

Dendrograma_Punto extra

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Dendrograma

Instalar paquete

```
install.packages("cluster.datasets")  
library(cluster.datasets)
```

Se renombra la matriz

```
data("mammal.dentition")  
MD=mammal.dentition  
MD
```

##	name	top.i	bottom.i	top.c	bottom.c	top.pm	bottom.pm	top.m
## 1	Opossum	5	4	1	1	3	3	4
## 2	Hairy tail mole	3	3	1	1	4	4	3
## 3	Common mole	3	2	1	0	3	3	3
## 4	Star nose mole	3	3	1	1	4	4	3
## 5	Brown bat	2	3	1	1	3	3	3
## 6	Silver hair bat	2	3	1	1	2	3	3
## 7	Pigmy bat	2	3	1	1	2	2	3
## 8	House bat	2	3	1	1	1	2	3
## 9	Red bat	1	3	1	1	2	2	3
## 10	Hoary bat	1	3	1	1	2	2	3
## 11	Lump nose bat	2	3	1	1	2	3	3
## 12	Armadillo	0	0	0	0	0	0	8
## 13	Pika	2	1	0	0	2	2	3
## 14	Snowshoe rabbit	2	1	0	0	3	2	3
## 15	Beaver	1	1	0	0	2	1	3
## 16	Marmot	1	1	0	0	2	1	3
## 17	Groundhog	1	1	0	0	2	1	3
## 18	Prairie Dog	1	1	0	0	2	1	3
## 19	Ground Squirrel	1	1	0	0	2	1	3
## 20	Chipmunk	1	1	0	0	2	1	3
## 21	Gray squirrel	1	1	0	0	1	1	3
## 22	Fox squirrel	1	1	0	0	1	1	3
## 23	Pocket gopher	1	1	0	0	1	1	3
## 24	Kangaroo rat	1	1	0	0	1	1	3
## 25	Pack rat	1	1	0	0	0	0	3
## 26	Field mouse	1	1	0	0	0	0	3

## 27	Muskrat	1	1	0	0	0	0	3
## 28	Black rat	1	1	0	0	0	0	3
## 29	House mouse	1	1	0	0	0	0	3
## 30	Porcupine	1	1	0	0	1	1	3
## 31	Guinea pig	1	1	0	0	1	1	3
## 32	Coyote	1	3	1	1	4	4	3
## 33	Wolf	3	3	1	1	4	4	2
## 34	Fox	3	3	1	1	4	4	2
## 35	Bear	3	3	1	1	4	4	2
## 36	Civet cat	3	3	1	1	4	4	2
## 37	Raccoon	3	3	1	1	4	4	3
## 38	Marten	3	3	1	1	4	4	1
## 39	Fisher	3	3	1	1	4	4	1
## 40	Weasel	3	3	1	1	3	3	1
## 41	Mink	3	3	1	1	3	3	1
## 42	Ferrer	3	3	1	1	3	3	1
## 43	Wolverine	3	3	1	1	4	4	1
## 44	Badger	3	3	1	1	3	3	1
## 45	Skunk	3	3	1	1	3	3	1
## 46	River otter	3	3	1	1	4	3	1
## 47	Sea otter	3	2	1	1	3	3	1
## 48	Jaguar	3	3	1	1	3	2	1
## 49	Ocelot	3	3	1	1	3	2	1
## 50	Cougar	3	3	1	1	3	2	1
## 51	Lynx	3	3	1	1	3	2	1
## 52	Fur seal	3	2	1	1	4	4	1
## 53	Sea lion	3	2	1	1	4	4	1
## 54	Walrus	1	0	1	1	3	3	0
## 55	Grey seal	3	2	1	1	3	3	2
## 56	Elephant seal	2	1	1	1	4	4	1
## 57	Peccary	2	3	1	1	3	3	3
## 58	Elk	0	4	1	0	3	3	3
## 59	Deer	0	4	0	0	3	3	3
## 60	Moose	0	4	0	0	3	3	3
## 61	Reindeer	0	4	1	0	3	3	3
## 62	Antelope	0	4	0	0	3	3	3
## 63	Bison	0	4	0	0	3	3	3
## 64	Mountain goat	0	4	0	0	3	3	3
## 65	Musk ox	0	4	0	0	3	3	3
## 66	Mountain sheep	0	4	0	0	3	3	3
##	bottom.m							
## 1	4							
## 2	3							
## 3	3							
## 4	3							
## 5	3							
## 6	3							
## 7	3							
## 8	3							
## 9	3							
## 10	3							
## 11	3							
## 12	8							
## 13	3							

