# UNIVERSIDAD AUTÓNOMA DE NUEVO LEÓN

# FACULTAD DE CIENCIAS FORESTALES

## LABORATORIO DOS

## IMPORTAR DATOS A R

**EMANUEL MOLINA MARCHAN**

**MATRÍCULA**

**2134498**

**SEPTIEMBRE, 2022**

# Laboratorio02_EmanuelMolina.R

Emanuel

2022-09-02

```
read.csv("DBH_1.csv", header = T)
```

```
##    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
## 11   11 24.1       2
## 12   12 14.5       2
## 13   13  7.7       2
## 14   14 15.6       2
## 15   15 15.9       2
## 16   16 10.0       2
## 17   17 17.5       2
## 18   18 20.5       2
## 19   19  7.8       2
## 20   20 27.3       2
## 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
```

```
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)

head(dbh)
```

```
## [1] 16.5 25.3 22.1 17.2 16.1  8.1
```

```
profepa_url <- "http://www.profepa.gob.mx/innovaportal/file/7635/1/accion
esInspeccionfoanp.csv"
```

```
profepa <- read.csv(profepa_url, header= T, fileEncoding = "Latin1")
head(profepa)
```

```
##               Entidad Inspección Recorrido Operativo
## 1      Aguascalientes          7         5         1
## 2     Baja California          0        12         3
## 3 Baja California Sur          5         9         3
## 4            Campeche          1         4         3
## 5             Chiapas          3        11         0
## 6           Chihuahua         48        25         2
```

```
library(repmis)
conjunto <- source_data("https://www.dropbox.com/s/hmsf07bbayxv6m3/cuadro
1.csv?dl=1")
```

```
## Downloading data from: https://www.dropbox.com/s/hmsf07bbayxv6m3/cuadr
o1.csv?dl=1
```

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

```
head(conjunto)
```

```
##   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
```

```
library(readr)
file <- paste0("https://raw.githubusercontent.com/mgtagle/",
               "202_Analisis_Estadistico_2020/master/cuadro1.csv")
inventario <- read.csv(file)
head(inventario)
```

```
##   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
```

```
trees <- read.csv("DBH_1.csv", header= TRUE)
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
## 7     7 34.3       1
## 8     8  5.4       1
## 9     9  5.7       1
## 10   10 11.2       1
## 11   11 24.1       2
## 12   12 14.5       2
## 13   13  7.7       2
## 14   14 15.6       2
## 15   15 15.9       2
## 16   16 10.0       2
## 17   17 17.5       2
## 18   18 20.5       2
## 19   19  7.8       2
## 20   20 27.3       2
## 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
```

```
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
```

