

## LABORATORIO-3-CORRECCION.R

maria

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```
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# 02.03.2021  
# Laboratorio 3
```

```
# Parte 1: Importacion de datos -----
```

```
conjunto <- read.csv("~/gtihob/PRINCIPIOS_ESTADISTICA2021/cuadro1.csv",  
header = TRUE)
```

```
head(conjunto)
```

##	Arbol	Fecha	Especie	Posicion	Vecinos	Diametro	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	Diametro	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

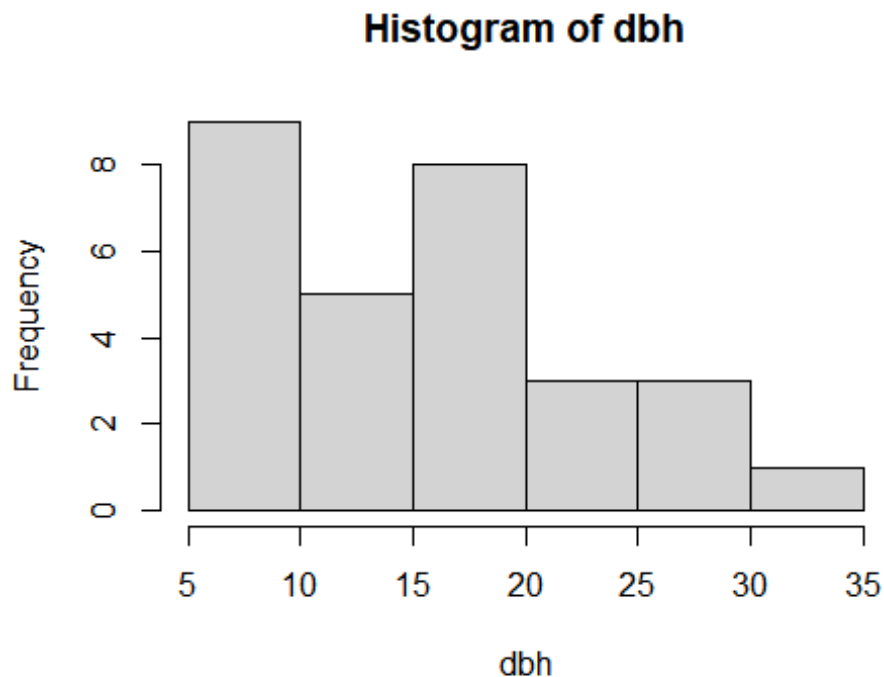
```
# Datos en consola -----
```

```
dbh <- c(16.5, 25.3, 22.1, 17.2, 16.1, 8.1, 34.3, 5.4, 5.7, 11.2, 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] 445.2
```

```
prod(dbh)
## [1] 8.820863e+32
hist(dbh)
```



```
# Datos URL -----

prof_url <-
"http://www.profepa.gob.mx/innovaportal/file/7635/1/accionesInspeccionfoa
np.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

*# EL total de Inspecciones realizadas es de 19*  
sum(profepa\$Inspecciones)

## [1] 19

*# EL total de operativos realizados es de 3*  
sum(profepa\$Operativos)

## [1] 3

*# EL total de Recorridos de vigilancia es de 21*  
sum(profepa\$Recorridos.de.vigilancia)

## [1] 21

*# Segundo URL*

```
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 del segundo URL -----*

```
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
```

```
head(conjunto.2)
```

##	Arbol	Fecha	Especie	Clase	Vecinos	Diametro	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

```
sum(conjunto.2$Vecinos)
```

```
## [1] 167
```

```
library(readr)
```

```
file <-
paste0("https://raw.githubusercontent.com/YuliaAbigail18/PrincipiosDeEstadistica2021/main/Cuadro1.csv")
```

```
inventario <- read.csv(file)
head(inventario)
```

##	Arbol	Fecha	Especie	Posicion	Vecinos	Diametro	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
```

*# Parte 2: Operaciones con La base de datos -----*

```
dbh
```

```
## [1] 16.5 25.3 22.1 17.2 16.1  8.1 34.3  5.4  5.7 11.2 14.5  7.7 15.6 15.9
10.0
```

```
## [16] 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] 15.35172
```

```
dbh < 10
```

```
## [1] FALSE FALSE FALSE FALSE FALSE  TRUE FALSE  TRUE  TRUE FALSE FALSE
TRUE
```

```
## [13] FALSE FALSE FALSE FALSE FALSE  TRUE FALSE  TRUE  TRUE FALSE  TRUE
FALSE
```

```
## [25] FALSE FALSE FALSE FALSE FALSE
```

```
sum(dbh < 10)
```

```
## [1] 8
```

```
which(dbh < 10)
```

```
## [1]  6  8  9 12 18 20 21 23
```

```
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"),]
```

