

DENDROGRAMA

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```
#Dendrograma  
##intalar paqueterias y subir la base de datos  
  
library(cluster.datasets)  
data("all.mammals.milk.1956")  
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
```

Calculo de la matriz de distancia de Mahalonobis

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

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)
```

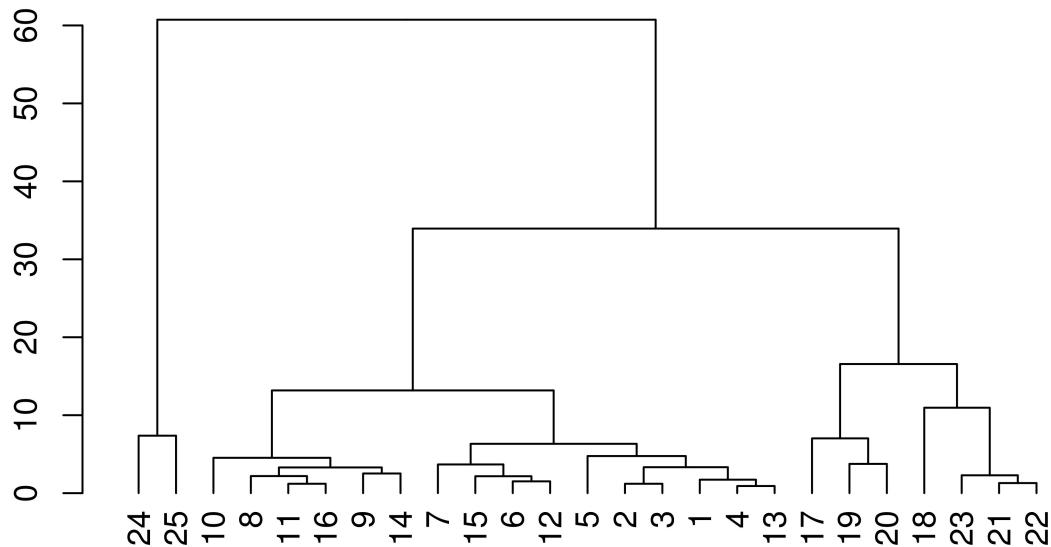
```
##      1     2     3     4     5     6  
## 1 0.000 3.327 2.494 1.226 4.759 4.107  
## 2 3.327 0.000 1.206 2.794 2.798 2.592  
## 3 2.494 1.206 0.000 2.375 3.716 2.348  
## 4 1.226 2.794 2.375 0.000 3.763 4.007  
## 5 4.759 2.798 3.716 3.763 0.000 4.176  
## 6 4.107 2.592 2.348 4.007 4.176 0.000
```

Calculo del dendrograma

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

Generacion del dendrograma

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



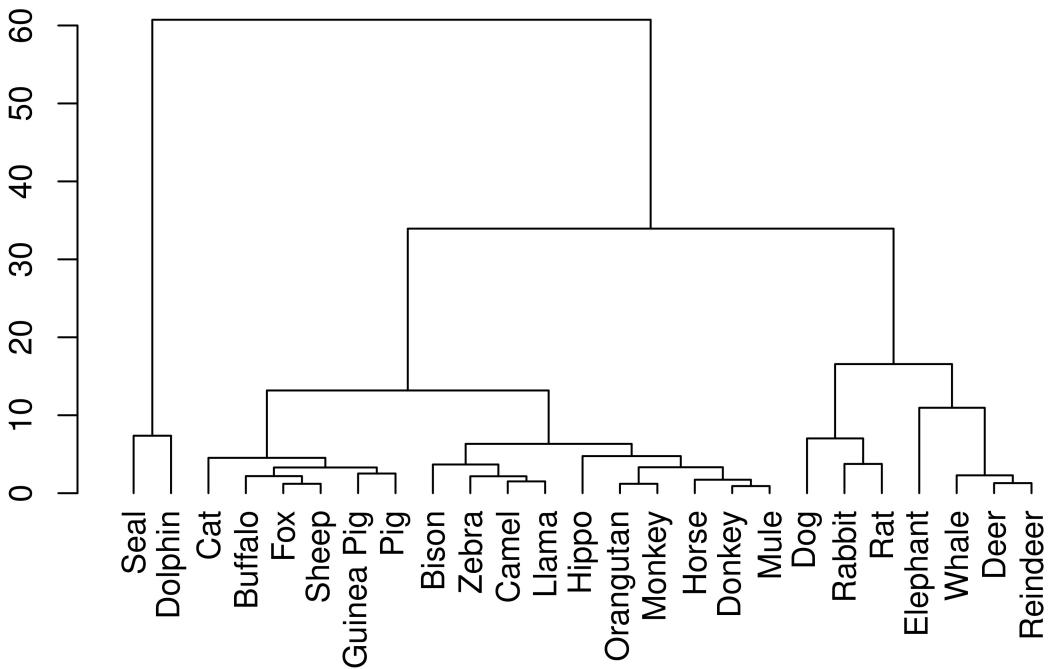
podemos ver un vistoso como seria la grafica

Agregar etiquetas al grafico

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

Construimos de nuevo el grafico

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



Modificar el dendrograma

cargo paquete

```
library(dendextend)
```

```
## Warning: package 'dendextend' was built under R version 4.1.3

##
## -----
## 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

```

Guardar las etiquetas en un objeto “L”

```

L=labels(dend.AMM)

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

```

cambiar el tamaño de las etiquetas

```

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

```

Dendrograma de mamíferos

