Final Assessment Test – November 2019

VIT
Vellore Institute of Technology

Course: BIT2001 - Analytical Bioinformatics

Class NBR(s): 0690 Slot: E2+TE2

Time: Three Hours Max. Marks: 100

KEEPING MOBILE PHONE/SMART WATCH, EVEN IN 'OFF' POSITION, IS EXAM MALPRACTICE

Answer ALL Questions

(10 X 10 = 100 Marks)

1. Discuss the importance of biological databases in bioinformatics. Give the layout of GenBank Flat File Format.

2. Let S1 = ATGCGCTTAA & S2 = ACATCGCTAT

   a) Build the complete dynamic programming table for these strings.

   b) What is the edit distance between S1 & S2?

3. Explain the working of BLAST based on your knowledge of sequence alignment. Define secondary databases and describe any one database of this category.

4. Describe the application of bioinformatics in phylogenetics and drug discovery.

5. Differentiate between Ab-Initio and homology methods of protein structure prediction. Explain the general homology prediction process in detail with neat diagram.

6. By using the following distance table for 5 sequences (a, b, c, d and e) as input, construct a phylogenetic tree following UPGMA algorithm.

	a	b	c	d	e
a	0	16	20	30	22
b	16	0	29	33	20
c	20	29	0	27	38
d	30	33	27	0	42
e	22	20	38	42	0

7. a) Write the significance of multiple sequence alignment in biological data analysis.

   b) Discuss iterative alignment method employed in multiple sequence alignment problems.

8. Perform global alignment of the two following sequences, CATTGCAA and CGATAACG and bring out one optimal alignment. (Match=+1, Mismatch=-1 and Gap score=-2 for scoring).

9. Elaborate on Maximum Parsimony algorithm and give its advantages.

10. Give an overview of structure based drug design and its challenges. How is it different from ligand based drug designing?