

AC

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#Análisis Canónico #Llamar a las paqueterias

```
library(tidyverse)
```

```
## -- Attaching packages ----- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.6      v purrr  0.3.4
```

```
## v tibble  3.1.7      v dplyr  1.0.9
```

```
## v tidyr   1.2.0      v stringr 1.4.0
```

```
## v readr   2.1.2      v forcats 0.5.1
```

```
## -- Conflicts ----- tidyverse_conflicts() --
```

```
## x dplyr::filter() masks stats::filter()
```

```
## x dplyr::lag()    masks stats::lag()
```

```
library(readxl)
```

Preparacion de la matriz

Se utiliza la matriz penguins.xlsx, importar la matriz de datos.

```
penguins <- read_excel("penguins.xlsx")
```

Exploracion de la matriz

```
dim(penguins)
```

```
## [1] 344  9
```

```
colnames(penguins)
```

```
## [1] "ID"          "especie"      "isla"         "largo_pico_mm"
```

```
## [5] "grosor_pico_mm" "largo_aleta_mm" "masa_corporal_g" "genero"
```

```
## [9] "año"
```

```
str(penguins)
```

```
## tibble [344 x 9] (S3: tbl_df/tbl/data.frame)
```

```
## $ ID          : chr [1:344] "i1" "i2" "i3" "i4" ...
```

```
## $ especie     : chr [1:344] "Adelie" "Adelie" "Adelie" "Adelie" ...
```

```
## $ isla        : chr [1:344] "Torgersen" "Torgersen" "Torgersen" "Torgersen" ...
```

```
## $ largo_pico_mm : num [1:344] 39.1 39.5 40.3 37.8 36.7 39.3 38.9 39.2 34.1 42 ...
```

```
## $ grosor_pico_mm : num [1:344] 18.7 17.4 18 18.1 19.3 20.6 17.8 19.6 18.1 20.2 ...
```

```
## $ largo_aleta_mm : num [1:344] 181 186 195 190 193 190 181 195 193 190 ...
```

```
## $ masa_corporal_g: num [1:344] 3750 3800 3250 3700 3450 ...
```

```
## $ genero      : chr [1:344] "male" "female" "female" "female" ...
## $ año        : num [1:344] 2007 2007 2007 2007 2007 ...

anyNA(penguins)

## [1] FALSE
```

Escalamiento de la matriz

Generacion de variables X

```
X <- penguins %>%
  select(grosor_pico_mm, largo_pico_mm) %>%
  scale()
head(X)

##      grosor_pico_mm largo_pico_mm
## [1,]      0.7863145      -0.8825216
## [2,]      0.1267012      -0.8093460
## [3,]      0.4311381      -0.6629947
## [4,]      0.4818776      -1.1203424
## [5,]      1.0907514      -1.3215754
## [6,]      1.7503647      -0.8459338
```

Generacion de variables Y

```
Y <- penguins %>%
  select(largo_aleta_mm, masa_corporal_g) %>% scale()
head(Y)

##      largo_aleta_mm masa_corporal_g
## [1,]      -1.4166210      -0.5646829
## [2,]      -1.0614850      -0.5022529
## [3,]      -0.4222402      -1.1889828
## [4,]      -0.7773762      -0.6271129
## [5,]      -0.5642946      -0.9392628
## [6,]      -0.7773762      -0.6895429
```

Analisis canonico con un par de variables

Libreria

```
library(CCA)

## Loading required package: fda
## Loading required package: splines
## Loading required package: fds
## Loading required package: rainbow
## Loading required package: MASS
```

```
##
## Attaching package: 'MASS'
## The following object is masked from 'package:dplyr':
##
##      select
## Loading required package: pcaPP
## Loading required package: RCurl
##
## Attaching package: 'RCurl'
## The following object is masked from 'package:tidyr':
##
##      complete
## Loading required package: deSolve
##
## Attaching package: 'fda'
## The following object is masked from 'package:graphics':
##
##      matplot
## Loading required package: fields
## Loading required package: spam
## Spam version 2.8-0 (2022-01-05) is loaded.
## Type 'help( Spam)' or 'demo( spam)' for a short introduction
## and overview of this package.
## Help for individual functions is also obtained by adding the
## suffix '.spam' to the function name, e.g. 'help( chol.spam)'.
##
## Attaching package: 'spam'
## The following objects are masked from 'package:base':
##
##      backsolve, forwardsolve
## Loading required package: viridis
## Loading required package: viridisLite
##
## Try help(fields) to get started.
```

