

Dendograma

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2022-06-03

Dendrograma.

1.- Se cargarán las librerías.

```
library(cluster.datasets)
```

2.- Bajamos la matriz de datos

```
data("all.mammals.milk.1956")
```

3.- Cambiamos el nombre de la matriz

```
AMM=all.mammals.milk.1956  
head(AMM)
```

```
##      name water protein fat lactose ash  
## 1   Horse  90.1     2.6 1.0    6.9 0.35  
## 2 Orangutan 88.5     1.4 3.5    6.0 0.24  
## 3   Monkey  88.4     2.2 2.7    6.4 0.18  
## 4   Donkey  90.3     1.7 1.4    6.2 0.40  
## 5   Hippo  90.4     0.6 4.5    4.4 0.10  
## 6   Camel  87.7     3.5 3.4    4.8 0.71
```

4.- Calculo de la matriz de distancia de Mahalanobis

```
dist.AMM<-dist(AMM[,2:6])
```

5.- Convertir los resultados del Calculo de la distancia a una matriz de datos y me indique 3 digitos.

```
round(as.matrix(dist.AMM)[1:6, 1:6],3)
```

```
##      1      2      3      4      5      6  
## 1 0.000 3.327 2.494 1.226 4.759 4.107  
## 2 3.327 0.000 1.206 2.794 2.798 2.592  
## 3 2.494 1.206 0.000 2.375 3.716 2.348  
## 4 1.226 2.794 2.375 0.000 3.763 4.007
```

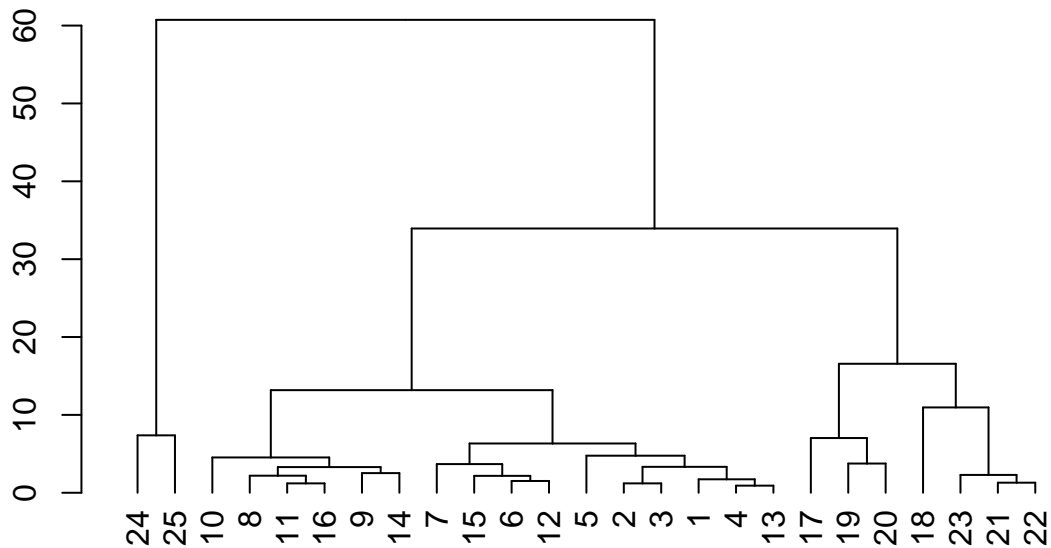
```
## 5 4.759 2.798 3.716 3.763 0.000 4.176
## 6 4.107 2.592 2.348 4.007 4.176 0.000
```

