

Factor Analysis of Mixed Data

reference: *Practical Guide to Principal Component Methods in R*

Introduction

Factor analysis of mixed data (FAMD) is a principal component method dedicated to analyze a data set containing both quantitative and qualitative variables (Pagès, 2004).

Quantitative and qualitative variables are normalized during the analysis in order to balance the influence of each set of variables.

Computation

R packages

```
[1] library("FactoMineR")
library("factoextra")
```

```
Loading required package: ggplot2
Welcome! Related Books: `Practical Guide To Cluster Analysis in R` at
https://goo.gl/13EFCZ
```

Data format

```
[2] # use the wine data set
data(wine)
df <- wine[, c(1, 2, 16, 22, 28, 29, 30, 31)]
head(df[, 1:7], 4)
```

	Label	Soil	Plante	Acidity	Intensity	Harmony	C
2EL	Saumur	Env1	2.000	2.107	2.857	3.143	3
1CHA	Saumur	Env1	2.000	2.107	2.893	2.964	3

	Label	Soil	Plante	Acidity	Intensity	Harmony	C
1FON	Bourgueuil	Env1	1.750	2.179	3.074	3.143	3
1VAU	Chinon	Env2	2.304	3.179	2.462	2.038	2

```
[3] str(df)
```

```
'data.frame': 21 obs. of 8 variables:
 $ Label      : Factor w/ 3 levels "Saumur","Bourgueuil",...: 1 1 2 3
1 2 2 1 3 1 ...
 $ Soil       : Factor w/ 4 levels "Reference","Env1",...: 2 2 2 3 1
1 1 2 2 3 ...
 $ Plante     : num  2 2 1.75 2.3 1.76 ...
 $ Acidity    : num  2.11 2.11 2.18 3.18 2.57 ...
 $ Intensity  : num  2.86 2.89 3.07 2.46 3.64 ...
 $ Harmony    : num  3.14 2.96 3.14 2.04 3.64 ...
 $ Overall.quality: num  3.39 3.21 3.54 2.46 3.74 ...
 $ Typical    : num  3.25 3.04 3.18 2.25 3.44 ...
```

R code

```
[4] res.famd <- FAMD(df, graph = FALSE)
print(res.famd)
```

*The results are available in the following objects:

name	description
1 "\$eig"	"eigenvalues and inertia"
2 "\$var"	"Results for the variables"
3 "\$ind"	"results for the individuals"
4 "\$quali.var"	"Results for the qualitative variables"
5 "\$quanti.var"	"Results for the quantitative variables"

Visualization and interpretation

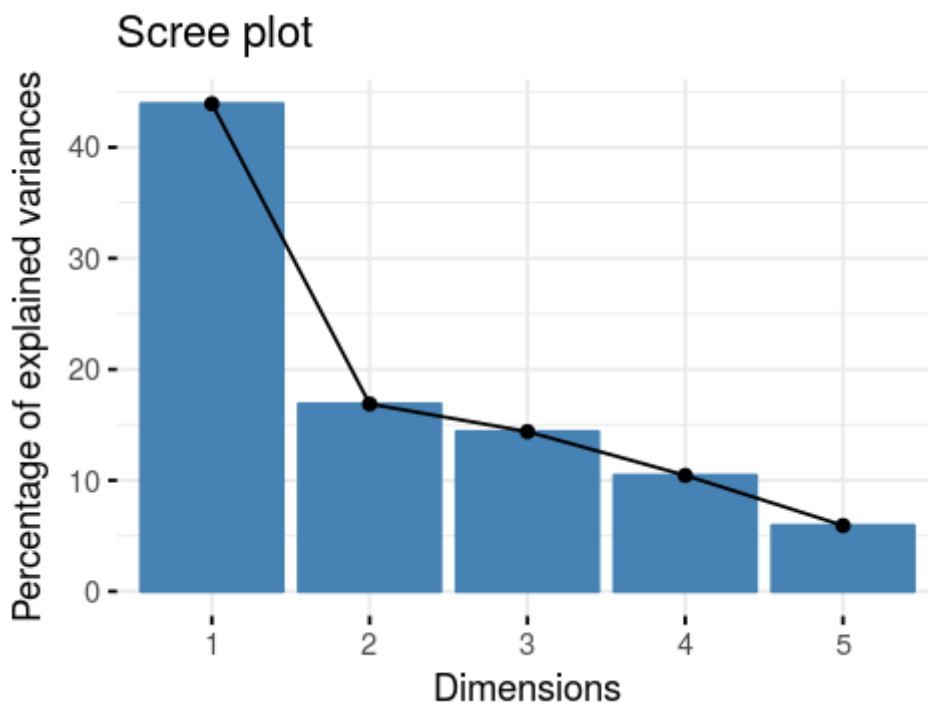
To help in the interpretation of FAMD, we highly recommend to read the interpretation of principal component analysis (Chapter 3) and multiple correspondence analysis (Chapter 5). Many of the graphs presented here have been already described in our previous chapters.

