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Calculator Application:

- a) Using with and without R objects on console.
- b) Using mathematical functions on console.
- c) Write an R script, to create R objects for calculator application and save in a specified location in disk.
- d) R Packages: tidyr, ggplot2, ggraph, glue, shiny.

a) Program:

```
# Without R objects 10
+ 5
20 - 7
8 * 3
15 / 3
```

Output:

```
[1] 15
[1] 13
[1] 24
[1] 5
```

```
# Using R objects
x <- 25
y <- 5
```

```
sum <- x + y
diff <- x - y
prod <- x * y
div <- x / y
```

```
print(sum)
print(diff)
print(prod)
print(div)
```

Output:

```
[1] 30
[1] 20
[1] 125
[1] 5
```

b) Program:

```
sqrt(16)    # Square root
exp(2)      # Exponential
log(10)     # Natural log
log10(1000) # Log base 10
sin(pi/2)   # Trigonometric function
abs(-45)    # Absolute value
```

Output:

```
[1] 4
[1] 7.389056
```

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```
[1] 2.302585
```

```
[1] 3
```

```
[1] 1
```

```
[1] 45
```

c) Program:

```
# Calculator script calculator
```

```
<- function(a, b) { result <-
```

```
list(
```

```
  Addition = a + b,
```

```
  Subtraction = a - b,
```

```
  Multiplication = a * b,
```

```
  Division = a / b
```

```
)
```

```
  return(result)
```

```
}
```

```
res <- calculator(20, 4)
```

```
print(res)
```

```
saveRDS(res, file = "calculator_output.rds")
```

```
read_res <- readRDS("calculator_output.rds")
```

```
print(read_res)
```

Output:

```
$Addition
```

```
[1] 24
```

```
$Subtraction
```

```
[1] 16
```

```
$Multiplication
```

```
[1] 80
```

```
$Division
```

```
[1] 5
```

```
$Addition
```

```
[1] 24
```

```
$Subtraction
```

```
[1] 16
```

```
$Multiplication
```

```
[1] 80
```

```
$Division
```

```
[1] 5
```

d) Program:

```
# Load essential packages
```

```
library(tidyr) # Data cleaning & reshaping
```

```
library(ggplot2) # Data visualization
```

```
library(ggraph) # Graph visualization
```

```
library(glue) # String interpolation
```

```
library(shiny) # Web applications in R
```

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Descriptive Statistics

- a) Write an R script to find basic descriptive statistics using summary().
 b) Write an R script to find subset of dataset by using subset().

a) Program:

```
data(iris)
summary(iris)
summary(iris$Sepal.Length)
```

Output:

```
Sepal.Length  Sepal.Width  Petal.Length  Petal.Width  Species
Min. :4.300  Min. :2.000  Min. :1.000  Min. :0.100  setosa      50
1st Qu.:5.100 1st Qu.:2.800 1st Qu.:1.600 1st Qu.:0.300 versicolor:50 Median
:5.800 Median :3.000 Median :4.350 Median :1.300 virginica :50
Mean :5.843 Mean :3.057 Mean :3.758 Mean :1.199 3rd
Qu.:6.400 3rd Qu.:3.300 3rd Qu.:5.100 3rd Qu.:1.800 Max.
:7.900 Max. :4.400 Max. :6.900 Max. :2.500
```

b) Program:

```
subset_data <- subset(iris, Sepal.Length > 5)
head(subset_data)
```

Output:

```
Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1      5.1      3.5      1.4      0.2  setosa
2      4.9      3.0      1.4      0.2  setosa
3      4.7      3.2      1.3      0.2  setosa
5      5.0      3.6      1.4      0.2  setosa
6      5.4      3.9      1.7      0.4  setosa
7      4.6      3.4      1.4      0.3  setosa
```

```
# Subset selecting only specific columns
subset_cols <- subset(iris, select = c(Sepal.Length, Species))
head(subset_cols)
```

Output:

```
Sepal.Length Specie
```

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```
s
1    5.1  setos
      a
2    4.9  setos
      a
3    4.7  setos
      a
4    4.6  setos
      a
5    5.0  setos
      a
6    5.4  setos
      a
```

```
# Subset with condition and selected columns
```

```
subset_cond <- subset(iris, Species == "setosa", select = c(Sepal.Length, Sepal.Width)) head(subset_cond)
```

