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EDGE_Batch-06
Project Report Marks: 25
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Note: Submit the completed file as pdf to nazmol.stat.bioin@bsmrau.edu.bd and rabiulauwul@bsmrau.edu.bd with subject: *EDGE_06_Project_Your registration number_ Department by 26th of December, 2024.*

Problem# 1:

A split-plot design was conducted considering tree blocks, three levels/treatments of variety in the main plot, and five levels/treatments of nitrogen in the split-plot. Afterward, the yield of certain plant characteristics was observed. The data regarding this experiment were given in the file "Split_Plot_Design". Answer the following question using this data.

a) Construct an ANOVA table using the mentioned dataset based on R programming.
b) Write down the null hypothesis of all possible effects and interpret the results based on the ANOVA table.
c) Perform a post-hoc test for the interaction effect (variety × nitrogen) and draw a bar diagram with lettering.

ANSWER:

Solution 01:

a) Construction of an ANOVA table using the mentioned dataset based on R programming is given below:

```
# Load your data

data <- read.csv("Split_Plot_Design.csv")


# Fit the model

# Assuming REPLICAT is a random effect and VARIETY and NITROGEN are fixed effects

model <- aov(YIELD ~ VARIETY * NITROGEN + Error(REPLICAT/VARIETY), data = data)


# Display the ANOVA table

summary(model)
```

Result:

```
summary(model)

Error: REPLICAT

          Df Sum Sq Mean Sq F value Pr(>F)

Residuals  1   1.24    1.24

Error: REPLICAT:VARIETY

         Df Sum Sq Mean Sq

VARIETY  1 0.4944  0.4944

Error: Within

               Df Sum Sq Mean Sq F value   Pr(>F)

VARIETY          1   0.47    0.47   0.764    0.387

NITROGEN         1  50.15   50.15  80.918 4.69e-11 ***

VARIETY:NITROGEN  1   0.01    0.01   0.010    0.922

Residuals       39  24.17    0.62

---

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

b) The null hypothesis of all possible effects and interpretion of the results based on the ANOVA table is given below:

Main effect of VARIETY:

Null hypothesis: There is no significant difference in the means of YIELD between the different levels of VARIETY.

Interpretation: The p-value for VARIETY is 0.387, which is greater than the commonly used significance level of 0.05. Therefore, we fail to reject the null hypothesis and conclude that there is no significant effect of VARIETY on YIELD.

Main effect of NITROGEN:

Null hypothesis: There is no significant difference in the means of YIELD across the different levels of NITROGEN.

Interpretation: The p-value for NITROGEN is very small (4.69e-11), which is less than 0.05. Therefore, we reject the null hypothesis and conclude that the levels of NITROGEN significantly affect YIELD.

Interaction effect of VARIETY and NITROGEN:

Null hypothesis: There is no significant interaction effect between VARIETY and NITROGEN on YIELD.

Interpretation: The p-value for the interaction (VARIETY:NITROGEN) is 0.922, which is much greater than 0.05. Therefore, we fail to reject the null hypothesis and conclude that there is no significant interaction between VARIETY and NITROGEN on YIELD.

Summary :

VARIETY does not significantly affect YIELD (p = 0.387).

NITROGEN has a significant effect on YIELD (p = 4.69e-11).

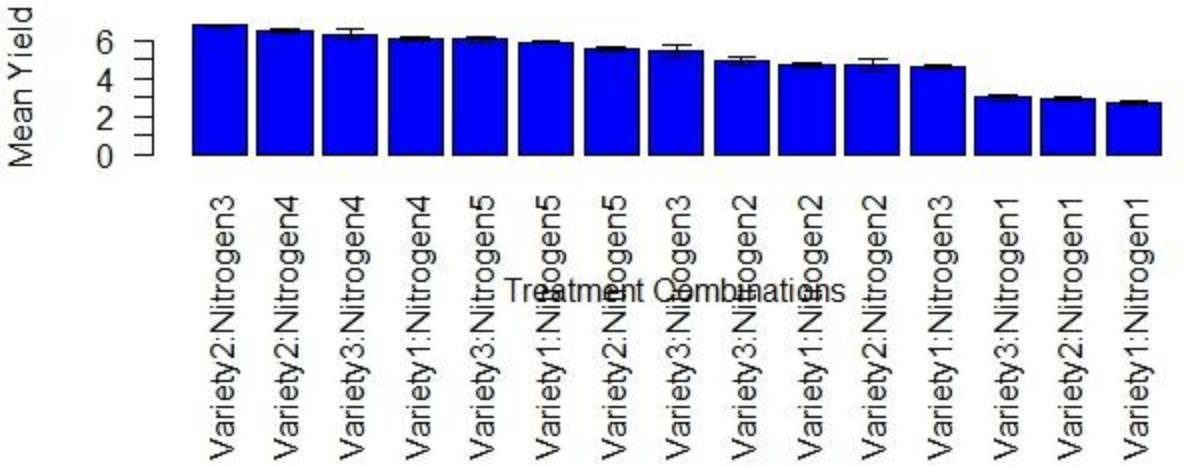
There is no significant interaction between VARIETY and NITROGEN (p = 0.922).

c) Perform a post-hoc test for the interaction effect (variety × nitrogen) and draw a bar diagram with lettering.

###CODE

