

Solucion_Lab3.R

marco

2021-03-04

```
# MAGT
# Laboratorio 3
# 03.03.2021

# Importar datos csv -----

conjunto <- read.csv("cuadro1.csv", header = TRUE)

head(conjunto)

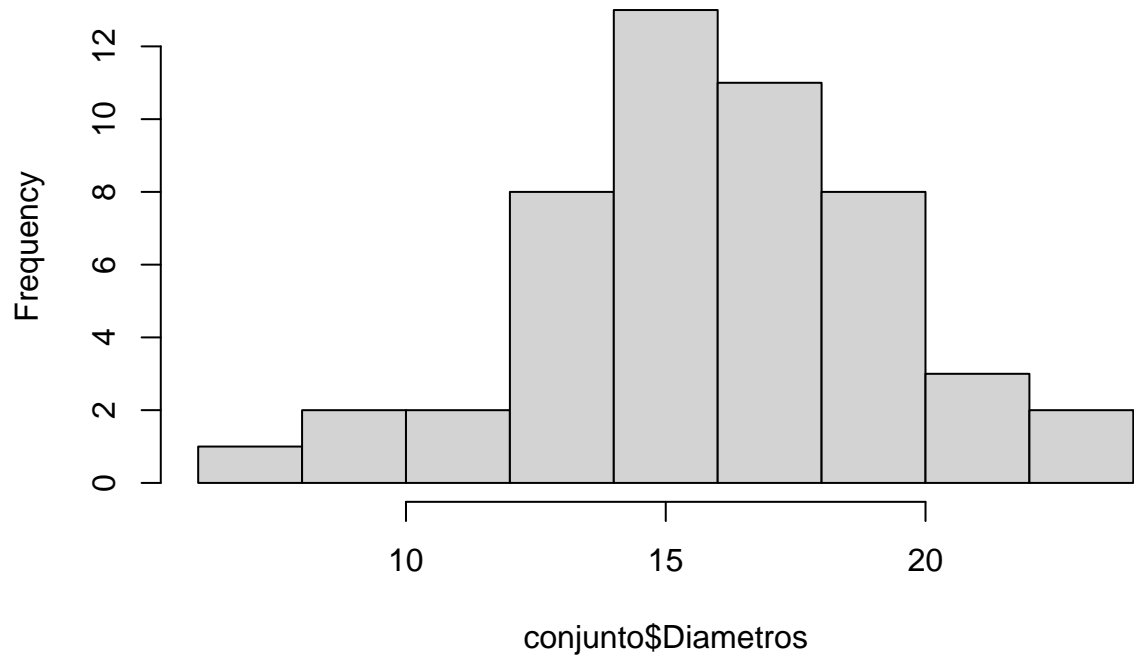
##      Arbol Fecha Especie Posicion Vecinos Diametros Altura
## 1      1     12      F      C      4      15.3  14.78
## 2      2     12      F      D      3      17.8  17.07
## 3      3      9      C      D      5      18.2  18.28
## 4      4      9      H      S      4       9.7   8.79
## 5      5      7      H      I      6      10.8  10.18
## 6      6     10      C      I      3      14.1  14.90

tail(conjunto)

##      Arbol Fecha Especie Posicion Vecinos Diametros Altura
## 45     45     24      C      I      4      10.2  13.93
## 46     46     23      F      I      3      14.4  12.68
## 47     47     24      C      S      6       7.7  10.00
## 48     48     25      C      S      5       9.9   8.69
## 49     49     25      H      D      1      20.4  16.73
## 50     50     24      H      D      3      20.9  16.25

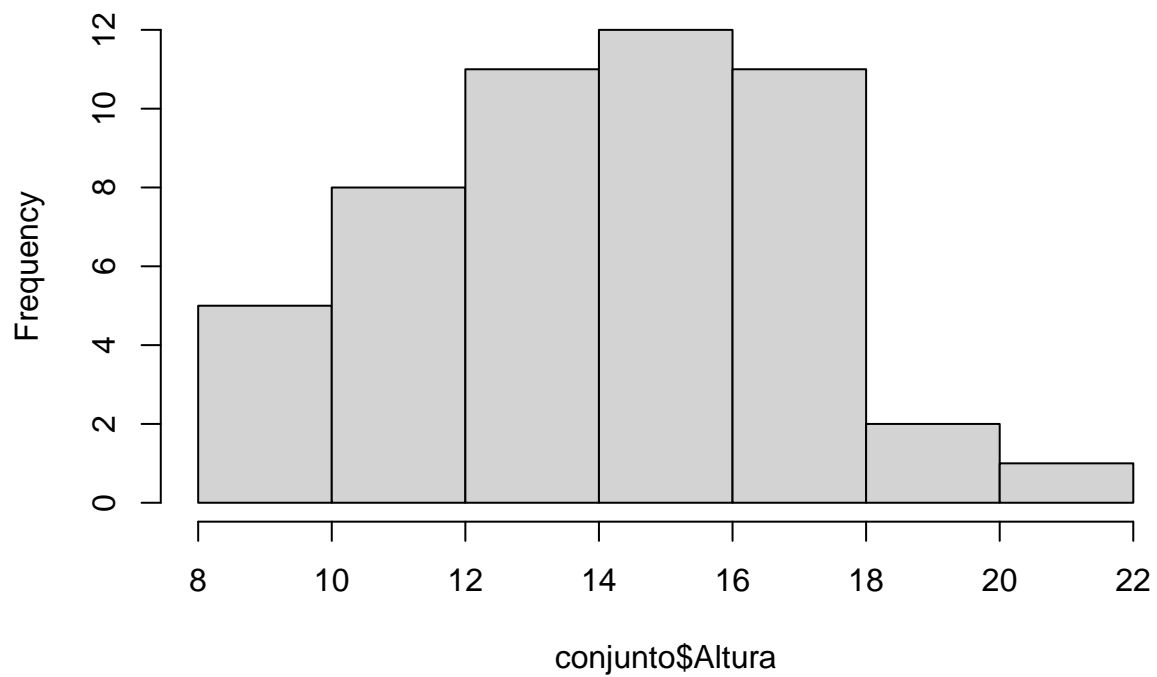
hist(conjunto$Diametros)
```