## 14	3
## 15	3
## 16	3
## 17	3
## 18	3
## 19	3
## 20	3
## 21	3
## 22	3
## 23	3
## 24	3
## 25	3
## 26	3
## 27	3
## 28	3
## 29	3
## 30	3
## 31	3
## 32	3
## 33	3
## 34	3
## 35	3
## 36	2
## 37	2
## 38	2
## 39	2
## 40	2
## 41	2
## 42	2
## 43	2
## 44	2
## 45	2
## 46	2
## 47	2
## 48	1
## 49	1
## 50	1
## 51	1
## 52	1
## 53	1
## 54	0
## 55	2
## 56	1
## 57	3
## 58	3
## 59	3
## 60	3
## 61	3
## 62	3
## 63	3
## 64	3
## 65	3
## 66	3

```
head(MD)
```

```
##           name top.i bottom.i top.c bottom.c top.pm bottom.pm top.m bottom.m
## 1      Opossum     5       4     1       1     3       3     4       4
## 2 Hairy tail mole  3       3     1       1     4       4     3       3
## 3   Common mole   3       2     1       0     3       3     3       3
## 4 Star nose mole  3       3     1       1     4       4     3       3
## 5   Brown bat    2       3     1       1     3       3     3       3
## 6 Silver hair bat 2       3     1       1     2       3     3       3
```

Cálculo de la matriz de distancia de Mahalanobis

```
dist.MD<-dist(MD[,1:8])
```

```
## Warning in dist(MD[, 1:8]): NAs introduced by coercion
```

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

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

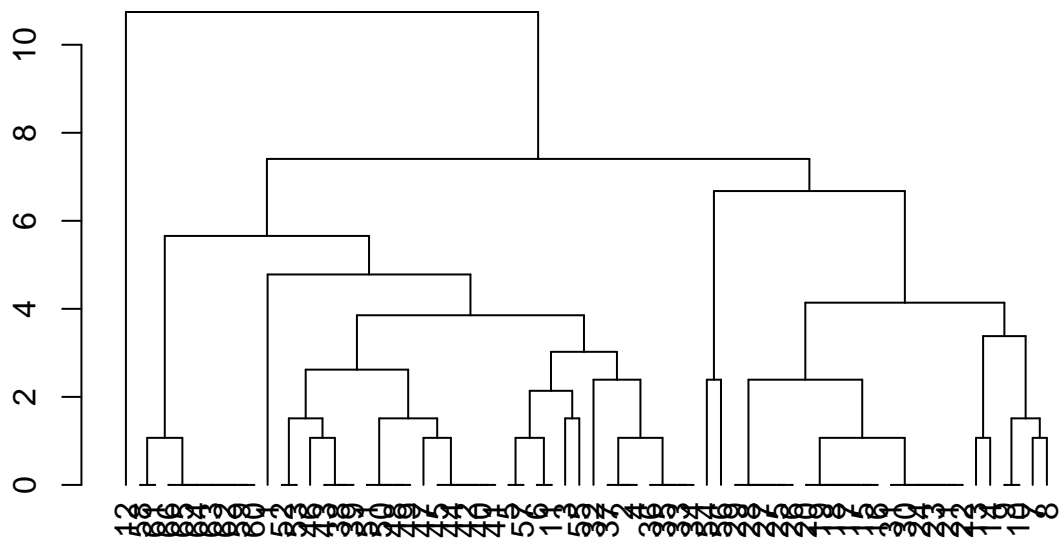
```
##           1       2       3       4       5       6
## 1 0.000 3.024 3.381 3.024 3.546 3.703
## 2 3.024 0.000 2.138 0.000 1.852 2.619
## 3 3.381 2.138 0.000 2.138 1.852 2.138
## 4 3.024 0.000 2.138 0.000 1.852 2.619
## 5 3.546 1.852 1.852 1.852 0.000 1.069
## 6 3.703 2.619 2.138 2.619 1.069 0.000
```