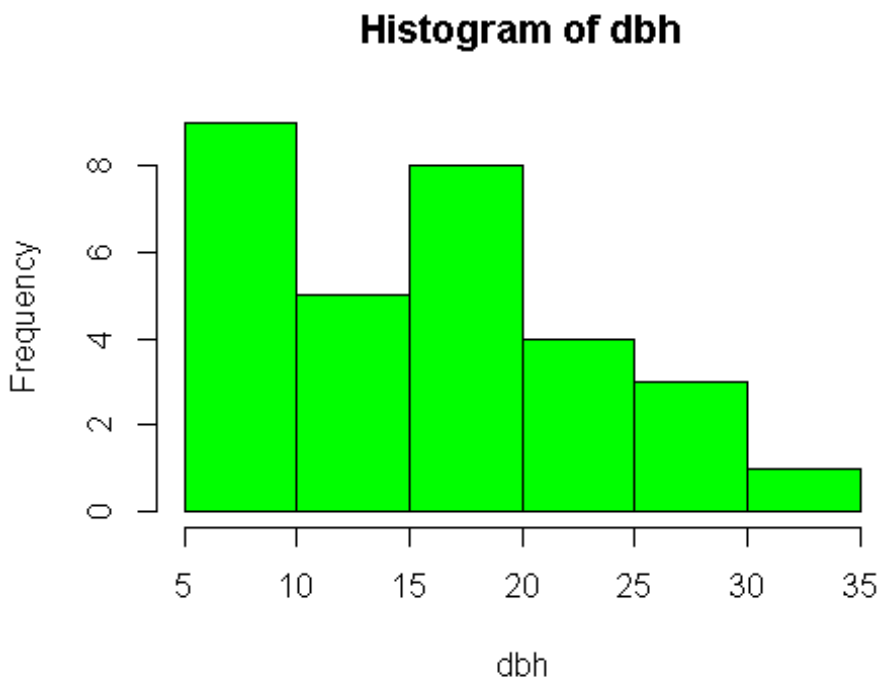
```
mean(trees$dbh)
```

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

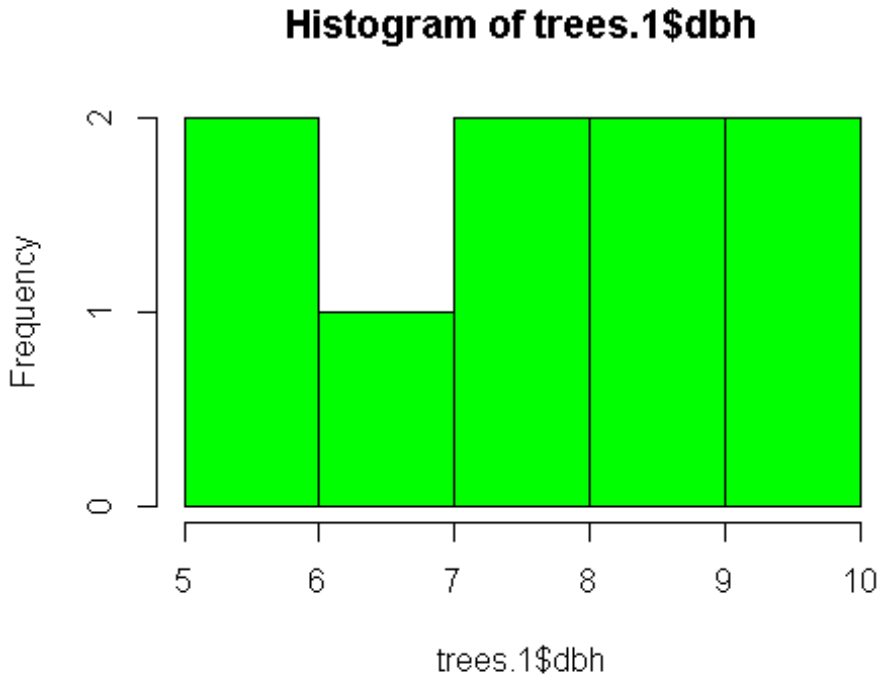
```
mean(trees.1$dbh)
```

```
## [1] 7.677778
```

```
hist(dbh, col = "green")
```

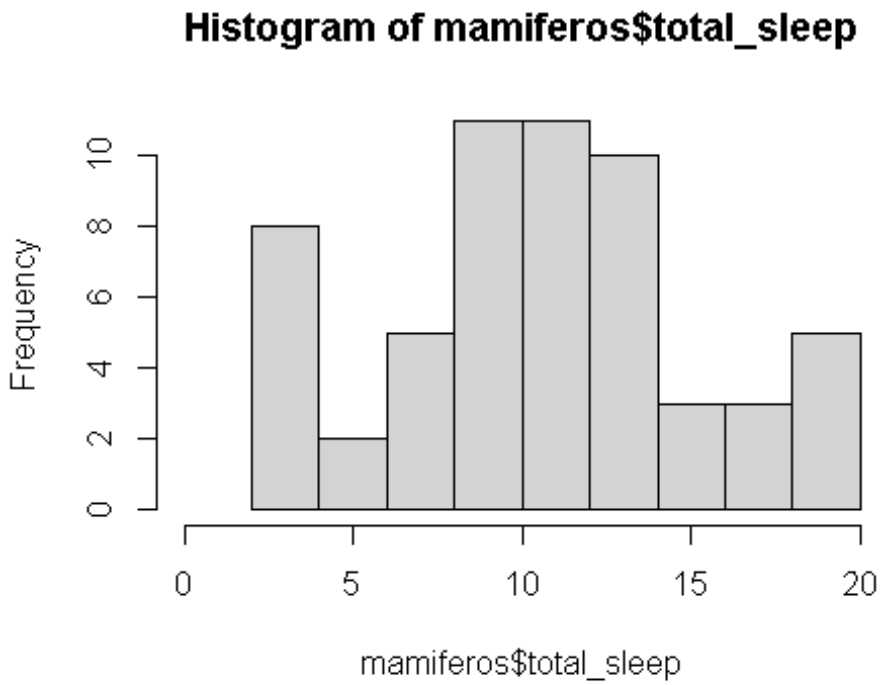



```
hist(trees.1$dbh, col = "green")
```