Histogram of conjunto\$Diametros



```
hist(conjunto$Altura)
```

Histogram of conjunto\$Altura



```
mean(conjunto$Diametros)
```

```
## [1] 15.794
```

```
mean(conjunto$Vecinos)
```

```
## [1] 3.34
```

```
range(conjunto$Vecinos)
```

```
## [1] 0 6
```

```
# Importar de la carpeta Datos el archivo cuadro2.csv
```

```
conjunto.2 <- read.csv("Datos/cuadro2.csv", header = TRUE)
```

```
# Directamente en consola -----
```

```
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)
```

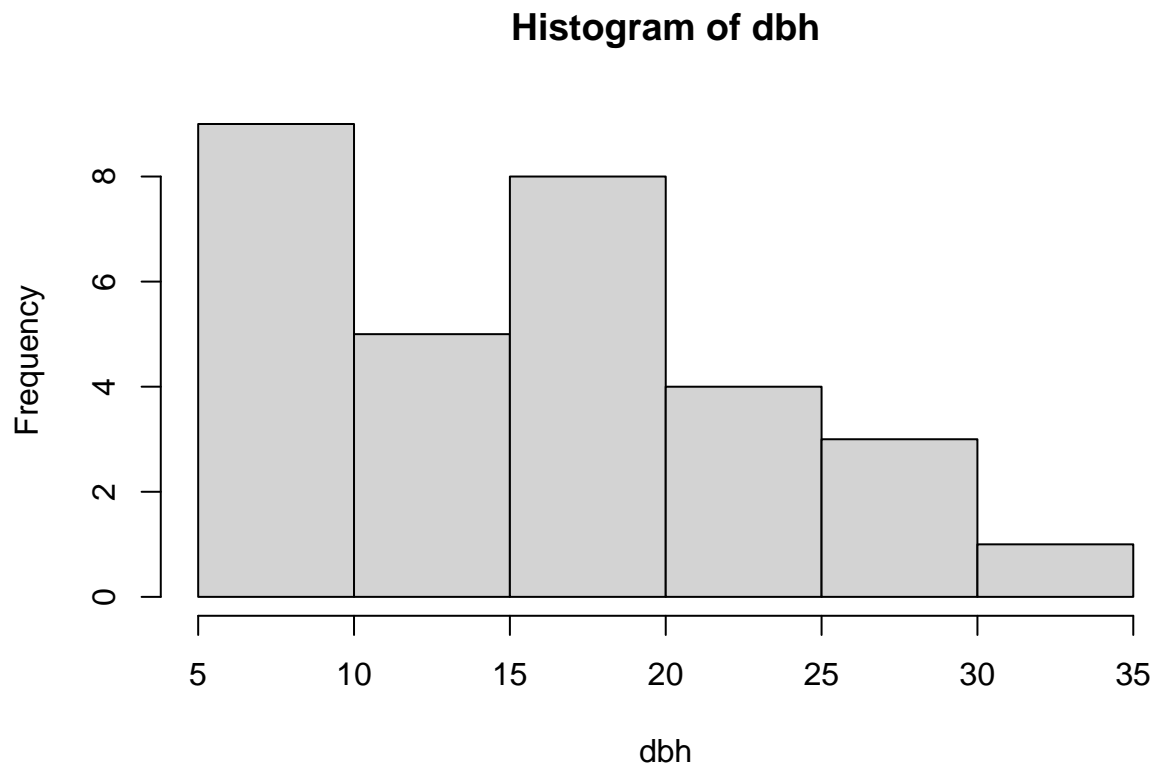
```
sum(dbh)
```

```
## [1] 469.3
```

```
prod(dbh)
```

```
## [1] 2.125828e+34
```

```
hist(dbh)
```



```
# Importar datos de una url -----
```

```
prof_url <- "http://www.profepa.gob.mx/innovaportal/file/7635/1/accionesInspeccionfoanp.csv"  
profepa <- read.csv(prof_url)  
head(profepa)
```

