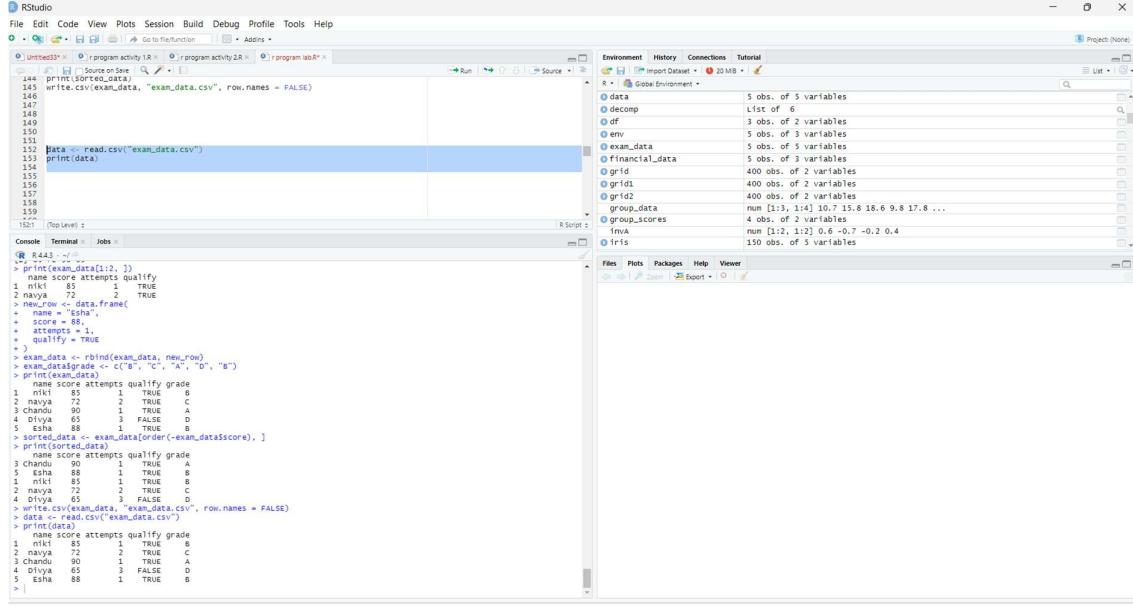


## 11. Write an R program to read a .csv file and display contents.

### CODE:

```
data <- read.csv("exam_data.csv")
print(data)
```

### OUTPUT:



The screenshot shows the RStudio interface with the following details:

- Code Editor:** Displays the R code for reading and printing the "exam\_data.csv" file.
- Environment View:** Shows the global environment with various objects and their types and sizes.
- Console:** Displays the output of the R code, showing the data frame structure with columns: name, score, attempts, qualify, and grade.

name	score	attempts	qualify	grade
nik1	85	1	TRUE	B
navya	72	2	TRUE	C
charan	90	1	TRUE	A
Divya	65	3	FALSE	D
Esha	88	1	TRUE	B

## 12. Perform data reshaping on airquality dataset: melt, cast, compute monthly averages for Ozone, Solar.R, Wind, and Temperature.

### CODE:

```
data(airquality)
monthly_avg <- aggregate(
  bbind(Ozone, Solar.R, Wind, Temp) ~ Month,
  data = airquality,
  FUN = mean,
  na.rm = TRUE
)
print(monthly_avg)
```

### OUTPUT:

The screenshot shows two R scripts open in RStudio:

- R program activity 1.R**:

```
1 #!/usr/bin/R  
2 library(tidyverse)  
3  
4 #> #> #> #> #> #>  
5  
6 #> data(airquality)  
7 monthly_avg <- aggregate(  
8   data ~ Month, data = airquality,  
9   FUN = mean,  
10   na.rm = TRUE  
11 )  
12  
13 print(monthly_avg)
```
- R program activity 2.R**:

```
1 #!/usr/bin/R  
2 library(tidyverse)  
3  
4 #> #> #> #> #> #>  
5  
6 #> sorted_data <- exan_data[order(-exan_datascore), ]  
7  
8 print(sorted_data)  
9  
10 #> write.csv(exan_data, "exan_data.csv", row.names = FALSE)  
11  
12 #> data <- read.csv("exan_data.csv")  
13  
14 print(data)  
15  
16 #> data(airquality)  
17 monthly_avg <- aggregate(  
18   cbind(Ozone, Solar.R, Wind, Temp) ~ Month,  
19   data = airquality,  
20   FUN = mean,  
21   na.rm = TRUE  
22 )  
23  
24 print(monthly_avg)
```

