

Second Assessment

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2024-05-31

```
#Q.no.6Ans:
# Load necessary libraries
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.3.3
```

```
# Set seed for reproducibility
set.seed(27)

# Generate random data
age <- sample(10:99, 200, replace = TRUE)
age
```

```
## [1] 78 63 82 92 25 42 34 42 66 10 62 12 84 87 65 26 85 87 24 33 37 28 42 97 52
## [26] 10 18 78 91 13 40 50 33 93 45 82 99 96 58 98 25 82 86 42 49 77 13 15 60 18
## [51] 40 64 38 55 76 30 36 91 69 13 46 92 40 48 45 46 63 69 57 66 30 51 92 99 94
## [76] 43 97 28 51 81 46 78 64 55 33 46 12 24 82 45 26 50 28 79 14 32 18 32 12 86
## [101] 31 53 90 72 84 35 82 28 40 14 50 36 11 93 80 81 72 88 74 43 50 44 86 29 87
## [126] 72 75 27 70 26 85 27 67 65 68 78 17 41 21 25 93 31 63 41 31 55 50 16 53 62
## [151] 73 55 44 65 64 72 36 79 39 35 13 13 40 48 44 13 11 79 34 89 68 57 20 63 19
## [176] 19 84 30 44 76 53 82 42 72 15 71 11 92 80 60 40 70 59 57 56 41 21 98 25 24
```

```
sex <- sample(c("male", "female"), 200, replace = TRUE)
sex
```

```
## [1] "female" "female" "male" "female" "male" "female" "male" "male"
## [9] "male" "female" "female" "female" "female" "female" "male" "female"
## [17] "female" "female" "female" "female" "male" "female" "female" "female"
## [25] "female" "female" "male" "male" "female" "female" "male" "female"
## [33] "female" "female" "male" "male" "female" "female" "female" "male"
## [41] "male" "female" "female" "male" "male" "male" "male" "female"
## [49] "female" "female" "female" "male" "male" "female" "female" "male"
## [57] "male" "female" "female" "male" "female" "male" "male" "male"
## [65] "male" "female" "male" "male" "male" "female" "female" "female"
## [73] "male" "male" "female" "female" "female" "female" "male" "female"
## [81] "female" "female" "female" "male" "male" "male" "male" "female"
## [89] "female" "male" "male" "male" "female" "male" "female" "male"
## [97] "male" "female" "male" "female" "female" "female" "female" "male"
## [105] "female" "female" "male" "female" "female" "male" "male" "male"
## [113] "male" "female" "female" "male" "male" "female" "male" "female"
```

```
## [121] "male" "male" "male" "female" "female" "male" "male" "female"
## [129] "female" "male" "male" "female" "male" "female" "male" "female"
## [137] "female" "male" "female" "male" "male" "female" "male" "female"
## [145] "female" "female" "female" "male" "male" "male" "female" "female"
## [153] "male" "male" "male" "male" "female" "female" "female" "male"
## [161] "female" "female" "female" "male" "male" "female" "male" "female"
## [169] "female" "female" "male" "male" "male" "female" "female" "female"
## [177] "male" "female" "female" "female" "male" "female" "male" "male"
## [185] "female" "male" "female" "female" "male" "female" "male" "female"
## [193] "female" "male" "female" "female" "female" "female" "female" "female"
```