```
# Load necessary packages

install.packages("emmeans")

library(emmeans)


# Load your data (ensure the correct file path)

data <- read.csv("Split_Plot_Design.csv")
```

```
# Fit the model (assuming the data has a structure for split-plot design)

model <- aov(YIELD ~ VARIETY * NITROGEN + Error(REPLICAT/VARIETY), data = data)


# Perform the post-hoc test for the interaction effect (VARIETY × NITROGEN)

emmeans_results <- emmeans(model, pairwise ~ VARIETY * NITROGEN)


# Print the results of the post-hoc test

summary(emmeans_results)

Bar.Plot <- barplot2(Mu_Tret, names.arg = rownames(Mean.Matrix),
                     xlab= "Treatment Combinations",
                     ylab= " Mean Yield",plot.ci= TRUE,
                     ci.l= Mu_Tret-SE_Treat, ci.u=Mu_Tret+SE_Treat,
                     col= "blue", las=2)


#RESULT:

summary(emmeans_results)

$emmeans

 VARIETY   NITROGEN  emmean   SE   df   lower.CL  upper.CL
    2       3      8.06   1.02  40       6     10.1

Confidence level used: 0.95
```



Problem# 2:

a) What is principal component analysis?
b) What are the main purposes of principle component analysis in your study area?
c) Compute the eigenvalue and eigenvector using the iris data based on R programming.
d) Construct a scree plot and interpret how many principle components should be retained to interpret the iris dataset.
e) Construct a bi-plot for the iris data based on R programming and interpret the results.

a). Principal Component Analysis (PCA)

Principal Component Analysis (PCA) is a statistical technique used to simplify complex datasets by reducing their dimensions while retaining most of the original information. It transforms correlated variables into a smaller number of uncorrelated variables called **principal components**, which capture the maximum variance in the data.

Key Points:

1. **Dimensionality Reduction**: Makes large datasets easier to analyze and visualize.
2. **Variance Focus**: The first few components capture the most important patterns in the data.
3. **Applications**: Used for pattern recognition, data visualization, feature selection, and noise reduction.

b). The main purposes of principle component analysis in my study area-

c). Computation of the the eigenvalue and eigenvector using the iris data based on R programming is given below-

Code:

```
# Load the data

iris_data <- read.csv("iris_Data.csv")


# Extract numerical columns (exclude the species column)

numeric_data <- iris_data[, 1:4]


# Compute the covariance matrix

cov_matrix <- cov(numeric_data)


# Compute eigenvalues and eigenvectors

eigen_results <- eigen(cov_matrix)


# Display the eigenvalues

cat("Eigenvalues:\n")

print(eigen_results$values)