| ## | Entidad | Inspecciones | Recorridos.de.vigilancia | Operativos |
|------|---------------------|--------------|--------------------------|------------|
| ## 1 | Aguascalientes | 0 | 1 | 0 |
| ## 2 | Baja California | 0 | 1 | 0 |
| ## 3 | Baja California Sur | 0 | 0 | 0 |
| ## 4 | Campeche | 0 | 0 | 0 |
| ## 5 | Chiapas | 0 | 0 | 0 |
| ## 6 | Chihuahua | 3 | 1 | 1 |

profepa

| ## | Entidad | Inspecciones | Recorridos.de.vigilancia | Operativos |
|-------|---------------------|--------------|--------------------------|------------|
| ## 1 | Aguascalientes | 0 | 1 | 0 |
| ## 2 | Baja California | 0 | 1 | 0 |
| ## 3 | Baja California Sur | 0 | 0 | 0 |
| ## 4 | Campeche | 0 | 0 | 0 |
| ## 5 | Chiapas | 0 | 0 | 0 |
| ## 6 | Chihuahua | 3 | 1 | 1 |
| ## 7 | Coahuila | 1 | 0 | 0 |
| ## 8 | Colima | 0 | 0 | 0 |
| ## 9 | Distrito Federal | 0 | 0 | 0 |
| ## 10 | Durango | 0 | 0 | 0 |
| ## 11 | Guanajuato | 0 | 0 | 0 |
| ## 12 | Guerrero | 0 | 0 | 0 |
| ## 13 | Hidalgo | 0 | 0 | 0 |
| ## 14 | Jalisco | 0 | 0 | 0 |
| ## 15 | México | 2 | 0 | 0 |
| ## 16 | Michoacán | 1 | 3 | 1 |
| ## 17 | Morelos | 2 | 0 | 1 |
| ## 18 | Nayarit | 0 | 1 | 0 |
| ## 19 | Nuevo León | 0 | 0 | 0 |
| ## 20 | Oaxaca | 0 | 0 | 0 |
| ## 21 | Puebla | 0 | 0 | 0 |
| ## 22 | Querétaro | 0 | 0 | 0 |
| ## 23 | Quintana Roo | 0 | 0 | 0 |
| ## 24 | San Luis Potosí | 0 | 0 | 0 |
| ## 25 | Sinaloa | 0 | 0 | 0 |
| ## 26 | Sonora | 0 | 0 | 0 |
| ## 27 | Tabasco | 0 | 0 | 0 |
| ## 28 | Tamaulipas | 0 | 0 | 0 |
| ## 29 | Tlaxcala | 4 | 2 | 0 |
| ## 30 | Veracruz | 0 | 1 | 0 |
| ## 31 | Yucatán | 0 | 0 | 0 |
| ## 32 | Zacatecas | 0 | 1 | 0 |
| ## 33 | Oficinas Centrales | 6 | 10 | 0 |

sum(profepa\$Inspecciones)

[1] 19

sum(profepa\$Operativos)

[1] 3

sum(profepa\$Recorridos.de.vigilancia)

