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Assignment 1

2024-02-02

```r
library(readr)
processes2 <- read_csv("C://Users//ujwal//Downloads//iris.csv")
```

```
## Rows: 150 Columns: 6
## -- Column specification ------------------------------------------------------
## Delimiter: ","
## chr (1): Species
## dbl (5): Id, SepalLengthCm, SepalWidthCm, PetalLengthCm, PetalWidthCm
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
View(processes2)
```

#Print out descriptive statistics for a selection of quantitative and categorical variables.

Define quantitative variables

```r
variable_1 <- c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")
```

Print out descriptive statistics for quantitative variables

```r
quant_desc <- summary(iris[, variable_1])
print("Descriptive statistics for quantitative variables:")
```

```
## [1] "Descriptive statistics for quantitative variables:"
```

```r
print(quant_desc)
```

```
##   Sepal.Length    Sepal.Width     Petal.Length    Petal.Width
## Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100
## 1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300
## Median :5.800   Median :3.000   Median :4.350   Median :1.300
## 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
```

Define categorical variable

```r
variable_2 <- "Species"
```

Print out descriptive statistics for categorical variable

```r
cat_counts <- table(iris[[variable_2]])
cat(paste("Descriptive statistics for", variable_2, ":"))
```

```
## Descriptive statistics for Species :
```

```r
cat("\n")
```

```r
print(cat_counts)
```

```
##
##     setosa versicolor  virginica
##         50         50         50
```

Define the variable to transform

```r
vars_to_trans <- "Sepal.Width"
```

## Perform the transformation (squaring each value)

```r
iris_trans <- iris
iris_trans[[vars_to_trans]] <- iris[[vars_to_trans]]^2
head(iris_trans)
```

```
##   Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 1          5.1       12.25          1.4         0.2  setosa
## 2          4.9        9.00          1.4         0.2  setosa
## 3          4.7       10.24          1.3         0.2  setosa
## 4          4.6        9.61          1.5         0.2  setosa
## 5          5.0       12.96          1.4         0.2  setosa
## 6          5.4       15.21          1.7         0.4  setosa
```

```r
library(ggplot2)
```

Plot histogram of Petal.Length

```
hist <- ggplot(iris, aes(x = Petal.Length)) +
  geom_histogram(binwidth = 0.4, fill = "blue", color = "black") +
  labs(title = "Histogram of Petal Length",
       x = "Petal Length",
       y = "Frequency")
print(hist)
```

Histogram of Petal Length
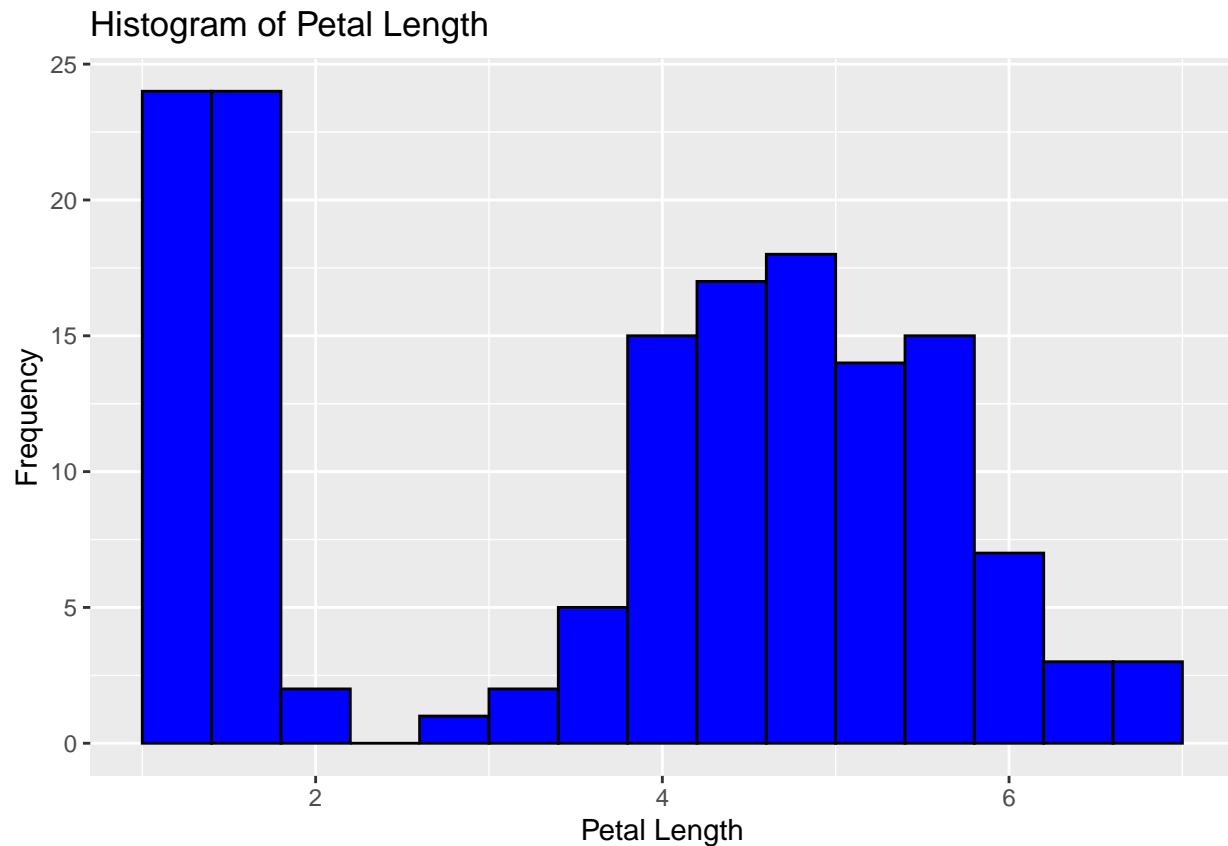
Create scatterplot of Petal.Length vs Petal.Width

```
scatplot <- ggplot(iris, aes(x = Petal.Length, y = Petal.Width)) +
  geom_point(color = "red") +
  labs(title = "Scatterplot of Petal Length vs Petal Width",
       x = "Petal Length",
       y = "Petal Width")
print(scatplot)
```

Scatterplot of Petal Length vs Petal Width