Analisis

```
ac<-cancor(X,Y)
```

Visualizacion de la matriz X

```
ac$xcoef
```

```
##           [,1]      [,2]
## grosor_pico_mm 0.03098538 0.04615243
## largo_pico_mm -0.03746177 0.04107014
```

Visualizacion de la matriz Y

```
ac$ycoef
```

```
##           [,1]      [,2]
## largo_aleta_mm -0.055220261 -0.0951545
## masa_corporal_g 0.001411466 0.1100076
```

Visualizacion de la correlacion canonica

```
ac$cor
```

```
## [1] 0.79268475 0.09867305
```

Obtencion de la matriz de variables canonicas Se obtiene multiplicando los coeficientes por cada una de las variables (X1 y Y1)

```
ac1_X <- as.matrix(X) %*% ac$xcoef[, 1]
ac1_Y <- as.matrix(Y) %*% ac$ycoef[, 1]
```

Visualizacion de los primeros 20 datos

```
ac1_X[1:20,]
```

```
## [1] 0.05742508 0.03424542 0.03819593 0.05690117 0.08330590 0.08592589
## [7] 0.04464608 0.07088939 0.08225809 0.06113346 0.04117935 0.04432371
## [13] 0.02642463 0.10015624 0.12599695 0.06040849 0.06488291 0.06556776
## [19] 0.08491867 0.05415894
```

```
ac1_Y[1:20,]
```

```
## [1] 0.07742915 0.05790657 0.02163800 0.04204177 0.02983476 0.04195365
## [7] 0.07720886 0.02414936 0.02987882 0.04301106 0.05702539 0.08126317
## [13] 0.07253771 0.03829586 0.01189829 0.06165247 0.02199048 0.01599667
## [19] 0.06491373 0.02723438
```

Correlacion canonica entre variable X1 y Y1

```
cor(ac1_X,ac1_Y)
```

```
##           [,1]
## [1,] 0.7926848
```

Verificacion de la correlacion canonica

```
assertthat::are_equal(ac$cor[1],
                      cor(ac1_X,ac1_Y)[1])
```

```
## [1] TRUE
```

Analisis canonico con dos pares de variables

Calculo de las variables X2 y Y2

```
ac2_X <- as.matrix(X) %*% ac$xcoef[, 2]
ac2_Y <- as.matrix(Y) %*% ac$ycoef[, 2]
```

Agregamos las variables generadas a la matriz original de penguins

```
ac_df <- penguins %>%
  mutate(ac1_X=ac1_X,
         ac1_Y=ac1_Y,
         ac2_X=ac2_X,
         ac2_Y=ac2_Y)
```

