



BRAINWARE UNIVERSITY

Term End Examination 2024-2025

Programme – M.Sc.(BT)-2024

Course Name – Genetics and Biostatistics

Course Code - MBT20204

(Semester II)

Full Marks : 60

Time : 2:30 Hours

[The figure in the margin indicates full marks. Candidates are required to give their answers in their own words as far as practicable.]

Group-A

(Multiple Choice Type Question)

1 x 15=15

1. Choose the correct alternative from the following :

- (i) Select the correct criterion to decide whether to use a histogram or a bar chart.
 - a) Use a histogram for discrete data and a bar chart for continuous data
 - b) Use a bar chart for discrete data and a histogram for continuous data
 - c) Both can be used interchangeably
 - d) Neither is suitable for data visualization
- (ii) Select the most suitable graph you would recommend for visualizing the correlation between two variables.
 - a) Bar chart
 - b) Histogram
 - c) Scatter plot
 - d) Box plot
- (iii) Write the most appropriate statistical measure you would recommend to determine the middle value of a dataset.
 - a) Mean
 - b) Median
 - c) Mode
 - d) Variance
- (iv) Write the correct classification for a dataset with a large difference between Q3 and Q1.
 - a) High variance
 - b) High standard deviation
 - c) High interquartile range
 - d) Low variability
- (v) Select the appropriate method to decide whether a dataset is positively skewed.
 - a) Check if the median is greater than the mean
 - b) Check if the mean is greater than the median
 - c) Look at the left tail of the distribution
 - d) Use a pie chart
- (vi) Classify the different modes of inheritance using pedigree analysis.
 - a) Autosomal dominant, autosomal recessive, X-linked dominant, X-linked recessive
 - b) Genetic drift, gene flow, mutation, selection

- c) Monohybrid, dihybrid, polygenic, epistatic d) Cladogram, phylogram, dendrogram, unrooted tree
- (vii) Recommend a method to measure gene flow between populations. b) F-statistics
- a) Hardy-Weinberg equation d) Sex ratio determination
- c) Pedigree analysis
- (viii) Decide which concept explains the movement of alleles between populations.
- a) Genetic drift b) Gene flow
- c) Natural selection d) Inbreeding
- (ix) Classify the different inheritance patterns observed in pedigree analysis.
- a) Autosomal dominant, autosomal recessive, X-linked dominant, X-linked recessive b) Mutations, recombination, gene flow, sex-linked
- c) Cladogram, phylogram, dendrogram, unrooted tree d) Phylogenetic trees, Hardy-Weinberg equilibrium, recombination
- (x) Decide whether correlation implies causation in statistical analysis.
- a) Yes b) No
- c) Only if $p < 0.05$ d) Only for parametric tests
- (xi) Decide which test is most appropriate for analyzing variance among multiple independent groups.
- a) t-test b) ANOVA
- c) Poisson regression d) Correlation
- (xii) Classify correlation coefficients based on the strength of the relationship.
- a) Weak, moderate, strong b) Small, medium, large
- c) High, low, average d) Positive, negative, neutral
- (xiii) Classify different types of regression models.
- a) Simple, multiple, logistic b) Linear, exponential, logarithmic
- c) Univariate, bivariate, multivariate d) All
- (xiv) Label which test is most suitable for analyzing categorical survey data.
- a) Chi-square test b) ANOVA
- c) Regression d) t-test
- (xv) Select the name of the statistical test used for comparing more than two group means.
- a) t-test b) Chi-square test
- c) ANOVA d) Correlation analysis

Group-B

(Short Answer Type Questions)

3 x 5=15

2. Calculate the skewness of a dataset where the mean is greater than the median. (3)
3. Classify different types of gene interactions that influence phenotypic expression. (3)
4. Classify different types of linear and nonlinear regression models. (3)
5. Illustrate how error propagation affects experimental data analysis. (3)
6. Create a box plot for the given dataset: 15, 21, 30, 42, 50, 55, 62, 70, 80. Identify the median, Q1, Q3, and IQR. (3)

OR

Construct a frequency distribution table for the following dataset: 8, 12, 15, 12, 18, 20, 15, 15, 12, 18, 22, 25, 22, 18, 12. (3)

Group-C

(Long Answer Type Questions)

5 x 6=30

7. Analyze the significance of Type I and Type II errors in hypothesis testing and their consequences in biomedical research. (5)
8. Report the effects of genetic bottlenecks on conservation efforts. (5)
9. Construct a frequency distribution table for the following dataset: 5, 10, 10, 15, 15, 20, 20, 25, 30, 35. (5)
10. Illustrate the concept of genetic correlation between two traits with a relevant example. (5)
11. Classify different types of factorial experiment designs. (5)
12. Illustrate the role of linkage disequilibrium in GWAS studies. (5)

OR

Summarize quantitative genetics models in predicting phenotypic traits. (5)

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