

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -2 EXAMINATION- 2024

B.Tech-IV Semester (BT)

COURSE CODE(CREDITS): 18B11BT413 (4)

MAX. MARKS: 25

COURSE NAME: Introduction to Bioinformatics

COURSE INSTRUCTORS: Dr. Raj Kumar

MAX. TIME: 1 Hour 30 Minutes

*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*

Q1. Jennifer Doudna and Emmanuelle Charpentier are pioneering scientists working on CRISPR gene editing. How will you search for relevant literature which they have collectively published on CRISPR? Write down the literature search scheme in a step-wise manner. (CO-2) [3]

Q2. Discuss the rationale of having two types of Gap penalties in scoring pairwise sequence alignments. (CO-3,4) [2]

Q3. Discuss the significance of Z-score in database similarity search? (CO-3,4) [2]

Q4. Calculate the sequence similarity score for the given alignment: (CO-3,4) [3]

```
A A T G A C G A - T G T G C C
|   | |   | | |   |   |   |
A G T G - C G A G T T T - A C
```

Q5. Given two sequences **Seq1**: ATGCT, **Seq2**: AGCT, and a scoring scheme **Match**: +1, **Mismatch**: -1, **Gap**: -2. Find out the suitable alignment using Needleman-Wunsch algorithm. (CO-3,4) [5]

Q6. Write short notes on:

- a) Entrez
- b) Uniprot
- c) PDB database
- d) Homologs Vs. Orthologs
- e) HSP

(CO-2,3,4) [2 × 5 = 10]