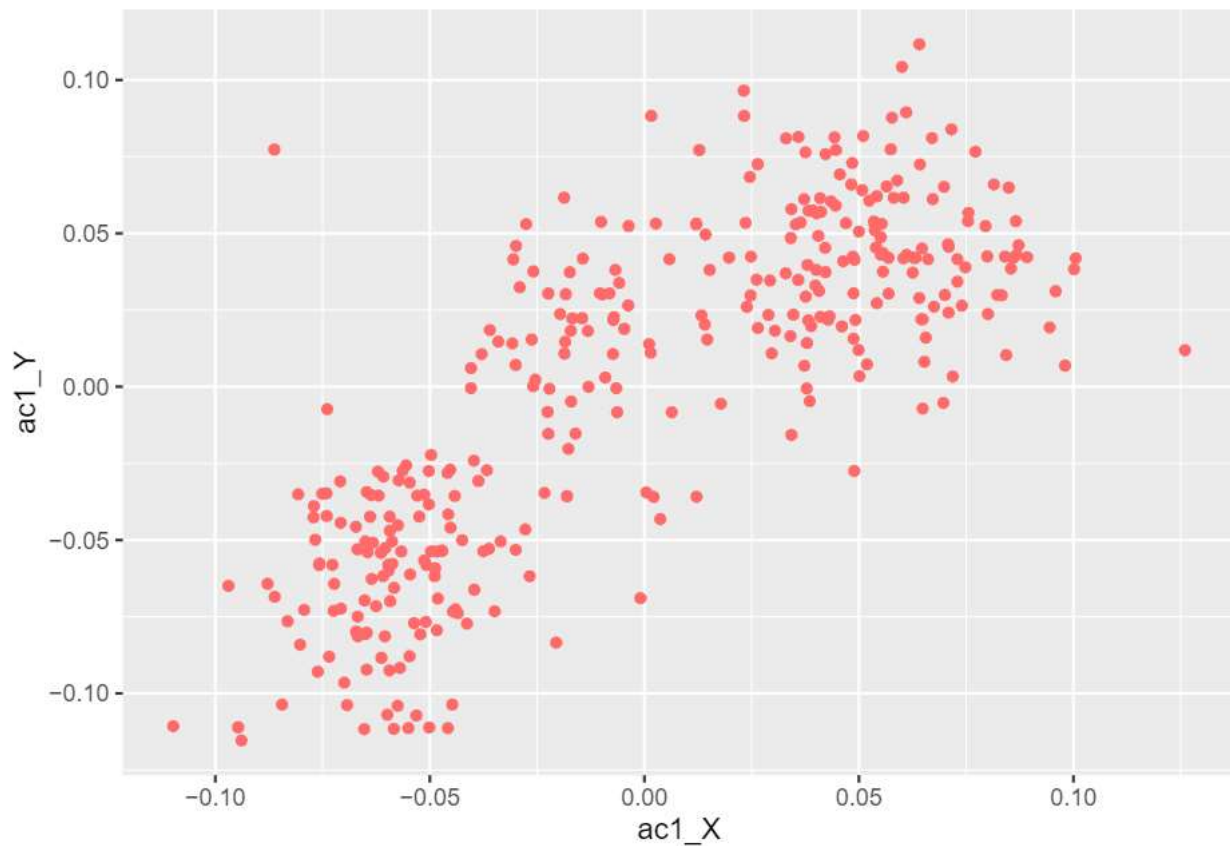
Visualizacion de los nombres de las variables

```
colnames(ac_df)
```

```
## [1] "ID"          "especie"      "isla"         "largo_pico_mm"
## [5] "grosor_pico_mm" "largo_aleta_mm" "masa_corporal_g" "genero"
## [9] "año"         "ac1_X"       "ac1_Y"       "ac2_X"
## [13] "ac2_Y"
```

Generacion del grafico scatter plot para la visualizacion de X1 y Y1

```
ac_df %>%
  ggplot(aes(x=ac1_X,y=ac1_Y))+
  geom_point(color="indianred1")
```

