

## Laboratorio-3.R

Andy

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```
# Andy Abril Ramos Villa
# 2026333
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# Ingresar datos directos en la consola -----
--

dbh <- c(16.5, 25.3, 22.1, 17.2, 16.1, 8.1, 34.3, 5.4, 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 seguras: Dropbox y Github -----
--

library(repmis)
conjunto <-
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)

##   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

# Operaciones con La base de datos -----
--

mean(trees$DBH)

## Warning in mean.default(trees$DBH): argument is not numeric or
logical:
## returning NA

## [1] NA

sd(trees$dbh)

## [1] NA

sum(trees$dbh < 10)

## [1] 0

which(trees$dbh < 10)

## integer(0)

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

## [1] Girth Height Volume
## <0 rows> (or 0-length row.names)

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

##   Girth Height Volume
## 6   10.8     83   19.7
## 8   11.0     75   18.2
## 12  11.4     76   21.0
## 15  12.0     75   19.1
## 18  13.3     86   27.4
## 20  13.8     64   24.9

mean(trees$dbh)

```

```
## Warning in mean.default(trees$dbh): argument is not numeric or
logical:
## returning NA

## [1] NA

mean(trees.1$dbh)

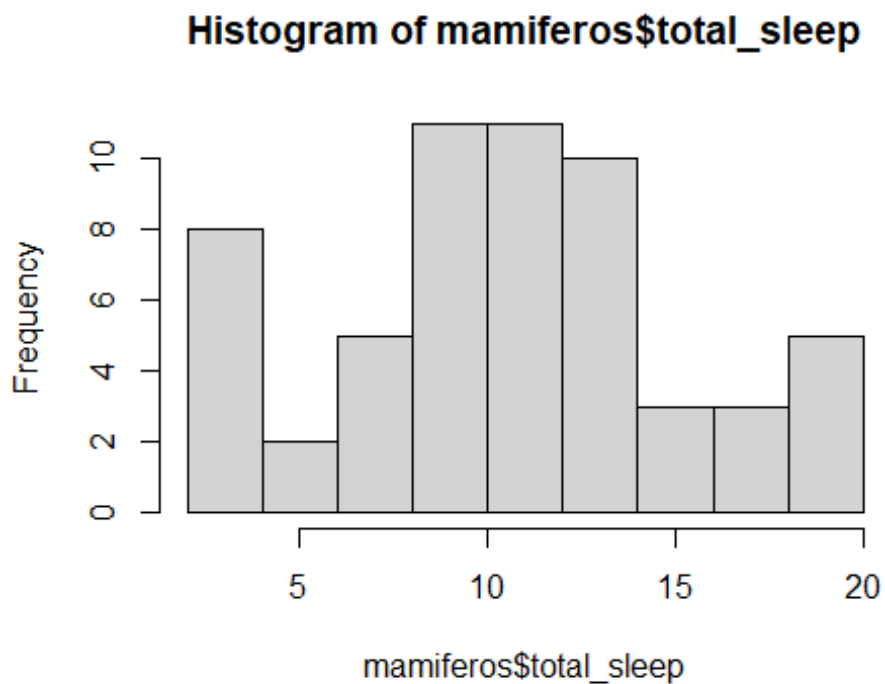
## Warning in mean.default(trees.1$dbh): argument is not numeric or
logical:
## returning NA

