BB-334

M. Sc. EXAMINATION, May 2017

(Second Semester)

(Main & Re-appear)

BT-508-MS

BIOTECHNOLOGY

Introduction to Bioinformatics

Time : 3 *Hours*]   [*Maximum Marks :* 100

Before answering the question-paper candidates should ensure that they have been supplied to correct and complete question-paper. No complaint, in this regard, will be entertained after the examination.

Note : Attempt *Five* questions in all, selecting at least *one* question from each Unit. All questions carry equal marks.

Unit I

1. Differentiate between : **4×5=20**

   (a) Windows, Unix and Linux operating systems.

   (b) Binary, octal and hexadecimal number systems.

   (c) Internet and Intranet.

   (d) Assemblers, interpreters and compilers.

2. (a) What are Databases ? Describe different forms of classification systems used for databases, giving examples of each type. **10**

   (b) How are structure database different from sequence databases ? Describe the salient features and organization of the three major databases. **10**

Unit II

3. (a) What do you mean by database similarity searching ? How does BLAST facilitate this ? **8**

   (b) Discuss the two major algorithms and scoring matrices used for pairwise sequence alignment. **12**

4. With the help of suitable examples, describe progressive, iterative and block-based methods of multiple sequence alignment. **20**

Unit III

5. What do you mean by phylogenetic analysis ? Describe in detail the steps and the software programmes used for phylogenetic data analysis. **20**

6. Give a detailed account of the various distance-based and character-based methods of tree construction. **20**

Unit IV

7. Describe in detail the various predictive methods used for nucleotide sequence annotation. **20**

8. Explain the hierarchial structural organization of proteins. Also discuss the predicture methods for protein sequences. **20**