

## ciencia\_\_dades\_\_iris.R

jcortes

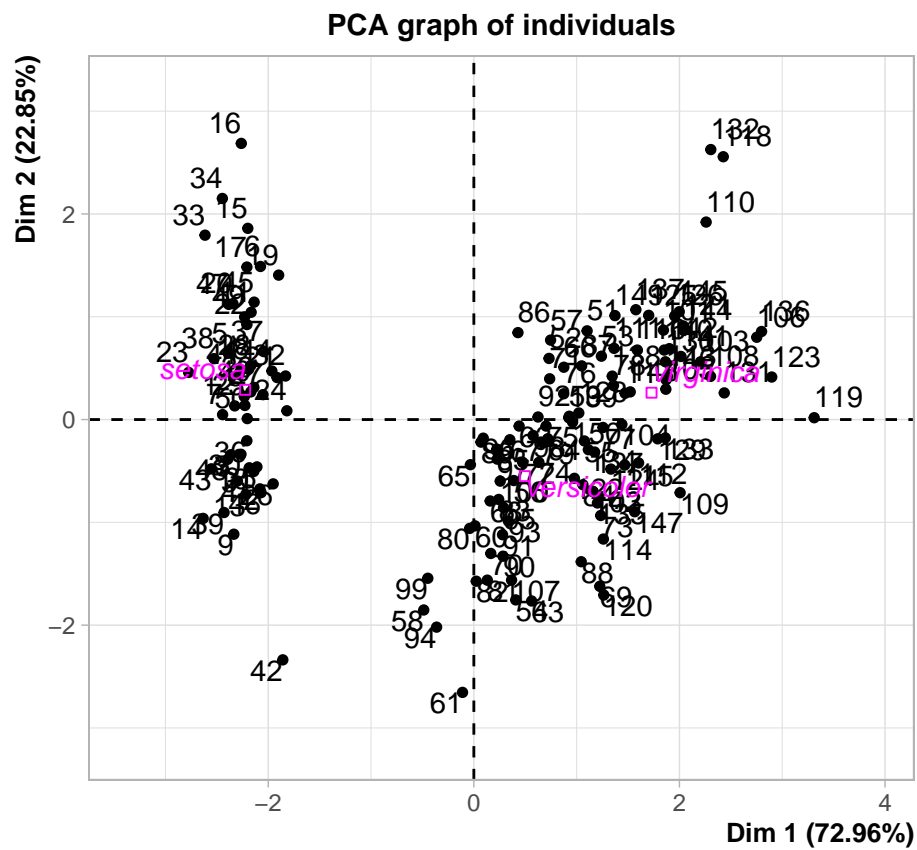
2023-11-30

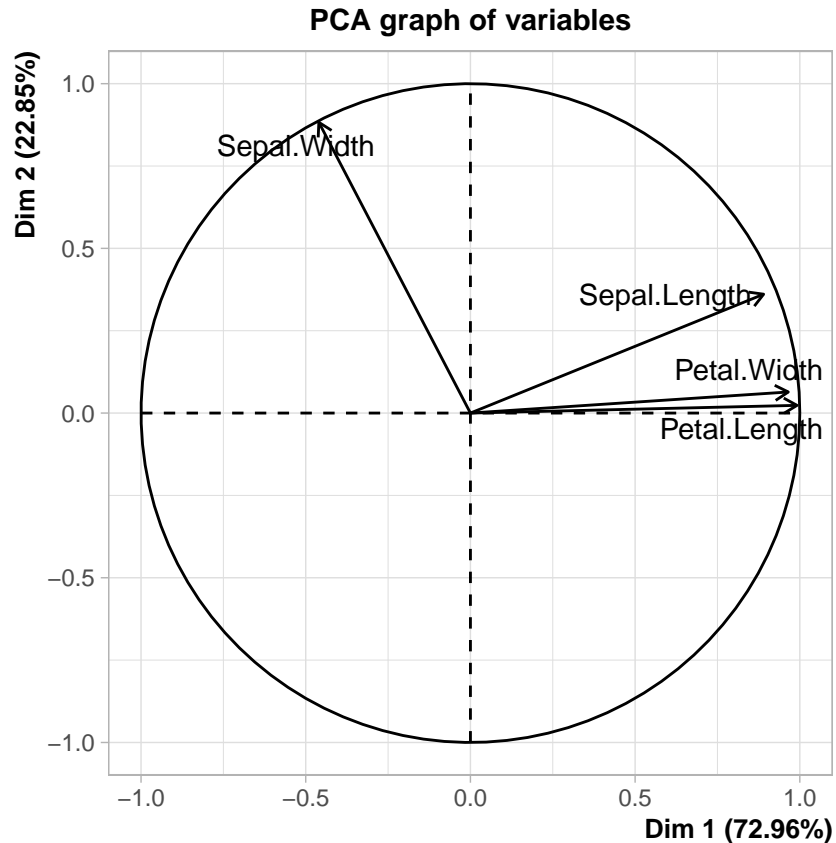
```
rm(list=ls())
```

```
library(FactoMineR)
```

```
d <- read.csv('https://raw.githubusercontent.com/jordicortes40/PE_Bloc_D/main/Dades/iris.csv')
# iris <- read.csv('../Dades/iris.csv')
```