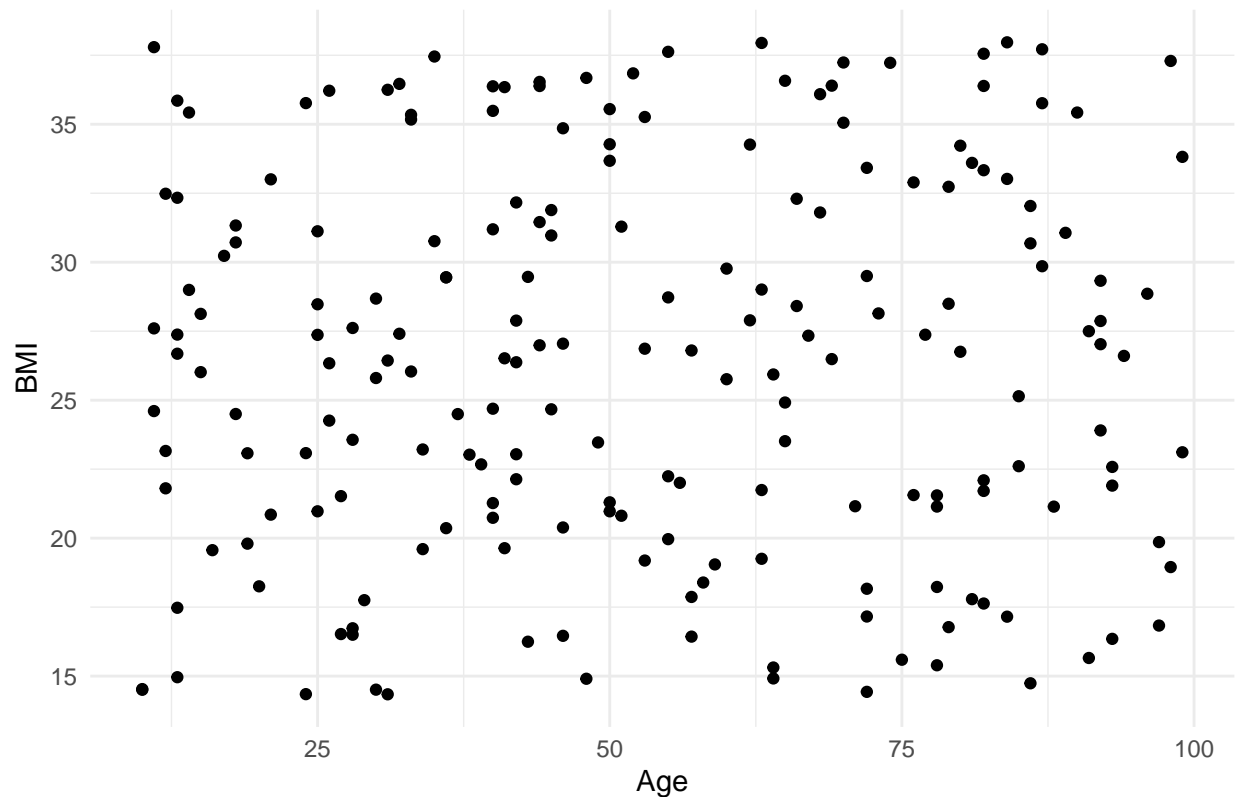
```
education <- sample(c("No education", "Primary", "Secondary", "Beyond secondary"), 200, replace = TRUE)
socio_economic <- sample(c("Low", "Middle", "High"), 200, replace = TRUE)
bmi <- runif(200, min = 14, max = 38)

#a Create dataset.
data <- data.frame(age, sex, education, socio_economic, bmi)

# b) Create scatter plot of age and BMI
scatter_plot <- ggplot(data, aes(x = age, y = bmi)) +
  geom_point() +
  labs(title = "Scatter Plot of Age and BMI",
       x = "Age",
       y = "BMI") +
  theme_minimal()

print(scatter_plot)
```

