Registration Number:

Date & session:

**ST. JOSEPH’S UNIVERSITY, BENGALURU -27**

**M.Sc (MICROBIOLOGY) – III SEMESTER**

**SEMESTER EXAMINATION: OCTOBER 2023**

**(Examination conducted in November/December 2023)**

**MB 9421: BIOSTATISTICS AND BIOINFORMATICS**

**(For current batch students only)**

**Time: 2 hours Max Marks: 50**

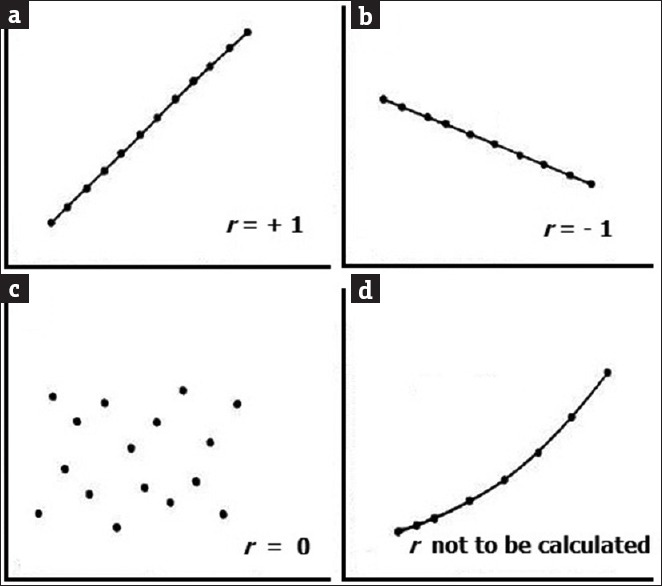
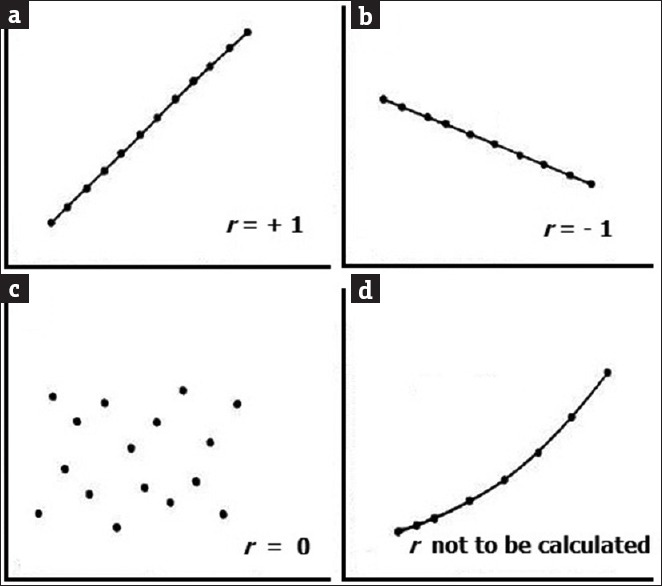
**This question paper contains 2 printed pages and 4 parts**

**I. Answer any Five of the following 5X3=15**

1. Correct the following statements: (a) A frequency histogram is constructed by connecting all midpoints of the top of the bars in a histogram by a straight line without displaying the bars. (b) The mean (arithmetic) does not use every value in the data and hence is a good representative of the data.
2. Identify the mode(s) in the following datasets:

(a) 7,2,5,8,1,9 (b) 2,2,2,6,7,8,4,4,4,1 (c) 4,3,8,2,6,7,7,5

1. Define descriptive statistics and inferential statistics.
2. Three coins are tossed simultaneously. What is the probability of getting no head?
3. what is the value of the correlation coefficient in the following plots?



6. Define sequence alignment.

7. What is EMBL? List the services provided by EMBL?

1. **Answer any Two of the following 2X5=10**

8.  Explain the principle of parsimony. Using a graph, depict the relations between number

of parameters, bias and variance.

9. Write a short note on likelihood approach.

10. What are the types of phylogenetic trees? Discuss the analysis methods of phyloge-

netic trees?

**III. Answer any Two of the following 2X10=20**

11. (a) Calculate the regression coefficients and obtain the equations (lines) of regression for the following data. X: 2, 3, 5, 6, 7, 8, 10; Y: 12, 14, 15, 16, 18, 21, 25.

(b) Explain the various datatypes in R and their uses.

12. Write a detailed note on the analysis and interpretation of results for HPLC.

13. What is Next Generation Sequencing? Explain RNA-Seq,

1. **Answer the following 1X5=5**

14. Draw the given matrix box in your answer sheet and use the steps in Needleman–Wunsch Algorithm to fill it with scores. Trace back the scores and find the final alignment of the given short sequences (ATGCT, AGCT).

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