

Ejercicio_Penguins

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Cargo los datos y las librerias utilizadas

```
#install.packages("palmerpenguins")
library(palmerpenguins)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
##
##     filter, lag
```

```
## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```
library(plyr)
```

```
## -----
```

```
## You have loaded plyr after dplyr - this is likely to cause problems.
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:
## library(plyr); library(dplyr)
```

```
## -----
```

```
##
## Attaching package: 'plyr'
```

```
## The following objects are masked from 'package:dplyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize
```

```
library(ggplot2)
library(patchwork)

data(package = 'palmerpenguins')
```

Ej 1) Número de individuos totales (1.1.), masculinos y femeninos por especie (1.2.).

```
species <- group_by(penguins, species)
dplyr::count(species)
```

```
## # A tibble: 3 x 2
## # Groups:   species [3]
##   species     n
##   <fct>     <int>
## 1 Adelie     152
## 2 Chinstrap   68
## 3 Gentoo     124
```

1.1.

1 Adelie 152 2 Chinstrap 68 3 Gentoo 124

```
sex <- group_by(penguins, sex)
dplyr::count(species, sex)
```

```
## # A tibble: 8 x 3
## # Groups:   species [3]
##   species   sex     n
##   <fct>     <fct> <int>
## 1 Adelie    female    73
## 2 Adelie    male     73
## 3 Adelie    <NA>      6
## 4 Chinstrap female    34
## 5 Chinstrap male     34
## 6 Gentoo    female    58
## 7 Gentoo    male     61
## 8 Gentoo    <NA>      5
```

1.2.

1 Adelie female 73 2 Adelie male 73 3 Adelie NA 6

4 Chinstrap female 34 5 Chinstrap male 34

6 Gentoo female 58 7 Gentoo male 61 8 Gentoo NA 5

1.3)La media, desviación estándar, valor mínimo y máximo de la longitud #y profundidad del pico, la longitud de la aleta y el tamaño.

Longitud Pico

```
media1 <- mean(penguins$bill_length_mm, na.rm = TRUE)
desvest1 <- sd(penguins$bill_length_mm, na.rm = TRUE)
minim1 <- min(penguins$bill_length_mm, na.rm = TRUE)
maxim1 <- max(penguins$bill_length_mm, na.rm = TRUE)

est_long_pico <- c(media1, desvest1, minim1, maxim1)
est_long_pico
```

```
## [1] 43.921930 5.459584 32.100000 59.600000
```

Profundidad Pico

```
media2 <- mean(penguins$bill_depth_mm, na.rm = TRUE)
desvest2 <- sd(penguins$bill_depth_mm, na.rm = TRUE)
minim2 <- min(penguins$bill_depth_mm, na.rm = TRUE)
maxim2 <- max(penguins$bill_depth_mm, na.rm = TRUE)

est_prof_pico <- c(media2, desvest2, minim2, maxim2)
est_prof_pico
```

```
## [1] 17.151170 1.974793 13.100000 21.500000
```

Longitud Aleta

```
media3 <- mean(penguins$flipper_length_mm, na.rm = TRUE)
desvest3 <- sd(penguins$flipper_length_mm, na.rm = TRUE)
minim3 <- min(penguins$flipper_length_mm, na.rm = TRUE)
maxim3 <- max(penguins$flipper_length_mm, na.rm = TRUE)

est_long_aleta <- c(media3, desvest3, minim3, maxim3)
est_long_aleta
```

```
## [1] 200.91520 14.06171 172.00000 231.00000
```

Tamaño (masa)

```
media4 <- mean(penguins$body_mass_g, na.rm = TRUE)
desvest4 <- sd(penguins$body_mass_g, na.rm = TRUE)
minim4 <- min(penguins$body_mass_g, na.rm = TRUE)
maxim4 <- max(penguins$body_mass_g, na.rm = TRUE)

est_body_weight <- c(media4, desvest4, minim4, maxim4)
est_body_weight
```