6.- Calculo del dendrograma

```
dend.AMM<-as.dendrogram(hclust(dist.AMM))
```

7.- Generacion del dendrograma

```
plot(dend.AMM)
```

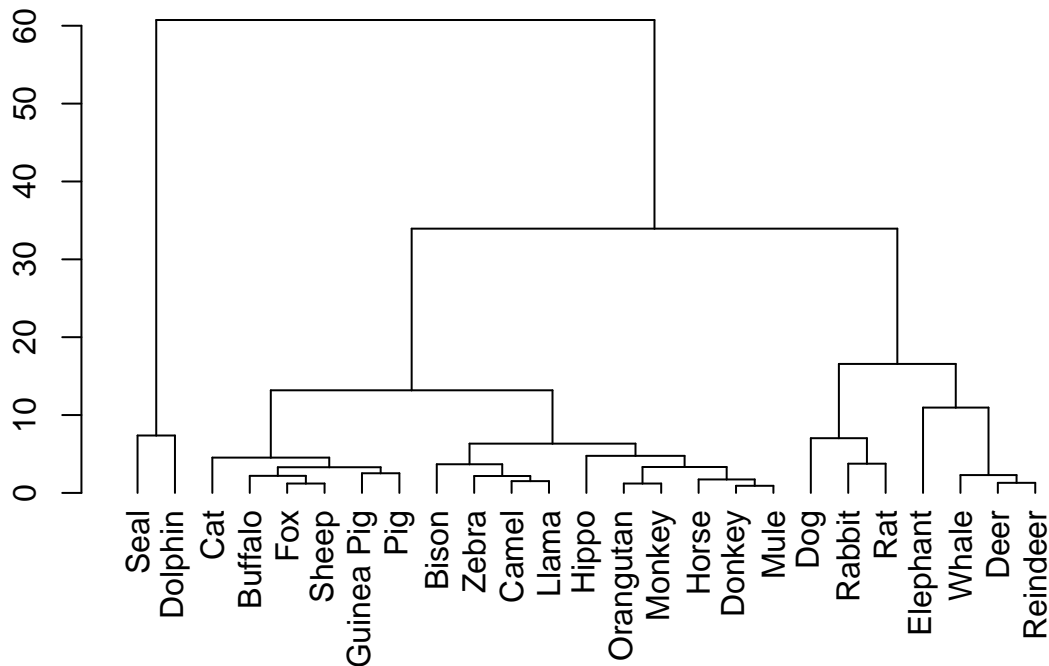


8.- Agregar etiquetas al Grafico

```
AMM.nombres=AMM
rownames(AMM.nombres)= AMM.nombres$name
AMM.nombres=AMM.nombres[, -1]
```

9.- Construimos de nuevo el Grafico

```
plot(as.dendrogram(hclust(dist(AMM.nombres))))
```



10.- Modificar el dendrograma

```
install.packages("dendextend")
```

```
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.2'
## (as 'lib' is unspecified)
```

```
library(dendextend)
```

```
##
## -----
## Welcome to dendextend version 1.15.2
## Type citation('dendextend') for how to cite the package.
##
## Type browseVignettes(package = 'dendextend') for the package vignette.
## The github page is: https://github.com/talgalili/dendextend/
##
## Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dendextend/issues
## You may ask questions at stackoverflow, use the r and dendextend tags:
##   https://stackoverflow.com/questions/tagged/dendextend
##
## To suppress this message use: suppressPackageStartupMessages(library(dendextend))
## -----
##
## Attaching package: 'dendextend'
##
## The following object is masked from 'package:stats':
##
##   cutree
```

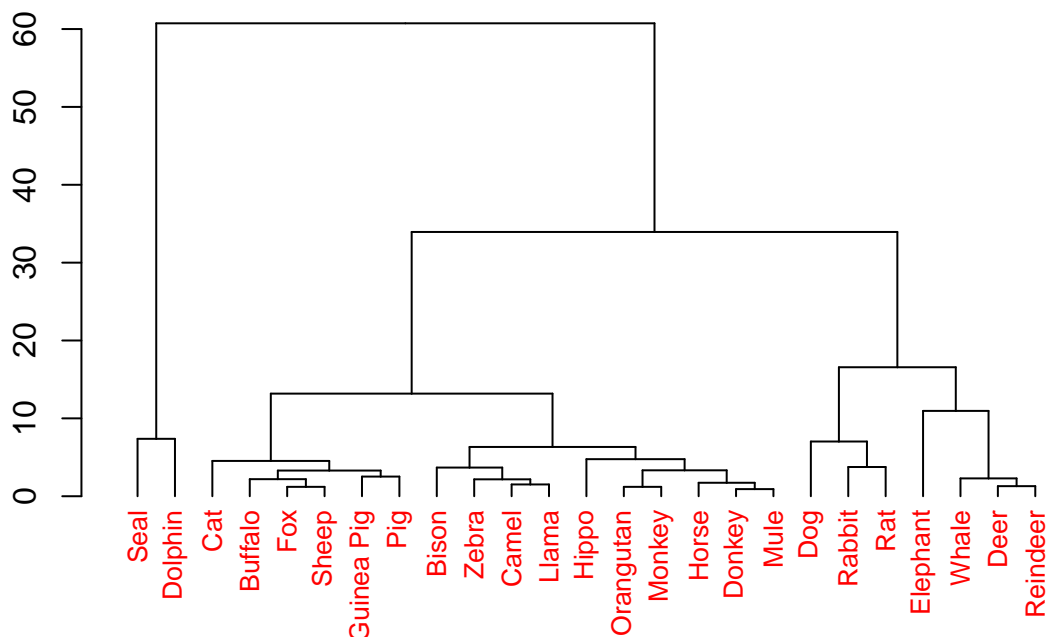
11.- Guardar las etiquetas en un objeto “L”

```
L=labels(dend.AMM)
labels(dend.AMM)=AMM$name[L]
```

12.- Cambiar el tamaño de las etiquetas

```
dend.AMM %>%
  set(what="labels_col", "red") %>% #Colores etiqueta
  set(what="labels_cex", 0.8) %>%
  plot(main="Dendrograma de Mamiferos")
```

Dendrograma de Mamiferos



13.- Dendrograma de Circulo

```
install.packages("circlize")
```

```
## Installing package into '/cloud/lib/x86_64-pc-linux-gnu-library/4.2'
## (as 'lib' is unspecified)
```

```
library("circlize")
```

```
## =====
## circlize version 0.4.15
## CRAN page: https://cran.r-project.org/package=circlize
## Github page: https://github.com/jokergoo/circlize
## Documentation: https://jokergoo.github.io/circlize\_book/book/
##
## If you use it in published research, please cite:
## Gu, Z. circlize implements and enhances circular visualization
```

```
## in R. Bioinformatics 2014.
##
## This message can be suppressed by:
## suppressPackageStartupMessages(library(circlize))
## =====
circlize_dendrogram(dend.AMM, labels_track_height=NA,
                    dend_track_height=0.1)
```

