

lab3.R

hp

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```
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trees <- dbh <- c(16.5, 25.3, 22.1, 17.2, 16.1, 8.1, 34.3, 5.4, 5.7,
11.2, 24.1, 14.5, 7.7, 15.6, 15.9, 10, 17.5, 20.5, 7.8, 27.3, 9.7, 6.5,
23.4, 8.2, 28.5, 10.4, 11.5, 14.3, 17.2, 16.8)
mean(dbh)

## [1] 15.64333

sum(dbh < 10)

## [1] 8

which(dbh < 10)

## [1]  6  8  9 13 19 21 22 24

trees.1 <- subset(trees, dbh<= 10)
head(trees.1)

## [1]  8.1  5.4  5.7  7.7 10.0  7.8

mean(dbh)

## [1] 15.64333

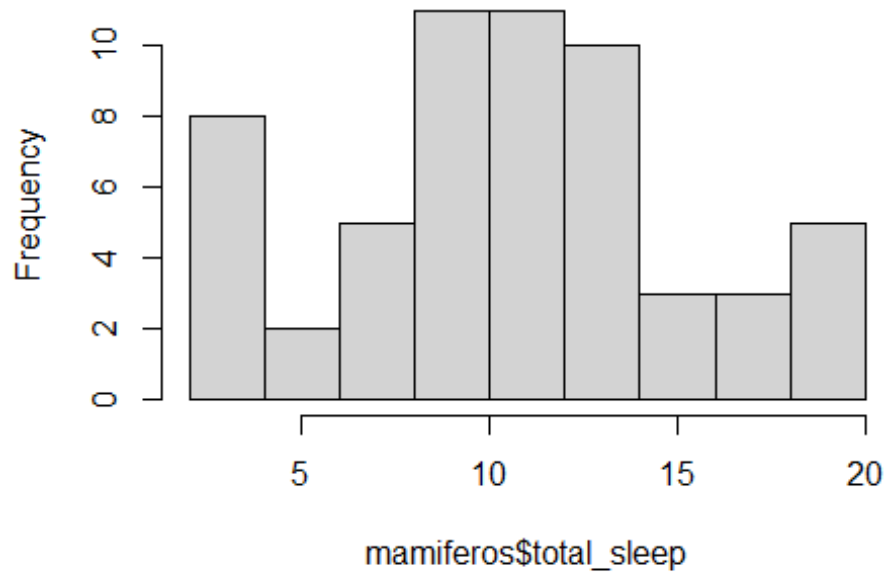
mean(trees.1)

## [1] 7.677778

# Parte 3. Representación gráfica -----
--

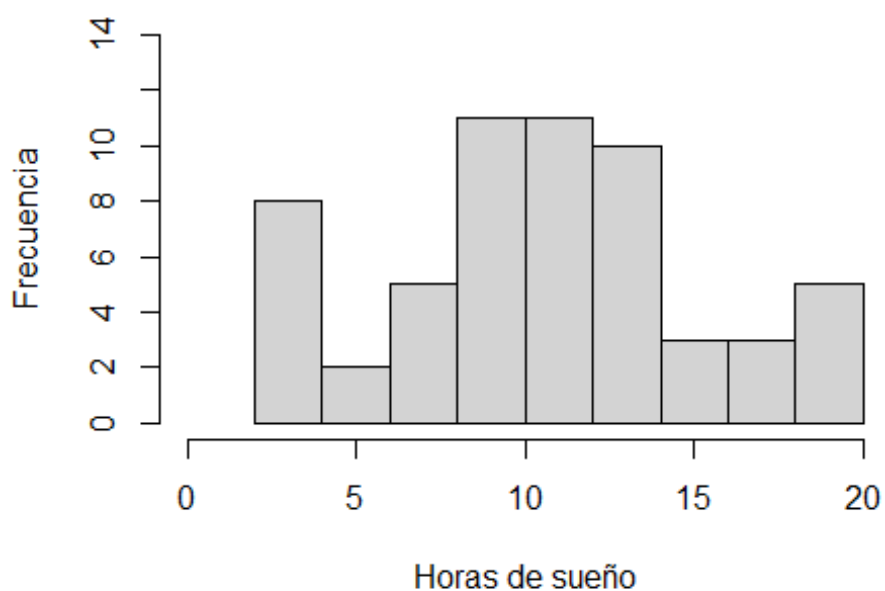
mamiferos <- read.csv("https://www.openintro.org/data/csv/mammals.csv")
hist(mamiferos$total_sleep)
```

Histogram of mamiferos\$total_sleep



```
hist(mamiferos$total_sleep,  
     xlim = c(0,20), ylim = c(0,14),  
     main = "Total de horas de sueño de las 39 especies",  
     xlab = "Horas de sueño",  
     ylab = "Frecuencia")
```

Total de horas de sueño de las 39 especies



```
# Barplot -----  
--  
  
data("chickwts")  
head(chickwts[c(1:2,42:43, 62:64), ])  
  
##      weight      feed  
## 1      179 horsebean  
## 2      160 horsebean  
## 42     226 sunflower  
## 43     320 sunflower  
## 62     379  casein  
## 63     260  casein  
  
feeds <- table(chickwts$feed)  
feeds  
  
##  
##      casein horsebean  linseed  meatmeal  soybean sunflower  
##          12         10         12         11         14         12  
  
barplot(feeds)
```



```
barplot(feeds[order(feeds, decreasing = TRUE)], col = "blue", horiz = 1)
```