Scatter Plot of Age and BMI

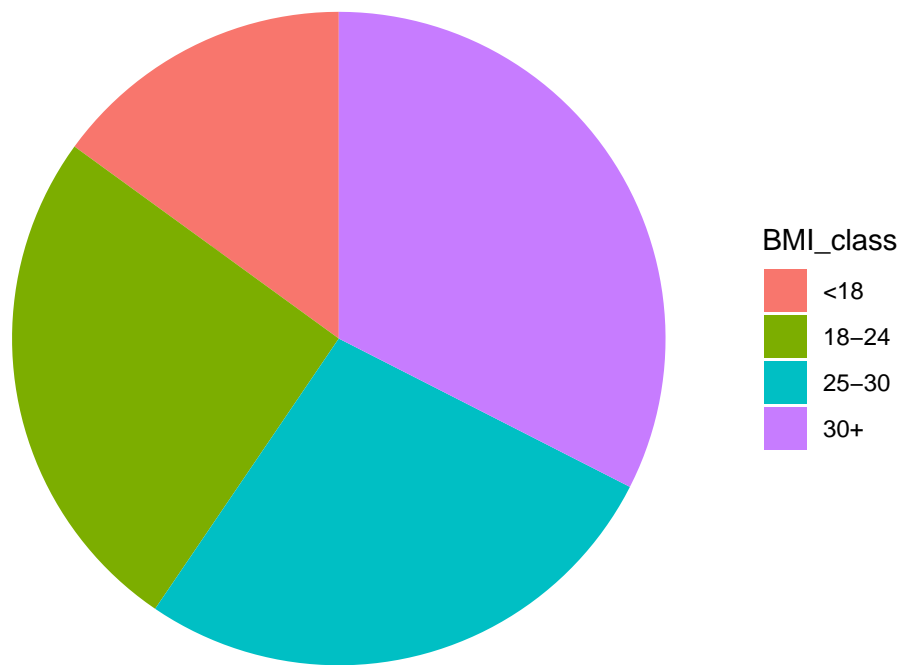


```
# c) Create class of BMI variable and pie chart
# Create BMI class
data$BMI_class <- cut(data$bmi, breaks = c(0, 18, 24, 30, Inf),
                      labels = c("<18", "18-24", "25-30", "30+"),
                      include.lowest = TRUE)

# Create pie chart
pie_chart <- ggplot(data, aes(x = "", fill = BMI_class)) +
  geom_bar(width = 1) +
  coord_polar("y", start = 0) +
  labs(title = "Pie Chart of BMI Classes") +
  theme_void() +
  theme(legend.position = "right")

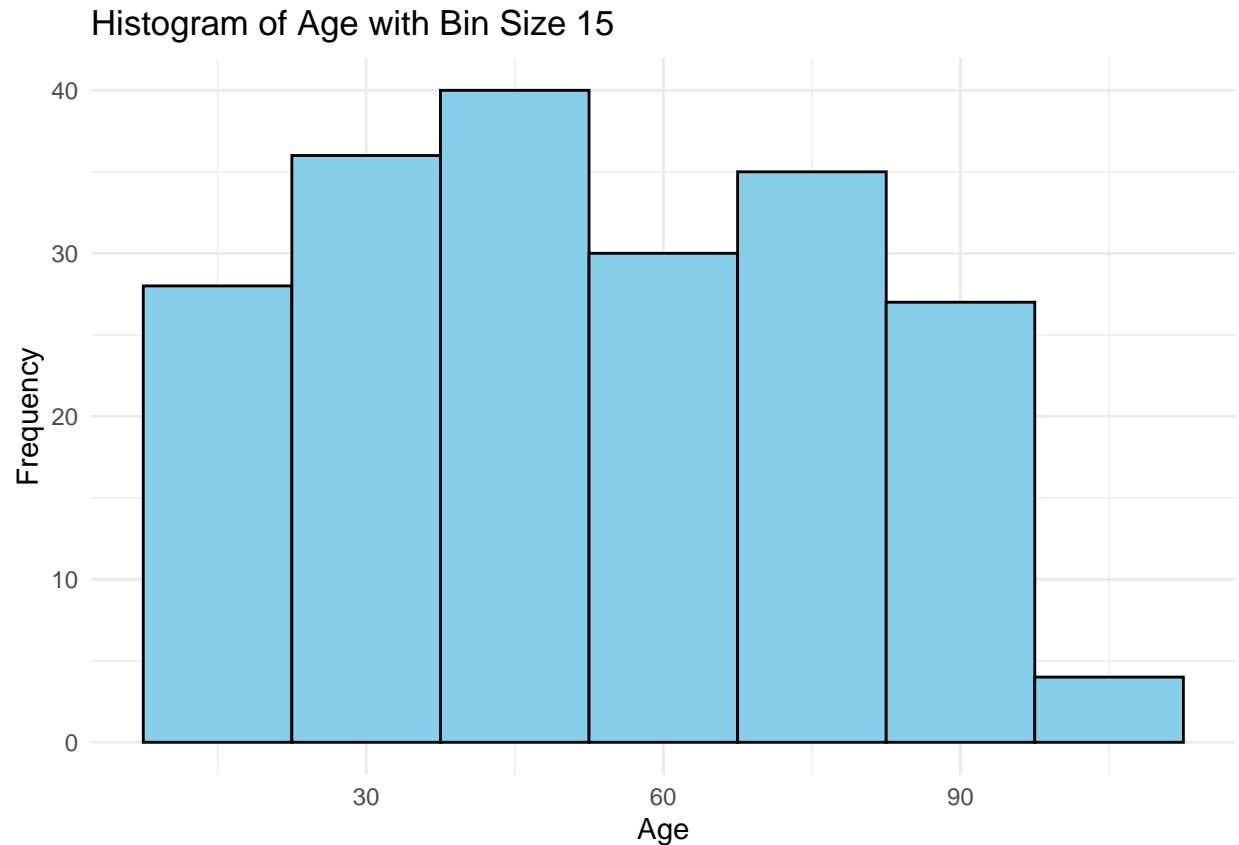
print(pie_chart)
```

Pie Chart of BMI Classes



```
# d) Create histogram of age variable
histogram <- ggplot(data, aes(x = age)) +
  geom_histogram(binwidth = 15, fill = "skyblue", color = "black") +
  labs(title = "Histogram of Age with Bin Size 15",
        x = "Age",
        y = "Frequency") +
  theme_minimal()

print(histogram)
```



#Interpretation:

#Scatter Plot (age vs BMI): This plot shows the relationship between age and BMI. By observing the scatter plot, we can see if there is a positive or negative correlation between the two variables.

#Pie Chart (BMI Classes): This chart represents the distribution of BMI classes within the dataset. It shows the proportion of individuals in each BMI category (Underweight, Normal weight, Overweight, Obese).

#Histogram (Age): The histogram illustrates the distribution of ages within the dataset with a bin size of 15. It shows the frequency of individuals in each age group.

#Q.no.7 Ans: using airquality dataset of R

#a)perform goodness-of-fit test on Temp variable to check if it follows normal distribution or not.

#b)perform goodness-of-fit test on temp variable by month variable to check if the variances of mpg are constant across months.

#c)Discuss which independent sample test must be used to compare "Temp" variable by "Month" variable categories.

#d)perform the best independent sample statistical test for this data and now interpret result carefully.

Load the airquality dataset

`data(airquality)`

a) Perform goodness-of-fit test on Temp variable to check if it follows normal distribution or not.