Output:

```
Sepal.Length Sepal.Width
```

```
1    5.1    3.5
2    4.9    3.0
3    4.7    3.2
4    4.6    3.1
5    5.0    3.6
6    5.4    3.9
```

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Reading and Writing Different Types of Datasets

- a) Reading different types of datasets (.txt, .csv) from web and disk and writing in file in specific disk location.
- b) Reading Excel dataset in R.
- c) Reading XML dataset in R.

a) Program:

```
# Writing a sample .txt file
write.table(iris[1:5, ], file = "sample.txt", sep = "\t", row.names = FALSE)
```

```
# Reading .txt file
txt_data <- read.table("sample.txt", header = TRUE, sep = "\t")
print(txt_data)
```

Output:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa

```
# Writing a sample .csv file
write.csv(iris[1:5, ], file = "sample.csv", row.names = FALSE)
```

```
# Reading .csv file
csv_data <- read.csv("sample.csv")
print(csv_data)
```

Output:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa

b) Program:

```
# Install package if not already installed #
install.packages("readxl")
```

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```
library(readxl)
```

```
# Assume an Excel file named "sample.xlsx" with iris data #
```

```
For demo, we first create one:
```

```
# (Requires openxlsx package to write) #
```

```
install.packages("openxlsx")
```

```
library(openxlsx)
```

```
write.xlsx(iris[1:5, ], "sample.xlsx")
```

```
# Read the Excel file
```

```
excel_data <- read_excel("sample.xlsx")
```

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```
print(excel_data)
```

Output:

```
# First 5 rows of iris data #
```

```
A tibble: 5 × 5
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
	<dbl>	<dbl>	<dbl>	<dbl>	<chr>
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa

c) Program:

```
# Install if not installed
```

```
# install.packages("xml2")
```

```
library(xml2)
```

```
# Create sample XML content
```

```
xml_content <- '<root>
```

```
<flower>
```

```
<Sepal.Length>5.1</Sepal.Length>
```

```
<Sepal.Width>3.5</Sepal.Width>
```

```
<Species>setosa</Species>
```

```
</flower>
```

```
<flower>
```

```
<Sepal.Length>4.9</Sepal.Length>
```

```
<Sepal.Width>3.0</Sepal.Width>
```

```
<Species>setosa</Species>
```

```
</flower>
```

```
</root>'
```

```
# Write XML file
```

```
writeLines(xml_content, "sample.xml")
```

```
# Read XML file
```

```
xml_file <- read_xml("sample.xml")
```

```
print(xml_file)
```

```
# Extract data
```

```
flowers <- xml_find_all(xml_file, "//flower")
```

```
for (f in flowers) {
```

```
  cat("Sepal.Length:", xml_text(xml_find_first(f, "Sepal.Length")),
```

```
    " Sepal.Width:", xml_text(xml_find_first(f, "Sepal.Width")),
```

```
    " Species:", xml_text(xml_find_first(f, "Species")), "\n")
```

```
}
```

Output:

```
{xml_document}
```

```
<root>
```

```
1. <flower>\n <Sepal.Length>5.1</Sepal.Length>\n <Sepal.Width>3.5</Sepal.Width>\n
<Species>setosa</Species>\n</flower>
```

```
2. <flower>\n <Sepal.Length>4.9</Sepal.Length>\n <Sepal.Width>3.0</Sepal.Width>\n
<Species>setosa</Species>\n</flower> Sepal.Length:
```

```
5.1 Sepal.Width: 3.5 Species: setosa
```

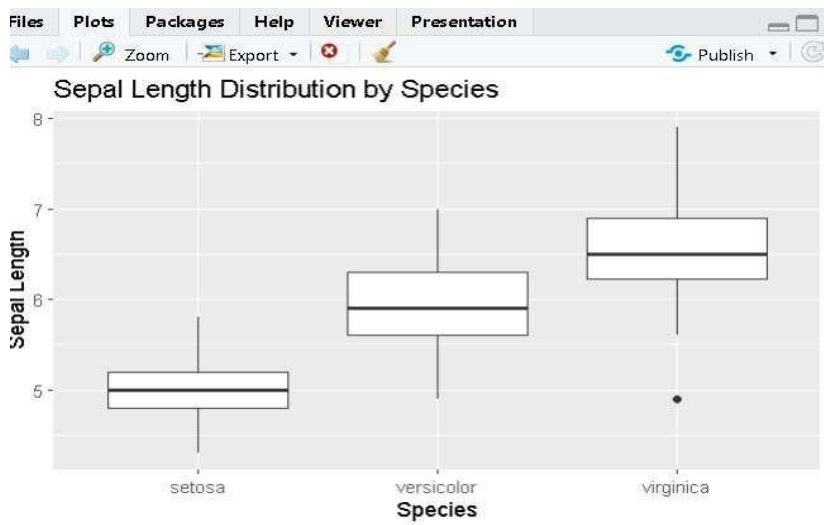
```
Sepal.Length: 4.9 Sepal.Width: 3.0 Species: setosa
```

TITLE:**DATE:****PAGE NO:****Visualizations**

- Find the data distributions using box plot and scatter plot.
- Find the outliers using plot().
- Plot the histogram, bar chart, and pie chart on sample data.

a) Program:

```
#box plot
library(ggplot2)
ggplot(data = iris, aes(x = Species, y = Sepal.Length)) +
  geom_boxplot() +
  labs(title = "Sepal Length Distribution by Species", x
        = "Species",
        y = "Sepal Length")
```

Output:

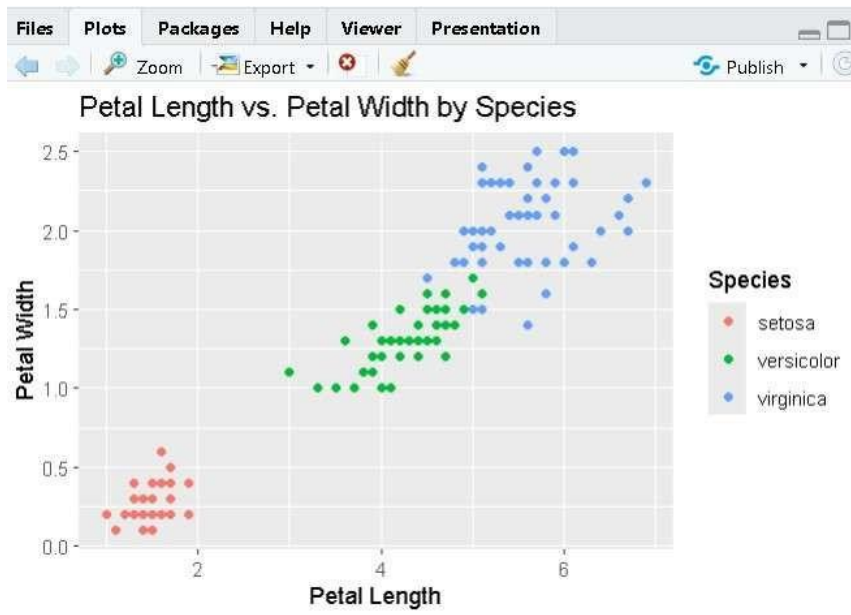
```
# scatter plot
library(ggplot2)
ggplot(data = iris, aes(x = Petal.Length, y = Petal.Width)) +
  geom_point(aes(color = Species)) +
  labs(title = "Petal Length vs. Petal Width by Species", x
        = "Petal Length",
        y = "Petal Width")
```

Output:

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**b) Program:**

Find the outliers using plot

```
data <- c(10, 12, 13, 15, 16, 18, 19, 33, 3, 36, 63, 99, 32, 15, 6, 20, 22, 100, 105)
```

```
# Create a boxplot
```

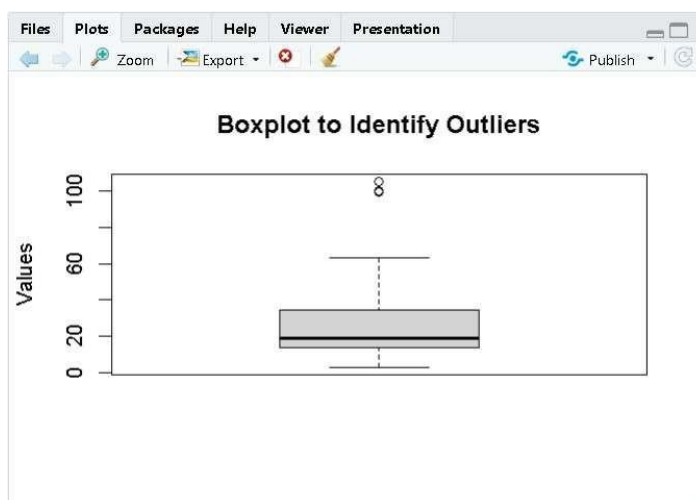
```
boxplot(data, main = "Boxplot to Identify Outliers", ylab = "Values") #
```

Optional: print outliers detected by boxplot.stats