*# Media de cada parcela dbh -----*

```
mean(tree.13$dbh)
```

```
## [1] 15.42
```

```
mean(tree.23$dbh)
```

```
## [1] 15.37
```

```
mean(tree.12$dbh)
```

```
## [1] 16.14
```

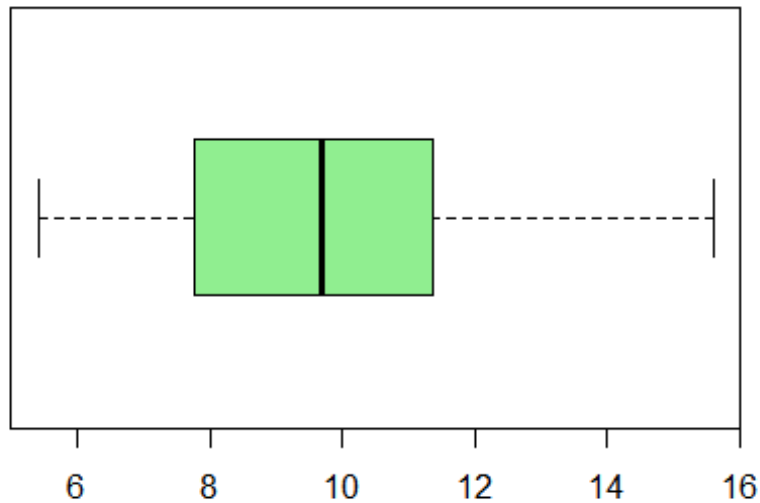
```

# Seleccion 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

# Representacion grafica de subconjuntos -----
boxplot(tree_mean$dbh, min = "DBH <= media", col = "Lightgreen",
        horizontal = TRUE)

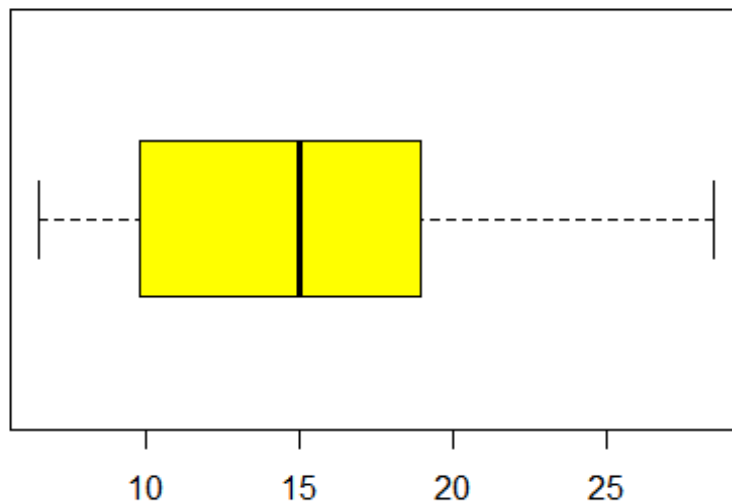
```



```

boxplot(tree.23$dbh, min= "DBH <= media", col = "yellow",
        horizontal = T)

```



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

```
## 50%
```

```
## 9.7
```

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

```
## 75%
```

```
## 11.35
```