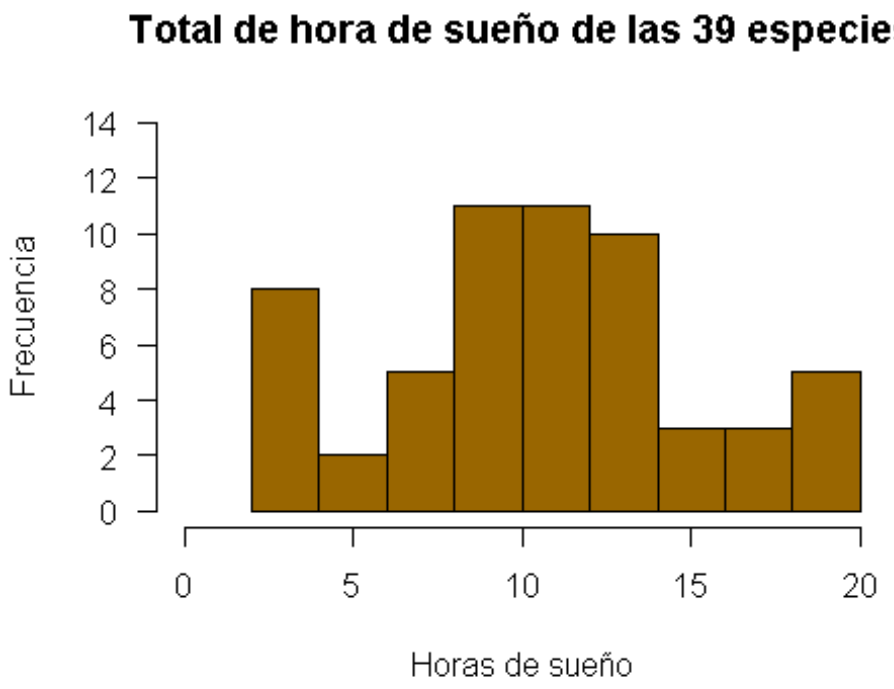



```
# Parte 3 ------------------------------------------------------------
--
```

```r
mamiferos <- read.csv("https://www.openintro.org/data/csv/mammals.csv")
hist(mamiferos$total_sleep, xlim= c(0,20))
```




```r
hist(mamiferos$total_sleep, xlim= c(0,20), ylim= c(0,14),
     main= "Total de hora de sueño de las 39 especies",
     xlab= "Horas de sueño",
     ylab= "Frecuencia",
     las= 1,
     col= "#996600")
```



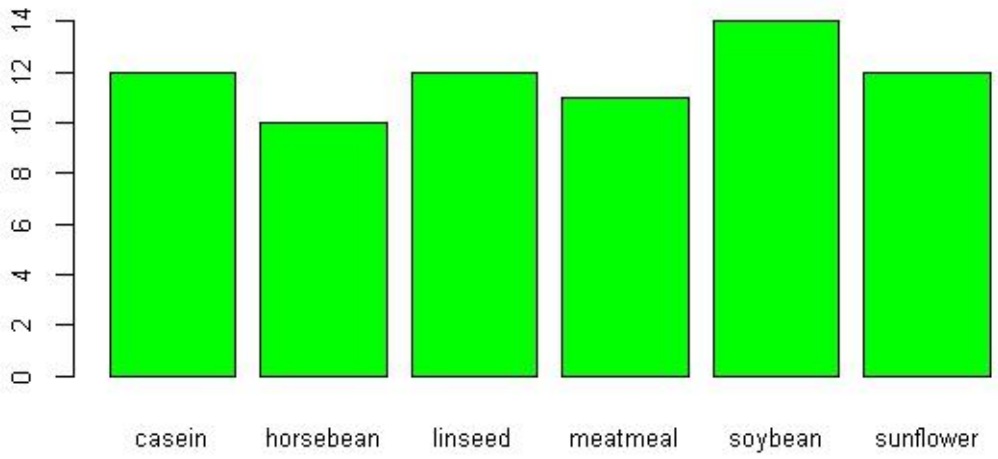

```
data("chickwts")

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
```

