Napping® VS. Classic sensorial analysis

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INTRODUCTION

The aim of this study is to compare two kinds of data collections. Napping® is a recent method which allows a direct product comparison on a tablecloth. The classical method analysis is a method based on the characterization of products.
We are comparing these two methods, and present the differences and similarities in the final conclusion.

This work begins with the Napping® method, and then is followed by the classic method. Preference mapping is also used in both as complement of the analysis.

I. DATA SETS

The data sets used here refer to 16 different cocktails evaluated by 12 panellists (11 for the Napping®). They can be divided into two data sets: "Napping® expert" and "Classical expert".

For the data frame "Napping® expert", each row represents one of the 16 products. Each couple (X_i,Y_i) represents the coordinates of the cocktail positioned on a tablecloth for each panellist. We also have the panelists' impressions of each juice.
For the data frame "Classical expert", each row represents one of the 16 product evaluated by one panellist during a given session.

II. NAPPING® DATA SET

1. *First of all…*

First, we would want to determine the **links** and **distances** between our 16 different types of juices. Which beverages are **similar**? **Different**?

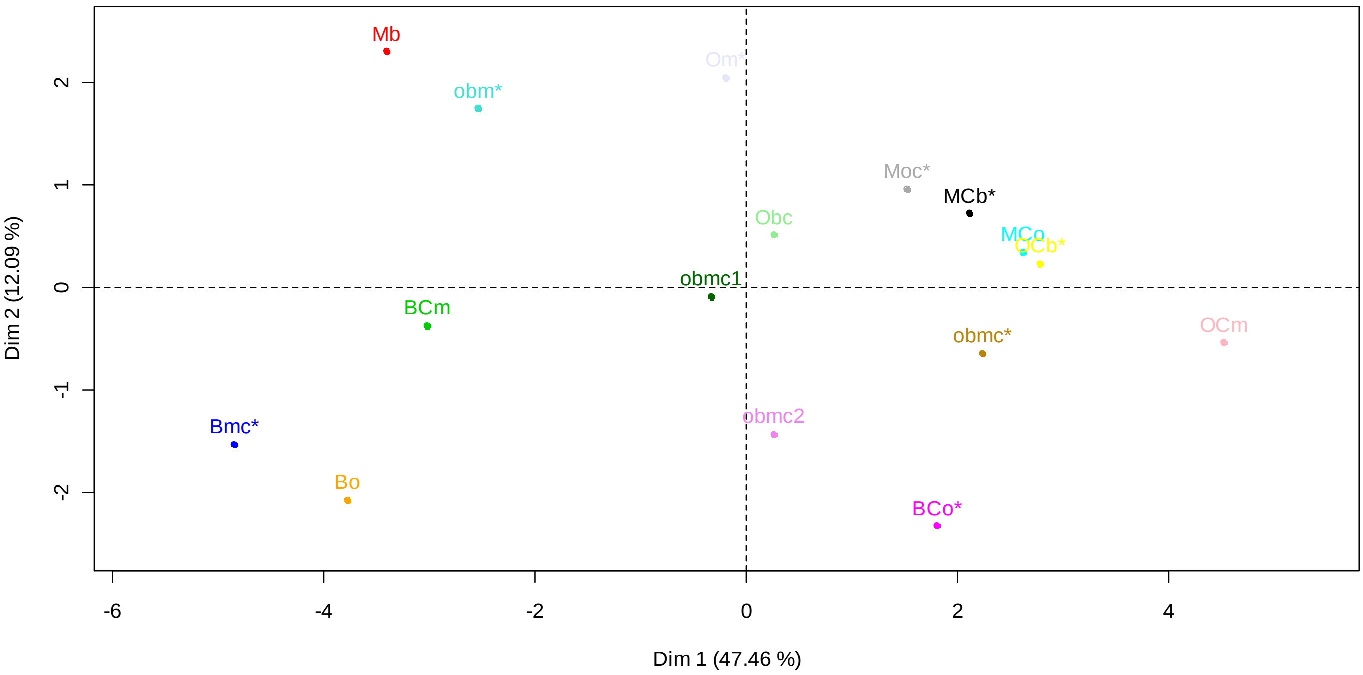
The Napping® data informs us on the distances between the juices and the vocabulary used by the panelist to describe each product. The classical sensorial data, on the other hand, is constituted of the tasters' judgments for all the descriptors such as the color intensity, the mango flavor, the acidity, the pulpiness, etc… ***(See. Data set presentation)***.

2. *Data set*

The Napping® data set is as follows:

JUICES	Panelist n°1				Panelist n°11		
	X_1	Y_1	$Words_1$		X_{11}	Y_{11}	$Words_{11}$
Mb	6.3	36.7	pineapple, sugar, mango…		10.5	29.2	banana, sugar, mango…
⋮				…			
BCm	23.95	21.55	acidty, banana, lemon…		52.6	34.2	acidty, banana, sugar…

3. *Results*

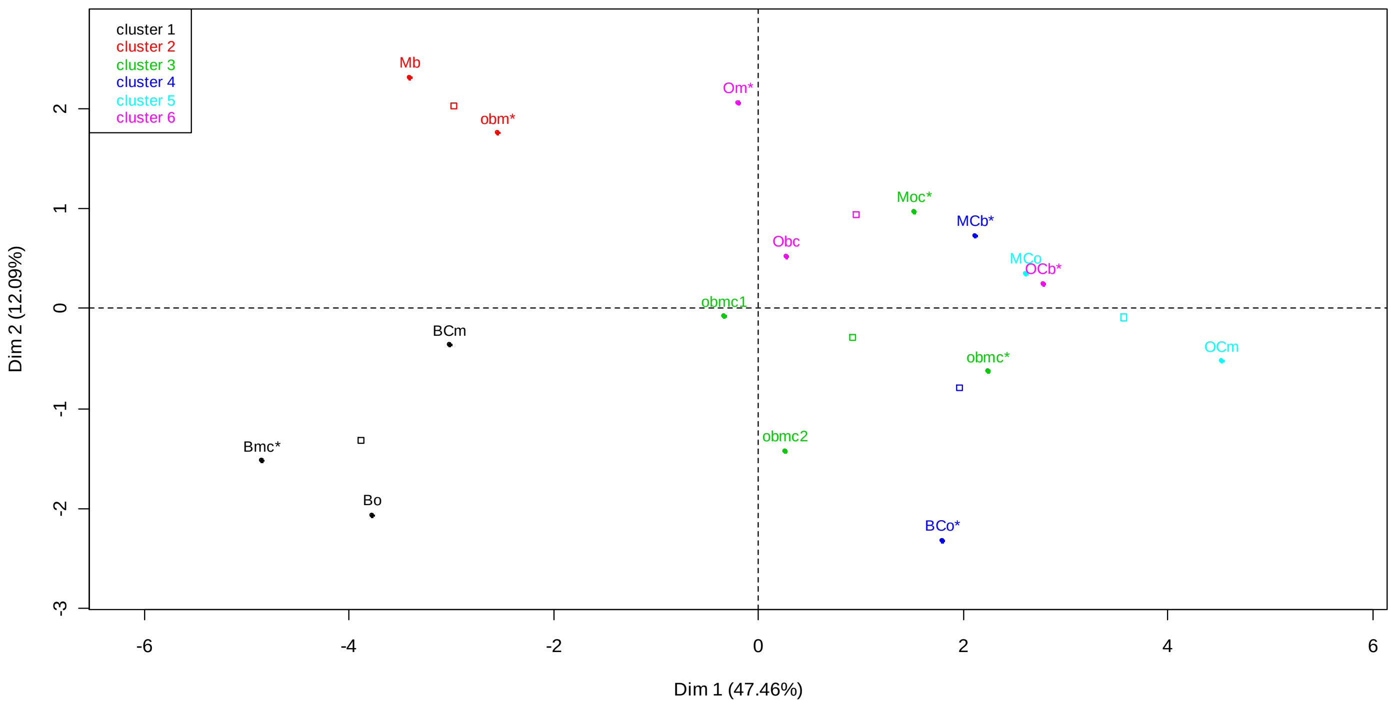


The **non-scaled** Multiple Factorial Analysis (**MFA**) below reveals **small distances** between the products *MCo*, *OCb*, *Moc*, MCb**; *Mb, obm** and *Bmc*, Bo*; which mean these products are **perceived similarly** by the 11 professional panelists.
Their names give also an indication on their composition. For example, a juice with more **O**range juice than **m**ango juice or **b**anana juice is coded as Omb*.