`shapiro.test(airquality$Temp)`

`##`

`## Shapiro-Wilk normality test`

`##`

`## data: airquality$Temp`

`## W = 0.97617, p-value = 0.009319`

```
# b) Perform goodness-of-fit test on Temp variable by Month variable to check if the variances of Temp
bartlett.test(Temp ~ Month, data = airquality)
```

```
##
## Bartlett test of homogeneity of variances
##
## data: Temp by Month
## Bartlett's K-squared = 12.023, df = 4, p-value = 0.01718
```

```
# c) Discuss which independent sample test must be used to compare "Temp" variable by "Month" variable
#the Bartlett test indicates whether the variances across different groups are equal or not, it helps d
#If the variances are equal, a parametric test like ANOVA can be used. If not, a non-parametric test li
```

```
# d) Perform the best independent sample statistical test for this data and now interpret the result ca
# Since Bartlett test indicates unequal variances, use the Kruskal-Wallis test.
kruskal.test(Temp ~ Month, data = airquality)
```

```
##
## Kruskal-Wallis rank sum test
##
## data: Temp by Month
## Kruskal-Wallis chi-squared = 73.328, df = 4, p-value = 4.496e-15
```

```
#Q.no.10 Ans:
# Load the iris dataset
data("iris")

# Take the first four variables (features) of the iris dataset
iris_features <- iris[, 1:4]
iris_features
```

```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1           5.1         3.5         1.4         0.2
## 2           4.9         3.0         1.4         0.2
## 3           4.7         3.2         1.3         0.2
## 4           4.6         3.1         1.5         0.2
## 5           5.0         3.6         1.4         0.2
## 6           5.4         3.9         1.7         0.4
## 7           4.6         3.4         1.4         0.3
## 8           5.0         3.4         1.5         0.2
## 9           4.4         2.9         1.4         0.2
## 10          4.9         3.1         1.5         0.1
## 11          5.4         3.7         1.5         0.2
## 12          4.8         3.4         1.6         0.2
## 13          4.8         3.0         1.4         0.1
## 14          4.3         3.0         1.1         0.1
## 15          5.8         4.0         1.2         0.2
## 16          5.7         4.4         1.5         0.4
## 17          5.4         3.9         1.3         0.4
## 18          5.1         3.5         1.4         0.3
## 19          5.7         3.8         1.7         0.3
## 20          5.1         3.8         1.5         0.3
```

## 21	5.4	3.4	1.7	0.2
## 22	5.1	3.7	1.5	0.4
## 23	4.6	3.6	1.0	0.2
## 24	5.1	3.3	1.7	0.5
## 25	4.8	3.4	1.9	0.2
## 26	5.0	3.0	1.6	0.2
## 27	5.0	3.4	1.6	0.4
## 28	5.2	3.5	1.5	0.2
## 29	5.2	3.4	1.4	0.2
## 30	4.7	3.2	1.6	0.2
## 31	4.8	3.1	1.6	0.2
## 32	5.4	3.4	1.5	0.4
## 33	5.2	4.1	1.5	0.1
## 34	5.5	4.2	1.4	0.2
## 35	4.9	3.1	1.5	0.2
## 36	5.0	3.2	1.2	0.2
## 37	5.5	3.5	1.3	0.2
## 38	4.9	3.6	1.4	0.1
## 39	4.4	3.0	1.3	0.2
## 40	5.1	3.4	1.5	0.2
## 41	5.0	3.5	1.3	0.3
## 42	4.5	2.3	1.3	0.3
## 43	4.4	3.2	1.3	0.2
## 44	5.0	3.5	1.6	0.6
## 45	5.1	3.8	1.9	0.4
## 46	4.8	3.0	1.4	0.3
## 47	5.1	3.8	1.6	0.2
## 48	4.6	3.2	1.4	0.2
## 49	5.3	3.7	1.5	0.2
## 50	5.0	3.3	1.4	0.2
## 51	7.0	3.2	4.7	1.4
## 52	6.4	3.2	4.5	1.5
## 53	6.9	3.1	4.9	1.5
## 54	5.5	2.3	4.0	1.3
## 55	6.5	2.8	4.6	1.5
## 56	5.7	2.8	4.5	1.3
## 57	6.3	3.3	4.7	1.6
## 58	4.9	2.4	3.3	1.0
## 59	6.6	2.9	4.6	1.3
## 60	5.2	2.7	3.9	1.4
## 61	5.0	2.0	3.5	1.0
## 62	5.9	3.0	4.2	1.5
## 63	6.0	2.2	4.0	1.0
## 64	6.1	2.9	4.7	1.4
## 65	5.6	2.9	3.6	1.3
## 66	6.7	3.1	4.4	1.4
## 67	5.6	3.0	4.5	1.5
## 68	5.8	2.7	4.1	1.0
## 69	6.2	2.2	4.5	1.5
## 70	5.6	2.5	3.9	1.1
## 71	5.9	3.2	4.8	1.8
## 72	6.1	2.8	4.0	1.3
## 73	6.3	2.5	4.9	1.5
## 74	6.1	2.8	4.7	1.2