Cálculo del dendrograma

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

Generación del dendrograma

```
plot(dend.MD)
```

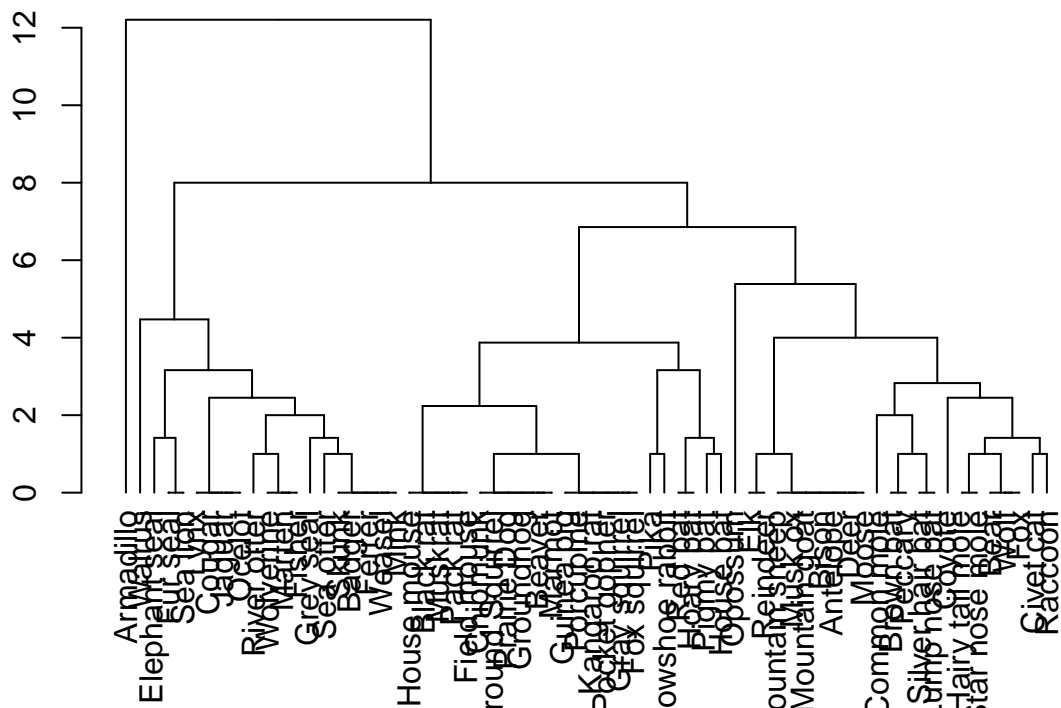


Agregar etiquetas al gráfico

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

Construimos de nuevo el gráfico

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



Modificar el dendrograma

Instalar paquete

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

Guardar las etiquetas en un objeto "L"

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

Cambiar el tamaño de las etiquetas

```
dend.MD %>%  
  set(what="labels_col", "blue") %>% #Colores etiqueta  
  set(what="labels_cex", 0.8) %>%  
  plot(main="Para cada animal el número de dientes en cada grupo principal")
```

Para cada animal el número de dientes en cada grupo principal

