QP Code : 76157

(2½ Hours) [Total Marks : 75

N.B. : (1) **All** questions are **compulsory.**
(2) **All** questions carry **equal marks.**
(3) Use of simple **calculator** is **permitted.**

1. (a) Calculate Karl Pearson's correlation between X and Y series from the given data : 7

X	12	9	8	10	11	13	7
Y	13	8	6	9	11	12	2

(b) With suitable example explain Null and Alternate hypothesis setting, what will be its Type I and Type II errors. 8

OR

1. (a) What is standard deviation and standard error? State their uses. 5
(b) What is sampling? Explain how sample size is decided for quantitative and qualitative data. 5
(c) Write a note on Null hypothesis. 5

2. (a) Elaborate on computer based patient record. 7
(b) Write a note on statistical software's with the help of suitable example. 8

OR

2. (a) Explain algorithm and its importance. 7
(b) Give the brief account of basic C programming. 8

3. (a) Explain briefly the organization of biological data in databases. 7
(b) Describe the methods and tools for identification of proteins from its sequence. 8

OR

3. (a) Discuss the databases and tools used for Multiple Sequence Alignment. 7
(b) Elaborate on global and local sequence alignment. 8

4. (a) Describe types of Microarrays and give their advantages and limitations. 8
(b) Elaborate on the techniques used for identification of proteins. 7

OR

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4. (a) With respect to microarray data analysis explain the following : 8
(1) Grouping of expression data; (2) Clustering method.
(b) What are the consensus sequences and sequence logos? Explain their role in human genome analysis. 7

5. Write short note on **any three** of the following : 15
(a) Chi Square test
(b) Spread sheets
(c) Friedman test
(d) Gateways to assess human genome
(e) Exon intron finder
