

Universidad Autónoma de Nuevo León

Facultad de Ciencias Forestales

Análisis Estadístico

Profesor: Dr. Marco A. González Tagle

Laboratorio 2: Importar datos a R

Jorge Alexis Luna Robles

Matricula: 2134500

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Laboratorio02_JorgeLuna.R

Alexis Luna

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```
# Importar desde archivos csv  
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
```

```
head(trees)
```

```
##      Girth Height Volume  
## 1      8.3     70  10.3  
## 2      8.6     65  10.3  
## 3      8.8     63  10.2  
## 4     10.5     72  16.4  
## 5     10.7     81  18.8  
## 6     10.8     83  19.7
```

#Ingresar datos directo en la 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)
```

Datos de URL no seguras (http)

```
prof_url <- "http://www.profepa.gob.mx/innovaportal/file/7635/1/accionesI  
nspeccionfoanp.csv"
```

```
profepa <- read.csv(prof_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
```

```
prof_url_2 <- paste0("http://www.profepa.gob.mx/innovaportal/",  
                    "file/7635/1/accionesInspeccionfoanp.csv")  
profepa2 <- read.csv(prof_url_2, header = T, fileEncoding = "Latin1")  
head(profepa2)
```

```
##           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
```

#Datos de URL seguras (https): Dropbox

```
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
```

#Datos de URL seguras (https): Github

```
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
```

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

--

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

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

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

```
sd(trees$dbh)
```

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

Selección mediante restricciones

```
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
```

Selección de una submuestra

```
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)
```

