Met_tarea2.R

Juan Carlos Delgado Garza

2025-11-27

```r
##########################################
#Base de datos iris
##########################################

#Base iris
data("iris")
head(iris)

##   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
## 6          5.4         3.9          1.7         0.4  setosa

summary(iris)

##   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
##        Species
## setosa    :50
## versicolor:50
## virginica :50
##
##
##

str(iris)

## 'data.frame':    150 obs. of  5 variables:
##  $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
##  $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
##  $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
##  $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
##  $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1
## 1 1 1 1 1 1 ...
```

```
####################################################################
#################
data_sub <- subset(iris, Species %in% c("versicolor", "virginica"))
table(data_sub$Species)

##
##     setosa versicolor  virginica
##          0         50         50

boxplot(data_sub)
```
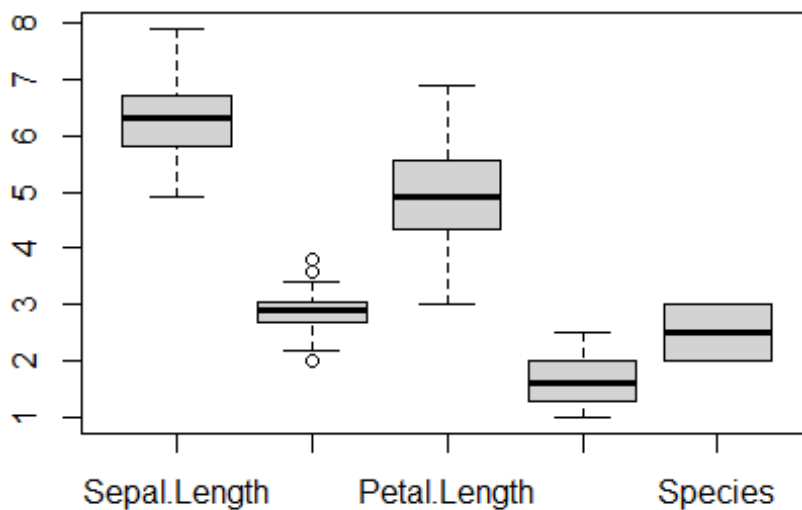


```
tapply(data_sub$Petal.Length, data_sub$Species, mean)

##     setosa versicolor  virginica
##         NA      4.260      5.552

tapply(data_sub$Petal.Length, data_sub$Species, sd)

##     setosa versicolor  virginica
##         NA  0.4699110  0.5518947

aggregate(Petal.Length ~ Species, data = data_sub, summary)

##      Species Petal.Length.Min. Petal.Length.1st Qu.
Petal.Length.Median
## 1 versicolor             3.000                4.000
4.350
## 2  virginica             4.500                5.100
```

```
5.550
##   Petal.Length.Mean Petal.Length.3rd Qu. Petal.Length.Max.
## 1            4.260                4.600              5.100
## 2            5.552                5.875              6.900
```

```r
var.test(Petal.Length ~ Species, data = data_sub)
```

```
##
##  F test to compare two variances
##
## data:  Petal.Length by Species
## F = 0.72497, num df = 49, denom df = 49, p-value = 0.2637
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.411402 1.277530
## sample estimates:
## ratio of variances
##           0.7249678
```

```r
t.test(Petal.Length ~ Species, data = data_sub, var.equal = TRUE)
```

```
##
##  Two Sample t-test
##
## data:  Petal.Length by Species
## t = -12.604, df = 98, p-value < 2.2e-16
## alternative hypothesis: true difference in means between group
versicolor and group virginica is not equal to 0
## 95 percent confidence interval:
##  -1.495426 -1.088574
## sample estimates:
## mean in group versicolor  mean in group virginica
##                    4.260                     5.552
```

```r
#Cohen's
versicolor <- data_sub$Petal.Llegth[data_sub$Species == "versicolor"]
versicolor <- data_sub$Petal.Llegth[data_sub$Species == "virginica"]


##################################################################################
###############

boxplot(Petal.Length ~ Species, data = data_sub,
        main = "Comparacion de Petal.Length entre especies",
        ylab = "Longitud del petalo(cm)",
        col = c("lightblue","peru"))
```

Comparacion de Petal.Length entre especies

Longitud del petalo(cm)

setosa   versicolor   virginica

Species