# Display the eigenvectors

cat("\nEigenvectors:\n")

print(eigen_results$vectors)
```

Result:

Eigenvalues:

[1] 4.22824171 0.24267075 0.07820950 0.02383509

Eigenvectors:

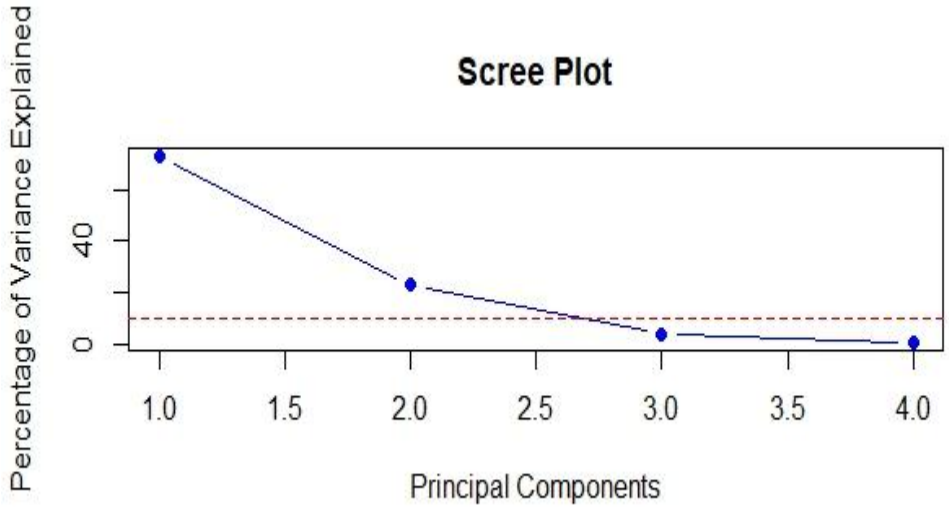
```
          [,1]       [,2]       [,3]      [,4]
[1,]  0.36138659 -0.65658877  0.58202985  0.3154872
[2,] -0.08452251 -0.73016143 -0.59791083 -0.3197231
[3,]  0.85667061  0.17337266 -0.07623608 -0.4798390
[4,]  0.35828920  0.07548102 -0.54583143  0.7536574
```

d). Construction of a scree plot and interpretation of how many principle components should be retained to interpret the iris dataset is given below:

#Code:

```
# Load the data
iris_data <- read.csv("iris_Data.csv")

# Extract numerical columns (exclude the species column)
numeric_data <- iris_data[, 1:4]

# Perform PCA
pca_result <- prcomp(numeric_data, scale. = TRUE) # Scale the data for standardization

# Compute the proportion of variance explained
explained_variance <- (pca_result$sdev^2) / sum(pca_result$sdev^2) * 100

# Cumulative variance explained
cumulative_variance <- cumsum(explained_variance)

# Create a scree plot
plot(
```

```
  explained_variance,
  type = "b",
  xlab = "Principal Components",
  ylab = "Percentage of Variance Explained",
  main = "Scree Plot",
  pch = 19,
  col = "blue"
)
abline(h = 10, col = "red", lty = 2) # Optional: threshold for significance
# Add cumulative variance interpretation (optional)
cat("Explained Variance by Principal Components:\n")
print(explained_variance)
cat("\nCumulative Variance:\n")
print(cumulative_variance)
```