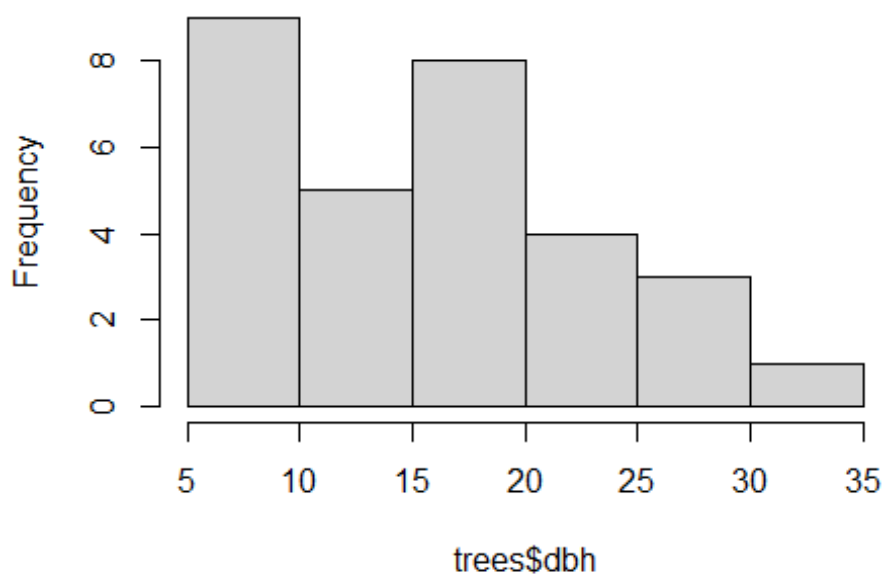
```
## [1] 15.64333
```

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

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

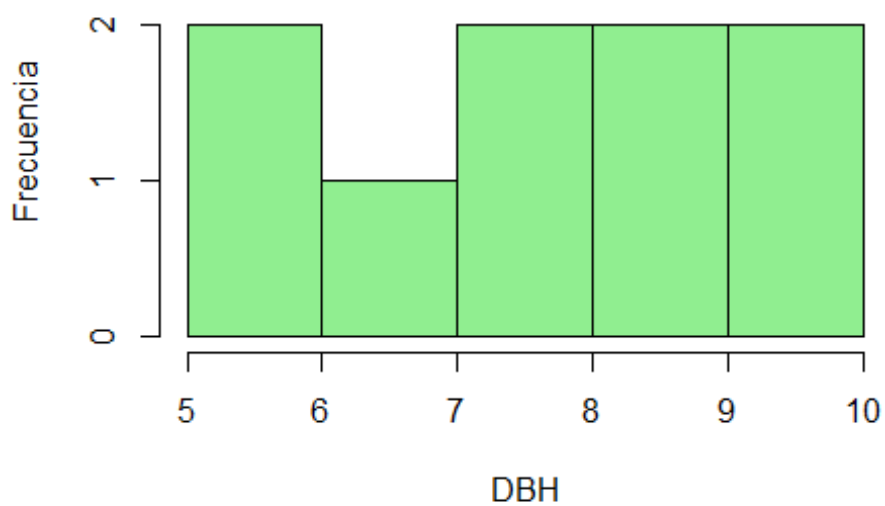
```
hist(trees$dbh)
```

Histogram of trees\$dbh

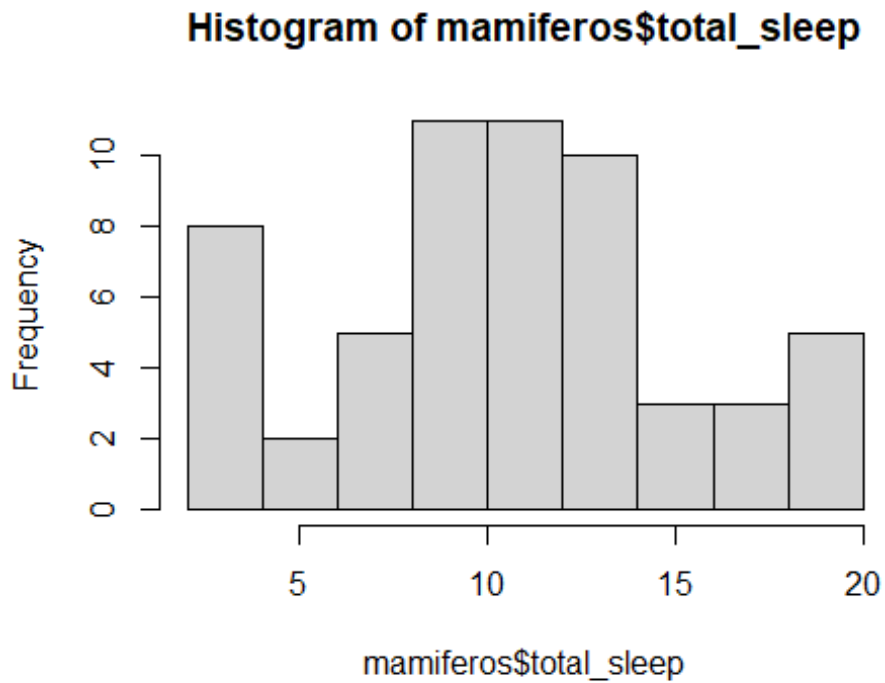


```
hist(trees.1$dbh, col = "lightgreen", ylab = "Frecuencia",  
xlab = "DBH", ylim= c(0, 2.5))
```

Histogram of trees.1\$dbh

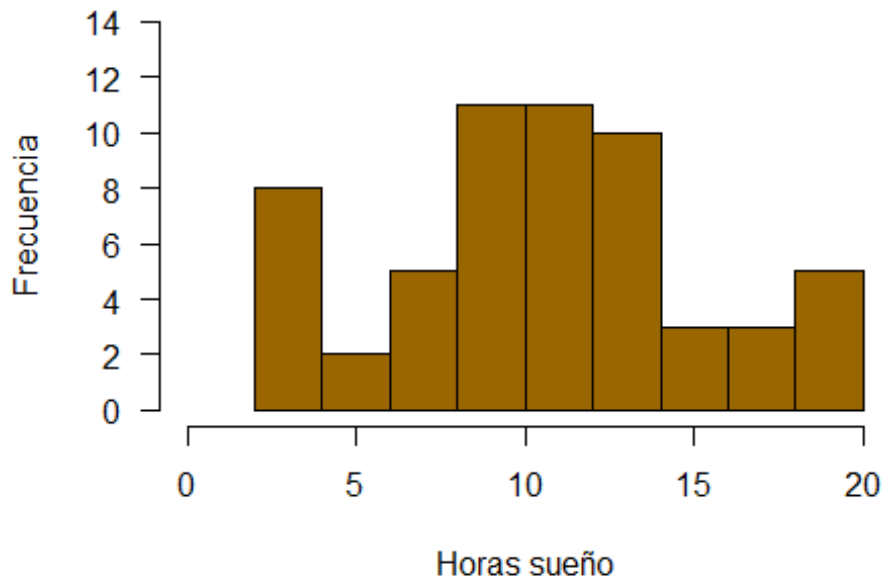


```
# Parte 3 Representación gráfica -----  
--  
  
# Histogramas  
mamiferos <- read.csv("https://www.openintro.org/data/csv/mammals.csv")  
  
hist(mamiferos$total_sleep)
```



