Laboratorio-2.R

User

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```r
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# 8/18/2021
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############

# Importar datos ------------------------------------------------------
#comando setwd especifica la ruta en donde se encuentran las bases de datos almacenados
setwd("C:/estadistica/Analisis-estadisticos-2021")

Trees <- read.csv("DBH_1.csv", header = TRUE)
head(Trees)
```

```
##   Tree  dbh parcela
## 1    1 16.5       1
## 2    2 25.3       1
## 3    3 22.1       1
## 4    4 17.2       1
## 5    5 16.1       1
## 6    6  8.1       1
```

```r
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,

## Accesar datos de internet

### Ejemplo 2
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  X
## 1       Aguascalientes            2                        2          0 NA
## 2       Baja California           0                        5          1 NA
## 3 Baja California Sur            1                        0          1 NA
## 4             Campeche            1                        2          2 NA
## 5              Chiapas            1                        1          0 NA
## 6             Chihuahua           14                       8          1 NA
```

```r
### Ejemplo 2
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  X
## 1       Aguascalientes            2                        2          0 NA
```

```
## 2      Baja California               0                       5        1 NA
## 3 Baja California Sur               1                       0        1 NA
## 4           Campeche                1                       2        2 NA
## 5            Chiapas                1                       1        0 NA
## 6          Chihuahua               14                       8        1 NA
```

Datos de URL seguras (https): Dropbox y Github

```r
library(repmis)
conjuntos <- source_data("https://www.dropbox.com/s/9iwqx34fzdh2rhw/cuadro1.csv?dl=1")
```

```
## Downloading data from: https://www.dropbox.com/s/9iwqx34fzdh2rhw/cuadro1.csv?dl=1
```

```
## SHA-1 hash of the downloaded data file is:
## 2bdde4663f51aa4198b04a248715d0d93498e7ba
```

```r
head(conjuntos)
```

```
##   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
```

```r
library(repmis)
```

```r
library(readr)
```

```
## Warning: package 'readr' was built under R version 4.1.1
```

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

```
## New names:
## * `12` -> `12...8`
## * F -> F...9
## * C -> C...10
## * `4` -> `4...11`
## * `12` -> `12...14`
## * ...
```

```
## Rows: 0 Columns: 307
```

```
## -- Column specification -------------------------------------------------
## Delimiter: ","
## chr (307): Arbol, Fecha, Especie, Clase, Vecinos, Diametro, Altura1, 12...8...
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
head(inventario)
```

```
## # A tibble: 0 x 307
## # ... with 307 variables: Arbol <chr>, Fecha <chr>, Especie <chr>, Clase <chr>,
## #   Vecinos <chr>, Diametro <chr>, Altura1 <chr>, 12...8 <chr>, F...9 <chr>,
```

```
## #   C...10 <chr>, 4...11 <chr>, 15.3 <chr>, 14.782 <chr>, 12...14 <chr>,
## #   F...15 <chr>, D...16 <chr>, 3...17 <chr>, 17.8...18 <chr>, 17.073 <chr>,
## #   9...20 <chr>, C...21 <chr>, D...22 <chr>, 5...23 <chr>, 18.2...24 <chr>,
## #   18.284 <chr>, 9...26 <chr>, H...27 <chr>, S...28 <chr>, 4...29 <chr>,
## #   9.7 <chr>, 8.795 <chr>, 7 <chr>, H...33 <chr>, I...34 <chr>, ...
# Operaciones con la base de datos --------------------------------------
```

```
mean(Trees$dbh)
```

```
## [1] 15.64333
```

```
sd(Trees$dbh)
```

```
## [1] 7.448892
```

```
sum(Trees$dbh < 10)
```

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

```
which(Trees$dbh < 10)
```

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

```
Trees.13 <- Trees[!(Trees$parcela=="2"),]
Trees.13
```

```
##    Tree  dbh parcela
## 1     1 16.5       1
## 2     2 25.3       1
## 3     3 22.1       1
## 4     4 17.2       1
## 5     5 16.1       1
## 6     6  8.1       1
## 7     7 34.3       1
## 8     8  5.4       1
## 9     9  5.7       1
## 10   10 11.2       1
## 21   21  9.7       3
## 22   22  6.5       3
## 23   23 23.4       3
## 24   24  8.2       3
## 25   25 28.5       3
## 26   26 10.4       3
## 27   27 11.5       3
## 28   28 14.3       3
## 29   29 17.2       3
## 30   30 16.8       3
```

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

```
##    Tree  dbh parcela
## 6     6  8.1       1
## 8     8  5.4       1
## 9     9  5.7       1
## 13   13  7.7       2
## 16   16 10.0       2
```