*# Parte 3: Representacion grafica -----*

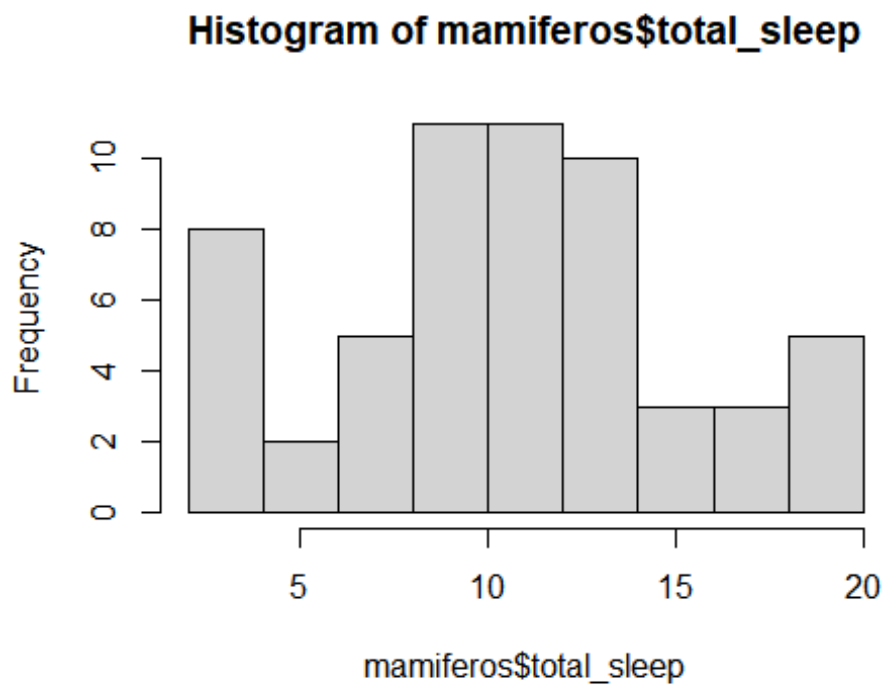
```
mamiferos <- read.csv("https://www.openintro.org/data/csv/mammals.csv")
head(mamiferos)
```

```
##           species  body_wt brain_wt non_dreaming dreaming
total_sleep
## 1   Africanelephant 6654.000   5712.0          NA         NA
3.3
## 2 Africangiantpouchedrat    1.000     6.6          6.3         2.0
8.3
## 3         ArcticFox    3.385    44.5          NA         NA
12.5
## 4  Arcticgroundsquirrel    0.920     5.7          NA         NA
16.5
## 5         Asianelephant 2547.000   4603.0          2.1         1.8
3.9
## 6             Baboon   10.550    179.5          9.1         0.7
```

9.8

```
##   life_span gestation predation exposure danger
## 1    38.6      645         3         5        3
## 2     4.5       42         3         1        3
## 3    14.0       60         1         1        1
## 4     NA       25         5         2        3
## 5    69.0     624         3         5        4
## 6    27.0     180         4         4        4
```

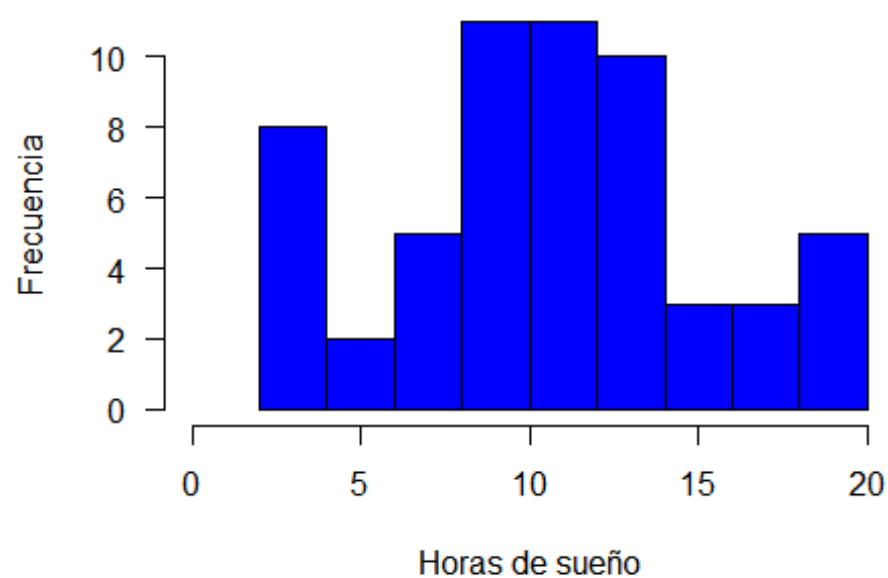
```
hist(mamiferos$total_sleep)
```



```
hist(mamiferos$total_sleep, xlim = c(0,20),
     main = "Total de horas de sueño de los 39 especies",
     xlab = "Horas de sueño", ylab = "Frecuencia", las= 1, col = "blue" )
```

