**PROGRAM:**

data(iris)

head(iris)

selected\_iris <- iris[, c("Sepal.Length", "Species")]

print("Selected Columns:")

print(head(selected\_iris))

filtered\_iris <- iris[iris$Sepal.Length > 5, ]

print("Filtered Rows (Sepal.Length > 5):")

print(head(filtered\_iris))

iris$Petal.Width[10] <- NA

cleaned\_iris <- na.omit(iris)

print("Cleaned Data (NA removed):")

print(head(cleaned\_iris))

hist(iris$Sepal.Length,

col = "lightgreen",

main = "Sepal Length Distribution",

xlab = "Sepal Length")

boxplot(Sepal.Width ~ Species,

data = iris,

col = c("pink", "skyblue", "lightyellow"),

main = "Sepal Width by Species",

xlab = "Species",

ylab = "Sepal Width")

plot(iris$Petal.Length, iris$Petal.Width,

col = iris$Species,

pch = 19,

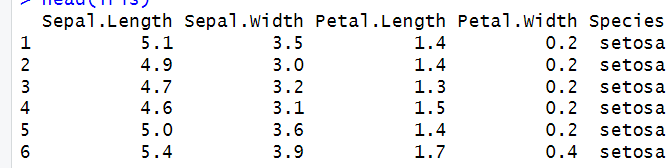
main = "Petal Length vs Petal Width",

xlab = "Petal Length",

ylab = "Petal Width")

**OUTPUT:**

**Head:**



**Selectedcolumns:**

**A screenshot of a computer

AI-generated content may be incorrect.**

**A screen shot of a number

AI-generated content may be incorrect.**

**Cleaned data:**

**A screen shot of a computer

AI-generated content may be incorrect.**

**A graph of different colored dots

AI-generated content may be incorrect.**