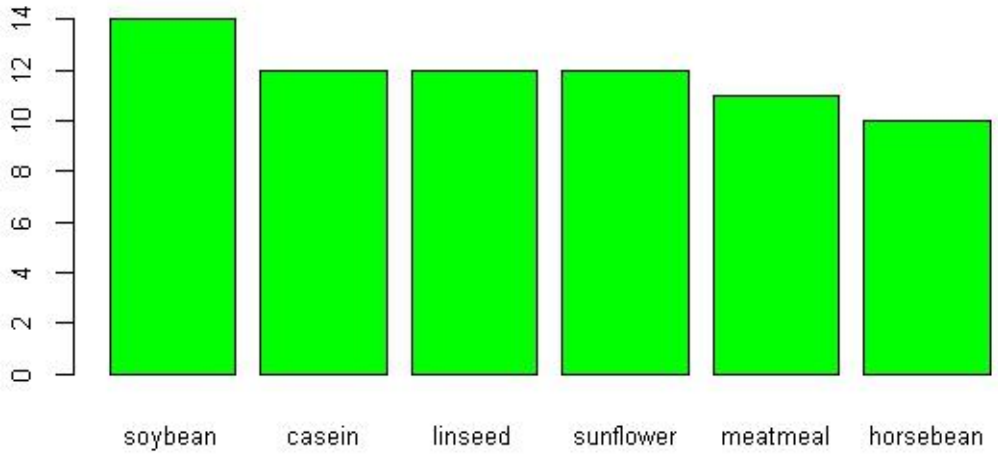
```
feeds <- table(chickwts$feed)
feeds
```

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

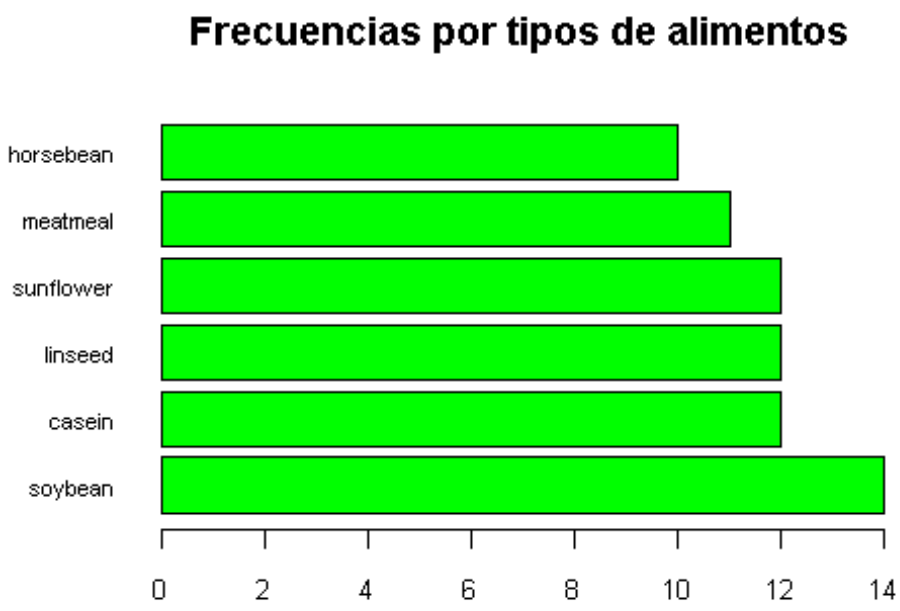
```
barplot(feeds, cex.names = 0.8, cex.axis = 0.8, col = "green")
```




```
barplot(feeds[order(feeds, decreasing = TRUE)], cex.axis = 0.8, cex.names
= 0.8, col = "green")
```




```
barplot(feeds[order(feeds, decreasing = TRUE)],
        horiz = TRUE, las = 1, col= "green", cex.axis = 0.8, cex.names =
0.7,
        main= "Frecuencias por tipos de alimentos")
```


Frecuencias por tipos de alimentos
horsebean
meatmeal
sunflower
linseed
casein
soybean
0
2
4
6
8
10
12
14