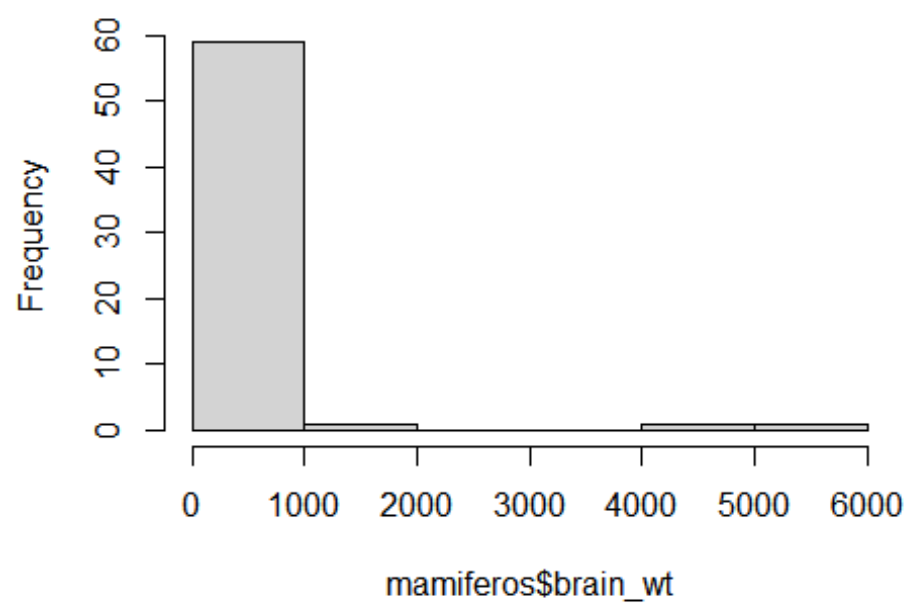


### Total de horas de sueño de los 39 especies



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

### Histogram of mamiferos\$brain\_wt



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

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

```
# Barplot o grafica de barras -----
```

```
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)
```

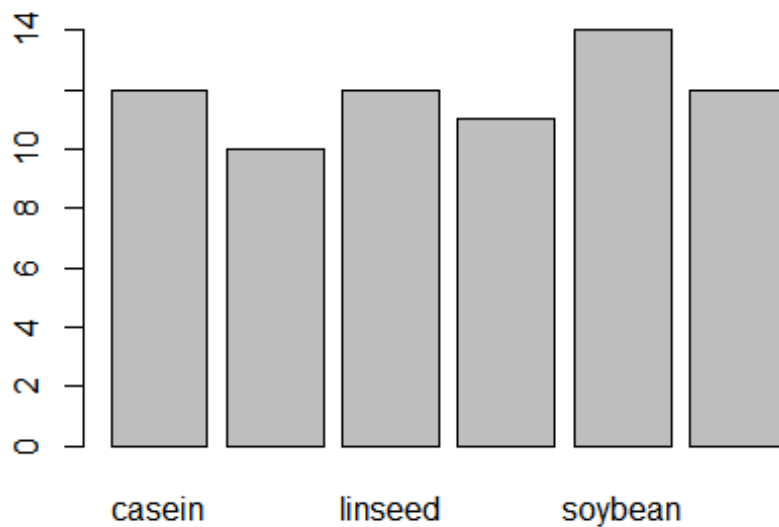
```
feeds
```

```
##
```

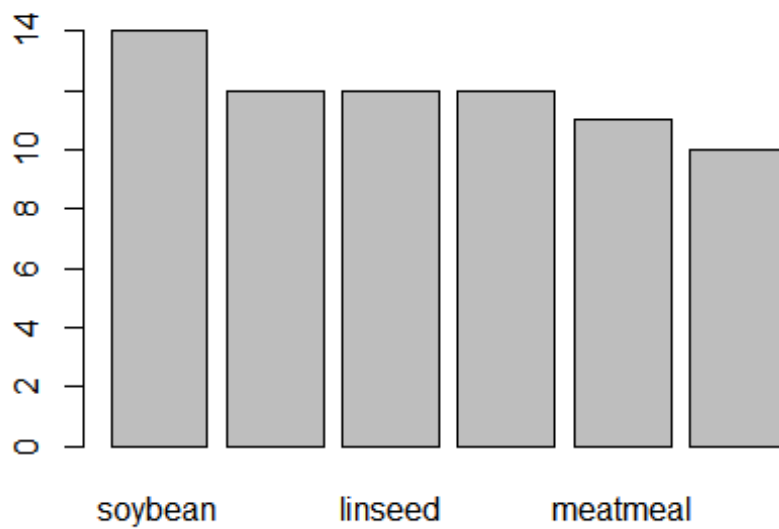
```
## casein horsebean linseed meatmeal soybean sunflower
```

```
## 12 10 12 11 14 12
```

```
barplot(feeds)
```



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



```
barplot(feeds[order(feeds, decreasing = TRUE)], horiz = T, las = 1,  
        col = "red", main = "Frecuencia por tipo de alimentacion",  
        xlab = "Numero de pollos")
```