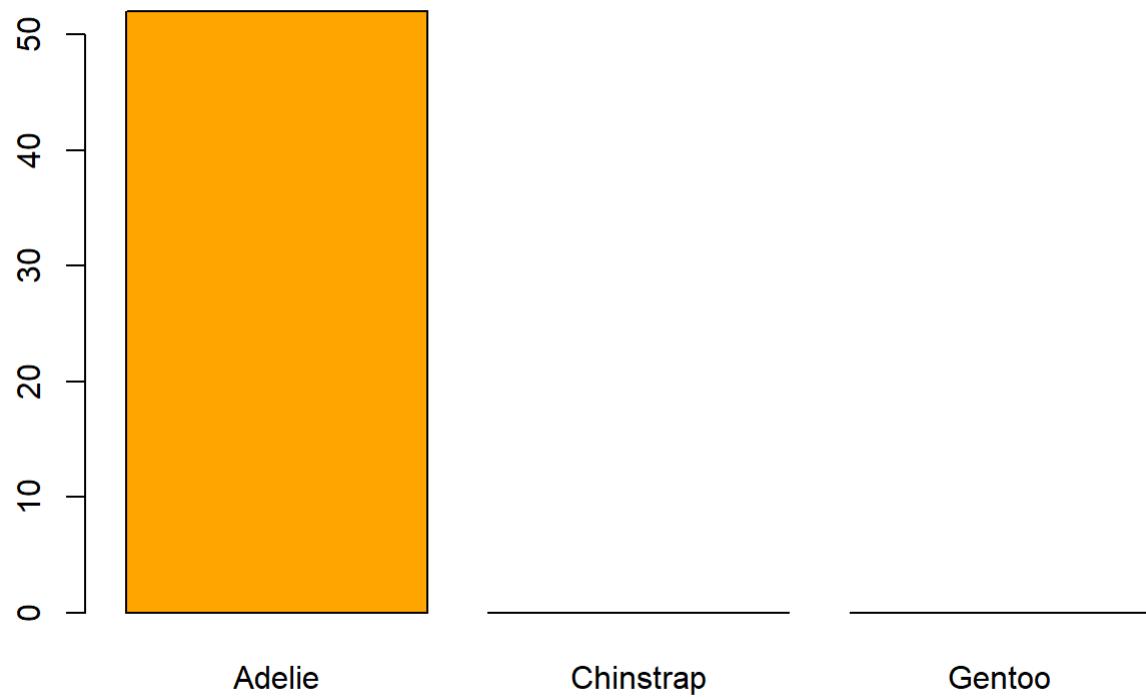
```
## [1] 4201.7544 801.9545 2700.0000 6300.0000
```

2) Un gráfico de barras que represente el número de individuos muestreados de cada especie en cada isla, ## representando las especies en diferentes colores (chinstrap – morado, gentoo – azul, adelie – naranja).

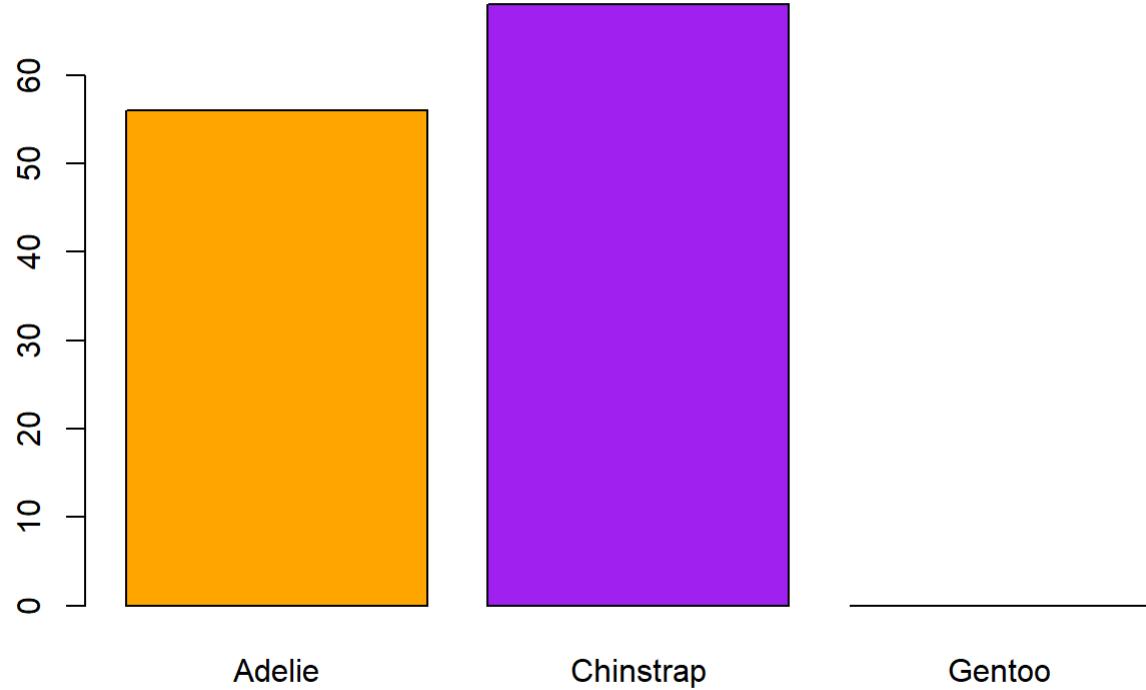
```
nombreIslas <- levels(penguins$island)

islaTorgen<- penguins[penguins$island == "Torgersen",]
islaDream <- penguins[penguins$island == "Dream",]
islaBiscoe <- penguins[penguins$island == "Biscoe",]

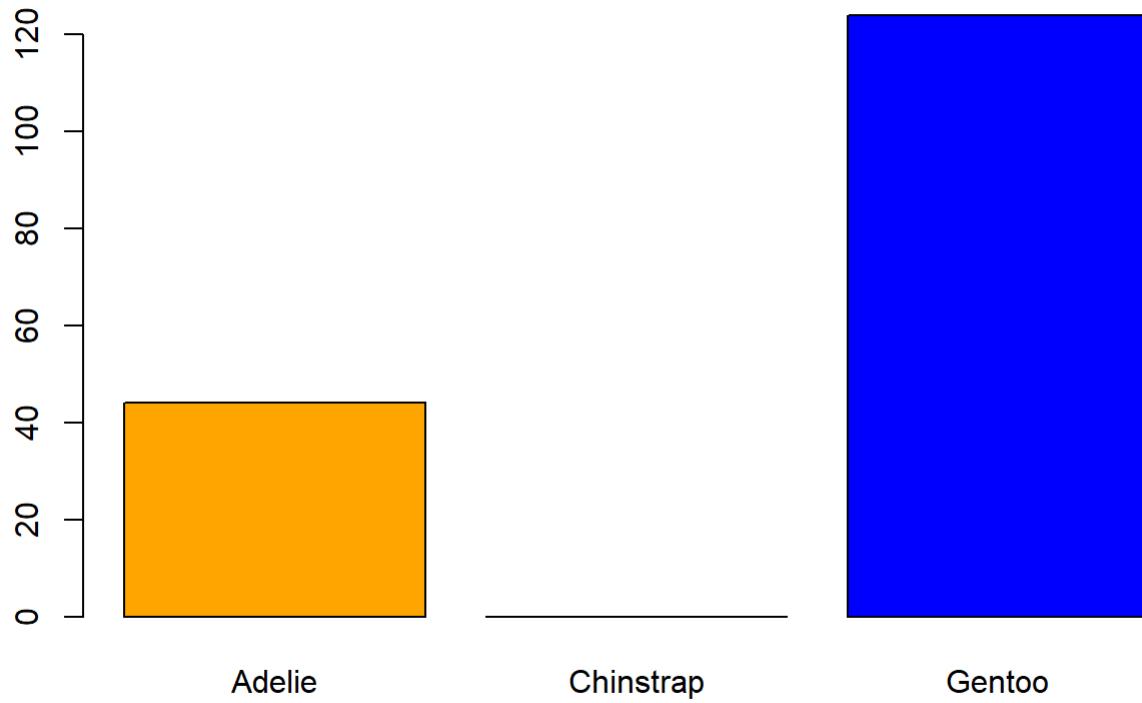
countTorgen <- table(islaTorgen$species)
barplot(countTorgen, col = c("orange", "purple", "blue"))
```



```
countDream <- table(islaDream$species)
barplot(countDream, col = c("orange", "purple", "blue"))
```



```
countBiscoe <- table(islaBiscoe$species)
barplot(countBiscoe, col= c("orange", "purple", "blue"))
```



a) ¿Qué especie se ha muestreado en las tres islas?

La especie muestreada en las tres islas es Adelie

b) ¿Cuántos individuos se han muestreado en la isla Dream?

```
dplyr::count(islaDream)
```

```
## # A tibble: 1 × 1
##       n
##   <int>
## 1    124
```

En la isla Dream se han muestreado 124 individuos.