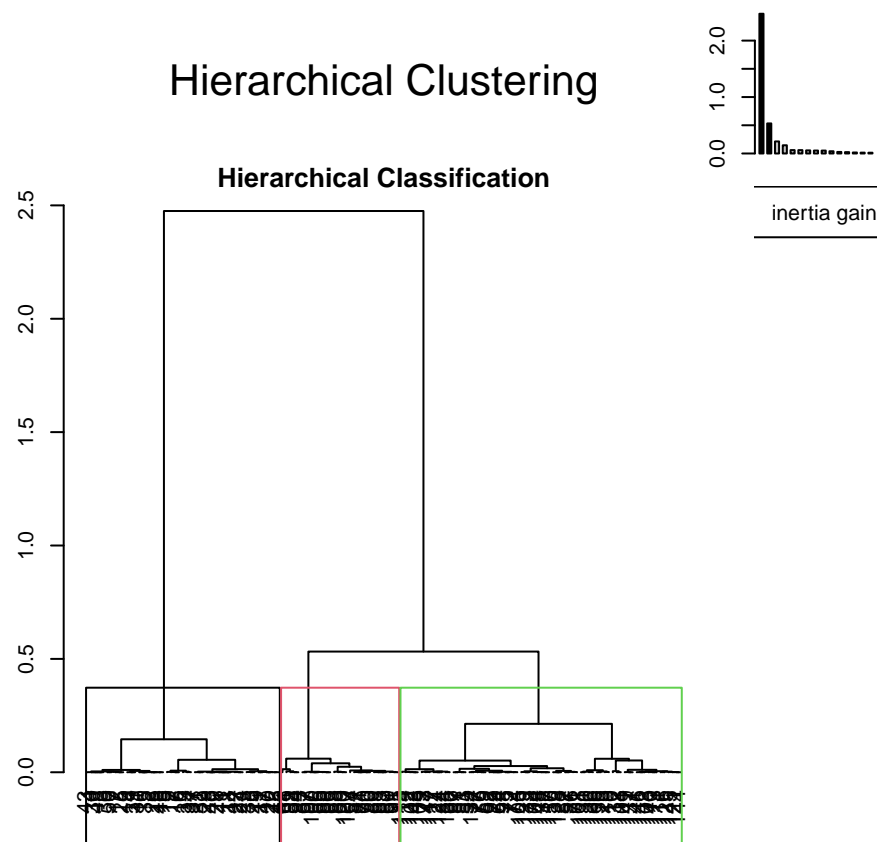
```
(pca.iris <- PCA(iris, quali.sup=c(5: 5)))
```



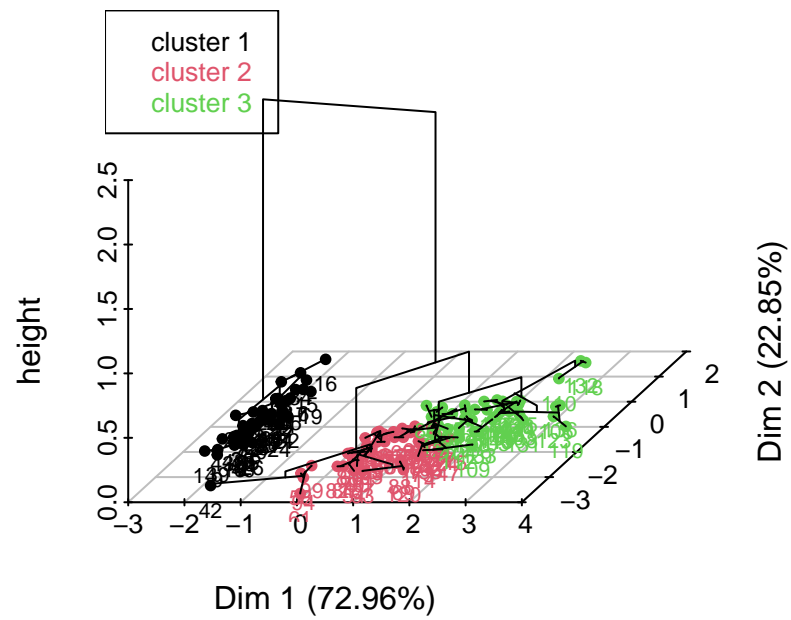


```
## **Results for the Principal Component Analysis (PCA)**
## The analysis was performed on 150 individuals, described by 5 variables
## *The results are available in the following objects:
##
##   name                description
## 1  "$eig"              "eigenvalues"
## 2  "$var"              "results for the variables"
## 3  "$var$coord"        "coord. for the variables"
## 4  "$var$cor"          "correlations variables - dimensions"
## 5  "$var$cos2"         "cos2 for the variables"
## 6  "$var$contrib"      "contributions of the variables"
## 7  "$ind"              "results for the individuals"
## 8  "$ind$coord"        "coord. for the individuals"
## 9  "$ind$cos2"         "cos2 for the individuals"
## 10 "$ind$contrib"      "contributions of the individuals"
## 11 "$quali.sup"         "results for the supplementary categorical variables"
## 12 "$quali.sup$coord"  "coord. for the supplementary categories"
## 13 "$quali.sup$v.test" "v-test of the supplementary categories"
## 14 "$call"              "summary statistics"
## 15 "$call$centre"      "mean of the variables"
## 16 "$call$ecart.type"  "standard error of the variables"
## 17 "$call$row.w"       "weights for the individuals"
## 18 "$call$col.w"       "weights for the variables"
```

