

# Dendrograma punto extra

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## Dendrograma

### Instalar paquete

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

## Matriz de datos

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

### Se renombra la matriz

```
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[,2:5])
```

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

```
round(as.matrix(dist.MD)[2:5, 2:5],3)
```

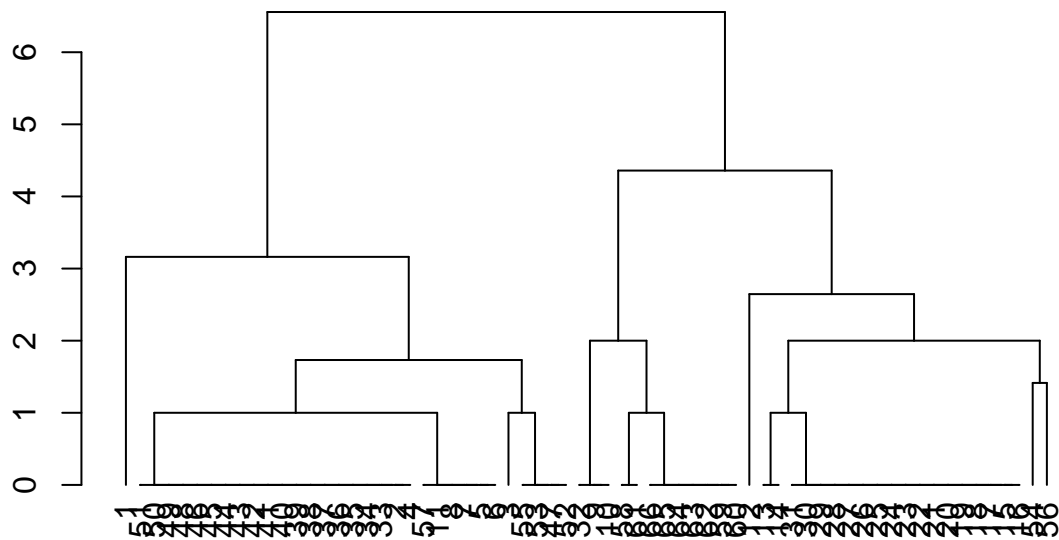
```
##           2      3      4      5
## 2 0.000 1.414 0.000 1.000
## 3 1.414 0.000 1.414 1.732
## 4 0.000 1.414 0.000 1.000
## 5 1.000 1.732 1.000 0.000
```

## Cálculo del dendrograma

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

## Generación del dendrograma

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

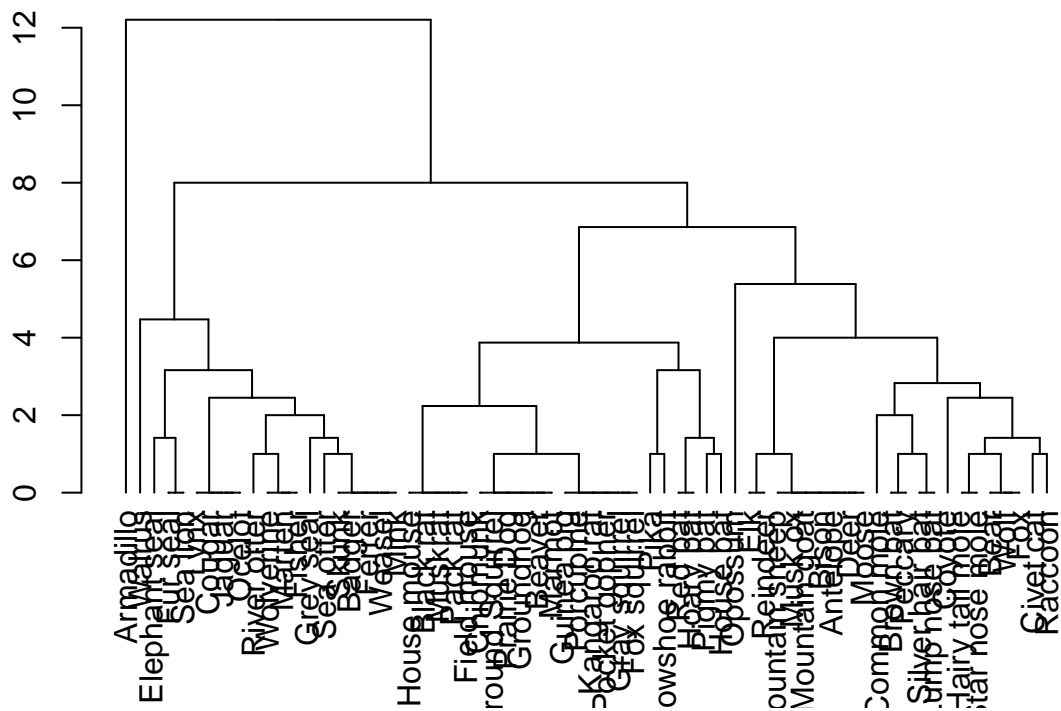


## Agregar etiquetas al gráfico

```
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 n?mero de dientes en cada grupo principal")
```

### Para cada animal el n?mero de dientes en cada grupo principal

