

**JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT**

**TEST -1 EXAMINATION- 2024**

**M.Sc - II Semester (BT/MM/Ph.D.)**

**COURSE CODE (CREDITS): 20MS1BT213 (2)**

**MAX. MARKS: 15**

**COURSE NAME: Bioinformatics**

**COURSE INSTRUCTORS: Dr. Shikha Mittal**

**MAX. TIME: 1 Hour**

*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. Describe dot matrix method of sequence alignment. Find the sequence having best optimal score using the values of match=1, mismatch=-1, and gap penalty=0.5 (3 marks)**

Sequence 1- ATGCGTGGTE

Sequence 2- ATGCGTGGT

**Q2. Briefly explain primary, secondary and tertiary biological databases with examples? (3 marks)**

**Q3. Define Sequence Alignment. What are the different types of Sequence Alignment? (3 marks)**

**Q4. Calculate sequence similarity and sequence identity for the given sequences (2 marks)**

Sequence 1- GTCCTCATAACTCTCTCTAG

Sequence 2- GTCGTCATAACACTCTCTAG

**Q5. Briefly explain – (4 marks)**

(a) Difference between homologs, paralogs and orthologs.

(b) Submission and retrieval tools for nucleotide databases