Set - C

Mode of Examination: Online

Unique Paper Code	: 107455
Name of the Paper	: Bioinformatics (LSPT – 409)
Name of the Course	: B.Sc. (Prog.) Life Sciences/ B.Sc. (Hons.) Zoology (3YUG)
Semester	: IV/VI
Duration	: 2 Hours
Maximum Marks	: 75

Instructions for Students

Write your Roll No., Name of the Paper, Course, Semester, and Date of examination on the first page of answer sheet.

Attempt ***ANY FOUR*** *questions. All questions carry equal marks.*

1. Define biological databases and classify them according to data source and data type. Describe the sequence retrieval system of databases.

2. Give salient features of the following databases in terms of resources at the databases, sequence/data submission and sequence data retrieval: EMBL and Swiss-Prot.

3. Expand MSA. What is progressive alignment? Step-wise describe how you would perform the MSA in CLUSTALW.

4. Describe various types of scoring matrices for aligning sequences. Differentiate between PAM and BLOSUM matrices. Enlist their advantages and disadvantages.

5. What is a phylogenetic tree? Elaborate steps involved in constructing a phylogenetic tree. Describe the various methods by which a phylogenetic tree can be constructed. How can you ascertain the consistency of molecular phylogeny prediction?

6. Describe in detail applications of bioinformatics particularly in the fields of drug discovery, microbial genomics and crop improvement giving suitable examples.