# Laboratorio_3.R

Usuario

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```
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# Laboratorio 3

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

sd(dbh)

## [1] 7.448892

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. Representacion grafica ----------------------------------------
--

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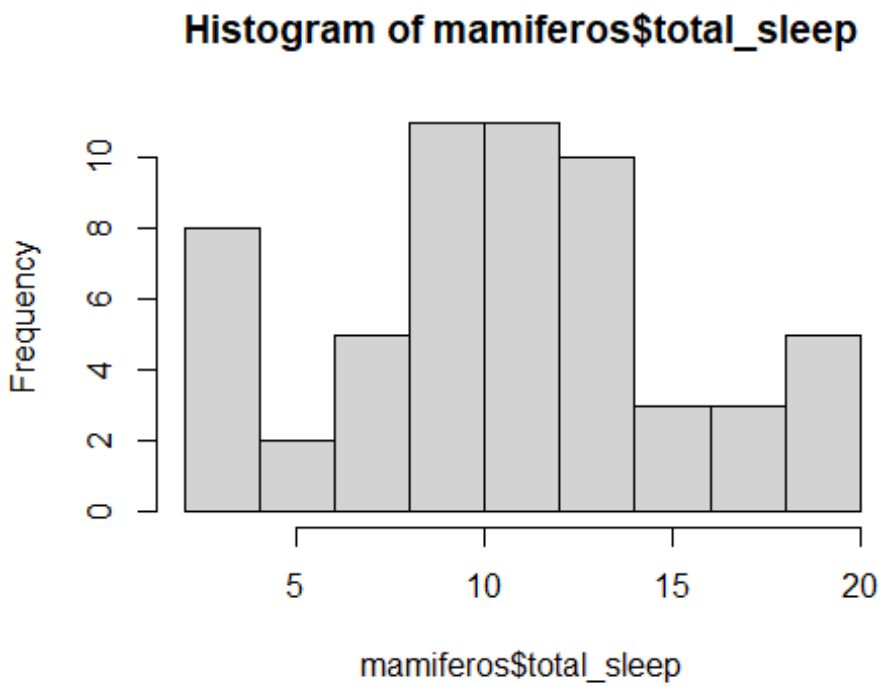
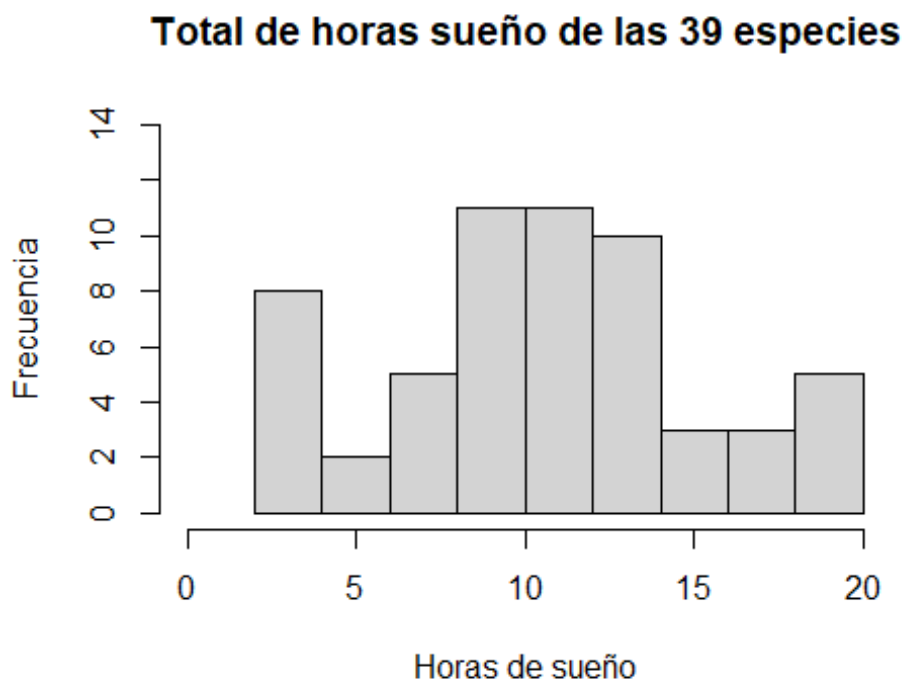
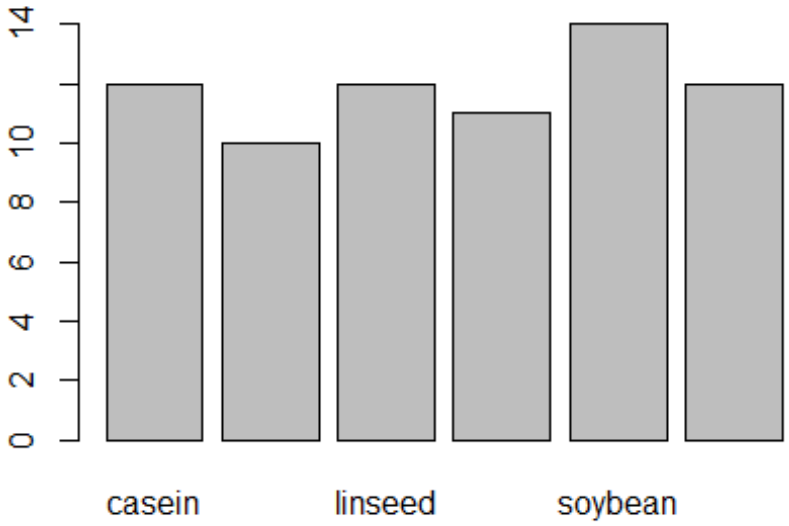




```r
hist(mamiferos$total_sleep,
     xlim = c(0,20), ylim = c(0,14),
     main = "Total de horas sueño de las 39 especies",
     xlab = "Horas de sueño",
     ylab = "Frecuencia")
```




```
# 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 = "green", horiz = 1)
```