```
## 19   19  7.8        2
```

```
mean(Trees$dbh)
```

```
## [1] 15.64333
```

```
mean(Trees.1$dbh)
```

```
## [1] 7.677778
```
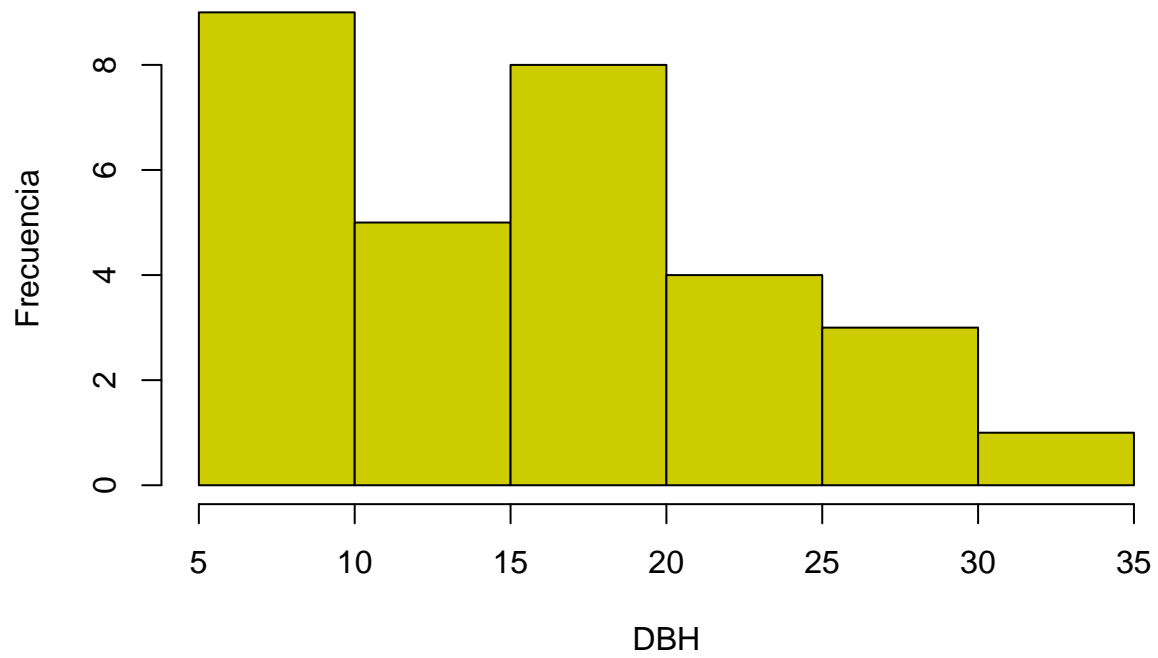
```
hist(Trees$dbh)
```

Histogram of Trees$dbh


```
hist(Trees.1$dbh)
```
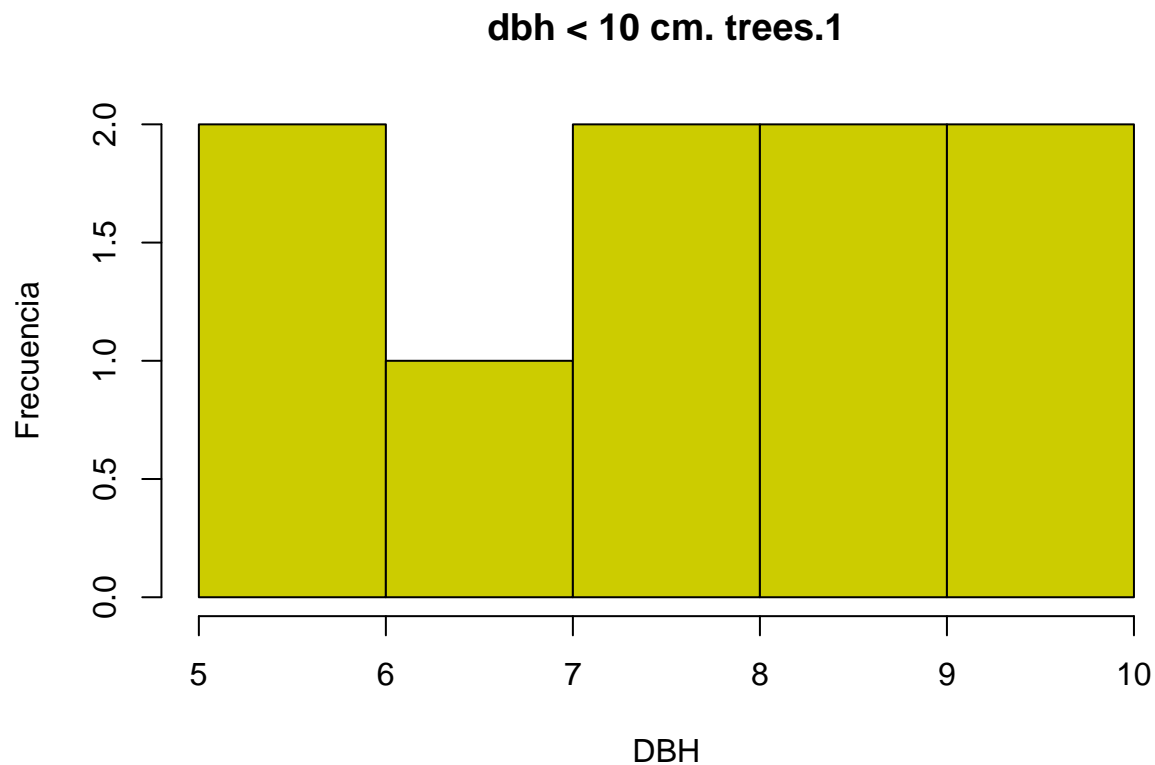
Histogram of Trees.1$dbh