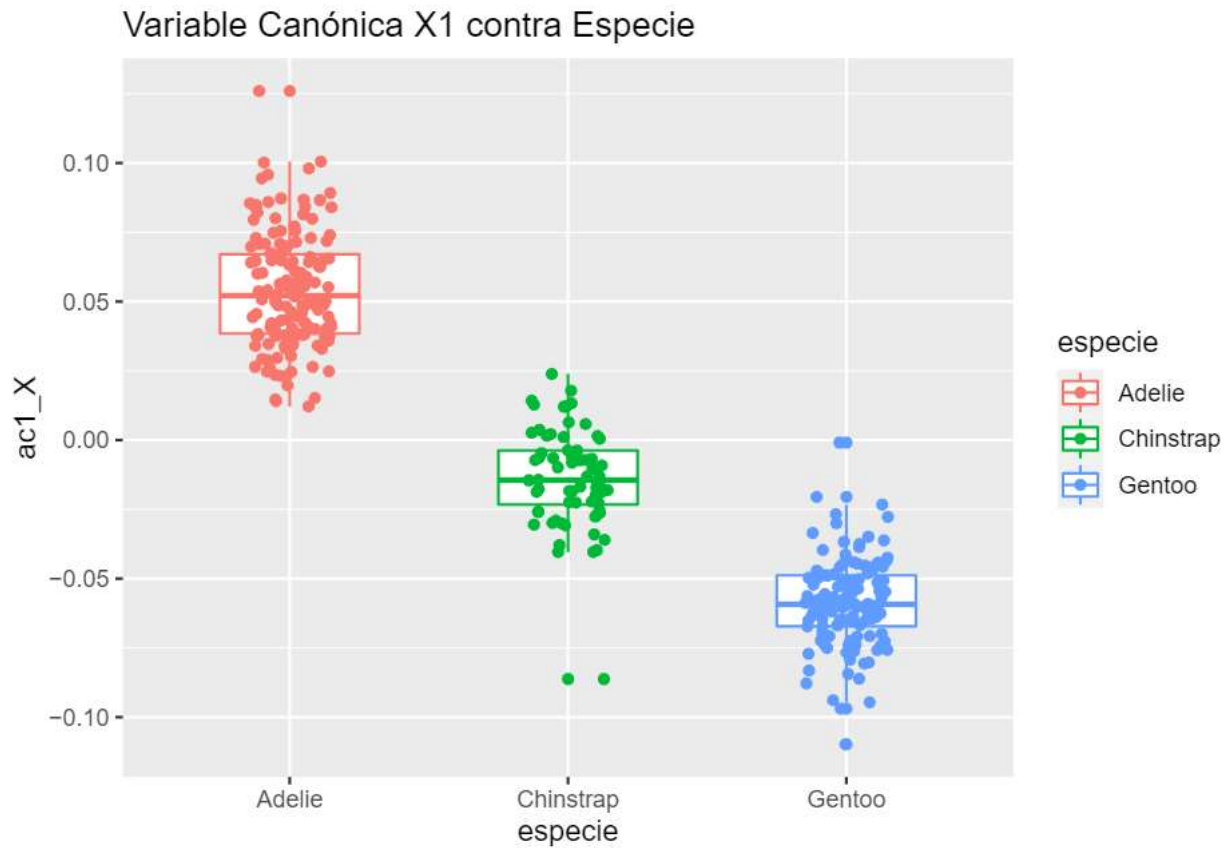


Generacion de un boxplot

```
ac_df %>%
  ggplot(aes(x=especie,y=ac1_X, color=especie))+
```

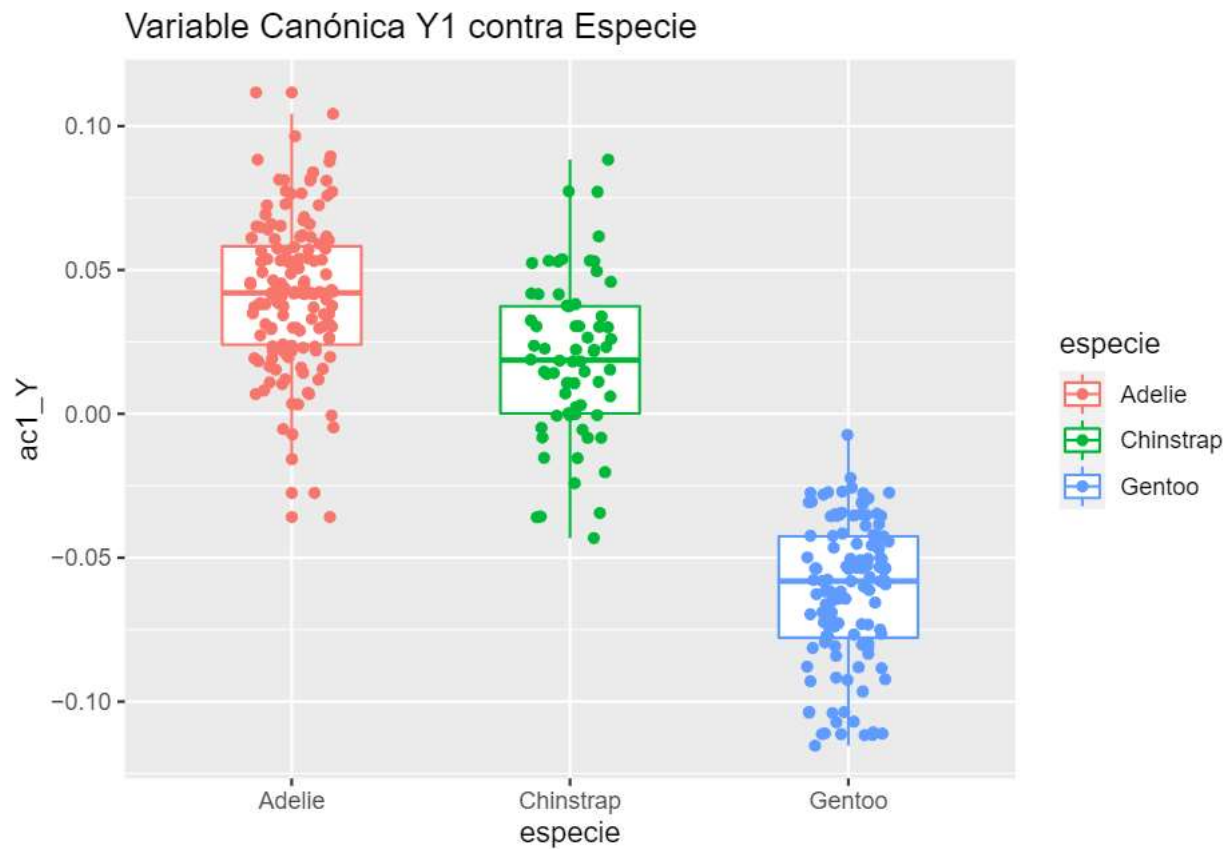


```
geom_boxplot(width=0.5)+
geom_jitter(width=0.15)+
ggtitle("Variable Canónica X1 contra Especie")
```