Eigenvalues / Variances

```
[5] eig.val <- get_eigenvalue(res.famd)
head(eig.val)
```

	eigenvalue	variance.percent	cumulative.variance.percent
Dim.1	4.8315174	43.922886	43.92289
Dim.2	1.8568797	16.880724	60.80361
Dim.3	1.5824794	14.386176	75.18979
Dim.4	1.1491200	10.446546	85.63633
Dim.5	0.6518053	5.925503	91.56183

```
[6] options(repr.plot.width=4, repr.plot.height=3)
fviz_screplot(res.famd)
```



Graph of variables

All variables

```
[7] var <- get_famd_var(res.famd)
var
```

FAMD results for variables

```
=====
Name      Description
```



```
1 "$coord"    "Coordinates"
2 "$cos2"     "Cos2, quality of representation"
3 "$contrib"  "Contributions"
```

```
[8] # Coordinates of variables
head(var$coord)
```

	Dim.1	Dim.2	Dim.3	Dim.4	Dir
Plante	0.7344160	0.060551966	0.105902048	0.004011299	0.0
Acidity	0.1732738	0.491118153	0.126394029	0.115376784	0.0
Intensity	0.6991811	0.134639254	0.065382234	0.023214984	0.0
Harmony	0.8943968	0.023628146	0.040124469	0.003653813	0.0
Overall.quality	0.9115699	0.005246728	0.009336677	0.005445276	0.0
Typical	0.7808611	0.027094327	0.001549791	0.083444627	0.0

```
[9] # Cos2: quality of representation on the factor map
head(var$cos2)
```

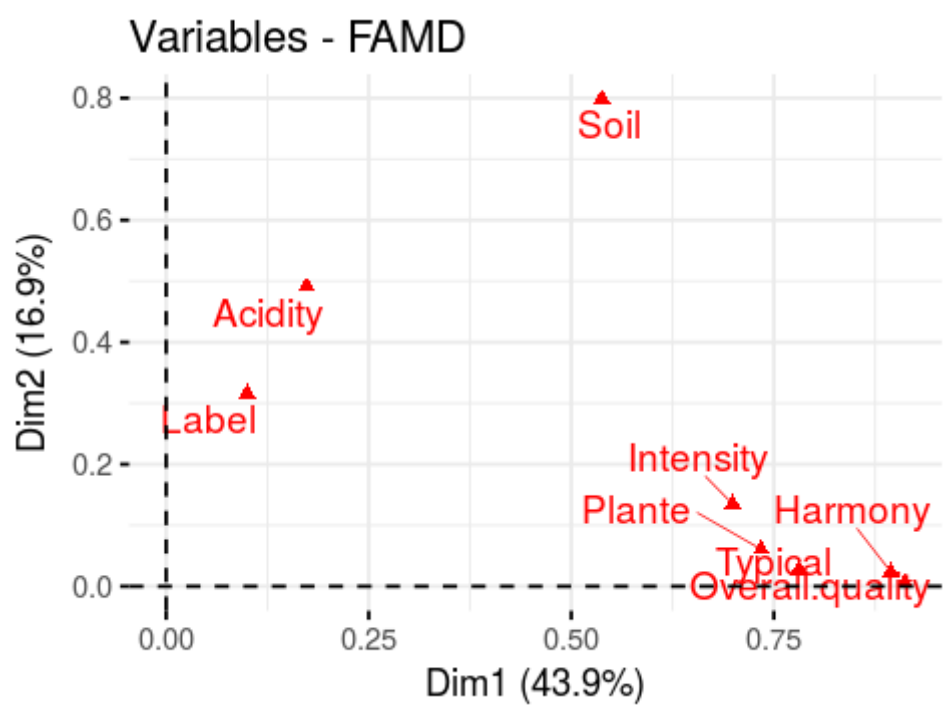
	Dim.1	Dim.2	Dim.3	Dim.4	Dim.5
Plante	0.53936692	3.666541e-03	1.121524e-02	1.609052e-05	1.069206
Acidity	0.03002381	2.411970e-01	1.597545e-02	1.331180e-02	2.103405
Intensity	0.48885427	1.812773e-02	4.274836e-03	5.389355e-04	4.190005
Harmony	0.79994566	5.582893e-04	1.609973e-03	1.335035e-05	7.503805
Overall.quality	0.83095973	2.752815e-05	8.717353e-05	2.965103e-05	6.339107
Typical	0.60974400	7.341026e-04	2.401853e-06	6.963340e-03	3.496207

```
[10] # Contributions to the dimensions
head(var$contrib)
```