```
hist(Trees$dbh, main = "Muestra original trees", ylab = "Frecuencia", xlab = "DBH", col = "#cccc00")
```

Muestra original trees


```
hist(Trees.1$dbh, main = "dbh < 10 cm. trees.1", ylab = "Frecuencia", xlab = "DBH", col = "#cccc00")
```

dbh < 10 cm. trees.1


```
# Representacion grafica ---------------------------------------------------

## Histogramas
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
```
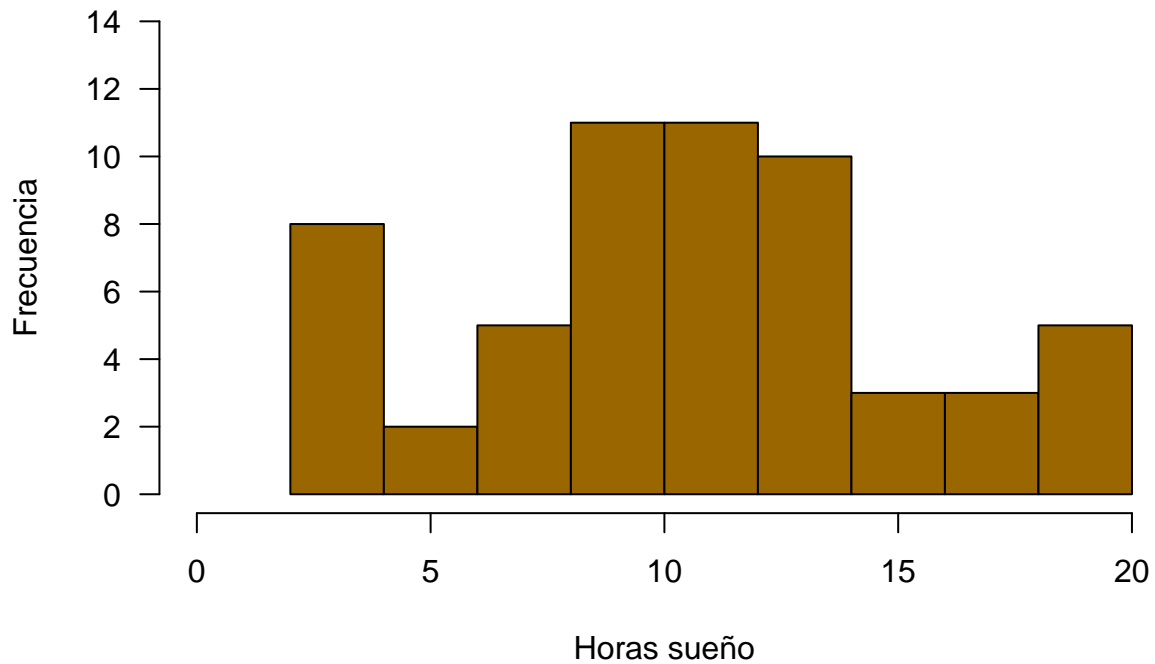
```
hist(mamiferos$total_sleep)
```

Histogram of mamiferos$total_sleep
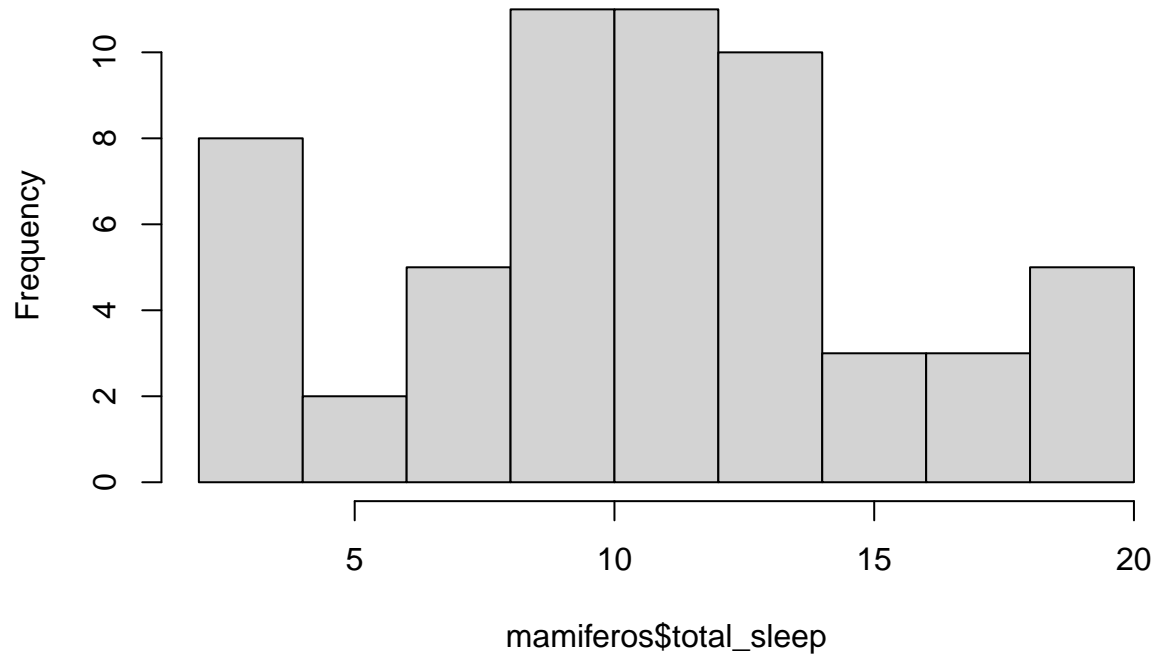