[1] 21

```

prof_url_2 <- paste0("http://www.profepa.gob.mx/innovaportal/",
                     "file/7635/1/accionesInspeccionfoanp.csv")
profepa2 <- read.csv(prof_url_2)
head(profepa2)

##           Entidad Inspecciones Recorridos.de.vigilancia Operativos
## 1    Aguascalientes           0                1           0
## 2    Baja California           0                1           0
## 3 Baja California Sur           0                0           0
## 4    Campeche                 0                0           0
## 5    Chiapas                  0                0           0
## 6    Chihuahua                3                1           1

# Importar datos de url seguras -----

library(repmis)

conjunto.2 <- source_data("https://www.dropbox.com/s/hmsf07bbayxv6m3/cuadro1.csv?dl=1")

## Downloading data from: https://www.dropbox.com/s/hmsf07bbayxv6m3/cuadro1.csv?dl=1
## SHA-1 hash of the downloaded data file is:
## 2bdde4663f51aa4198b04a248715d0d93498e7ba

sum(conjunto.2$Vecinos)

## [1] 167

library(readr)

file <- paste0("https://raw.githubusercontent.com/mgtagle/",
               "202_Analisis_Estadistico_2020/master/cuadro1.csv")
inventario <- read_csv(file)

##
## -- Column specification -----
## cols(
##   Arbol = col_double(),
##   Fecha = col_double(),
##   Especie = col_character(),
##   Clase = col_character(),
##   Vecinos = col_double(),
##   Diametro = col_double(),
##   Altura = col_double()
## )

sum(inventario$Vecinos)

## [1] 167

# Parte II: -----

# Selección mediante restricciones

dbh

## [1] 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
## [16] 10.0 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
dbh < 10

## [1] FALSE FALSE FALSE FALSE FALSE TRUE FALSE TRUE TRUE FALSE FALSE FALSE
## [13] TRUE FALSE FALSE FALSE FALSE FALSE TRUE FALSE TRUE TRUE FALSE TRUE
## [25] FALSE FALSE FALSE FALSE FALSE FALSE

sum(dbh < 10)

## [1] 8
which(dbh < 10)

## [1] 6 8 9 13 19 21 22 24
dbh.url <- "https://raw.githubusercontent.com/mgtagle/PrincipiosEstadistica2021/main/DBH_1.csv"
parcelas <- read.csv(dbh.url)

tree.13 <- parcelas[!(parcelas$parcela == "2"),]
tree.23 <- parcelas[!(parcelas$parcela == "1"),]
tree.12 <- parcelas[!(parcelas$parcela == "3"),]

# Revisar las medias del dbh en cada combinación de parcelas

mean(tree.12$dbh); mean(tree.13$dbh); mean(tree.23$dbh)

## [1] 16.14
## [1] 15.42
## [1] 15.37

# Selección de submuestras -----

tree_mean <- subset(parcelas, dbh <= mean(parcelas$dbh))
tree.up <- subset(parcelas, dbh >= mean(parcelas$dbh))

mean(tree_mean$dbh); mean(tree.up$dbh)

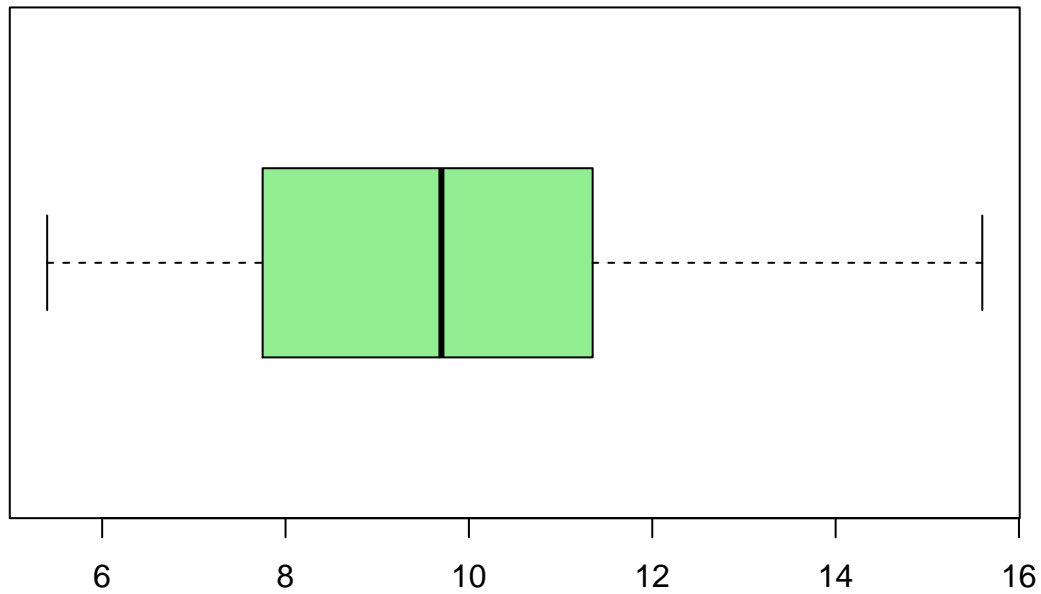
## [1] 9.773333
## [1] 21.51333

# Representación gráfica de los dos subconjuntos

boxplot(tree_mean$dbh, main = "DBH <= media", col = "lightgreen", horizontal = TRUE)

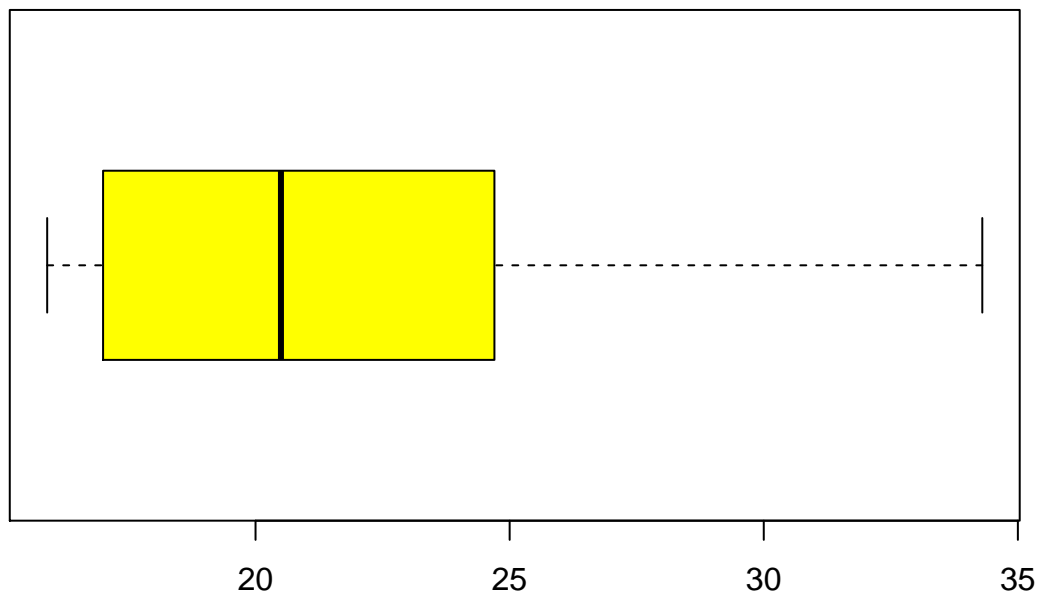
```