The right pane shows the RStudio environment with variables defined in both scripts:

- jan\_1st**: List of 3
- na1**: int [1:2, 1:2] 1 2 3 4 5 6
- na2**: int [1:2, 1:2] 7 8 9 10 11 12
- market**: 4 obs. of 2 variables
- market\_share\_data**: 4 obs. of 2 variables
- nat**: int [1:3, 1:3] 1 2 3 4 5 6 7 8 9
- nat1**: int [1:5, 1:4] 1 5 9 13 17 2 6 10 14 18 ...
- nat2**: int [1:3, 1:3] 1 2 3 4 5 6 7 8 9
- nat3**: int [1:2, 1:2] 1 3 2 4
- model**: List of 30
- model\_humidity**: List of 12
- model\_wind**: List of 12
- monthly\_avg**: 5 obs. of 5 variables

### **13. Combine multiple arrays row-wise.**

## **CODE:**

```
a1 <- matrix(1:6, nrow=2)
```

```
a2 <- matrix(7:12, nrow=2)
```

```
combined <- rbind
```

```
print(comb)
```

## OUTPUT:

The screenshot shows the RStudio interface with several windows open:

- Code Editor:** Displays R code for calculating monthly averages and creating a CSV file.
- Console:** Shows the execution of the R code, including the creation of data frames and writing them to a CSV file.
- Environment:** Shows the global environment with various objects like `combined`, `consumer_data`, `data`, etc.
- Plots:** Shows a histogram of ozone levels.
- Packages:** Shows available packages: `grid`, `gridExtra`, `gridSVG`, `gridBase`, `gridText`, `gridUnit`.
- Help:** Shows help documentation for `grid`.
- Viewer:** Shows the generated `exan_data.csv` file.

14. Explore and manipulate ChickWeight dataset (sorting, melting, casting by Diet).

## **CODE:**

```
data(ChickWeight)  
head(ChickWeight)  
sorted <- ChickWeight[order(ChickWeight$Diet),]  
library(reshape2)  
melted <- melt(ChickWeight, id=c("Chick", "Diet"))  
dcast(melted, Diet ~ variable, mean)
```

## **OUTPUT:**

**15. Perform EDA on iris dataset: dimensions, summary, standard deviation, quantiles, grouping by**

**Species, pivot table, categorical grouping with Sepal.Length categories.**

## **CODE:**

```
data(iris)  
dim(iris)  
summary(iris)  
sd(iris$Sepal.Length)  
quantile(iris$Sepal.Length)  
aggregate(. ~ Species, iris, mean)  
table(cut(iris$Sepal.Length, breaks=3), iris$Species)
```

## **OUTPUT:**

```

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146 data(iris)
147 summary(iris)
148 sd(iris$Sepal.Length)
149 sd(iris$Petal.Length)
150 aggregate(~ Species, iris, mean)
151 table(cut(iris$Sepal.Length, breaks=3), iris$Species)
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```

RStudio

```

206
207 Data(USArrests)
208 summary(USArrests)
210 rownames(USArrests)[which.max(USArrests$Rape)]
211 USArrests$Murder <- min(USArrests$Murder)
212 cor(USArrests)
213 USArrests$Assault <- median(USArrests$Assault)
214 USArrests$Murder <- quantile(USArrests$Murder,0.25,]
215 hist(USArrests$Murder, USArrests$Assault)
216 plot(USArrests$Murder, USArrests$Assault)
217 barplot(USArrests$Rape, names.arg=rownames(USArrests), las=2)
218
219
220
221
222
223 
```

Console Terminal Jobs