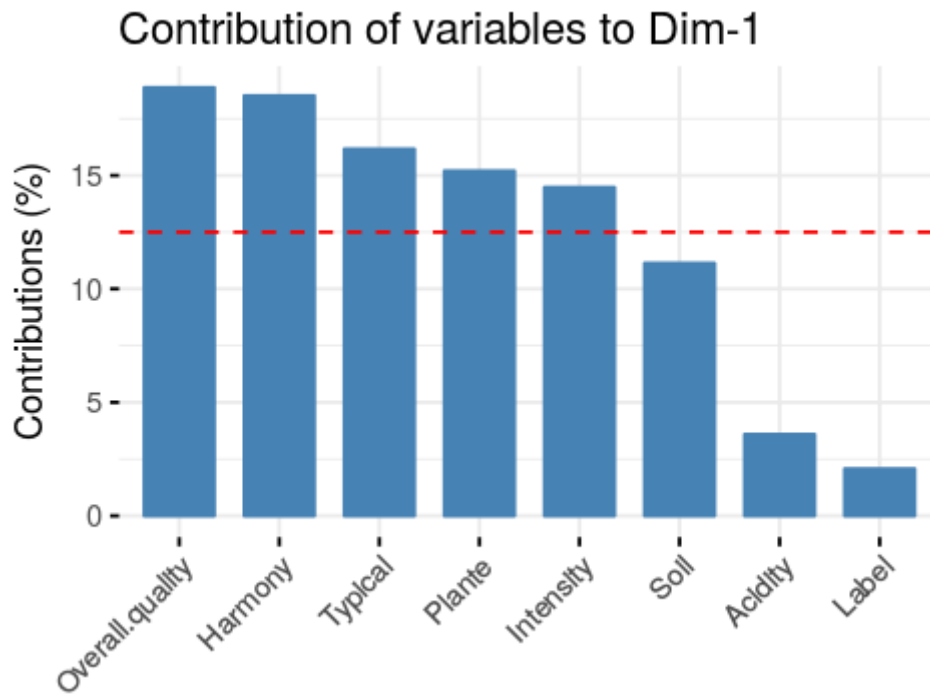
	Dim.1	Dim.2	Dim.3	Dim.4	Dim.5
Plante	15.200526	3.2609526	6.69215972	0.3490757	0.1586

	Dim.1	Dim.2	Dim.3	Dim.4	Dim.5
Acidity	3.586323	26.4485720	7.98708850	10.0404466	0.7036
Intensity	14.471254	7.2508336	4.13163258	2.0202401	0.9930
Harmony	18.511716	1.2724651	2.53554453	0.3179662	1.3289
Overall.quality	18.867156	0.2825562	0.59000304	0.4738648	0.1221
Typical	16.161818	1.4591321	0.09793437	7.2617850	0.0907

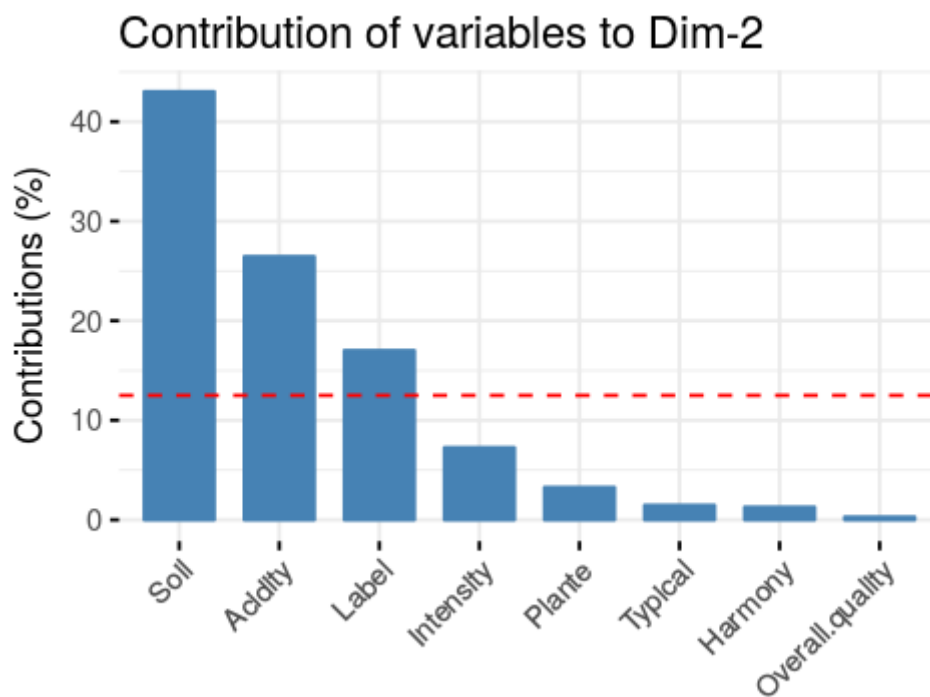
```
[11] # Plot of variables
fviz_famd_var(res.famd, repel = TRUE)
```



```
[12] # Contribution to the first dimension
fviz_contrib(res.famd, "var", axes = 1)
```



```
[13] # Contribution to the second dimension
fviz_contrib(res.famd, "var", axes = 2)
```