## 75	6.4	2.9	4.3	1.3
## 76	6.6	3.0	4.4	1.4
## 77	6.8	2.8	4.8	1.4
## 78	6.7	3.0	5.0	1.7
## 79	6.0	2.9	4.5	1.5
## 80	5.7	2.6	3.5	1.0
## 81	5.5	2.4	3.8	1.1
## 82	5.5	2.4	3.7	1.0
## 83	5.8	2.7	3.9	1.2
## 84	6.0	2.7	5.1	1.6
## 85	5.4	3.0	4.5	1.5
## 86	6.0	3.4	4.5	1.6
## 87	6.7	3.1	4.7	1.5
## 88	6.3	2.3	4.4	1.3
## 89	5.6	3.0	4.1	1.3
## 90	5.5	2.5	4.0	1.3
## 91	5.5	2.6	4.4	1.2
## 92	6.1	3.0	4.6	1.4
## 93	5.8	2.6	4.0	1.2
## 94	5.0	2.3	3.3	1.0
## 95	5.6	2.7	4.2	1.3
## 96	5.7	3.0	4.2	1.2
## 97	5.7	2.9	4.2	1.3
## 98	6.2	2.9	4.3	1.3
## 99	5.1	2.5	3.0	1.1
## 100	5.7	2.8	4.1	1.3
## 101	6.3	3.3	6.0	2.5
## 102	5.8	2.7	5.1	1.9
## 103	7.1	3.0	5.9	2.1
## 104	6.3	2.9	5.6	1.8
## 105	6.5	3.0	5.8	2.2
## 106	7.6	3.0	6.6	2.1
## 107	4.9	2.5	4.5	1.7
## 108	7.3	2.9	6.3	1.8
## 109	6.7	2.5	5.8	1.8
## 110	7.2	3.6	6.1	2.5
## 111	6.5	3.2	5.1	2.0
## 112	6.4	2.7	5.3	1.9
## 113	6.8	3.0	5.5	2.1
## 114	5.7	2.5	5.0	2.0
## 115	5.8	2.8	5.1	2.4
## 116	6.4	3.2	5.3	2.3
## 117	6.5	3.0	5.5	1.8
## 118	7.7	3.8	6.7	2.2
## 119	7.7	2.6	6.9	2.3
## 120	6.0	2.2	5.0	1.5
## 121	6.9	3.2	5.7	2.3
## 122	5.6	2.8	4.9	2.0
## 123	7.7	2.8	6.7	2.0
## 124	6.3	2.7	4.9	1.8
## 125	6.7	3.3	5.7	2.1
## 126	7.2	3.2	6.0	1.8
## 127	6.2	2.8	4.8	1.8
## 128	6.1	3.0	4.9	1.8

## 129	6.4	2.8	5.6	2.1
## 130	7.2	3.0	5.8	1.6
## 131	7.4	2.8	6.1	1.9
## 132	7.9	3.8	6.4	2.0
## 133	6.4	2.8	5.6	2.2
## 134	6.3	2.8	5.1	1.5
## 135	6.1	2.6	5.6	1.4
## 136	7.7	3.0	6.1	2.3
## 137	6.3	3.4	5.6	2.4
## 138	6.4	3.1	5.5	1.8
## 139	6.0	3.0	4.8	1.8
## 140	6.9	3.1	5.4	2.1
## 141	6.7	3.1	5.6	2.4
## 142	6.9	3.1	5.1	2.3
## 143	5.8	2.7	5.1	1.9
## 144	6.8	3.2	5.9	2.3
## 145	6.7	3.3	5.7	2.5
## 146	6.7	3.0	5.2	2.3
## 147	6.3	2.5	5.0	1.9
## 148	6.5	3.0	5.2	2.0
## 149	6.2	3.4	5.4	2.3
## 150	5.9	3.0	5.1	1.8

a) Fit a k-means clustering model in the data with $k=2$ and $k=3$

```
set.seed(27) # for reproducibility
```

```
kmeans_model_k2 <- kmeans(iris_features, centers = 2)
```

```
kmeans_model_k2
```

```
## K-means clustering with 2 clusters of sizes 97, 53
```

##

```
## Cluster means:
```

```
## Sepal.Length Sepal.Width Petal.Length Petal.Width
```

##	1	6.301031	2.886598	4.958763	1.695876
----	---	----------	----------	----------	----------

```
## 2      5.005660      3.369811      1.560377      0.290566
```

##

```
## Clustering vector:
```

```
##      [1] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
```

```
## [38] 2 2 2 2 2 2 2 2 2 2 2 2 2 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
```

```
## [75] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 2 1 1 1 1 1 1 1 1
```

[illegible]

```
## [112] 1 1
## [149] 1 1
```

##

```
## Within cluster sum of squares by cluster:
```

```
## [1] 123.79588 28.55208
```

```
## (between SS / total SS = 77.6 %)
```