```

# R 4.4.3 ->
Florida 15.4 335 80 31.9
Georgia 17.4 211 60 25.8
Illinois 10.4 249 83 21.0
Louisiana 15.4 249 66 22.2
Maryland 11.3 300 67 27.8
Michigan 12.1 253 74 21.1
Mississippi 16.1 259 44 17.1
Missouri 9.0 178 70 28.2
Nevada 11.4 285 82 20.0
New Mexico 11.4 285 70 32.1
New York 11.1 254 86 26.1
North Carolina 13.0 337 41 13.1
Rhode Island 3.4 174 87 8.3
South Carolina 14.2 248 65 21.8
Tennessee 13.2 188 59 26.9
Texas 12.7 201 80 25.5
wyoming 6.8 163 60 15.6
> USArrests$Murder <- quantile(USArrests$Murder,0.25,]
Murder Assault UrbanPop Rape
Connecticut 3.8 110 77 11.1
Idaho 2.6 120 54 14.2
Iowa 2.1 88 57 11.3
Maine 2.1 83 51 8.8
Minnesota 2.7 72 66 14.9
New Hampshire 2.7 57 58 11.5
North Dakota 0.8 45 44 7.3
Rhode Island 3.4 174 87 8.3
South Dakota 1.2 66 45 8.8
utah 3.2 120 80 22.9
vermont 2.0 48 32 11.2
washington 4.0 145 73 26.2
wisconsin 2.6 53 66 10.8
> hist(USArrests$Murder)
> plot(density(USArrests$Assault))
> plot(USArrests$Murder, USArrests$Assault)
> barplot(USArrests$Rape, names.arg=rownames(USArrests), las=2)
> hist(USArrests$Murder) 
```

R Graphics: Device 2 (ACTIVE)

RStudio

```

206
207
208 Data(USArrests)
209 summary(USArrests)
210 rownames(USArrests)[which.max(USArrests$Rape)]
211 max(USArrests$Murder); min(USArrests$Murder)
212 cor(USArrests)
213 USArrests$Assault > median(USArrests$Assault)
214 USArrests$Murder <- quantile(USArrests$Murder,0.25,]
215 hist(USArrests$Murder, USArrests$Assault)
216 plot(USArrests$Murder, USArrests$Assault)
217 barplot(USArrests$Rape, names.arg=rownames(USArrests), las=2)
218
219
220
221
222
223 
```

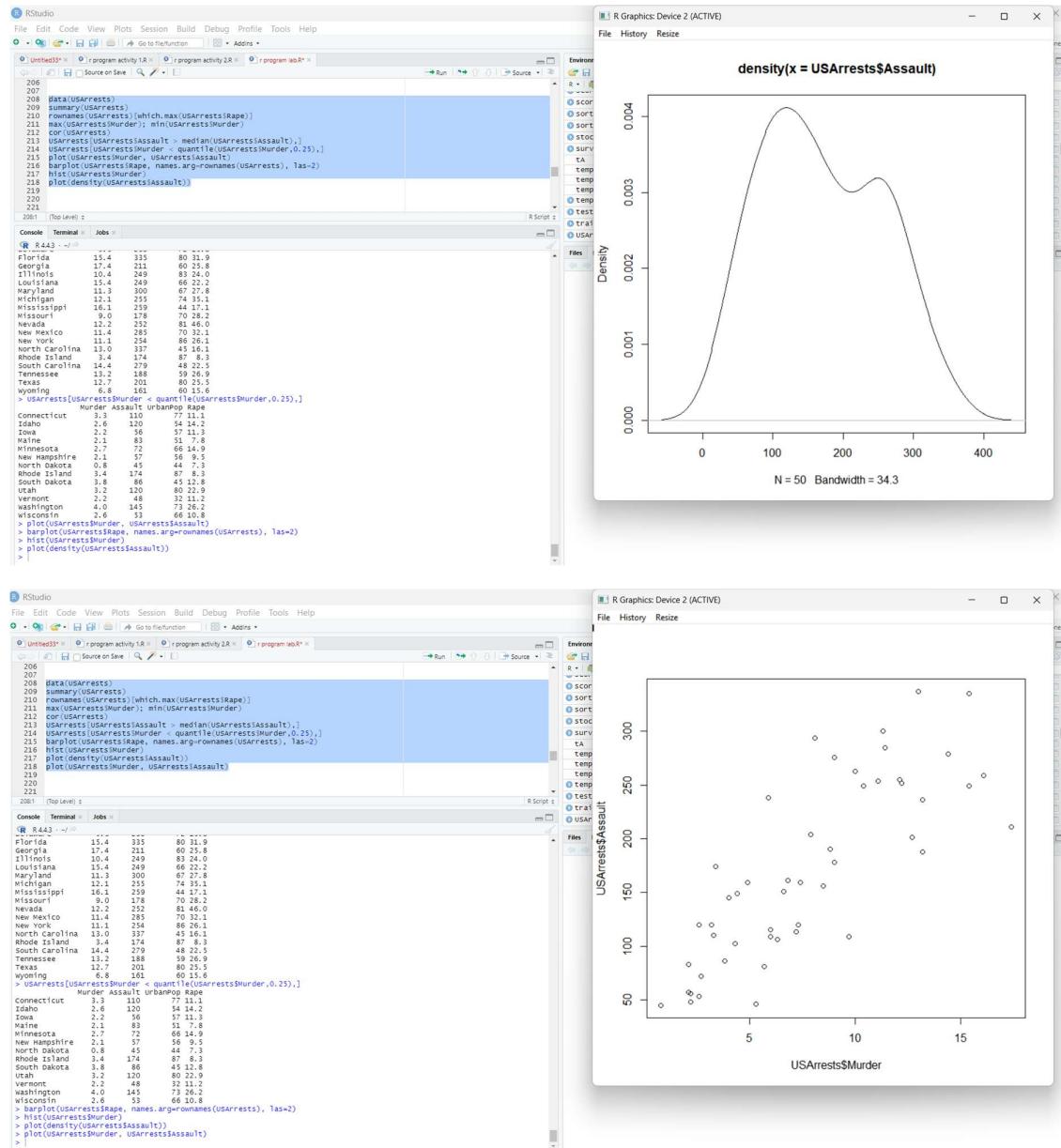
Console Terminal Jobs