DBH <= media



```
boxplot(tree.up$dbh, main = "DBH >= media", col = "yellow", horizontal = T)
```

DBH >= media



```
quantile(tree_mean$dbh, 0.5)
```

```
## 50%
```

```
## 9.7
```

```
quantile(tree_mean$dbh, 0.75)
```

```
## 75%
```

```
## 11.35
```

```
# Parte 3: representación gráfica -----

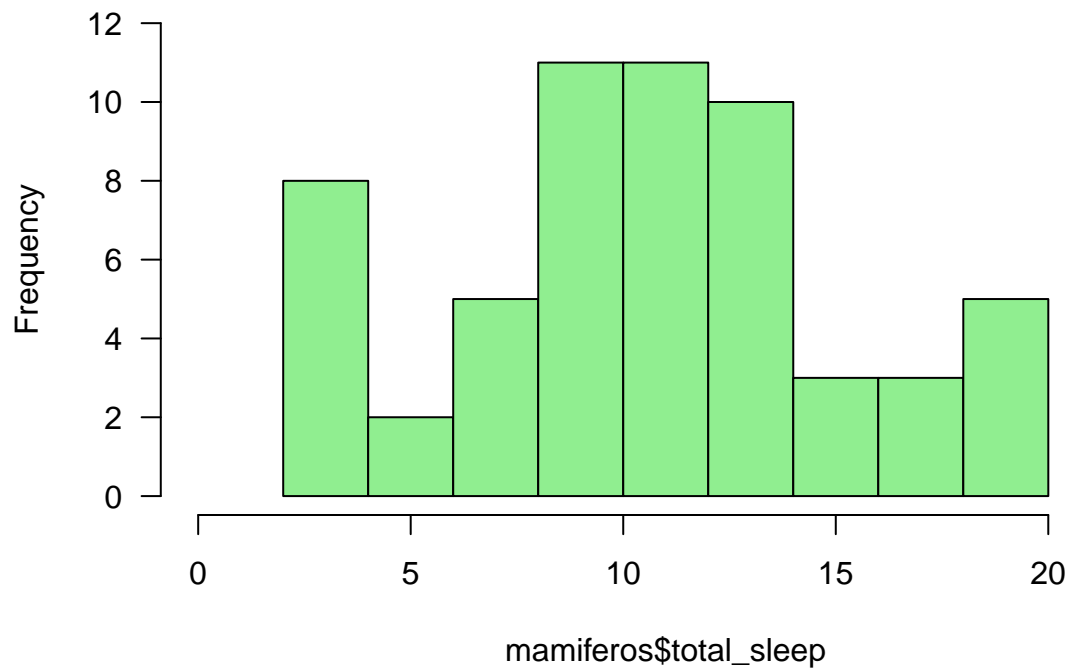
mamiferos <- read.csv("https://www.openintro.org/data/csv/mammals.csv")

mean(mamiferos$brain_wt)

## [1] 283.1342

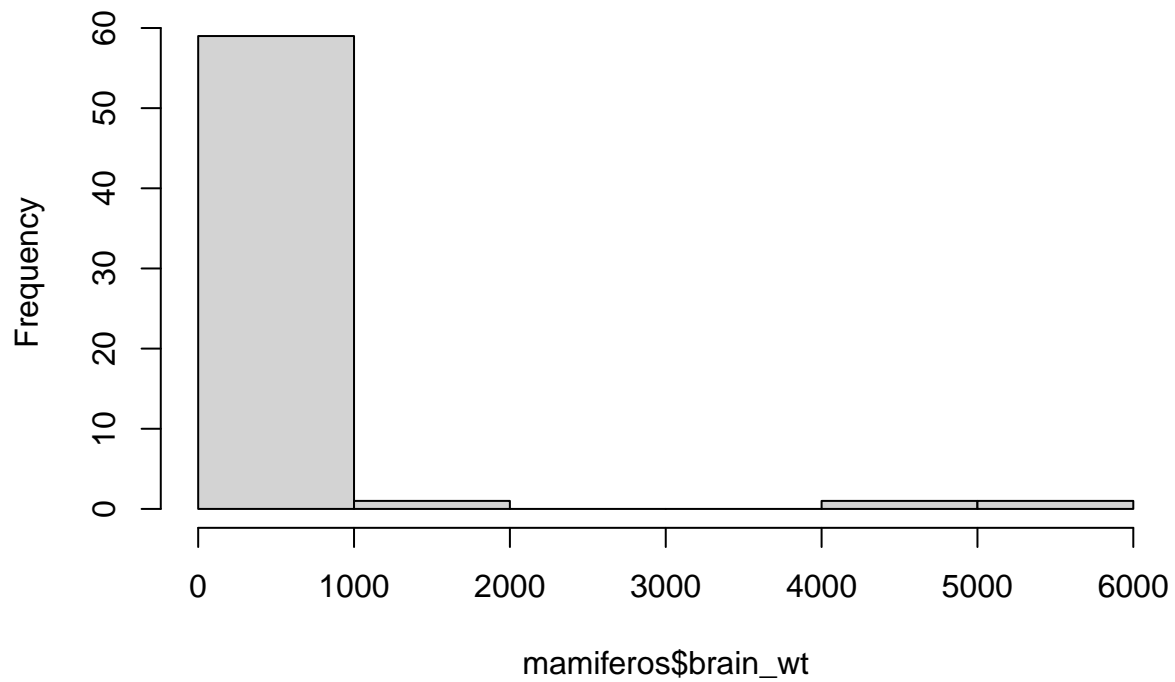
hist(mamiferos$total_sleep, col="lightgreen",
      ylim = c(0, 12), xlim = c(0, 22),
      las = 1)
```

