Roll No. | | | | | | | | | | | | **Total No. of Pages : 02**

Total No. of Questions : 09

B.Sc. (BT) (Sem.–6)

BIOINFORMATICS

Subject Code : BSBT-149-18

M.Code : 79460

Date of Examination : 05-01-2023

Time : 3 Hrs. **Max. Marks : 40**

INSTRUCTIONS TO CANDIDATES :

1. **SECTION-A is COMPULSORY consisting of TEN questions carrying ONE mark each.**
2. **SECTION-B contains FIVE questions carrying $2^1/_2$ (Two and Half) marks each and students has to attempt any FOUR questions.**
3. **SECTION-C contains THREE questions carrying TEN marks each and students has to attempt any TWO questions.**

SECTION-A

1. Write short notes on :

a) File format

b) Heuristic methods

c) Global alignment

d) Gap penalties

e) Rooted tree

f) Patterns

g) TBLASTX

h) Docking

i) Cladogram

j) GRAIL.

SECTION-B

2. Give an overview on the applications of Bioinformatics.

3. Describe briefly the Dot matrix method for pairwise sequence alignment.

4. Discuss any protein structure database in brief.

5. Elaborate on the use of Neural networks for protein structure prediction.

6. Discuss the UPGMA method for phylogenetic analysis.

SECTION-C

7. Write a note on the Chou-Fasman and GOR method for protein structure prediction.

8. Discuss the Needleman-Wunsch algorithm for sequence alignment.

9. Elaborate on the different methods used for Multiple sequence alignment.

NOTE : Disclosure of Identity by writing Mobile No. or Marking of passing request on any paper of Answer Sheet will lead to UMC against the Student.