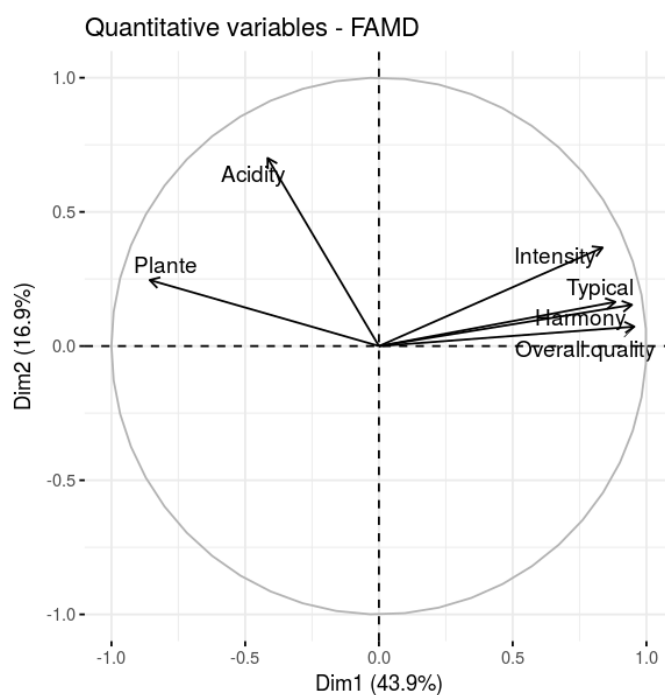
The red dashed line on the graph above indicates the expected average value, If the contributions were uniform

```
[14] quanti.var <- get_famd_var(res.famd, "quanti.var")
      quanti.var
```

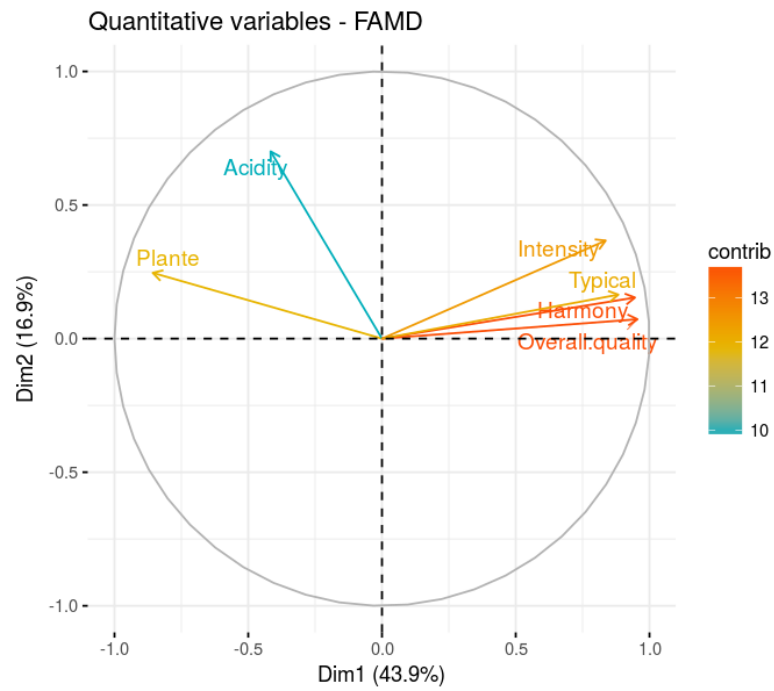
FAMD results for quantitative variables

```
=====
      Name      Description
1 "$coord"    "Coordinates"
2 "$cos2"     "Cos2, quality of representation"
3 "$contrib"  "Contributions"
```

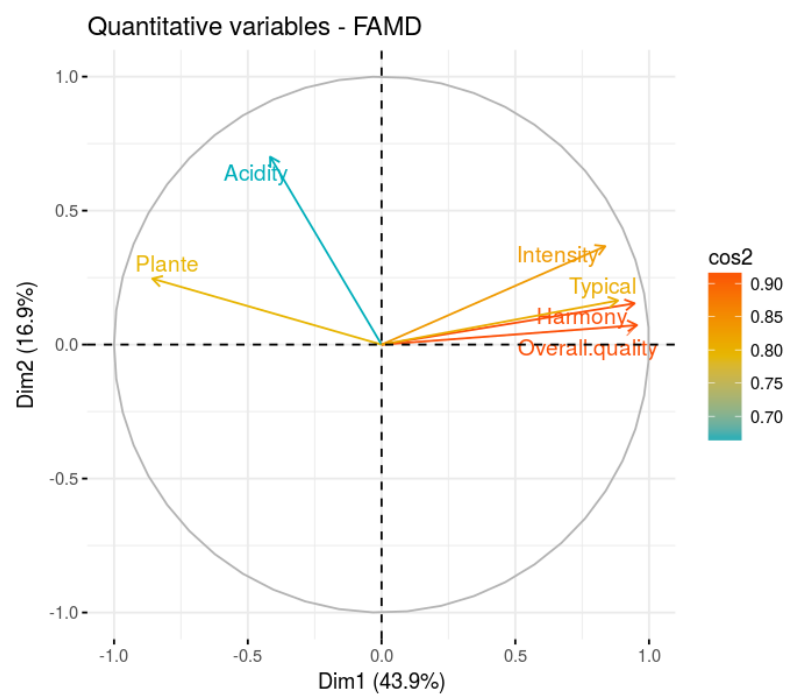
```
[15] options(repr.plot.width=9, repr.plot.height=5)
      fviz_famd_var(res.famd, "quanti.var", repel = TRUE,
                    col.var = "black")
```



```
[16] fviz_famd_var(res.famd, "quanti.var", col.var= "contrib",
              gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
              repel = TRUE)
```



```
[17] # Color by cos2 values: quality on the factor map
fviz_famd_var(res.famd, "quanti.var", col.var = "cos2",
  gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
  repel = TRUE)
```



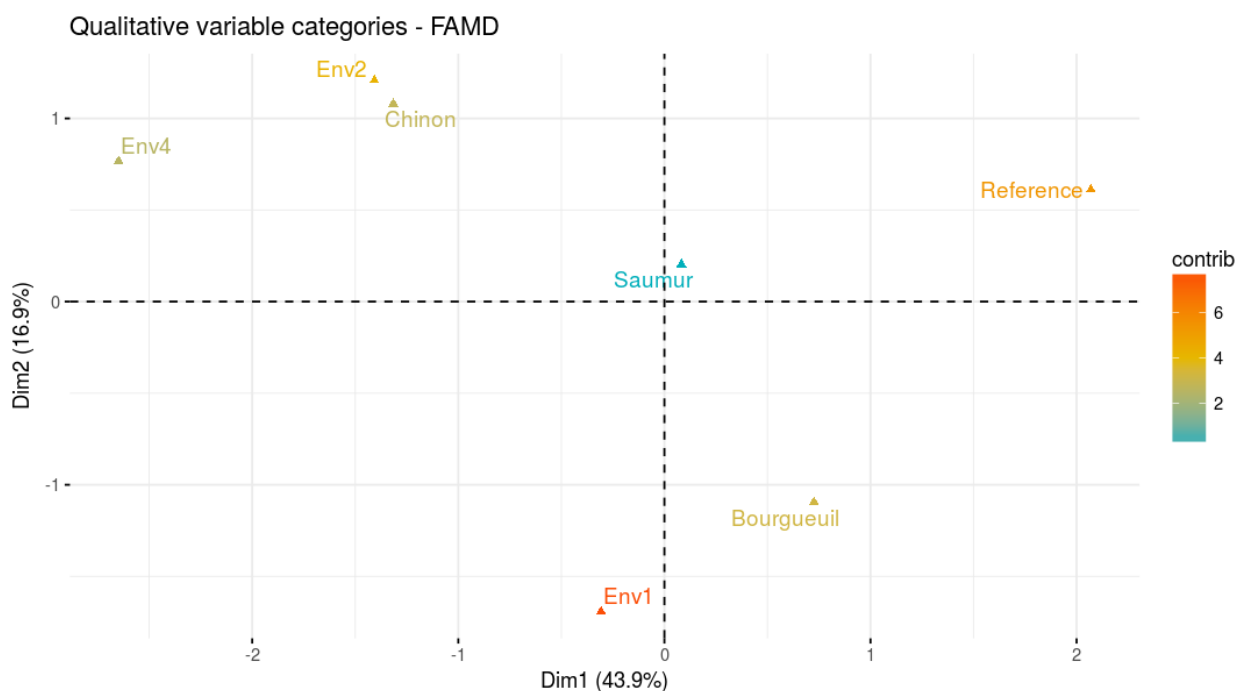
Graph of qualitative variables

```
[18] quali.var <- get_famd_var(res.famd, "quali.var")
quali.var
```


FAMD results for qualitative variable categories

```
=====
Name      Description
1 "$coord" "Coordinates"
2 "$cos2"  "Cos2, quality of representation"
3 "$contrib" "Contributions"
```

```
[19] fviz_famd_var(res.famd, "quali.var", col.var="contrib",
               gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
               repel = TRUE)
```



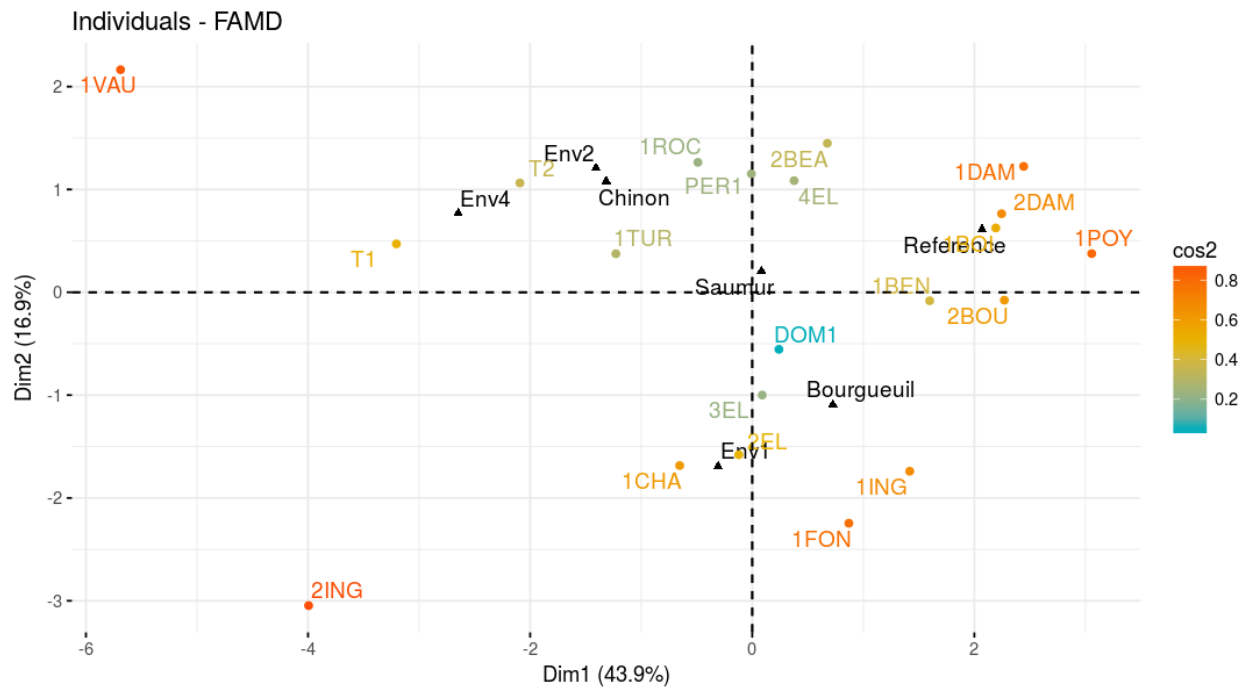
Graph of individuals

```
[20] ind <- get_famd_ind(res.famd)
ind
```

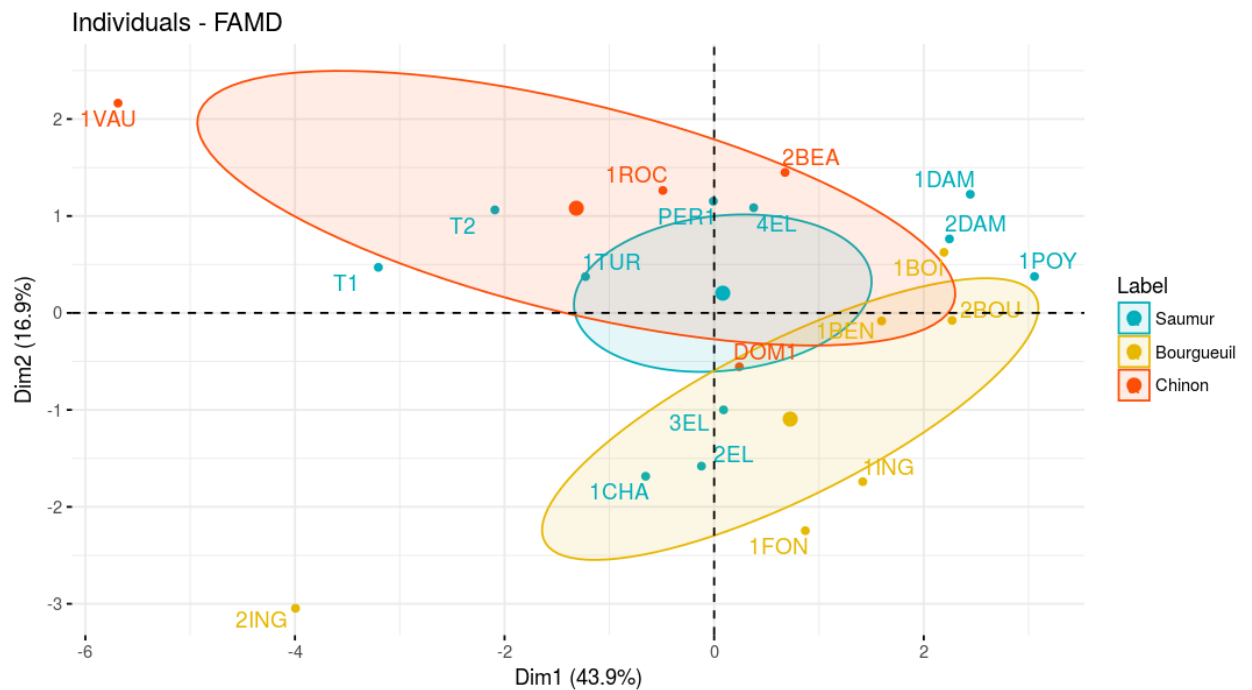
FAMD results for individuals

```
=====
Name      Description
1 "$coord" "Coordinates"
2 "$cos2"  "Cos2, quality of representation"
3 "$contrib" "Contributions"
```

```
[21] fviz_famd_ind(res.famd, col.ind = "cos2",
               gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
               repel = TRUE)
```

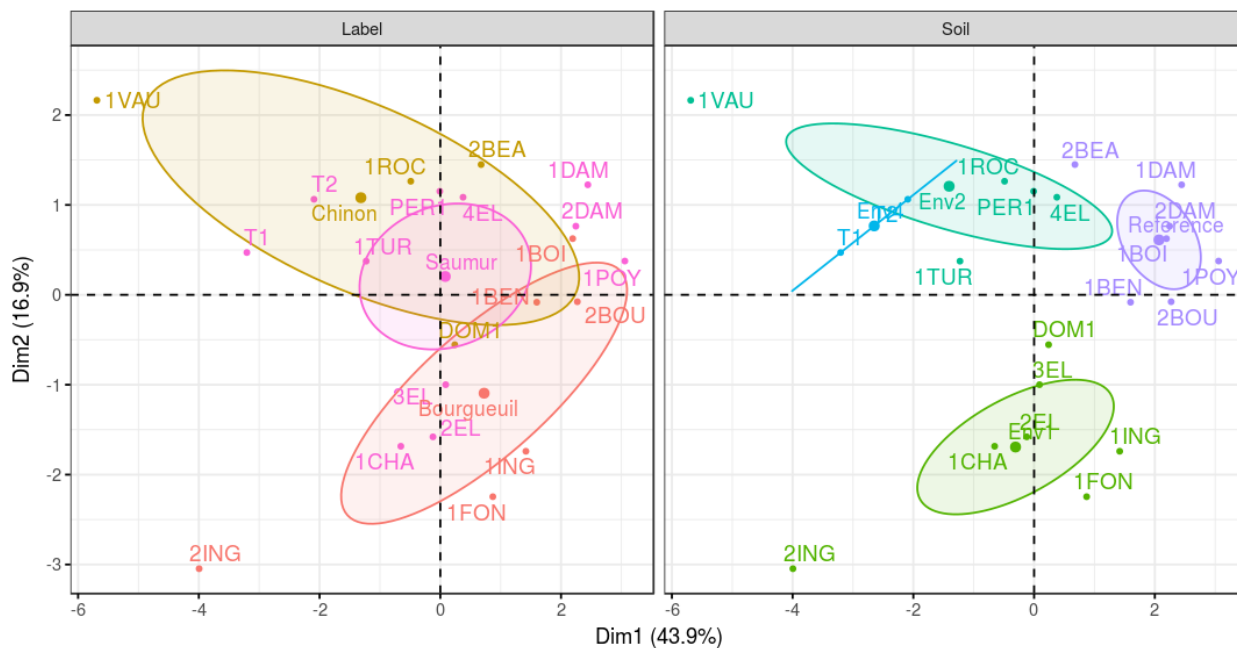


```
[24] fviz_mfa_ind(res.famd,
  habillage = "Label", # color by groups
  palette = c("#00AFBB", "#E7B800", "#FC4E07"),
  addEllipses = TRUE, ellipse.type = "confidence",
  repel = TRUE # Avoid text overlapping
)
```