Histogram of mamiferos\$total_sleep



```
hist(mamiferos$brain_wt)
```


Histogram of mamiferos\$brain_wt



```
fivenum(mamiferos$brain_wt)
```

```
## [1] 0.14 4.00 17.25 169.00 5712.00
```

```
data("chickwts")
```

```
head(chickwts)
```

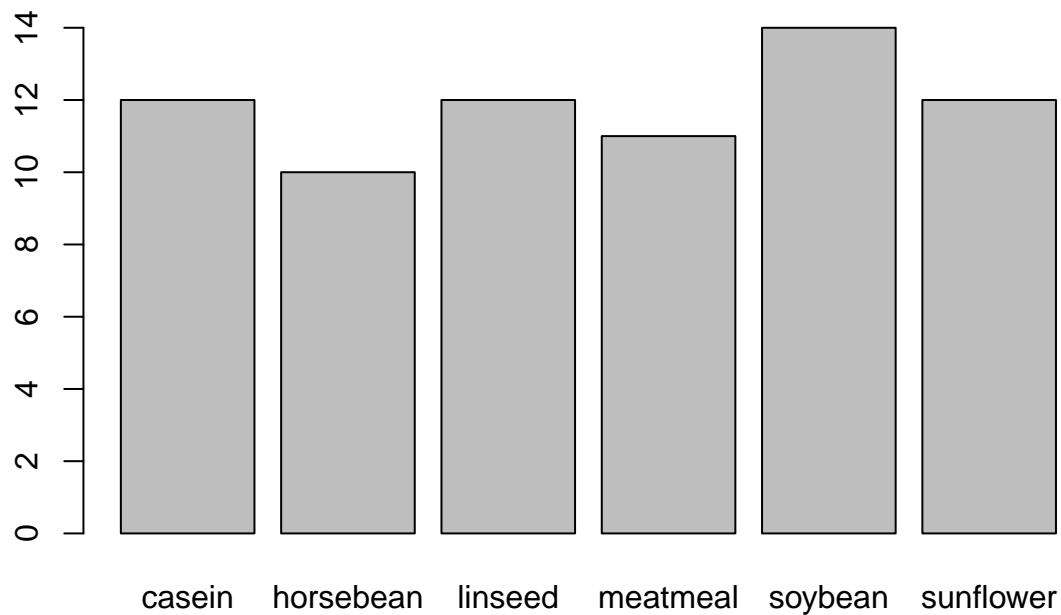
```
## weight feed
## 1 179 horsebean
## 2 160 horsebean
## 3 136 horsebean
## 4 227 horsebean
## 5 217 horsebean
## 6 168 horsebean
```

```
alimentación <- table(chickwts$feed)
```