##

```
## Available components:
```

##

```
## [1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
```

```
## [6] "betweenss"      "size"           "iter"           "ifault"
```

```
kmeans_model_k3 <- kmeans(iris_features, centers = 3)
```

```
kmeans_model_k3
```

```

## K-means clustering with 3 clusters of sizes 38, 62, 50
##
## Cluster means:
##   Sepal.Length Sepal.Width Petal.Length Petal.Width
## 1      6.850000      3.073684      5.742105      2.071053
## 2      5.901613      2.748387      4.393548      1.433871
## 3      5.006000      3.428000      1.462000      0.246000
##
## Clustering vector:
##   [1] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
##  [38] 3 3 3 3 3 3 3 3 3 3 3 3 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
##  [75] 2 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 2 1 1 1 1 2 1 1 1
## [112] 1 1 2 2 1 1 1 1 2 1 2 1 2 1 1 2 2 1 1 1 1 2 1 1 1 1 2 1 1 1 2 1
## [149] 1 2
##
## Within cluster sum of squares by cluster:
## [1] 23.87947 39.82097 15.15100
## (between_SS / total_SS =  88.4 %)
##
## Available components:
##
## [1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
## [6] "betweenss"    "size"         "iter"         "ifault"

```

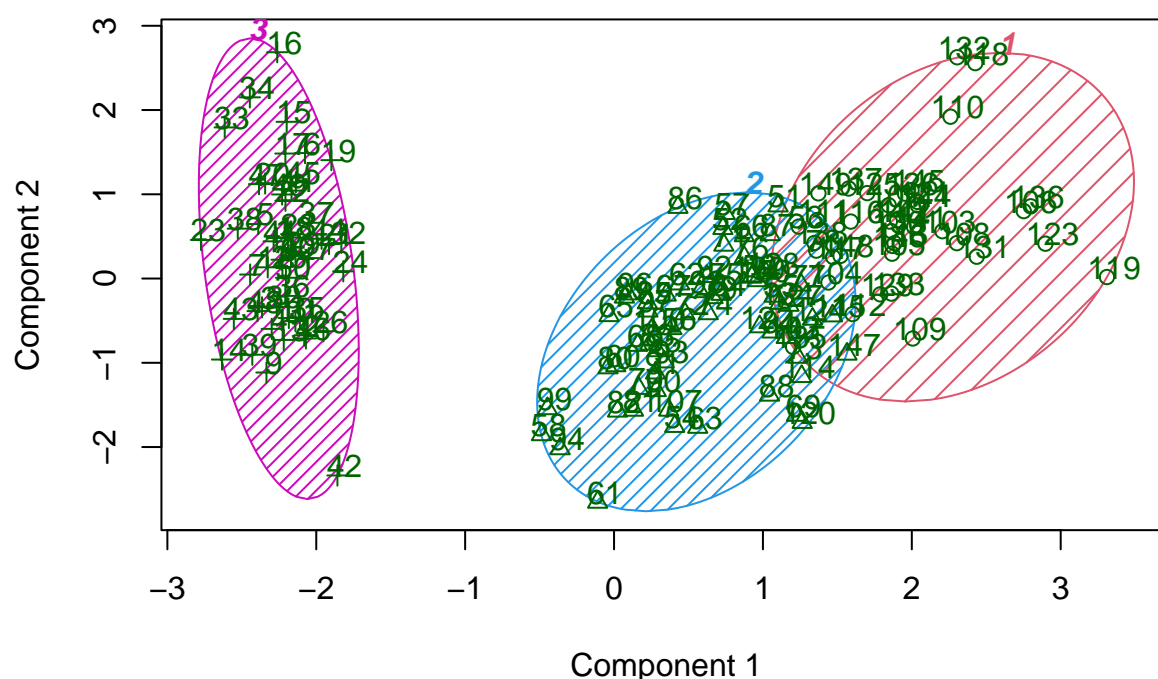
b) Plot the clusters formed with k=3 in a single graph and interpret them carefully

```

library(cluster)
clusplot(iris_features, kmeans_model_k3$cluster, color = TRUE, shade = TRUE, labels = 2, lines = 0)

```

CLUSPLOT(iris_features)



These two components explain 95.81 % of the point variability.

Interpretation:

The clusterplot visualizes the clusters formed by k-means with k=3.