## [1] NA

# Representación gráfica -----
--

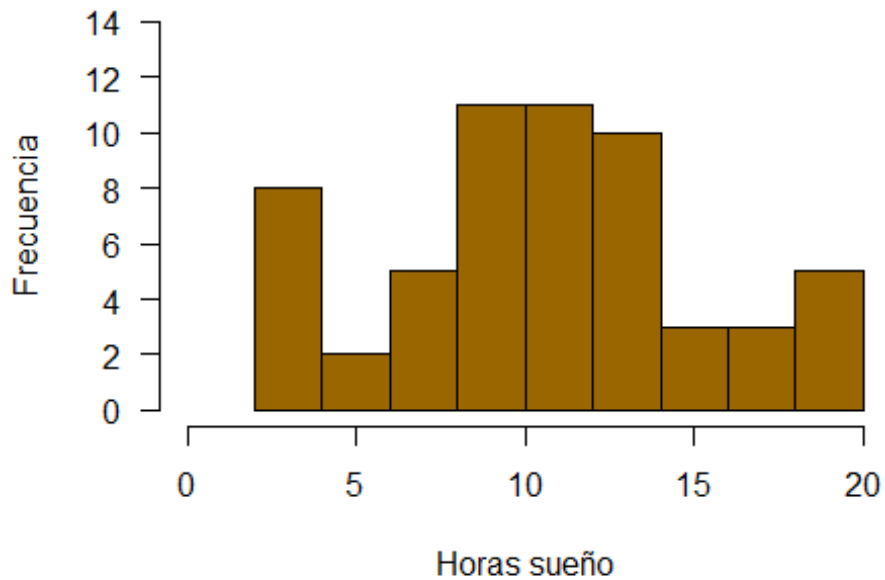
# Histogramas -----
--

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



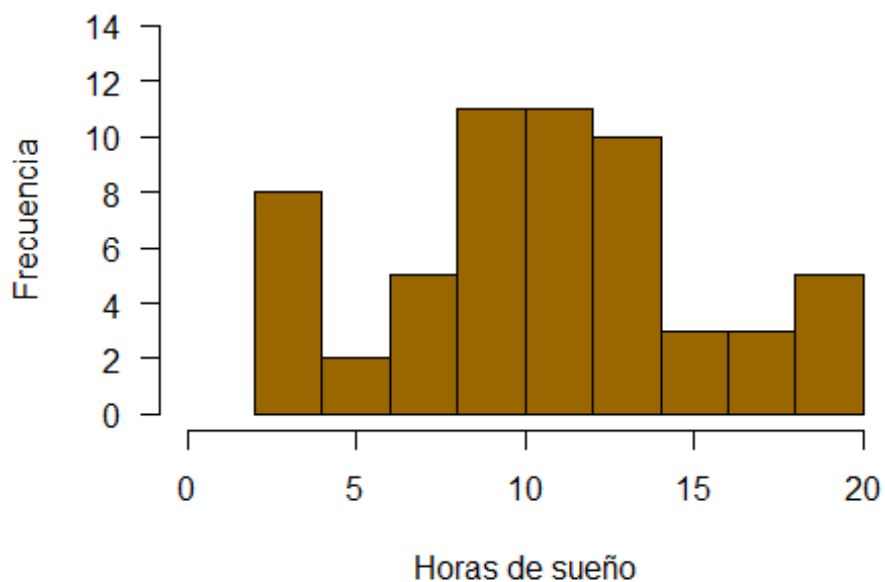
```
hist(mamiferos$total_sleep, xlim = c(0, 20), ylim = c(0,14),
     main = "Total de horas sueño de las 39 especies",
     xlab = "Horas sueño", ylab = "Frecuencia", las = 1, col = "#996600")
```

### Total de horas sueño de las 39 especies



```
# Datos -----  
--  
  
hist(mamiferos$total_sleep,  
      xlim = c(0,20), ylim = c(0,14), # Cambiar los límites de x & y,  
      main = "Total de horas de sueño de 39 especies ", # Cambiar el  
      titulo,  
      xlab = "Horas de sueño", # Cambiar eje de las x,  
      ylab = "Frecuencia", # Cambiar eje de las y,  
      las = 1, # Cambiar orientación de y,  
      col = "#996600") # Cambiar color de las barras
```

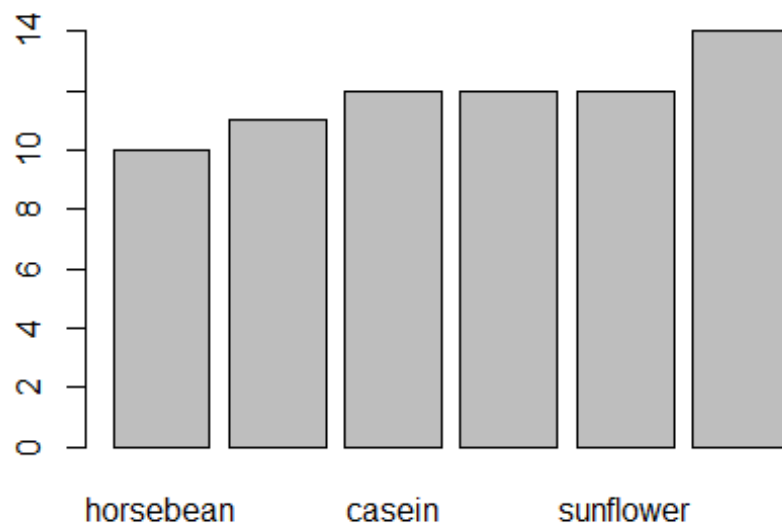
## Total de horas de sueño de 39 especies



```
# Barplots -----  
--  
  
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 = FALSE)])
```



```
# Personalizar histograma -----
--
```

```
barplot(sort(feeds), horiz = TRUE,  
        main = "Frecuencia de alimentacion",  
        las = 1, xlab = "Numeros de pollos",  
        col = c("purple", "pink", "green", "brown", "blue", "yellow"))
```