```

# R 4.4.3 ->
Florida 15.4 335 80 31.9
Georgia 17.4 211 60 25.8
Illinois 10.4 249 83 21.0
Louisiana 15.4 249 66 22.2
Maryland 11.3 300 67 27.8
Michigan 12.1 253 74 21.1
Mississippi 16.1 259 44 17.1
Missouri 9.0 178 70 28.2
Nevada 11.4 285 82 20.0
New Mexico 11.4 285 70 32.1
New York 11.1 254 86 26.1
North Carolina 13.0 337 41 13.1
Rhode Island 3.4 174 87 8.3
South Carolina 14.2 248 65 21.8
Tennessee 13.2 188 59 26.9
Texas 12.7 201 80 25.5
wyoming 6.8 163 60 15.6
> USArrests$Murder <- quantile(USArrests$Murder,0.25,]
Murder Assault UrbanPop Rape
Connecticut 3.8 110 77 11.1
Idaho 2.6 120 54 14.2
Iowa 2.1 88 57 11.3
Maine 2.1 83 51 8.8
Minnesota 2.7 72 66 14.9
New Hampshire 2.7 57 58 11.5
North Dakota 0.8 45 44 7.3
Rhode Island 3.4 174 87 8.3
South Dakota 1.2 66 45 8.8
utah 3.2 120 80 22.9
vermont 2.0 48 32 11.2
washington 4.0 145 73 26.2
wisconsin 2.6 53 66 10.8
> hist(USArrests$Murder)
> plot(density(USArrests$Assault))
> plot(USArrests$Murder, USArrests$Assault)
> barplot(USArrests$Rape, names.arg=rownames(USArrests), las=2)
> hist(USArrests$Murder) 
```

R Graphics: Device 2 (ACTIVE)

### Histogram of USArrests\$Murder

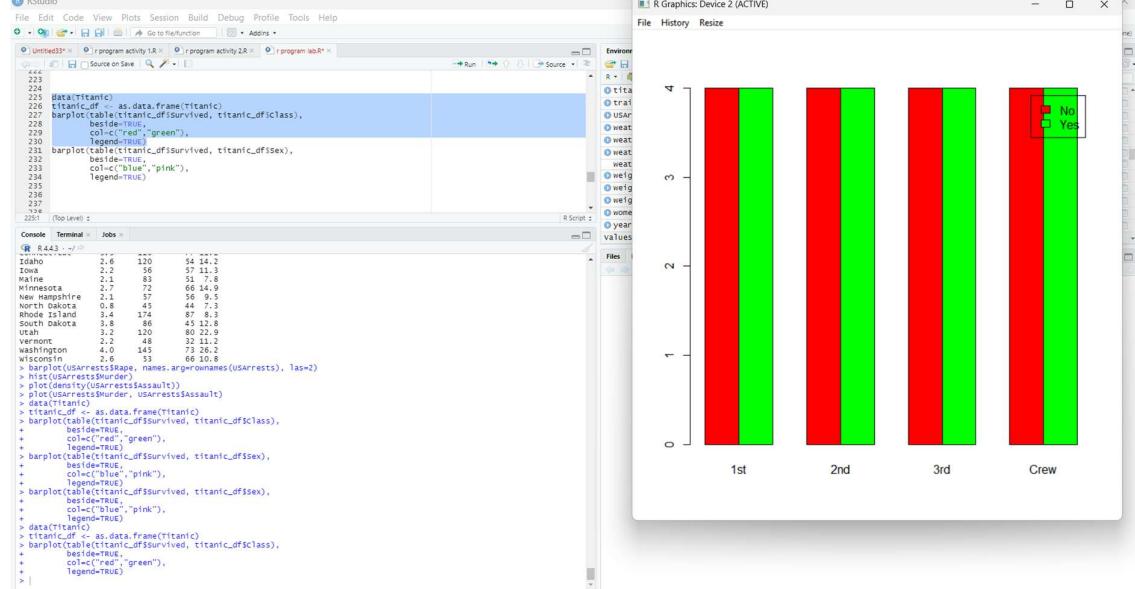
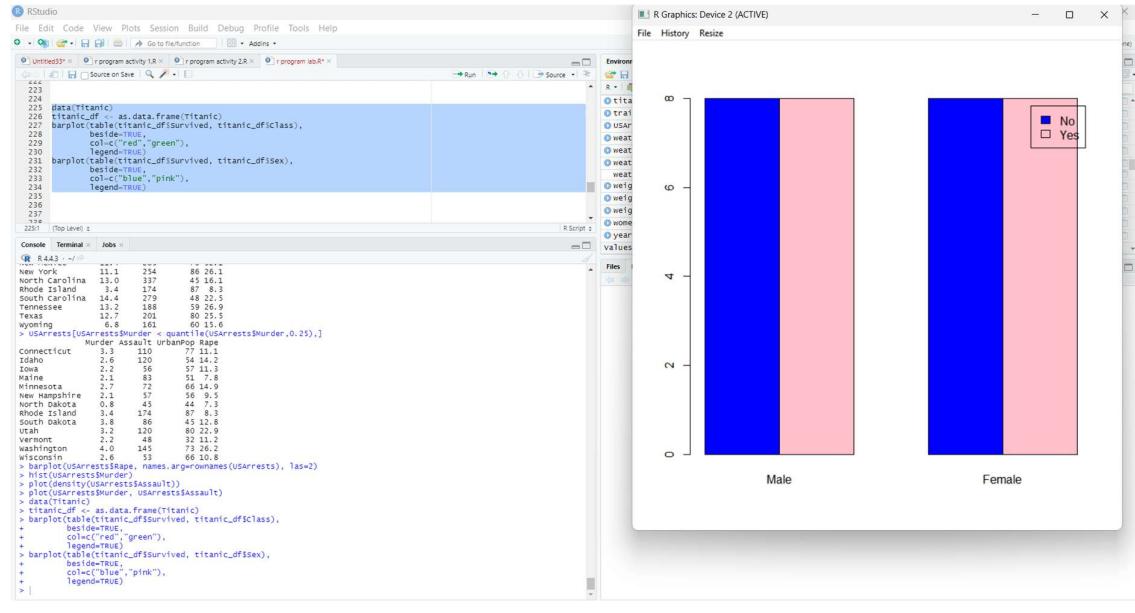