```
outliers <- boxplot.stats(data)$out print(paste("Outliers:",
```

```
paste(outliers, collapse = ", ")))
```

Output:



```
[1] "Outliers: 99, 100, 105"
```

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c) Program:

Plot the histogram, bar chart and pie chart on sample data #pie
chart

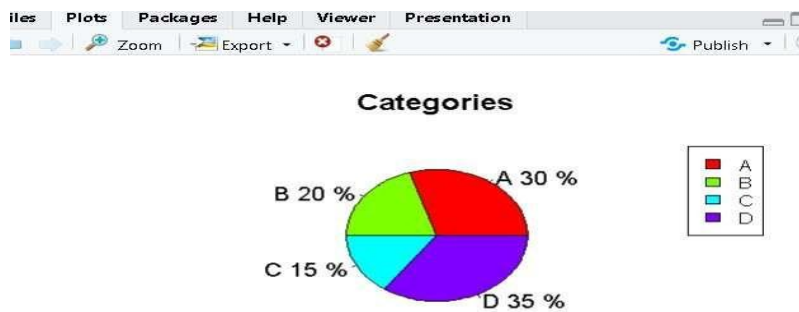
```
slices <- c(30, 20, 15, 35) labels
```

```
<- c("A", "B", "C", "D")
```

```
piepercent<- round(100 * slices / sum(slices), 1)
```

```
pie(slices, labels=paste(labels, piepercent, "%"), main="Categories", col=rainbow(length(slices)))
```

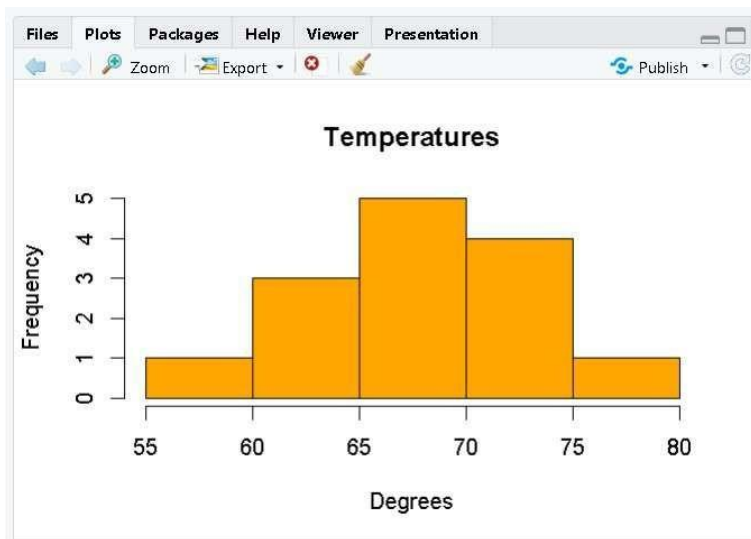
```
legend("topright", labels, fill=rainbow(length(slices)), cex=0.8)
```

Output:

```
#histogram
```

```
temperatures <- c(67, 72, 74, 62, 76, 66, 65, 59, 61, 69, 70, 71, 75, 68)
```