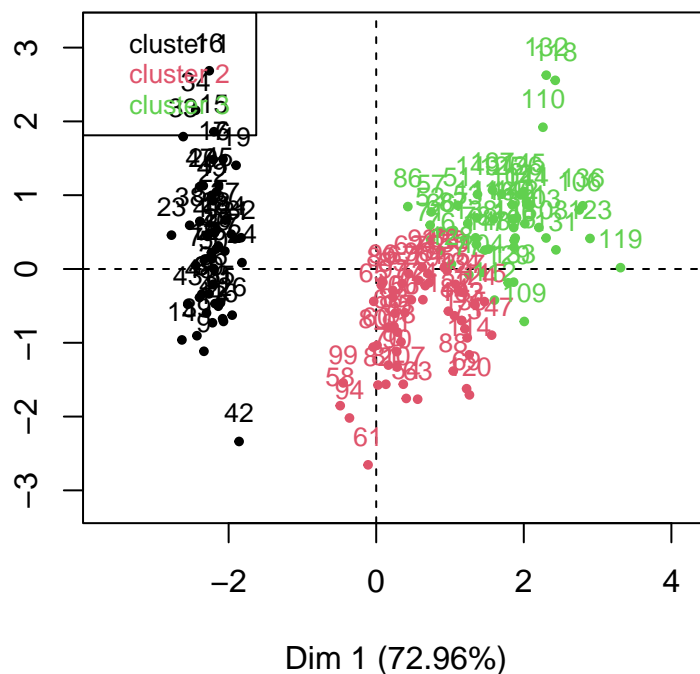
```
(hcpc.iris <- HCPC(pca.iris,nb.clust=-1))
```



## Hierarchical clustering on the factor map



## Factor map



```
## **Results for the Hierarchical Clustering on Principal Components**
##   name
## 1  "$data.clust"
## 2  "$desc.var"
## 3  "$desc.var$quanti.var"
## 4  "$desc.var$quanti"
## 5  "$desc.var$test.chi2"
## 6  "$desc.axes$category"
## 7  "$desc.axes"
## 8  "$desc.axes$quanti.var"
## 9  "$desc.axes$quanti"
## 10 "$desc.ind"
## 11 "$desc.ind$para"
## 12 "$desc.ind$dist"
## 13 "$call"
## 14 "$call$t"
##   description
## 1  "dataset with the cluster of the individuals"
## 2  "description of the clusters by the variables"
## 3  "description of the cluster var. by the continuous var."
## 4  "description of the clusters by the continuous var."
## 5  "description of the cluster var. by the categorical var."
## 6  "description of the clusters by the categories."
## 7  "description of the clusters by the dimensions"
## 8  "description of the cluster var. by the axes"
## 9  "description of the clusters by the axes"
```

```
## 10 "description of the clusters by the individuals"
## 11 "parangons of each clusters"
## 12 "specific individuals"
## 13 "summary statistics"
## 14 "description of the tree"
```

```
table(hcpc.iris$data.clust[,ncol(hcpc.iris$data.clust)],iris$Species)
```

```
##
##      setosa versicolor virginica
## 1      50           0           0
## 2       0          39          14
## 3       0          11          36
```

```
iris2 <- iris[,1:4]
km.iris <- kmeans(iris2,centers=3,nstart=10)
table(km.iris$cluster,iris$Species)
```

```
##
##      setosa versicolor virginica
## 1       0          48          14
## 2       0           2          36
## 3      50           0           0
```

```
# Representacio en components principals del K-means -----
pr.comp <- princomp(iris2)
x <- pr.comp$scores[,1]
y <- pr.comp$scores[,2]
plot(x,y,pch=19,col=km.iris$cluster)
```