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

Total de horas sueño de las 39 especies



#Barplot o gráfico de barras

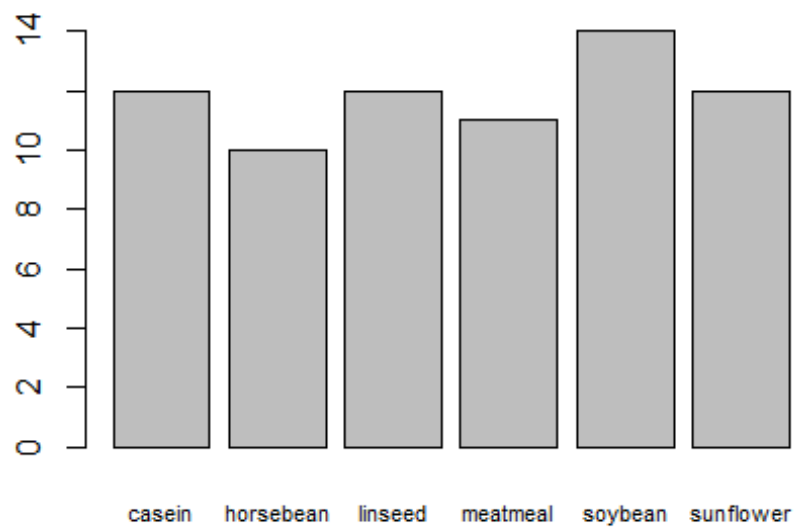
```
data("chickwts")
head(chickwts[c(1:2,42:43, 62:64), ])

##   weight    feed
## 1    179 horsebean
## 2    160 horsebean
## 42   226 sunflower
## 43   320 sunflower
## 62   379  casein
## 63   260  casein

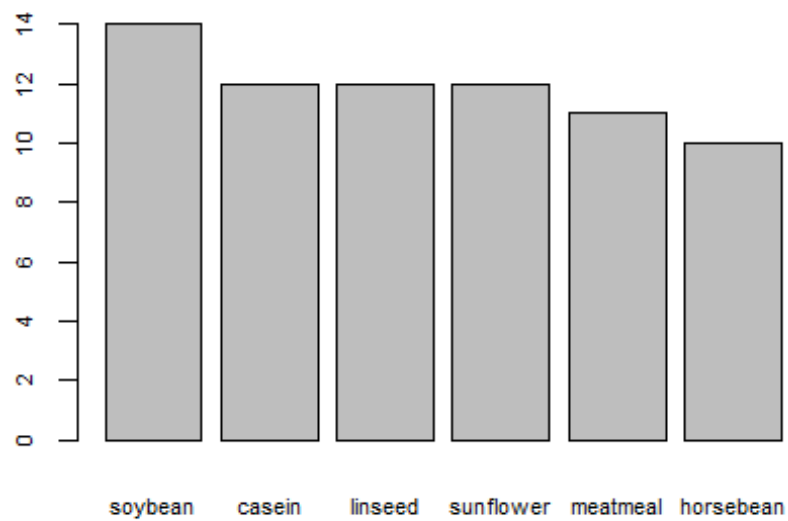
feeds <- table(chickwts$feed)
feeds

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

barplot(feeds, cex.names = 0.7)
```

```
barplot(feeds[order(feeds, decreasing = TRUE)], cex.axis = 0.7, cex.names = 0.7)
```



```
barplot(feeds[order(feeds, decreasing = TRUE)], horiz = TRUE,  
        las= 1, col = "yellow", xlab = "Número de pollos", cex.names = 0.  
8,  
        main= "Frecuencias por tipos de alimentos")
```