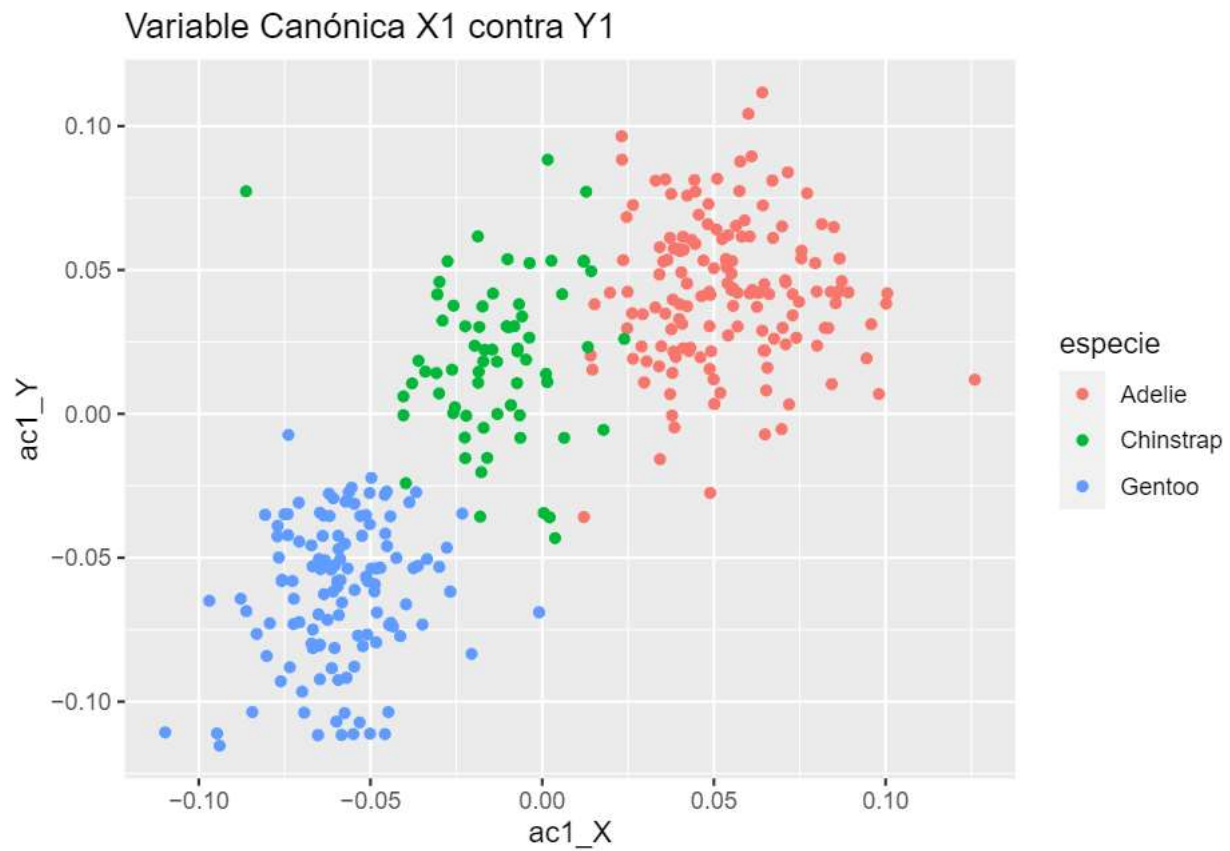


Interpretación: se observa una correlación entre la variable canónica X1 y la variable latente Especie

```
ac_df %>%
ggplot(aes(x=especie,y=ac1_Y, color=especie))+
geom_boxplot(width=0.5)+
geom_jitter(width=0.15)+
ggtitle("Variable Canónica Y1 contra Especie")
```