```
hist(temperatures, main="Temperatures", xlab="Degrees", breaks=5, col="orange")
```

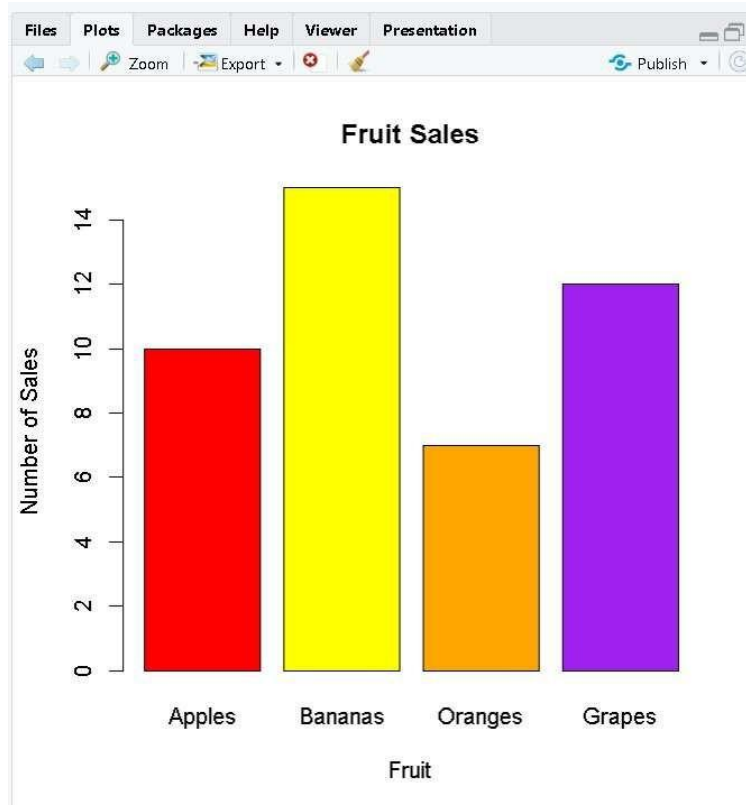
Output:

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```
#barchart  
categories <- c("Apples", "Bananas", "Oranges", "Grapes")  
values <- c(10, 15, 7, 12)  
barplot(values, names.arg = categories, main = "Fruit Sales",  
        xlab = "Fruit", ylab = "Number of Sales",  
        col = c("red", "yellow", "orange", "purple"))
```

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Correlation and Covariance

- Develop a program to find the correlation matrix on *iris* data.
- Plot the correlation plot on dataset and visualize, giving an overview of relationships among data on *iris* data.
- Analysis of covariance: variance (ANOVA) if data has categorical variables on *iris* data.

a) Program:

```
# Take only numeric columns from iris
num_data <- iris[, 1:4]

# Correlation matrix cor_matrix
<- cor(num_data)
print(cor_matrix)
```

Output:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
Sepal.Length	1.0000000	-0.1175698	0.871753	0.817941
h			8	1
Sepal.Width	-0.1175698	1.0000000	-0.4284401	-0.366125
h				9
Petal.Length	0.8717538	-0.4284401	1.0000000	0.962865
h				4
Petal.Width	0.8179411	-0.3661259	0.9628654	1.000000
				0

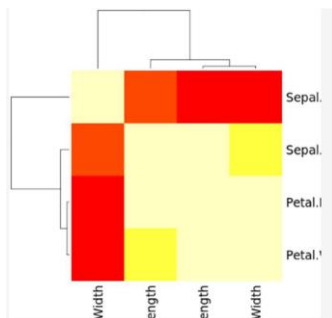
b) Program:

```
# install.packages("corrplot") # run once if not installed
library(corrplot)

corrplot(cor_matrix, method = "circle", type = "upper",
         tl.col = "black", tl.cex = 0.8)
```

Output:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
Sepal.Length	1.0000000	-0.1175698	0.8717538	0.8179411
Sepal.Width	-0.1175698	1.0000000	-0.4284401	-0.3661259
Petal.Length	0.8717538	-0.4284401	1.0000000	0.9628654
Petal.Width	0.8179411	-0.3661259	0.9628654	1.0000000



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c) Program:

```
# Compare Sepal.Length across species using ANOVA
anova_model <- aov(Sepal.Length ~ Species, data = iris)
summary(anova_model)
```

Output:

```
      Df Sum Sq Mean Sq F value Pr(>F)
Species    2  63.21  31.606  119.3 <2e-16 ***
Residuals 147   38.96   0.265
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05
```

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6) Write an R-script that detects file type (.csv, .txt, .xlsx, .xml) and reads it accordingly.

Program:

```
read_file <- function(filename) { #
  Extract file extension
  ext <- tools::file_ext(filename)

  if(ext == "csv") {
    data <- read.csv(filename)
  } else if (ext == "txt") {
    data <- read.table(filename, header = TRUE)
  } else if (ext == "xlsx")
    { library(readxl)
      data <- read_excel(filename)
    } else if (ext == "xml")
    { library(xml2)
      data <- read_xml(filename)
    } else {
      stop("Unsupported file type!")
    }
  }
  return(data)
}

# Example usage
write.csv(iris[1:5, ], "iris_sample.csv", row.names = FALSE)
result <- read_file("iris_sample.csv")
print(result)
```

Output:

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa