How to use ClustersAnalysis Package

Contents

Introduction

This is a demonstration of using the R package ClustersAnalysis. You will see how to analyze classes according to one or more variables. The group variable must be of the type factor or character and the exploratory variables can be quantitative or qualitative. In this demonstration we are going to use natives dataset from R such as “iris”, “infert” or “esoph”.

Short Descriptions of datasets

Iris :

The data set consists of 50 samples from each of three species of Iris (Iris setosa, Iris virginica and Iris versicolor). Four features were measured from each sample: the length and the width of the sepals and petals, in centimeters. Based on the combination of these four features, Fisher developed a linear discriminant model to distinguish the species from each other.

```
summary(iris)
```

```
##   Sepal.Length    Sepal.Width     Petal.Length    Petal.Width   
##  Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100  
##  1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300  
##  Median :5.800   Median :3.000   Median :4.350   Median :1.300  
##  Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199  
##  3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800  
##  Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500  
##        Species  
##  setosa    :50  
##  versicolor:50  
##  virginica :50  
##                 
##                 
## 
```

Infert :

This is a matched case-control study dating from before the availability of conditional logistic regression.

```
summary(infert)
```

```
##    education        age             parity         induced      
##  0-5yrs : 12   Min.   :21.00   Min.   :1.000   Min.   :0.0000  
##  6-11yrs:120   1st Qu.:28.00   1st Qu.:1.000   1st Qu.:0.0000  
##  12+ yrs:116   Median :31.00   Median :2.000   Median :0.0000  
##                Mean   :31.50   Mean   :2.093   Mean   :0.5726  
##                3rd Qu.:35.25   3rd Qu.:3.000   3rd Qu.:1.0000  
##                Max.   :44.00   Max.   :6.000   Max.   :2.0000  
##       case          spontaneous        stratum      pooled.stratum 
##  Min.   :0.0000   Min.   :0.0000   Min.   : 1.00   Min.   : 1.00  
##  1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:21.00   1st Qu.:19.00  
##  Median :0.0000   Median :0.0000   Median :42.00   Median :36.00  
##  Mean   :0.3347   Mean   :0.5766   Mean   :41.87   Mean   :33.58  
##  3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:62.25   3rd Qu.:48.25  
##  Max.   :1.0000   Max.   :2.0000   Max.   :83.00   Max.   :63.00  
```

Esoph :

Data from a case-control study of (o)esophageal cancer in Ille-et-Vilaine, France. This is a data frame with records for 88 age/alcohol/tobacco combinations.

```
summary(esoph)
```

```
##    agegp          alcgp         tobgp        ncases         ncontrols
##  25-34:15   0-39g/day:23   0-9g/day:24   Min.   : 0.000   Min.   : 1.00
##  35-44:15   40-79    :23   10-19    :24   1st Qu.: 0.000   1st Qu.: 3.00
##  45-54:16   80-119   :21   20-29    :20   Median : 1.000   Median : 6.00
##  55-64:16   120+     :21   30+      :20   Mean   : 2.273   Mean   :11.08
##  65-74:15                                 3rd Qu.: 4.000   3rd Qu.:14.00
##  75+  :11                                 Max.   :17.000   Max.   :60.00
```

Import ClustersAnalysis from Github (using devtools)

```
#Use the below line to install devtools if necessary
#install.packages("devtools")
#library(devtools)

#install package from github
#Use the below line to install ClustersAnalysis if necessary
#devtools::install_github("clepadellec/ClustersAnalysis")

#load package
library(ClustersAnalysis)
```

How to access to help

You can juste use the fonction help(function name) to see all the documentation about your function.

```
help("u_plot_size_effect")
```

Univariate Analysis for qualitatives variariables

To begin we will try to understand, for each qualitative explanatory variable, if it affects the group variable. It's necessary to create an object of univariate type. You can use the constructor **Univariate_object**.

```
#Creation of univariate object using esoph dataframe and "agegp" (first column) as the group variable
u_esoph<-Univariate_object(esoph,1)

#detail of attributes associated with the object
print(u_esoph)
```

```
## $ind.qual
##     agegp     alcgp     tobgp    ncases ncontrols
##      TRUE      TRUE      TRUE     FALSE     FALSE
##
## $ind.quan
##     agegp     alcgp     tobgp    ncases ncontrols
##     FALSE     FALSE     FALSE      TRUE      TRUE
```

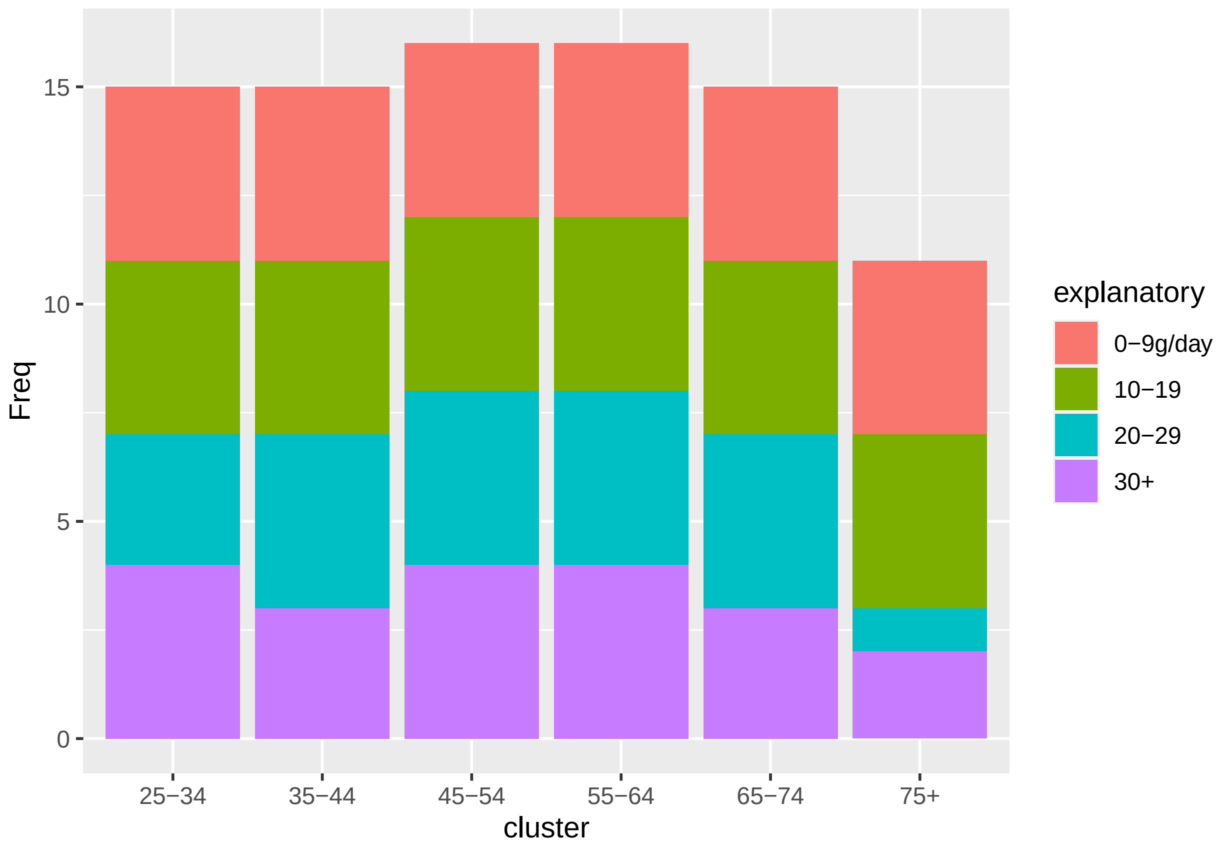
```
##
## $df
##    agegp     alcgp    tobgp ncases ncontrols
## 1  25-34 0-39g/day 0-9g/day      0        40
## 2  25-34 0-39g/day    10-19      0        10
## 3  25-34 0-39g/day    20-29      0         6
## 4  25-34 0-39g/day      30+      0         5
## 5  25-34     40-79 0-9g/day      0        27
## 6  25-34     40-79    10-19      0         7
## 7  25-34     40-79    20-29      0         4
## 8  25-34     40-79      30+      0         7
## 9  25-34    80-119 0-9g/day      0         2
## 10 25-34    80-119    10-19      0         1
## 11 25-34    80-119      30+      0         2
## 12 25-34      120+ 0-9g/day      0         1
## 13 25-34      120+    10-19      1         1
## 14 25-34      120+    20-29      0         1
## 15 25-34      120+      30+      0         2
## 16 35-44 0-39g/day 0-9g/day      0        60
## 17 35-44 0-39g/day    10-19      1        14
## 18 35-44 0-39g/day    20-29      0         7
## 19 35-44 0-39g/day      30+      0         8
## 20 35-44     40-79 0-9g/day      0        35
## 21 35-44     40-79    10-19      3        23
## 22 35-44     40-79    20-29      1        14
## 23 35-44     40-79      30+      0         8
## 24 35-44    80-119 0-9g/day      0        11
## 25 35-44    80-119    10-19      0         6
## 26 35-44    80-119    20-29      0         2
## 27 35-44    80-119      30+      0         1
## 28 35-44      120+ 0-9g/day      2         3
## 29 35-44      120+    10-19      0         3
## 30 35-44      120+    20-29      2         4
## 31 45-54 0-39g/day 0-9g/day      1        46
## 32 45-54 0-39g/day    10-19      0        18
## 33 45-54 0-39g/day    20-29      0        10
## 34 45-54 0-39g/day      30+      0         4
## 35 45-54     40-79 0-9g/day      6        38
## 36 45-54     40-79    10-19      4        21
## 37 45-54     40-79    20-29      5        15
## 38 45-54     40-79      30+      5         7
## 39 45-54    80-119 0-9g/day      3        16
## 40 45-54    80-119    10-19      6        14
## 41 45-54    80-119    20-29      1         5
## 42 45-54    80-119      30+      2         4
## 43 45-54      120+ 0-9g/day      4         4
## 44 45-54      120+    10-19      3         4
## 45 45-54      120+    20-29      2         3
## 46 45-54      120+      30+      4         4
## 47 55-64 0-39g/day 0-9g/day      2        49
## 48 55-64 0-39g/day    10-19      3        22
## 49 55-64 0-39g/day    20-29      3        12
## 50 55-64 0-39g/day      30+      4         6
## 51 55-64     40-79 0-9g/day      9        40
## 52 55-64     40-79    10-19      6        21
## 53 55-64     40-79    20-29      4        17
## 54 55-64     40-79      30+      3         6
## 55 55-64    80-119 0-9g/day      9        18
## 56 55-64    80-119    10-19      8        15
## 57 55-64    80-119    20-29      3         6
## 58 55-64    80-119      30+      4         4
## 59 55-64      120+ 0-9g/day      5        10
## 60 55-64      120+    10-19      6         7
## 61 55-64      120+    20-29      2         3
## 62 55-64      120+      30+      5         6
## 63 65-74 0-39g/day 0-9g/day      5        48
## 64 65-74 0-39g/day    10-19      4        14
## 65 65-74 0-39g/day    20-29      2         7
## 66 65-74 0-39g/day      30+      0         2
## 67 65-74     40-79 0-9g/day     17        34
## 68 65-74     40-79    10-19      3        10
## 69 65-74     40-79    20-29      5         9
## 70 65-74    80-119 0-9g/day      6        13
## 71 65-74    80-119    10-19      4        12
## 72 65-74    80-119    20-29      2         3
## 73 65-74    80-119      30+      1         1
## 74 65-74      120+ 0-9g/day      3         4
## 75 65-74      120+    10-19      1         2
## 76 65-74      120+    20-29      1         1
## 77 65-74      120+      30+      1         1
## 78   75+ 0-39g/day 0-9g/day      1        18
## 79   75+ 0-39g/day    10-19      2         6
## 80   75+ 0-39g/day      30+      1         3
## 81   75+     40-79 0-9g/day      2         5
## 82   75+     40-79    10-19      1         3
## 83   75+     40-79    20-29      0         3
## 84   75+     40-79      30+      1         1
## 85   75+    80-119 0-9g/day      1         1
## 86   75+    80-119    10-19      1         1
## 87   75+      120+ 0-9g/day      2         2
## 88   75+      120+    10-19      1         1
##
## $group
## [1] 1
##
## $name_group
## [1] "agegp"
##
## $lst_quali
## [1] "agegp" "alcgp" "tobgp"
##
## $lst_quanti
## [1] "ncases"    "ncontrols"
##
## $multiple_var
## [1] TRUE
```

Contingency table and size effect

The first thing we can do is to create a contingency table between the explanatory variable and the group variable and then visualize lines/columns profils. In our case the explanatory variable is "tobgp" which is the tobacco consumption (gm/day). To do this you can use the **u__desc__profils**

```r
#use intecract=TRUE to show an interactive graphique with widgets like zoom, comparisons...
ClustersAnalysis::u_desc_profils(u_esoph,3,interact=FALSE)
```

```
## [1] "Tableau de contingence : "
##
##         0-9g/day 10-19 20-29 30+
##   25-34        4     4     3   4
##   35-44        4     4     4   3
##   45-54        4     4     4   4
##   55-64        4     4     4   4
##   65-74        4     4     4   3
##   75+          4     4     1   2
## [1] "Profils lignes : "
##
##            0-9g/day 10-19 20-29 30+   Total
##   25-34     26.7     26.7  20.0  26.7 100.0
##   35-44     26.7     26.7  26.7  20.0 100.0
##   45-54     25.0     25.0  25.0  25.0 100.0
##   55-64     25.0     25.0  25.0  25.0 100.0
##   65-74     26.7     26.7  26.7  20.0 100.0
##   75+       36.4     36.4   9.1  18.2 100.0
##   Ensemble  27.3     27.3  22.7  22.7 100.0
## [1] "Profils colonnes : "
##
##         0-9g/day 10-19  20-29  30+    Ensemble
##   25-34  16.67    16.67  15.00  20.00  17.05
##   35-44  16.67    16.67  20.00  15.00  17.05
##   45-54  16.67    16.67  20.00  20.00  18.18
##   55-64  16.67    16.67  20.00  20.00  18.18
##   65-74  16.67    16.67  20.00  15.00  17.05
##   75+    16.67    16.67   5.00  10.00  12.50
##   Total 100.00   100.00 100.00 100.00 100.00
```



The distributions don't show any particular phenomena. The most represented classes are the 35-44 and 55-64 years. Then we can see that there are more than a half that smokes less than 20 g/days. The only fact that we can see is that the 75+ people are close to 75% to don't smoke a lot.

Now we are going to see in details if there is a size effect between these two variables. To do this we can use **u_desc_size_effect** which return the test statistic vt (comparison between proportions). Then we can also use **u_plot_size_effect** which create a mosaic plot.

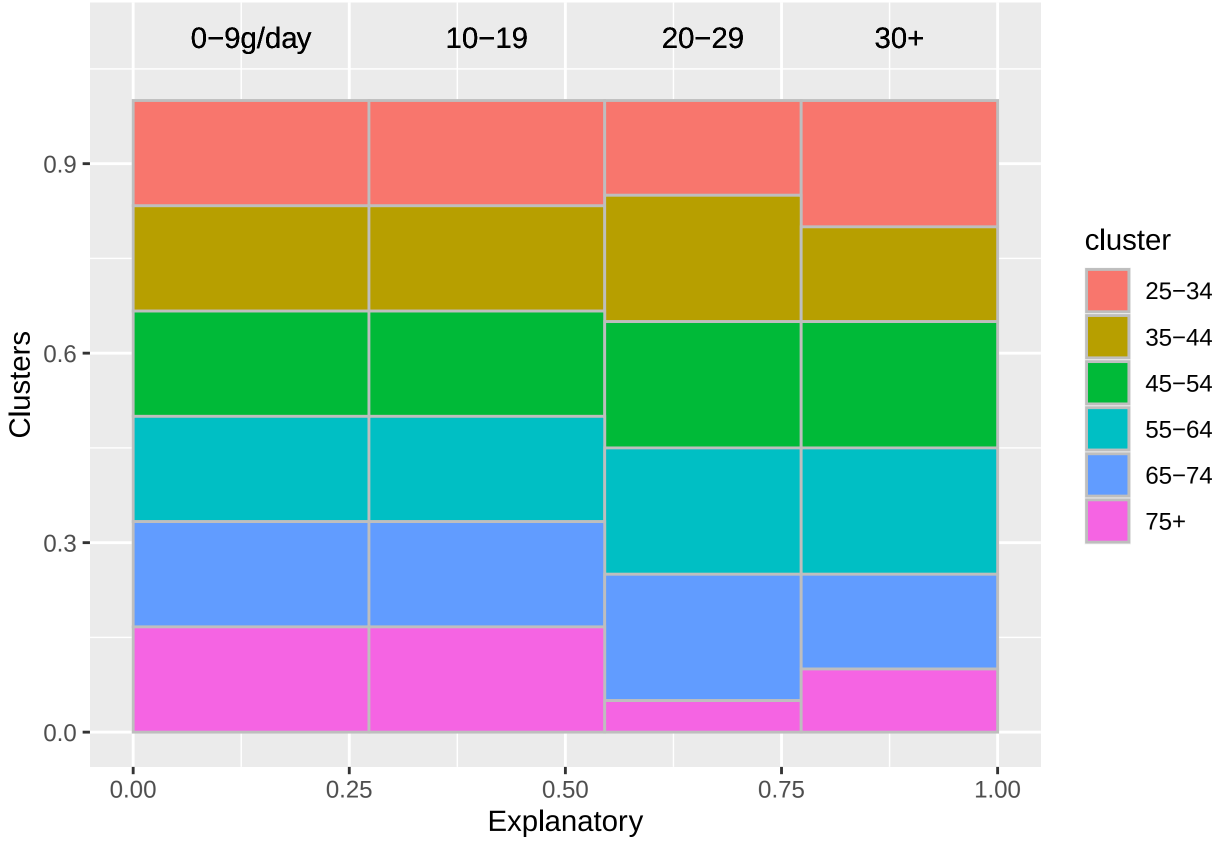
```
u_desc_size_effect(u_esoph,3)
```

```
##
##         0-9g/day 10-19 20-29 30+ Sum
##   25-34        4     4     3   4  15
##   35-44        4     4     4   3  15
##   45-54        4     4     4   4  16
##   55-64        4     4     4   4  16
##   65-74        4     4     4   3  15
##   75+          4     4     1   2  11
##   Sum         24    24    20  20  88
```

```
##
##           0-9g/day      10-19      20-29        30+
##   25-34 -0.1291915 -0.1291915 -0.6565969  0.9484178
##   35-44 -0.1291915 -0.1291915  0.9484178 -0.6565969
##   45-54 -0.5038193 -0.5038193  0.5690195  0.5690195
##   55-64 -0.5038193 -0.5038193  0.5690195  0.5690195
##   65-74 -0.1291915 -0.1291915  0.9484178 -0.6565969
##   75+    1.6158165  1.6158165 -2.7373833 -0.9124611
```

```
#use intecract=TRUE to show an interactive graphique with widgets like zoom, comparisons...
u_plot_size_effect(u_esoph,3,interact=FALSE)
```

```
## Warning: Ignoring unknown aesthetics: width
```



If we refer to the results we can see that the biggest “vt” values are for 75+ peoples who smokes 0-9g/day or 10-19 g/day. So this is for these two combinations that one can most easily conclude that there is an over-representation. We can use the mosaic plot to confirm our comment.

You can do the sames analyses for the variable “tobgp”.

Chisq test

We can now use **u_chisq_test_all** which is use to calculate the p-avlue for a chisq test between the group variable and each qualitatives variables.

```
u_chisq_test_all(u_esoph)
```

```
##   var.groupement var.explicative p.value.chisq.test   interpretation
## 1          agegp           alcgp  0.999997088517426 non significatif
## 2          agegp           tobgp  0.999902175028874 non significatif
##   intensité(v cramer)
## 1                <NA>
## 2                <NA>
```

Here we can see that the p-avlues are very high which mean that we accept the null hypothesis and the variables are independant. Because of this, it's useless to calculate v-cramer.

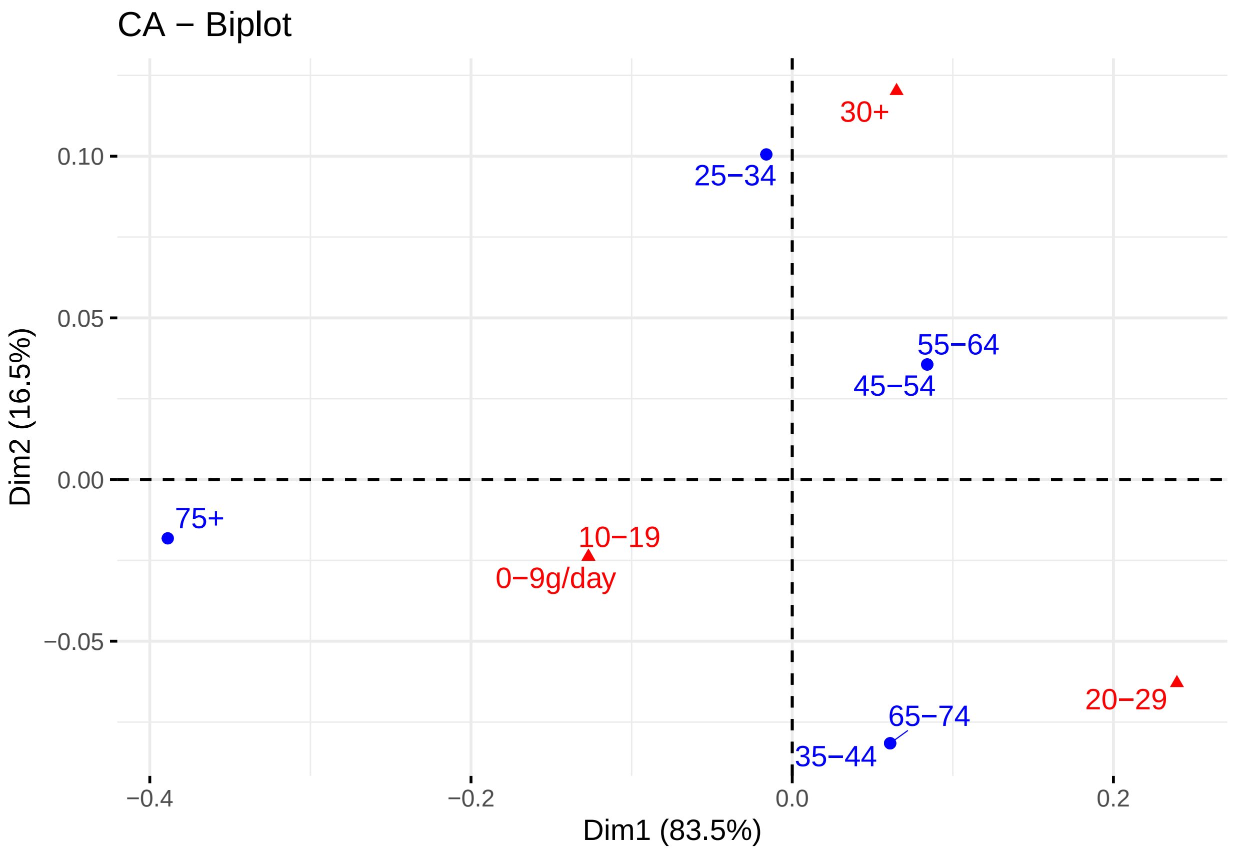
If you want to see significant results you can run the code below, the aim is to predict the sexe according to many qualitatives attributs. We can see that for each chisq.test, we can conclude that the sex depends on the attributs. But the attributs which has the most influence is "qualif".

```r
#install.packages("questionr")
#library(questionr)
# data(hdv2003)
# d<- hdv2003[,3:8]
# u_chisq_test_all(Univariate_object(d,1))
```

Correspondence analysis

To better visualize if some groups are close to a particular modality we can use correspondence analysis. The **u_afc_plot** function return a biplot to visualize our results.

```r
u_afc_plot((Univariate_object(esoph,1)),3)
```



In our case the principal information that we can see is that the 25-34 peoples are quite close to 30+g/day. It's a new information that we didn't have before.

Univariate Analysis for quantitatives variables

Now we are going to use the famous iris dataset. The aim si to understand how the Species can be described.

```
#Creation of univariate object with the "Species" as group variable
u_iris <-Univariate_object(iris,5)
```

Means comparisons (using student test)

To begin we are going to search for each group and each explanatory variable if the fact to belong to a species or not have an influence on the length and the width of Petal/Sepal. To do this we use **u_ttest_all**, this function for each group, separates the group variable into two modalities : target modality or others modality. Then we verify normality hypothesis and if it's possible we use a student test to define if it's significative or not.

```
 u_ttest_all(u_iris)
```

```
##            Sepal.Length       Sepal.Width        Petal.Length
## setosa     "significatif"     "significatif"     "significatif"
## versicolor "non significatif" "significatif"     "significatif"
## virginica  "significatif"     "non significatif" "significatif"
##            Petal.Width
## setosa     "significatif"
## versicolor "non significatif"
## virginica  "significatif"
```

Here we can see that each group have one or many significatives variables which mean that the fact to belong to setosa,versicolor or virginica have an influence on the attributs.

Fisher Test

```
u_fisher_test_all(u_iris)
```

```
##                   Eta2 Test_value p_value
## Sepal.Length 0.6187057  119.26450       0
## Sepal.Width  0.4007828   49.16004       0
## Petal.Length 0.9413717 1180.16118       0
## Petal.Width  0.9288829  960.00715       0
```

Test Value for clustering (for only one explanatory variable)

```
d<-iris[,c(1,5)]

u_test_value(Univariate_object(d,2))
```

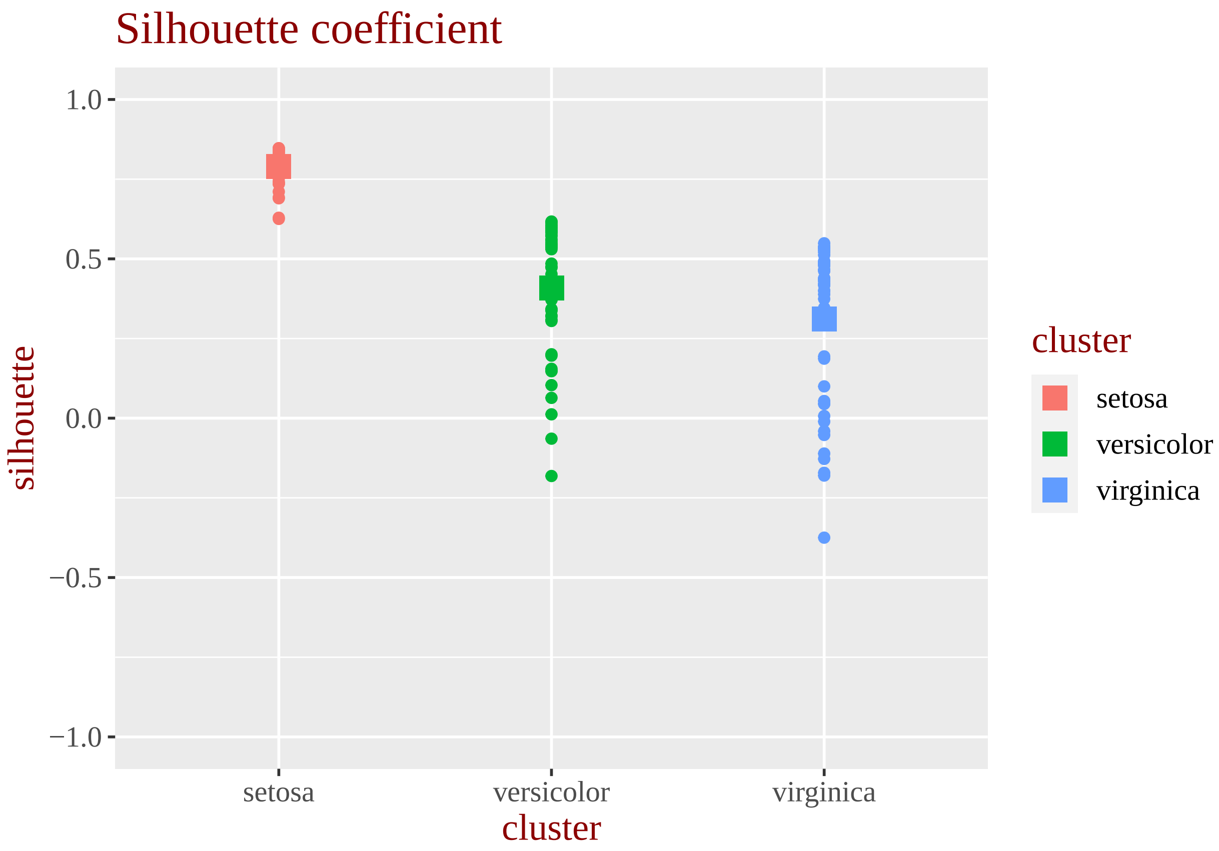
```
##                                  setosa      pvalue
## object.df...object.ind.quan. -8.757174 2.00206e-18
```

Silhouettes indices

```
u_silhouette_ind(u_iris)
```

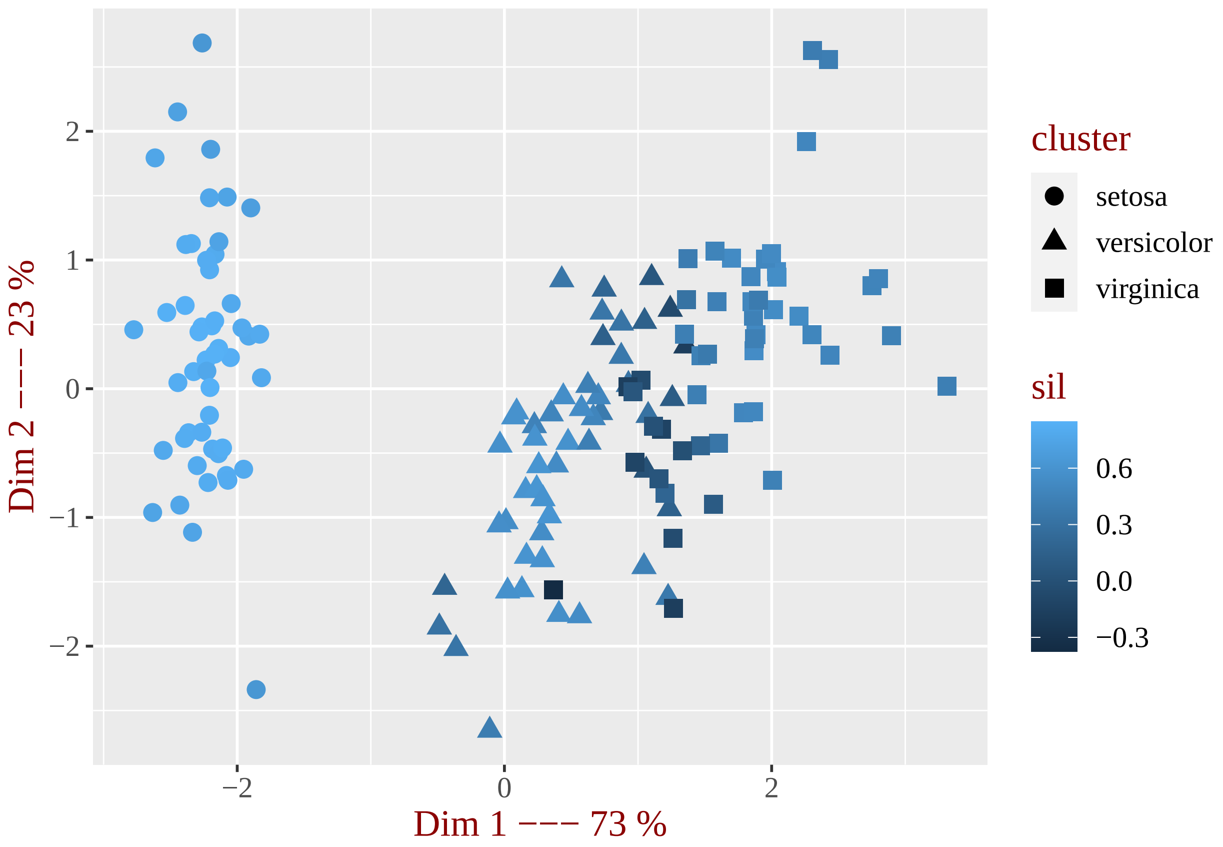
```
##   [1]  0.846469167  0.807398624  0.822366948  0.796876817  0.842846154
##   [6]  0.736507297  0.814515322  0.847356179  0.742514780  0.817476712
##  [11]  0.794022278  0.828702784  0.802439759  0.737078463  0.689960878
##  [16]  0.628999725  0.766148464  0.844448086  0.692395962  0.812505487
##  [21]  0.773274497  0.818253227  0.785451525  0.784113653  0.764467842
##  [26]  0.789153491  0.825818819  0.834753090  0.836562949  0.809910370
##  [31]  0.806887667  0.789361476  0.752791405  0.710627128  0.821092541
##  [36]  0.825165104  0.784801580  0.835250278  0.759758982  0.843495197
##  [41]  0.843051188  0.625304380  0.778506146  0.791253901  0.734990902
##  [46]  0.801610336  0.805121738  0.811665590  0.809962469  0.845574752
##  [51]  0.063715563  0.340711283 -0.064281513  0.561473318  0.305000462
##  [56]  0.530022415  0.200545585  0.308661268  0.319555176  0.543435800
##  [61]  0.406053695  0.550061016  0.537256657  0.385789403  0.571311879
##  [66]  0.321608094  0.472621711  0.605407613  0.372686019  0.603296093
##  [71]  0.147370132  0.583675548  0.154964703  0.424476170  0.485144208
##  [76]  0.371265559  0.103724987 -0.181429615  0.475130100  0.556363272
##  [81]  0.583818539  0.574789098  0.617045132  0.012110302  0.452127963
##  [86]  0.342655400  0.148502744  0.439260455  0.584909351  0.589378605
##  [91]  0.544467525  0.430746508  0.616053311  0.337310169  0.596447444
##  [96]  0.586870976  0.596975798  0.536457716  0.196223138  0.612465204
## [101]  0.486842095  0.044986135  0.532358573  0.420690626  0.536542484
## [106]  0.462715960 -0.374840516  0.479717476  0.437605428  0.484479316
## [111]  0.313233908  0.346347201  0.511927944 -0.040778258  0.186761261
## [116]  0.433115124  0.438175908  0.416637998  0.419567558 -0.180048546
## [121]  0.539110752 -0.110879955  0.436867338 -0.010490659  0.526019728
## [126]  0.491425863 -0.127795281 -0.052646866  0.487318513  0.439510070
## [131]  0.479010718  0.399922091  0.492761852  0.006878731  0.193836006
## [136]  0.466476643  0.462003014  0.420618071 -0.171385023  0.482116062
## [141]  0.531199096  0.388712742  0.044986135  0.548803450  0.520693164
## [146]  0.429514550  0.099807524  0.374300521  0.399617217  0.053972269
```

```
u_silhouette_plot(u_iris, interact=FALSE)
```



Principal component analysis

```
u_sil_pca_plot(u_iris,interact = FALSE)
```



Rand Index

```
u_kmean_rand_index(u_iris)
```

```
## [1] 0.8322148
```

Multivariate Analysis