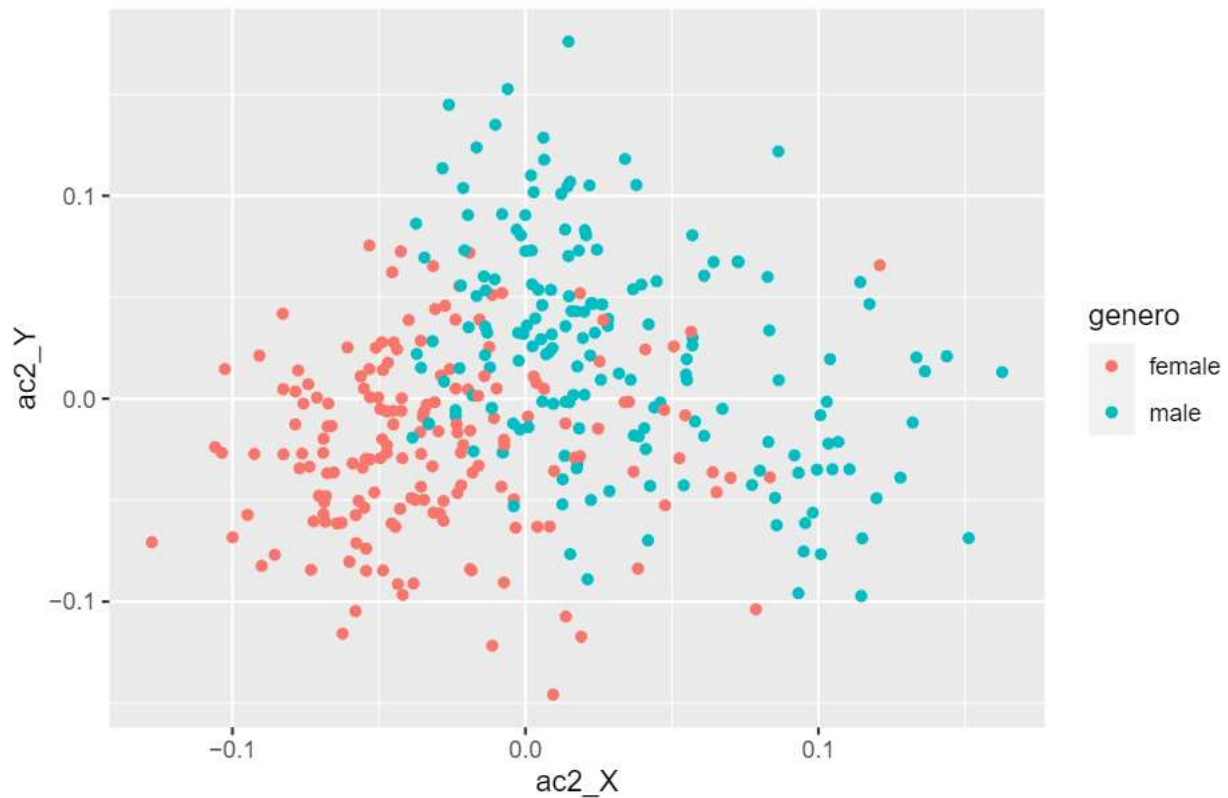
```
ac_df %>%  
  ggplot(aes(x=ac1_X,y=ac1_Y, color=especie))+  
  geom_point()+  
  ggtitle("Variable Canónica X1 contra Y1")
```



Scarter plot con las variables canonicas X2 y Y2 separadas por genero.

```
ac_df %>%
  ggplot(aes(x=ac2_X,y=ac2_Y, color=genero))+
  geom_point()+
  ggtitle("Variable Canónica X2 contra Y2")
```


Variable Canónica X2 contra Y2



Interpretacion: No se identifica correlación entre el conjunto de variables X2 y Y2 separadas por género.

#Generacion canonica

```
ac$xcoef
```

```
##                [,1]      [,2]
## grosor_pico_mm  0.03098538 0.04615243
## largo_pico_mm  -0.03746177 0.04107014
```

```
ac$ycoef
```

```
##                [,1]      [,2]
## largo_aleta_mm -0.055220261 -0.0951545
## masa_corporal_g  0.001411466  0.1100076
```

```
view(ac_df)
```