```

barplot(table(titanic_df$Survived, titanic_df$Sex),
       beside=TRUE,
       col=c("blue","pink"),
       legend=TRUE)

```

## OUTPUT:



## 18. Create graphs in R: boxplot, histogram, bar plot, line chart, scatter plot.

### CODE:

```
boxplot(iris$Sepal.Length)
```

```
hist(iris$Petal.Length)
```

```

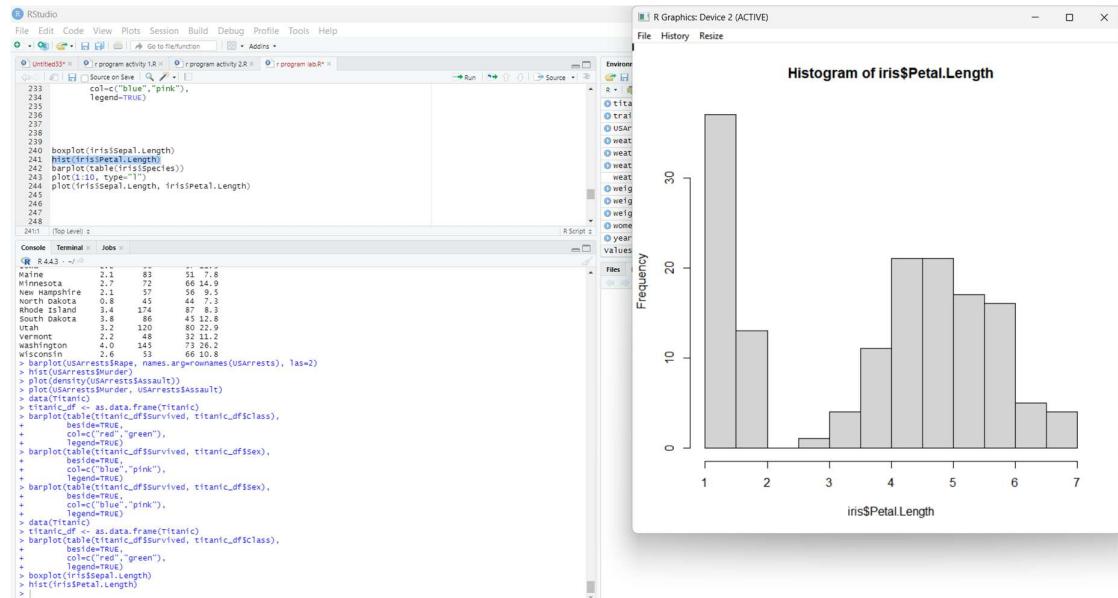
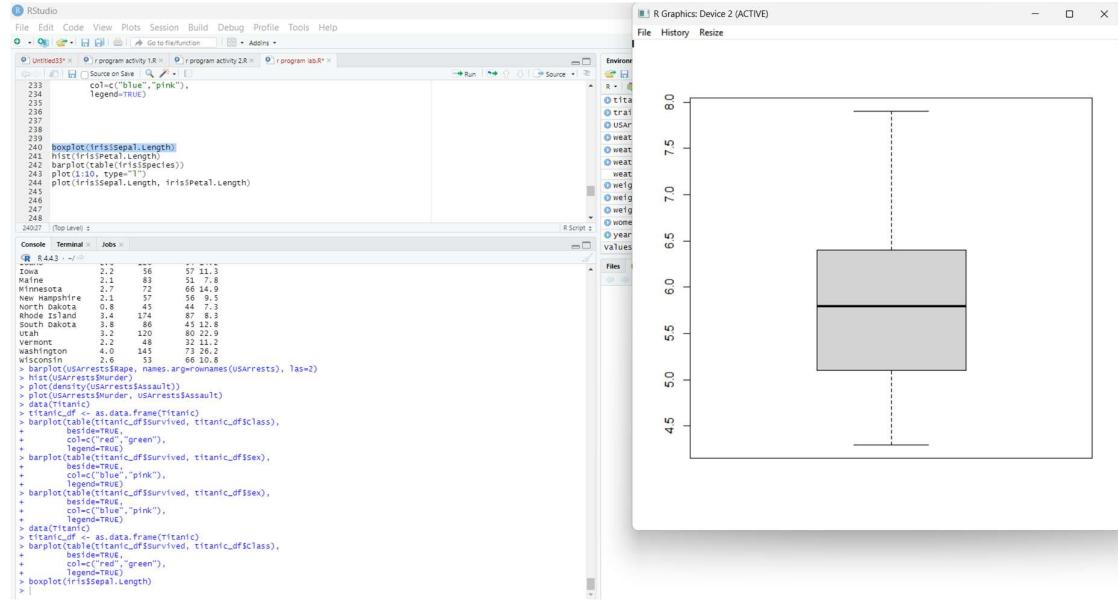
barplot(table(iris$Species))

