

**VIT**

Vellore Institute of Technology

REG.NO.:

SCHOOL OF BIOSCIENCES AND TECHNOLOGY
CONTINUOUS ASSESSMENT TEST - I
WINTER SEMESTER 2025-2026

Programme Name & Branch : MSI Biotechnology
Course Code and Course Name : TBIT304L, Bioinformatics
Slot(s) : B2 +TB2
Faculty Name(s) : Dr. Kuntal Pal
Class Number(s) : 3476
Date of Examination : 28.01.26
Exam Duration : 90 minutes
Maximum Marks: 50

General instruction(s):

- Answer All Questions

Q. No	Question	M
1.	Explain the role of biological databases in bioscience research.	10
2.	Identify the databases used to fetch the following information: a) Genetic variation in clinical samples b) Introns/Exon gene sequences c) Post-translational modification data. d) Protein structural data. e) Protein classification based upon structure. f) Single-nucleotide polymorphism g) Somatic mutations in cancer h) Human variation database from IIT-Madras i) Protein classification based upon family j) Protein isoform data	10
3.	a) Explain the dot-plot matrix used for sequence alignment. Discuss the features of a diagonal. b) Distinguish the Smith-Waterman algorithm from the Needleman-Wunsch algorithm.	5 5
4.	a) Interpret the different types of approaches used in multiple sequence alignment (MSA) b) Differentiate Clustal Omega from Clustal W in their approach for MSA	5 5
5.	Compare different types of scoring matrices used for sequence alignment.	10