The first two axes have a total inertia of **59.55%**, which is enough to interpret both axes because of the number of panelists.

Axis 1 contrasts juice *Bmc*,* which contains a lot of banana juice, to juice *OCm*; a juice with more citrus fruit (Orange, Lemon). On the right is **the citrus taste** and on the left is the **banana taste**, which represents the comparison between the **lemons' acidity** and the **bananas' sweetness**.
Axis one has an eigenvalue of 7,21 (1,43 for the second one) and it **is common** to all the panelists.

Axis 2 compares products **with** mango juice *(Mb, obm*)* to products **without** mango juice (BCo*).

To emphasize the juice groups, we chose to launch a Hierarchical Classification on Principal Components (**HCPC**).

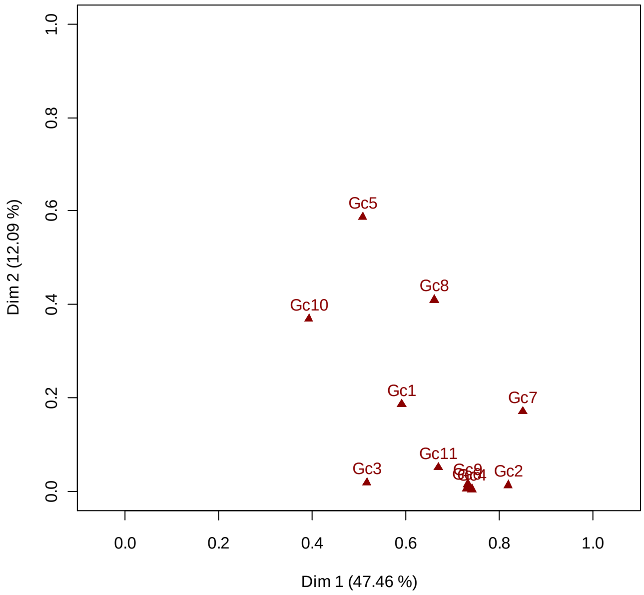


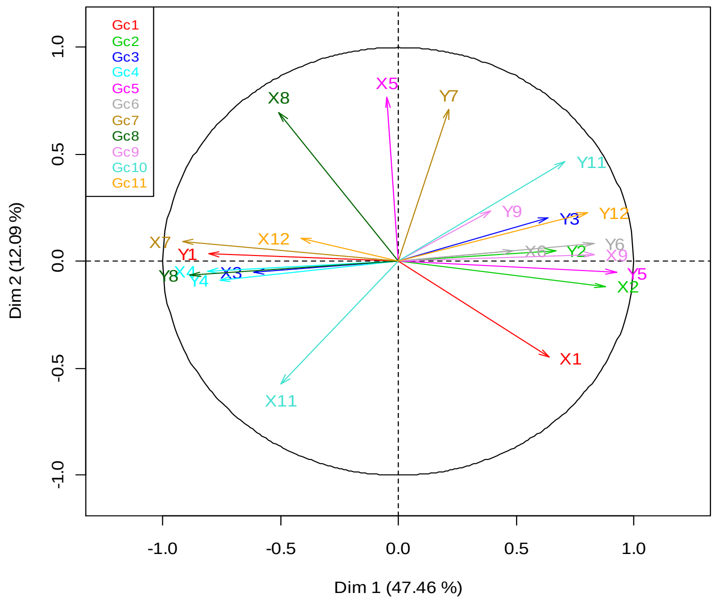
There are **6 major** groups that are emphasized;

