency** — **Expected Frequency** A-A — 0.2 — 0.15 A-G — 0.05 — 0.08	CO-II	(02)
Q4.	Explain the following – **a)** Homologs and orthologs **b)** Accession number **c)** Difference between sequence similarity and sequence identity with the help of an example	CO-I & CO-II	(06)

JUIT TEST-1 EXAMINATION- AUG-2025