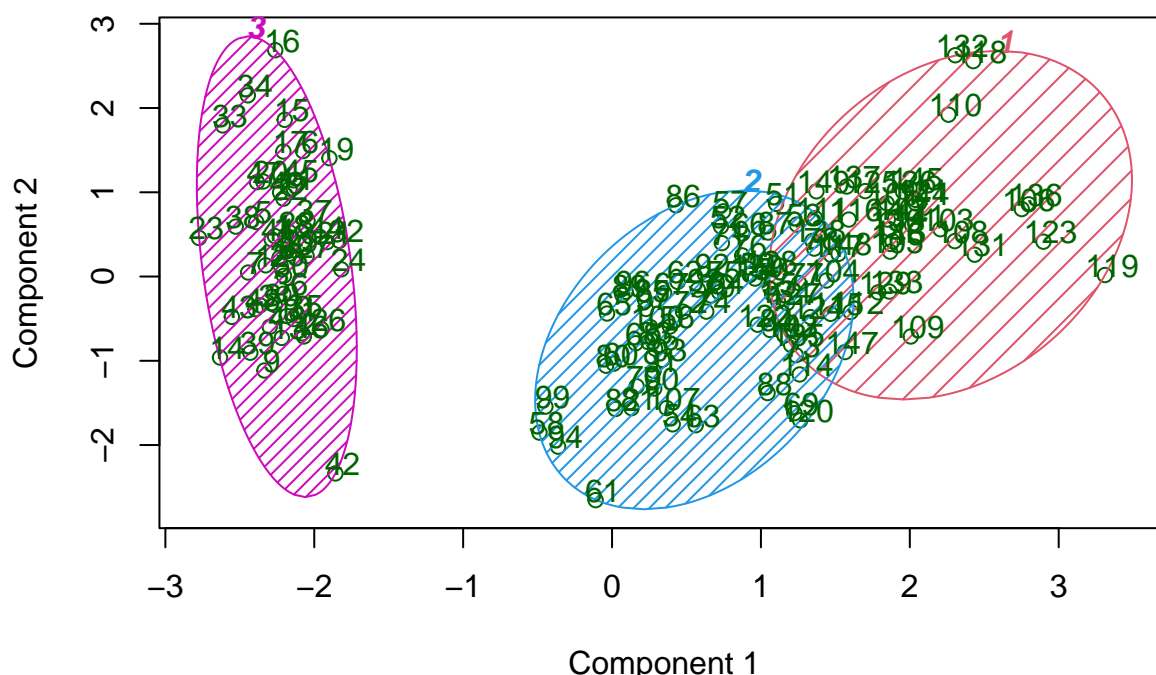
Each point represents an observation (flower) colored according to its assigned cluster.

The plot provides insights into the separation of clusters based on the first two principal component.

c) Add cluster centers for the plot of cluster formed with k=3 above and interpret it carefully

```
clusplot(iris_features, kmeans_model_k3$cluster, color = TRUE, shade = TRUE, labels = 2, lines = 0, plot.points(kmeans_model_k3$centers, col = 1:3, pch = 8, cex = 2))
```

CLUSPLOT(iris_features)



These two components explain 95.81 % of the point variability.

Interpretation:

In addition to the previous plot, this plot adds cluster centers represented by large triangles.

Each triangle represents the centroid of a cluster.

The plot allows for a clearer understanding of the location of the cluster centers relative to the data points.

d) Compare the k=3 cluster variable with species variable of iris data using confusion matrix and int
`table(iris$Species, kmeans_model_k3$cluster)`

```
##
##           1  2  3
## setosa      0  0 50
## versicolor  2 48  0
## virginica   36 14  0
```

Interpretation:

The confusion matrix compares the species variable of the original iris dataset with the clusters formed by the k-means algorithm.

Each row represents the true species, while each column represents the assigned cluster.

The numbers in the cells represent the counts of observations falling into each category.

By comparing the clusters with the true species, we can assess how well the clustering algorithm performed.

#Q.no.7 Ans: using airquality dataset of R

Load the airquality dataset

`data(airquality)`

```
# a) Perform goodness-of-fit test on Temp variable to check if it follows normal distribution or not.  
shapiro.test(airquality$Temp)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: airquality$Temp  
## W = 0.97617, p-value = 0.009319
```

```
# b) Perform goodness-of-fit test on Temp variable by Month variable to check if the variances of Temp  
bartlett.test(Temp ~ Month, data = airquality)
```

```
##  
## Bartlett test of homogeneity of variances  
##  
## data: Temp by Month  
## Bartlett's K-squared = 12.023, df = 4, p-value = 0.01718
```

```
# c) Discuss which independent sample test must be used to compare "Temp" variable by "Month" variable  
#the Bartlett test indicates whether the variances across different groups are equal or not, it helps d  
#If the variances are equal, a parametric test like ANOVA can be used. If not, a non-parametric test li
```

```
# d) Perform the best independent sample statistical test for this data and now interpret the result ca  
# Since Bartlett test indicates unequal variances, use the Kruskal-Wallis test.  
kruskal.test(Temp ~ Month, data = airquality)
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: Temp by Month  
## Kruskal-Wallis chi-squared = 73.328, df = 4, p-value = 4.496e-15
```

```
#Q.no.9 Ans:using iris dataset
```