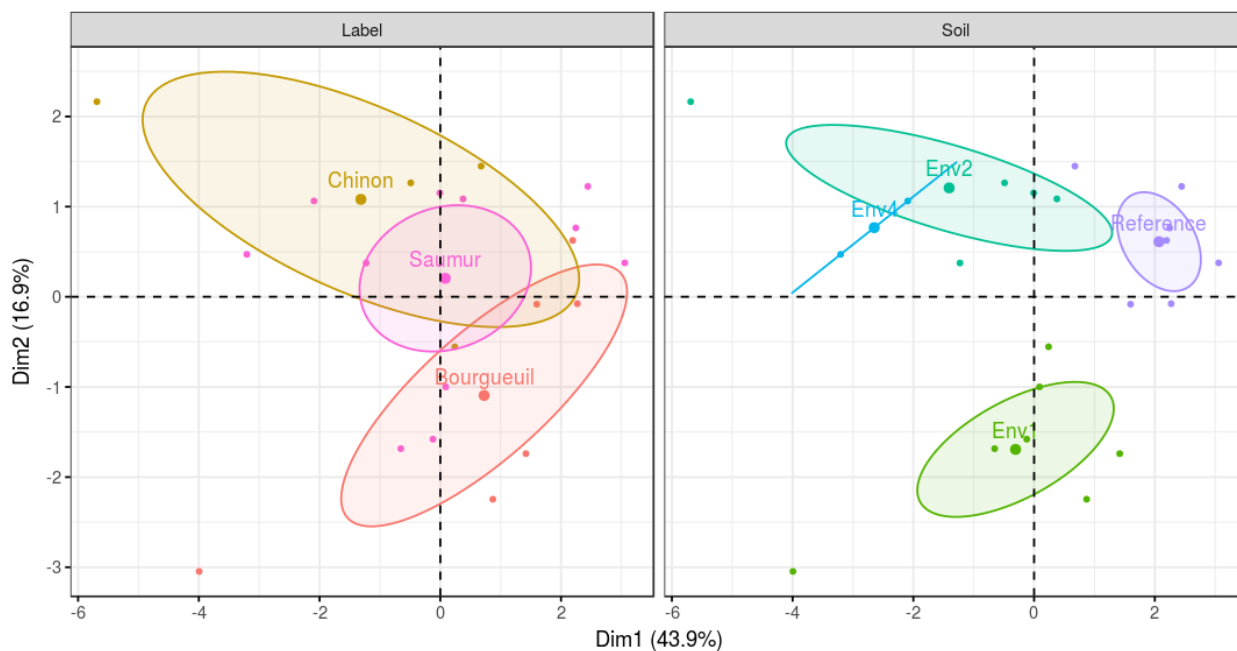
```
[25] fviz_ellipses(res.famd, c("Label", "Soil"), repel = TRUE)
```

FAMD factor map



```
[26] fviz_ellipses(res.famd, 1:2, geom = "point")
```

FAMD factor map



Summary

The factor analysis of mixed data (FAMD) makes it possible to analyze a data set, in which individuals are described by both qualitative and quantitative variables. In this article, we described how to perform and interpret FAMD using FactoMineR and factoextra R packages.