3) Gráfico multipanel de cajas y bigotes del tamaño de los pingüinos según su sexo, donde aparezca un panel para cada especie.

```
levels(penguins$species)
```

```
## [1] "Adelie"    "Chinstrap" "Gentoo"
```

```
chinstrap <- penguins[penguins$species == "Chinstrap",]

p1 <- ggplot(chinstrap, aes(y= body_mass_g, group= sex, x= sex, fill= sex))+  
  geom_boxplot()+ ylim(c(2500, 6500))+ ylab("Masa corporal (g)") +xlab("Sexo")

adelie <- penguins[penguins$species == "Adelie",]

p2 <- ggplot(adelie, aes(y= body_mass_g, group= sex, x= sex, fill= sex))+  
  geom_boxplot()+ ylim(c(2500, 6500))+ ylab("Masa corporal (g)") +xlab("Sexo")

gentoo <- penguins[penguins$species == "Gentoo",]

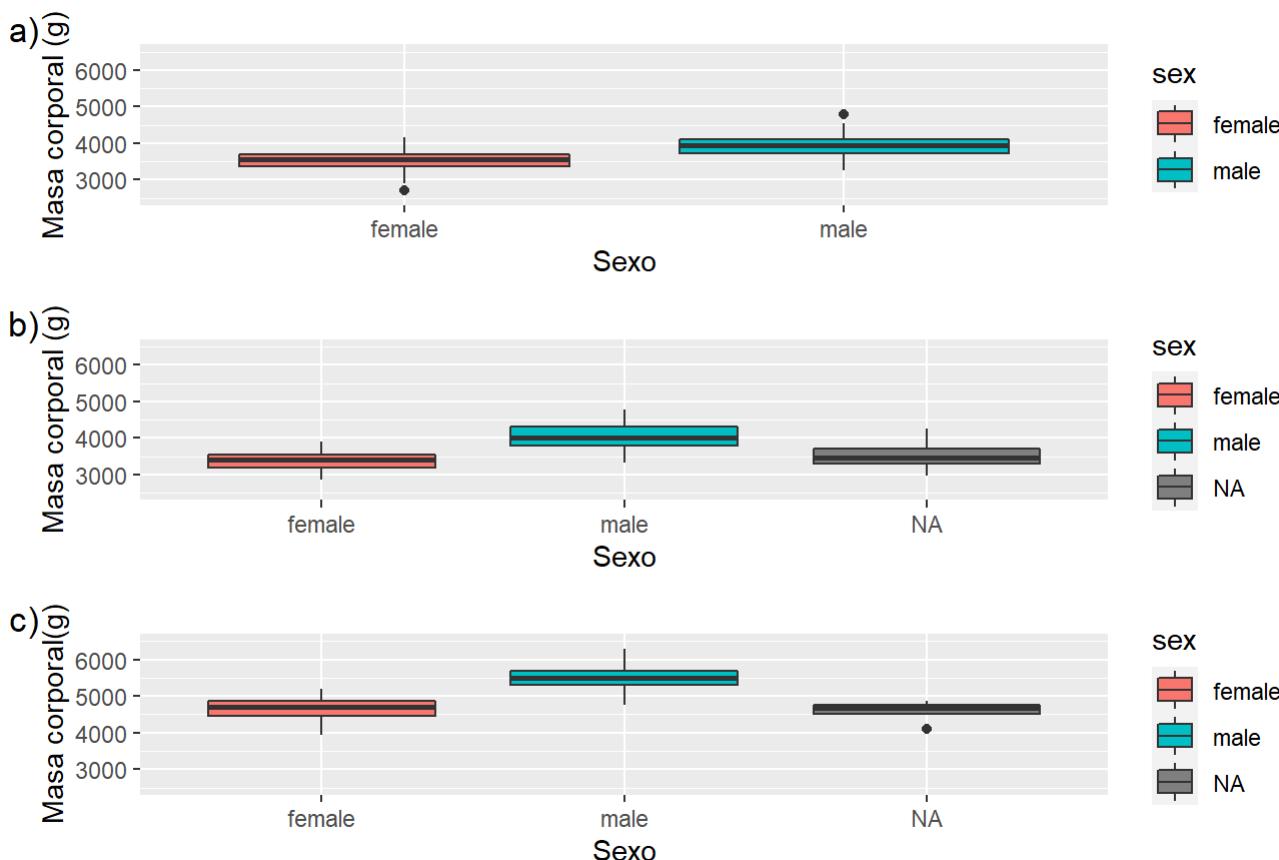
p3 <- ggplot(gentoo,aes(y= body_mass_g, x= sex, fill= sex), ylim= c(2500, 6500))+  
  geom_boxplot()+ ylim(c(2500, 6500))+ ylab("Masa corporal(g)")+xlab("Sexo")

p1 / p2 / p3 + plot_annotation(title = "Body mass by species (a for Chinstrap, b for Adelie, c for Gentoo)",tag_levels = "a", tag_suffix="")
```

```
## Warning: Removed 1 rows containing non-finite values (stat_boxplot).
```

```
## Warning: Removed 1 rows containing non-finite values (stat_boxplot).
```

Body mass by species (a for Chinstrap, b for Adelie, c for Gentoo)



3.1) ¿Qué especie tiene mayor tamaño?

Gentoo

3.2) ¿En qué especie las hembras y los machos tienen un tamaño más similar?

En la especie Chinstrap