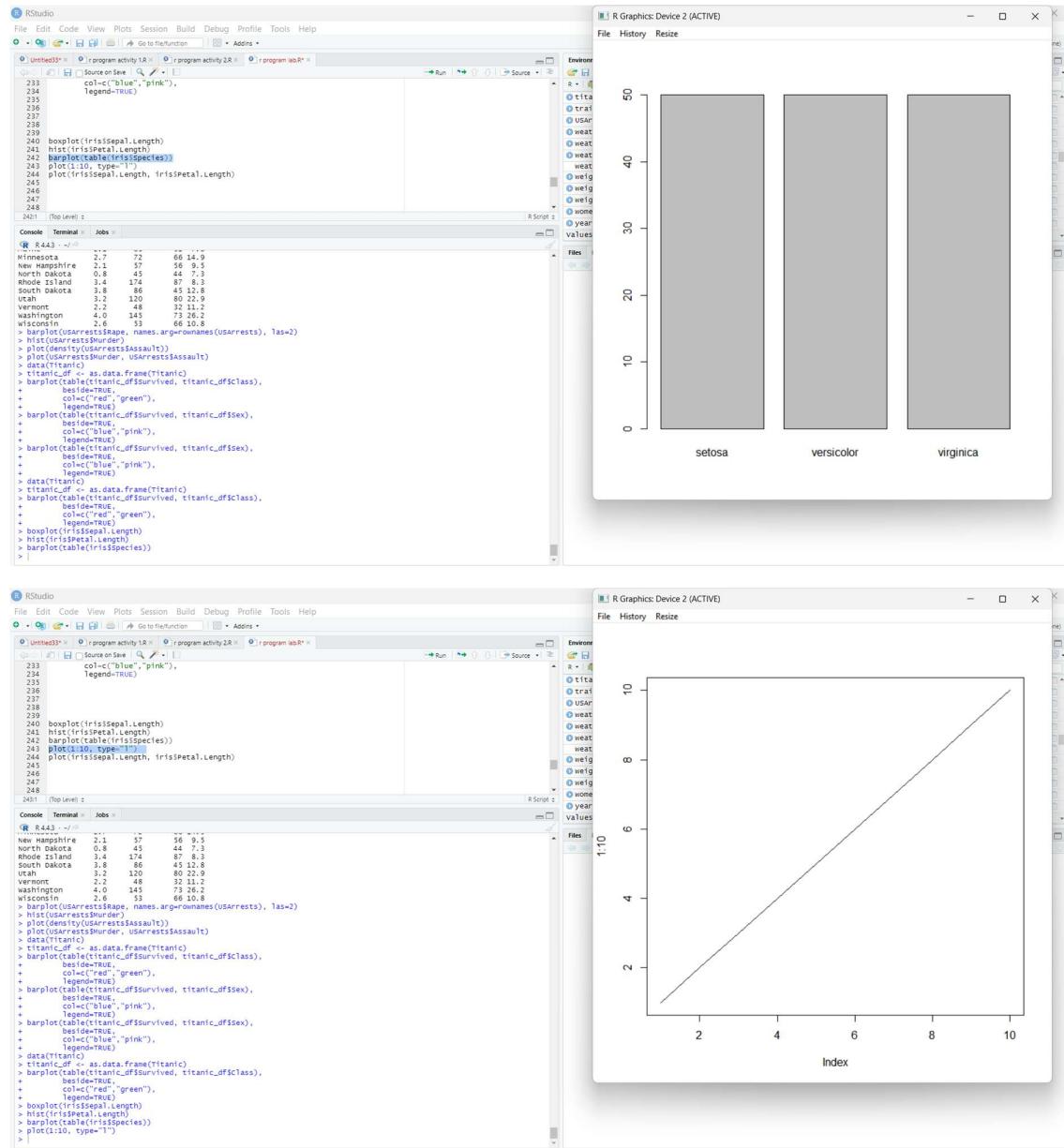
plot(1:10, type="l")

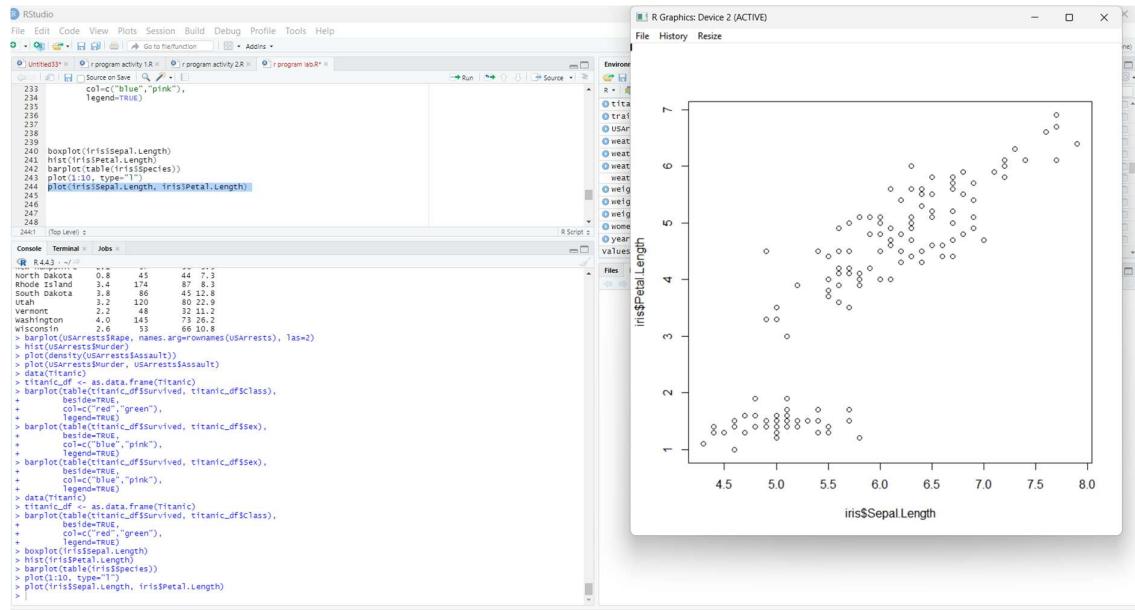
plot(iris$Sepal.Length, iris$Petal.Length)

```

## OUTPUT:







## 19. Build a regression model on advertising dataset (Sales ~ Spend) and predict Sales.

**CODE:**

