Exam. Code : 206603
Subject Code : 4619

M.Sc. Bio-Informatics Semester—III
GENOMICS AND PROTEOMICS
Paper : BI–631

Time Allowed—3 Hours]   [Maximum Marks—75

SECTION—A

Note :—All questions are compulsory and each question carries 1½ marks.

1.   Name a technique used for gene expression analysis.

2.   What are sequence repeats ?

3.   How MUMer differs from VISTA ?

4.   What is Homophila database ?

5.   Define a linkage map.

6.   What is SSCP ?

7.   Which spectrometry is used in proteomics ?

8.   How pharmacology differs from pharmacogenomics ?

9.   What is the significance of databases and networks ?

10. What is BioGRID ?

SECTION—B

Note :—Attempt any **one** question from each part and each question carries **12** marks.

1. Elaborate on characteristics of human genome and the significance of characters.

OR

Explain the principle, design and analysis of DNA microarray.

2. Discuss in detail the importance of genome databases with two examples.

OR

Discuss in detail HOBACGEN and XREFdb databases.

3. Explain the practical uses of genome maps.

OR

Comment on the importance of genetic markers in molecular studies.

4. Discuss at least five current applications of proteomics.

OR

Which modern field of science has revolutionized the field of pharmacology and how ?

5. Explain the functions and applications of one each a network, database and software in the field of PPIs.

OR

What is MINT ? Comment on its uses and applications.

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