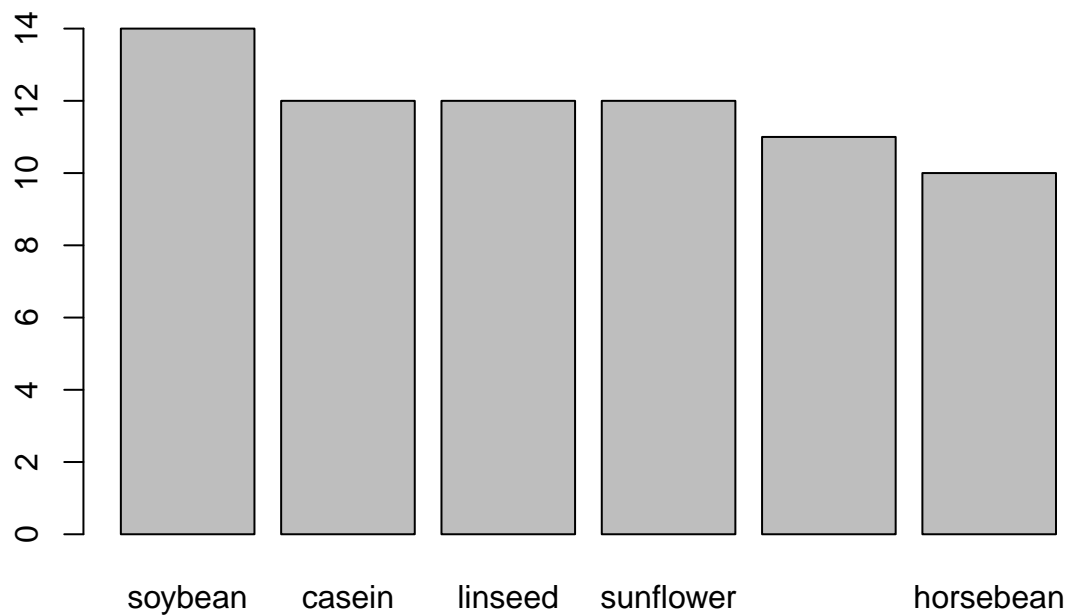
```
alimentación
```

```
##
## casein horsebean linseed meatmeal soybean sunflower
## 12 10 12 11 14 12
```

```
barplot(alimentación)
```



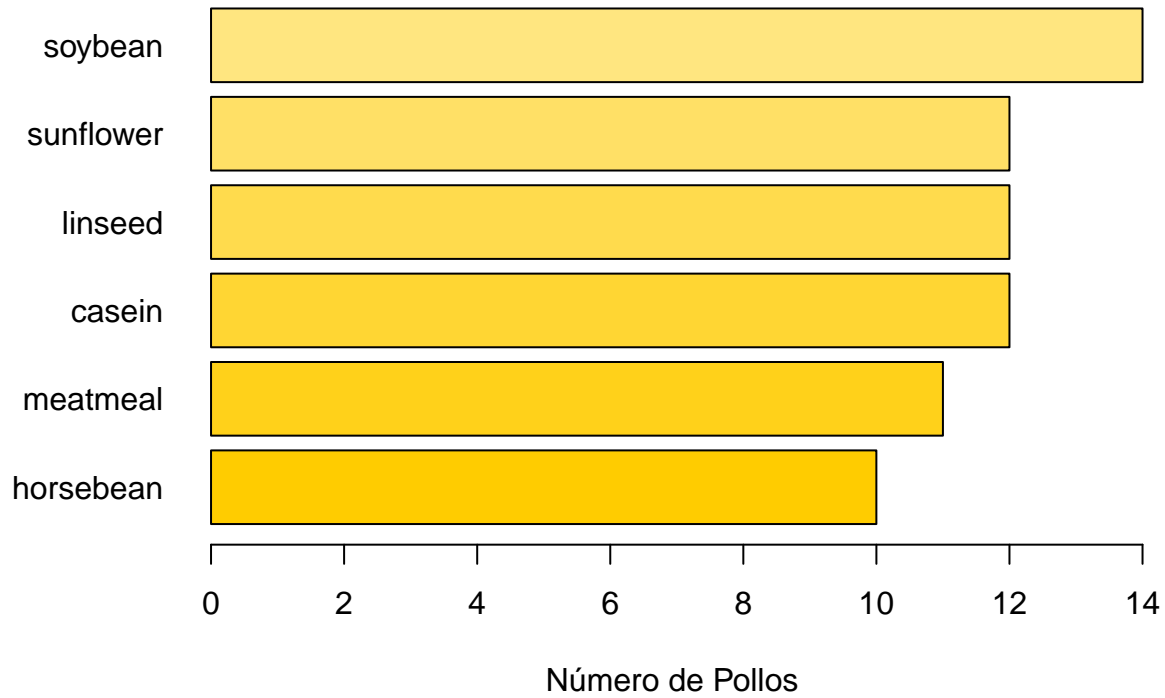
```
barplot(alimentación[order(alimentación, decreasing = TRUE)])
```



```
orig.par <- par() # Originales de las gráficas
par(oma=c(1,1,1,1))
par(mar=c(4,5,2,1))

barplot(alimentación[order(alimentación)],
        horiz = TRUE,
        las = 1,
        col = c("#ffcc00", "#ffd11a", "#ffd633", "#ffdb4d", "#ffe066", "#ffe680"),
        main = "Frecuencias por tipos de
alimentación",
        xlab = "Número de Pollos")
```