```
advertising <- data.frame(
  Spend = c(100,150,200,250,300),
  Sales = c(10,15,22,28,35)
)

model <- lm(Sales ~ Spend, data=advertising)

summary(model)

predict(model, data.frame(Spend=200))
```

**OUTPUT:**

The screenshot displays the RStudio interface with two open projects:

- Program Activity 1:** Contains R code for data analysis. It includes:
  - Data loading: `advertising` (data frame), `Spend` (vector), `Sales` (vector).
  - EDA: Boxplots for Spend and Sales.
  - Modeling: A linear regression model `model` is fitted with `lm(Sales ~ Spend, data=advertising)`.
  - Prediction: A prediction is made for a spending level of 200.
- Program Activity 2:** Contains R code for data manipulation and visualization. It includes:
  - Data loading: `iris` (data frame).
  - EDA: A histogram for the `Petal.Length` column.
  - Modeling: A linear model `model1` is fitted with `lm(Sales ~ Spend, data=advertising)`.

The right pane also shows the environment and global variables for both projects.

**20. Create multiple regression model using ChickWeight dataset with “Time” and “Diet” as predictors; predict weight and compute model error.**

## CODE:

```
data(ChickWeight)
```

```
model2 <- lm(weight ~ Time + Diet, data=ChickWeight)
```

```
pred <- predict(model2, ChickWeight)
```

```
mean((ChickWeight$weight - pred)^2)
```

### **OUTPUT:**

RStudio

The screenshot shows an RStudio interface with several windows open:

- Code Editor:** Displays R code for a linear model. It includes imports for `lm`, `predict`, and `data.table`. The main body of the script defines `model2` as a linear model with `Time` and `Diet` as predictors, and `pred` as the predicted values. A `mean` function is used to calculate the difference between the observed `chickweight` and the predicted `pred`.
- Console:** Shows the execution of the R code. It starts with the command `R 4.4.3: ./`, followed by various library imports like `base`, `tidyverse`, `gridExtra`, and `data.table`. Then it runs `iris` and `advertising` datasets. The `lm` function is used to fit a model with `Sales` as the dependent variable and `advertising` as the independent variable. The `summary` function is then called on the resulting `model`. The output shows the call, residuals, coefficients, and a summary of the linear regression results.
- Environment:** Shows the global environment with variables like `math_seq`, `max_x`, `mean_values`, `mean_x`, `n11_x`, `mod`, `n`, `name`, `names`, `num`, `pct_change`, `pos`, `preca`, `precB`, and `pred`.
- Plots:** Not visible in the screenshot.
- Packages:** Not visible in the screenshot.
- Help:** Not visible in the screenshot.
- Viewer:** Not visible in the screenshot.

**21. Randomly split iris dataset into train/test (80/20), build logistic regression (Species ~ Petal.Length +**

Petal.Width), predict, and evaluate with confusion matrix

**CODE:**

```
set.seed(1)
data(iris)
iris2 <- subset(iris, Species != "setosa")
iris2$Species <- factor(iris2$Species)
train_index <- sample(1:nrow(iris2), 0.8*nrow(iris2))
train <- iris2[train_index,]
test <- iris2[-train_index,]
model <- glm(Species ~ Petal.Length + Petal.Width,
              data=train, family=binomial)
prob <- predict(model, test, type="response")
pred <- ifelse(prob > 0.5,
                levels(train$Species)[2],
                levels(train$Species)[1])
table(Predicted=pred, Actual=test$Species)
```

### **OUTPUT:**

