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**BRAINWARE UNIVERSITY**

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Brainware University
Barasat, Kolkata -700125

Term End Examination 2025-2026**Programme – B.Tech.(BT)-2024****Course Name – Biostatistics****Course Code - BTB40111****(Semester IV)****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) Choose the correct classification for a dataset with multiple modes.
 - a) Unimodal
 - b) Bimodal
 - c) Multimodal
 - d) No mode
- (ii) Decide which factor increases genetic variation in a population.
 - a) Mutation
 - b) Genetic drift
 - c) Founder effect
 - d) Inbreeding
- (iii) 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
- (iv) Decide which assumption is NOT part of the Hardy-Weinberg equilibrium.
 - a) No mutation
 - b) Large population size
 - c) Non-random mating
 - d) No gene flow
- (v) Recommend the best method to determine evolutionary relationships between species.
 - a) Pedigree analysis
 - b) Hardy-Weinberg equation
 - c) Phylogenetic tree
 - d) PCR analysis
- (vi) Decide which factor plays the biggest role in non-random mating.
 - a) Genetic drift
 - b) Selective breeding
 - c) Gene flow
 - d) Mutation
- (vii) Decide which type of genetic disorder is most likely inherited in an autosomal recessive manner.
 - a) Huntington's disease
 - b) Cystic fibrosis
 - c) Hemophilia A
 - d) Rett syndrome

- (viii) Recommend a way to track the inheritance of genetic disorders in a family.
- Hardy-Weinberg principle
 - Phylogenetic tree
 - Pedigree analysis
 - Genetic drift model
- (ix) Classify the different types of mutations based on their effects on protein function.
- Silent, missense, nonsense, frameshift
 - Autosomal, X-linked, mitochondrial, polygenic
 - Positive, negative, neutral, lethal
 - Directional, stabilizing, disruptive, balancing
- (x) Classify the different types of genetic variance.
- Additive, dominance, epistatic
 - Structural, functional, regulatory
 - Genotypic, environmental, epigenetic
 - Autosomal, sex-linked, mitochondrial
- (xi) Recommend the best probability distribution for modeling the number of mutations in a gene per generation.
- Binomial
 - Poisson
 - Normal
 - Exponential
- (xii) Recommend an appropriate regression model for predicting enzyme concentration based on substrate concentration.
- Linear Regression
 - Logistic Regression
 - Poisson Regression
 - Chi-square Test
- (xiii) Decide how to interpret a correlation coefficient of -0.85.
- Strong negative correlation
 - Weak negative correlation
 - No correlation
 - Positive correlation
- (xiv) Classify the type of hypothesis that suggests a significant effect exists.
- Null hypothesis
 - Alternative hypothesis
 - Descriptive hypothesis
 - Non-statistical hypothesis
- (xv) Label which test should be used for analyzing variance across different groups.
- ANOVA
 - t-test
 - Regression
 - Chi-square test

Group-B

(Short Answer Type Questions)

3 x 5=15

- Summarize the assumptions required for performing a Z-test and its applications in large sample studies. (3)
- Illustrate the difference between a bar chart and a histogram using a real-world example. (3)
- Calculate the allele frequencies in a population where 36% of individuals exhibit a recessive trait. (3)
- Summarize the role of populations and samples in statistical inference. (3)
- Illustrate the role of counting principles in probability with suitable examples. (3)

OR

- Summarize the characteristics of Binomial, Poisson, and Normal distributions. (3)

Group-C

(Long Answer Type Questions)

5 x 6=30

- Calculate the interquartile range (IQR) for the dataset: 10, 15, 20, 25, 30, 35, 40, 45, 50. (5)
- Report the effects of genetic bottlenecks on conservation efforts. (5)
- Analyze the role of QTL mapping in identifying genes related to complex traits. (5)
- Analyze how Bayesian inference improves genetic risk prediction. (5)
- Summarize the steps involved in performing a correlation analysis in biological studies. (5)
- Create a step-by-step explanation of how to conduct a hypothesis test using a t-test for small samples. (5)

OR

Evaluate the advantages and limitations of using ANOVA instead of multiple t-tests when comparing multiple groups. (5)

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