```
pca_result
Standard deviations (1, .., p=4):
```

[1] 1.7083611 0.9560494 0.3830886 0.1439265

Rotation (n x k) = (4 x 4):

	PC1	PC2	PC3	PC4
Sepal.Length	0.5210659	-0.37741762	0.7195664	0.2612863
Sepal.Width	-0.2693474	-0.92329566	-0.2443818	-0.1235096
Petal.Length	0.5804131	-0.02449161	-0.1421264	-0.8014492
Petal.Width	0.5648565	-0.06694199	-0.6342727	0.5235971

Explained Variance by Principal Components:

[1] 72.9624454 22.8507618 3.6689219 0.5178709

Cumulative Variance:

[1] 72.96245 95.81321 99.48213 100.00000

Interpretation:

Scree Plot Insight:

In the scree plot, observed a sharp drop in variance explained from PC1 to PC2, and then the curve flattens after PC2. This suggests that **two principal components** would be adequate to interpret the dataset.

It can be choosen to retain **two components** for dimensionality reduction, as this will capture most of the variance without losing much information.

##The scree plot shows the **percentage of variance explained** by each principal component (PC):

1. **PC1** (first component):
    - Explains the largest variance (around 72.96% as per your data).
    - Represents the most significant pattern in the dataset.
2. **PC2** (second component):
    - Adds a significant amount of variance (around 22.85%, bringing the cumulative variance to 95.81%).

- Together, PC1 and PC2 capture the majority of the information (approximately 96%).

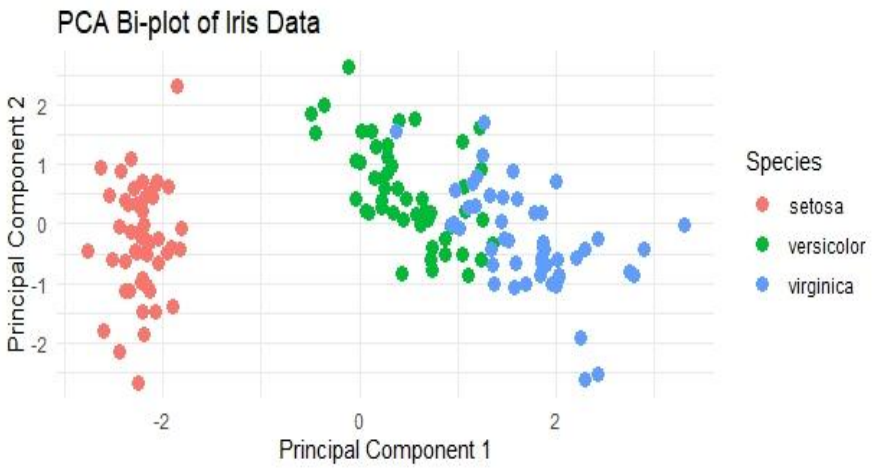
3. **PC3 and PC4**:
    - Contribute very little additional variance (3.67% and 0.52%, respectively).
    - These components are not significant for explaining the variability in the data.

Retain PC1 and PC2: These two components explain around **96% of the total variance**, which is sufficient to summarize the dataset effectively.
Discard PC3 and PC4: These components add minimal new information and can be ignored in most analyses.

e). Construction a bi-plot for the iris data based on R programming and interpretion of the the results is given below:

```
# Load the iris dataset
data(iris)

# Perform PCA on the numerical columns of the iris dataset (excluding the Species column)
pca_result <- prcomp(iris[, 1:4], center = TRUE, scale. = TRUE)

# Plot the bi-plot
biplot(pca_result, main = "Bi-plot of Iris Data")

# Optionally, you can customize the plot with different colors for each species
library(ggplot2)
pca_data <- data.frame(pca_result$x, Species = iris$Species)

# Plot with ggplot2 for better customization
ggplot(pca_data, aes(PC1, PC2, color = Species)) +
  geom_point(size = 3) +
  labs(title = "PCA Bi-plot of Iris Data", x = "Principal Component 1", y = "Principal Component 2") +
  theme_minimal()
```

Ans:



Interpretion:

- **Species Labels**: Each point is labeled with its species (setosa, versicolor, or virginica), making it easy to see how the species are distributed along the principal components.
- **Cluster Separation**: To observe clear separation of points between species (e.g., setosa may cluster in one part of the plot while versicolor and virginica cluster in other parts), this suggests that the principal components (PC1 and PC2) capture the variation that distinguishes these species.
- **Principal Components**: The arrows in the bi-plot represent the loadings of the original variables (sepal length, sepal width, petal length, and petal width) on the principal components.