```
hist(mamiferos$total_sleep, xlim = c(0,20), ylim = c(0,14), main = "Total de horas sueño de las 39 espec
```

Total de horas sueño de las 39 especies


```r
## Barplot o grafico 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
```

```r
feeds <- table(chickwts$feed)
feeds
```
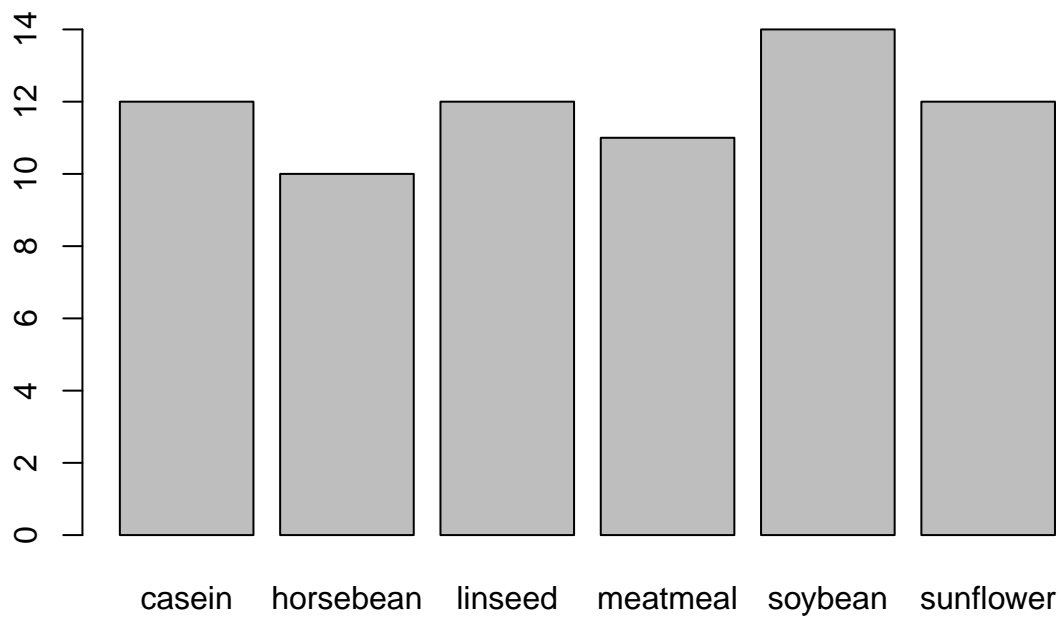
```
##
##    casein horsebean   linseed  meatmeal   soybean sunflower
##        12        10        12        11        14        12
```

```r
## Grafica
barplot(feeds)
```

```
barplot(feeds[order(feeds, decreasing = TRUE)], xlab = "Numero de pollos", main = "Frecuencias por tipo
```

Frecuencias por tipos de alimentación

Numero de pollos