

Dendrograma

Cargar paquetería

```
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
```

Cálculo de la matriz de distancia de Mahalanobis

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

Convertir los resultados del cálculo de la distancia a una matriz de datos y me indique 3 dígitos.

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

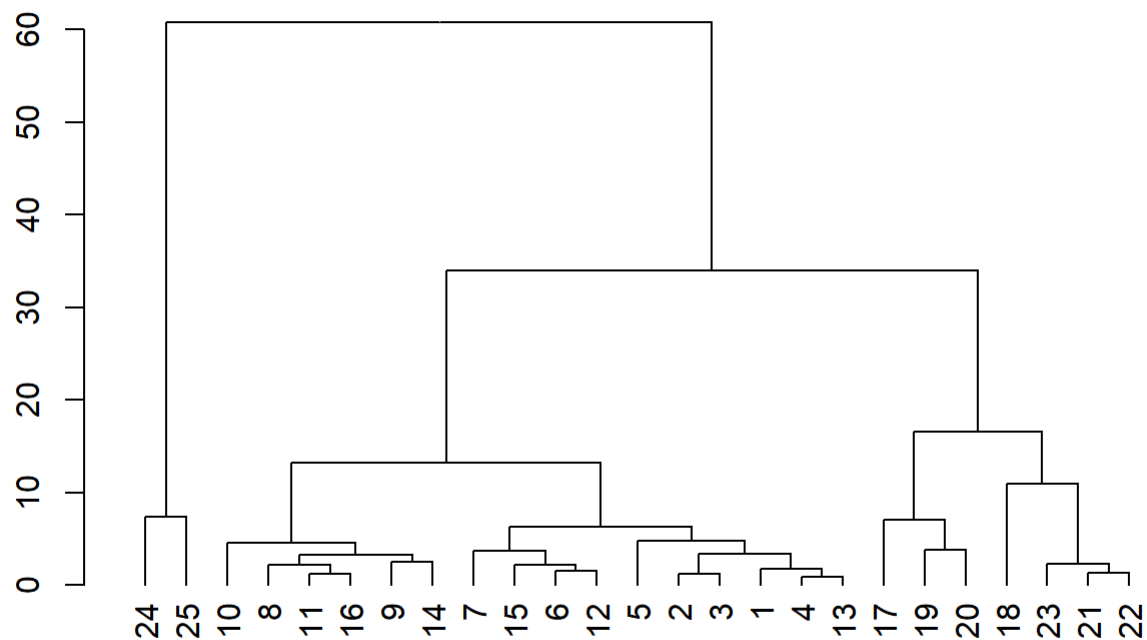
```
##      1      2      3      4      5      6  
## 1 0.000 3.327 2.494 1.226 4.759 4.107  
## 2 3.327 0.000 1.206 2.794 2.798 2.592  
## 3 2.494 1.206 0.000 2.375 3.716 2.348  
## 4 1.226 2.794 2.375 0.000 3.763 4.007  
## 5 4.759 2.798 3.716 3.763 0.000 4.176  
## 6 4.107 2.592 2.348 4.007 4.176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

Calculo del dendrograma

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

Generacion del dendrograma

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

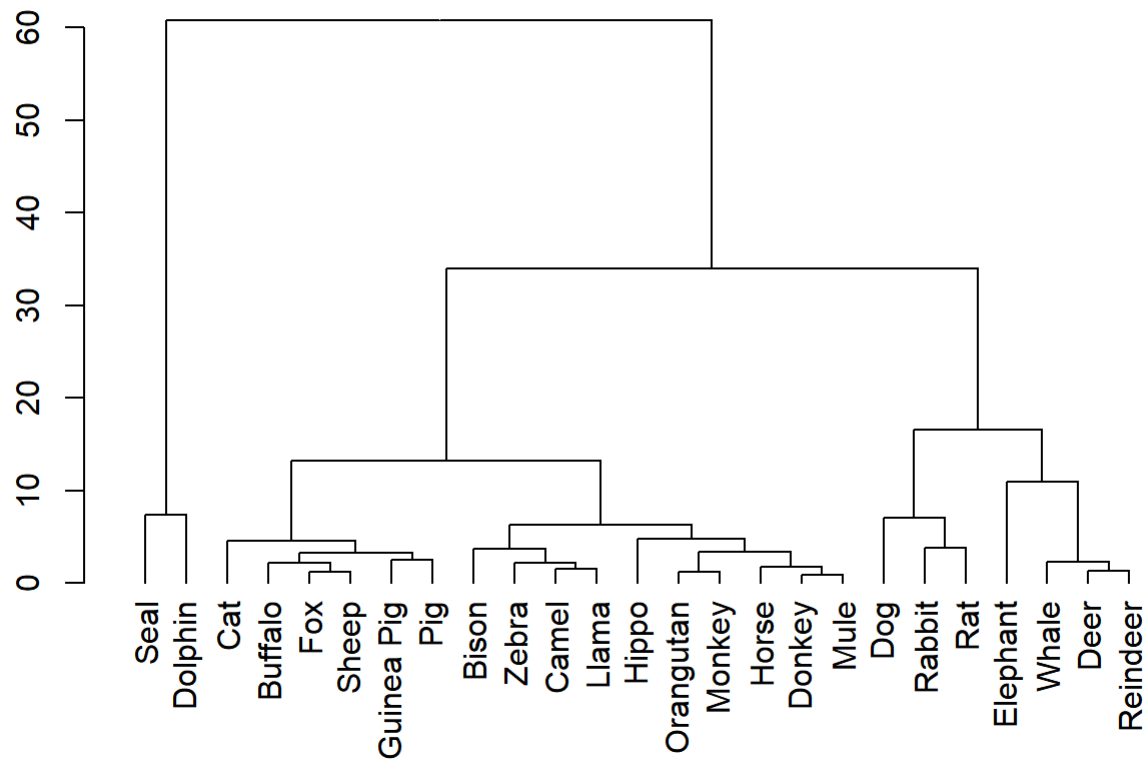


Agregar etiquetas al gráfico

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

Construimos de nuevo el gráfico

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



Modificar el dendrograma

Cargar paquetería

```
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
```

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 mamiferos")
```

Dendrograma de mamiferos