Frecuencias por tipos de alimentación



```
orig.par
```

```
## $xlog
## [1] FALSE
##
## $ylog
## [1] FALSE
##
## $adj
## [1] 0.5
##
## $ann
## [1] TRUE
##
## $ask
## [1] FALSE
##
## $bg
## [1] "transparent"
##
## $bty
## [1] "o"
##
## $cex
## [1] 1
##
## $cex.axis
## [1] 1
##
```

```

## $cex.lab
## [1] 1
##
## $cex.main
## [1] 1.2
##
## $cex.sub
## [1] 1
##
## $cin
## [1] 0.15 0.20
##
## $col
## [1] "black"
##
## $col.axis
## [1] "black"
##
## $col.lab
## [1] "black"
##
## $col.main
## [1] "black"
##
## $col.sub
## [1] "black"
##
## $cra
## [1] 10.8 14.4
##
## $crt
## [1] 0
##
## $csi
## [1] 0.2
##
## $cxy
## [1] 0.2155894 1.0631579
##
## $din
## [1] 6.5 4.5
##
## $err
## [1] 0
##
## $family
## [1] ""
##
## $fg
## [1] "black"
##
## $fig
## [1] 0 1 0 1
##

```

```

## $fin
## [1] 6.5 4.5
##
## $font
## [1] 1
##
## $font.axis
## [1] 1
##
## $font.lab
## [1] 1
##
## $font.main
## [1] 2
##
## $font.sub
## [1] 1
##
## $lab
## [1] 5 5 7
##
## $las
## [1] 0
##
## $lend
## [1] "round"
##
## $lheight
## [1] 1
##
## $ljoin
## [1] "round"
##
## $lmitre
## [1] 10
##
## $lty
## [1] "solid"
##
## $lwd
## [1] 1
##
## $mai
## [1] 1.02 0.82 0.82 0.42
##
## $mar
## [1] 5.1 4.1 4.1 2.1
##
## $mex
## [1] 1
##
## $mfcol
## [1] 1 1
##

```

```

## $mfg
## [1] 1 1 1 1
##
## $mfrow
## [1] 1 1
##
## $mgp
## [1] 3 1 0
##
## $mkh
## [1] 0.001
##
## $new
## [1] FALSE
##
## $oma
## [1] 0 0 0 0
##
## $omd
## [1] 0 1 0 1
##
## $omi
## [1] 0 0 0 0
##
## $page
## [1] TRUE
##
## $pch
## [1] 1
##
## $pin
## [1] 5.26 2.66
##
## $plt
## [1] 0.1261538 0.9353846 0.2266667 0.8177778
##
## $ps
## [1] 12
##
## $pty
## [1] "m"
##
## $smo
## [1] 1
##
## $srt
## [1] 0
##
## $tck
## [1] NA
##
## $tcl
## [1] -0.5
##

```

```
## $usr
## [1] -0.08  7.48 -0.14 14.00
##
## $xaxp
## [1] 0 7 7
##
## $xaxs
## [1] "r"
##
## $xaxt
## [1] "s"
##
## $xpd
## [1] FALSE
##
## $yaxp
## [1] 0 14 7
##
## $yaxs
## [1] "r"
##
## $yaxt
## [1] "s"
##
## $ylbias
## [1] 0.2
```