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

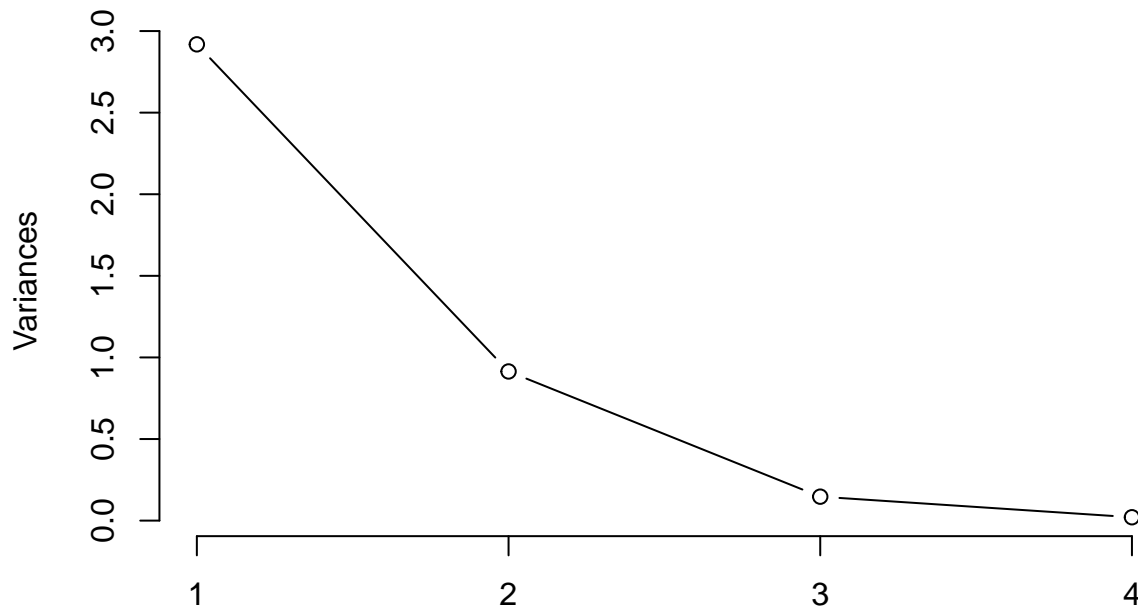
```
# a) Create a "flower scale" of the first four variables of iris dataset using PCA.  
iris_pca <- prcomp(iris[,1:4], scale. = TRUE)
```

```
# b) Compute the eigenvalues and interpret the PCA result carefully using Kaiser's criteria.  
eigenvalues <- iris_pca$sdev^2  
kaisers_criteria <- sum(eigenvalues >= 1)  
print(kaisers_criteria)
```

```
## [1] 1
```

```
# c) Show the scree plot and decide on the number of components to retain with careful interpretation.  
screeplot(iris_pca, type = "line", main = "Scree Plot of Iris PCA")
```

Scree Plot of Iris PCA



```
# d) Revise the flower scale with 3 components using VARIMAX rotation and interpret the result carefully.  
library(psych)
```

```
## Warning: package 'psych' was built under R version 4.3.3
```

```
##
```

```
## Attaching package: 'psych'
```

```
## The following objects are masked from 'package:ggplot2':
```

```
##
```

```
##    %+%, alpha
```

```
iris_pca_varimax <- principal(iris[,1:4], nfactors = 3, rotate = "varimax")  
print(iris_pca_varimax)
```

```
## Principal Components Analysis
```

```
## Call: principal(r = iris[, 1:4], nfactors = 3, rotate = "varimax")
```

```
## Standardized loadings (pattern matrix) based upon correlation matrix
```

```
##           RC1  RC3  RC2  h2      u2 com
```

```
## Sepal.Length  0.55  0.84  0.01 1.00 0.00141 1.7
```

```
## Sepal.Width  -0.18 -0.03  0.98 1.00 0.00032 1.1
```

```
## Petal.Length  0.79  0.53 -0.28 0.99 0.01331 2.0
```

```
## Petal.Width   0.90  0.39 -0.20 0.99 0.00568 1.5
```

```
##
```

```

##              RC1  RC3  RC2
## SS loadings      1.76 1.14 1.08
## Proportion Var    0.44 0.28 0.27
## Cumulative Var    0.44 0.72 0.99
## Proportion Explained 0.44 0.29 0.27
## Cumulative Proportion 0.44 0.73 1.00
##
## Mean item complexity = 1.6
## Test of the hypothesis that 3 components are sufficient.
##
## The root mean square of the residuals (RMSR) is 0
## with the empirical chi square 0.03 with prob < NA
##
## Fit based upon off diagonal values = 1

```

#Interpretation:

a)PCA was performed on the first four variables of the iris dataset.

#b) The eigenvalues represent the amount of variance explained by each principal component. Kaiser's cr

#c) The scree plot displays the eigenvalues for each principal component. By observing the scree plot, ,

#d) VARIMAX rotation is applied to the PCA to improve interpret ability by maximizing the variance of t

#Q.no.8 Ans: Using "Arrests" dataset of car package.

#a)Divide the Arrests data into the train and test the datasets with 80:20 random splits with 27.