- Mb and obm*
- Bmc*, Bo and BCm
- BCo* and MCb*
- obmc1, obmc2, Moc* and obmc*
- MCo and OCm
- MCb* and BCo*

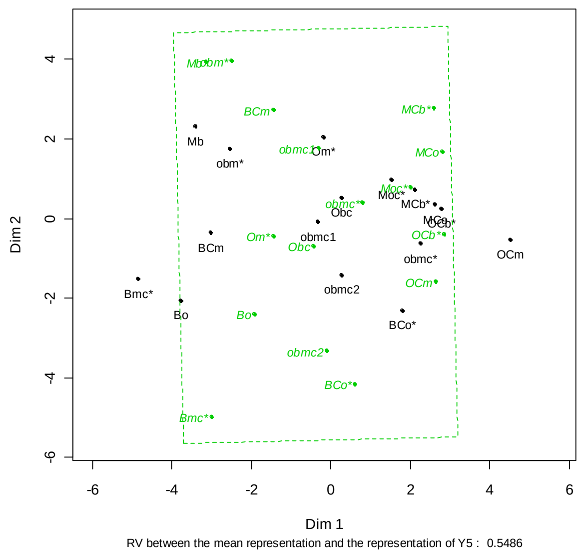
4. *Panelists' points of view*

Each group of the MFA corresponds to one taster and one X,Y coordinate.
The graphs below are obtained from the Napping® data MFA.
We notice that panelists **5** *(Contribution to axis 2: 31,99%)*, **8** *(Contribution to axis 2: 22,30%)*, and **10** *(Contribution to axis 2: 20,14%)* are bidimensional. They are different from the rest of the tasters, which means that **they do not have the same opinions of the juices** as panelists 2, 11, or 3 do.





These differences between the panelists could be validated by the representation of panelist n°5's tablecloth *(black)* in comparison with the average tablecloth *(green)* and by the partial individual plot.



As we said, panelist n°5 is **much different** than the rest of the tasters.

5. *Characterization of the products*

In order to characterize all of the products, we chose to add the vocabulary information. Then we launched a Correspondence Analysis (**CA**) in **SPAD** which allows one to obtain specific words for each juice.
The **WORDS** method creates a vocabulary base and then the **VOSPEC** method finishes the characterization.

The table below shows the descriptors which were most used for each juice (P-Value < 0,05).

JUICES	POSITIVE DESCRIPTORS *(V-TEST ++)*	NEGATIVE DESCRIPTORS *(V-TEST --)*
MCb*	LEMON	
Mb	SUGARY, PINEAPPLE, MANGO	SOUR
BCm	BANANA	ORANGE
Bmc*	BANANA, MOUTH, THICK	
MCo	SPICY	BANANA
BCo*	PERSISTANT, UNUSUAL	
Moc*	MANGO, TYPICAL	BANANA
obmc*	GREEN, LIME, ORANGE	
obmc1	SWEET, SUGARY	
obmc2		
obm*	SUGARY	SOUR
Bo	BANANA	SOUR
OCm	SOUR, LEMON	BANANA
Om*	ORANGE, GRAPEFRUIT, YELLOW, BRIGHT	
OCb*	BITTER, MOUTH ULCER, SOUR	
Obc	ORANGE ACIDTY, ORANGE	

We notice again, the **opposition** between the words “Banana” and “Sweet” versus “Lemon”, “Sour”, and “Orange”.

6. R-code

The data set is named "*AFM nappes*" and can be downloaded from AGROCAMPUS OUEST website.

```
Cocktail <- read.table("C:/.../AFM nappes.txt", header=TRUE,
  sep="\t", na.strings="NA", dec=",", strip.white=TRUE,row.names=1)
summary(Cocktail)

# Napping® results #
Cocktail.MFA<-Cocktail[, c("X1", "Y1", "X2", "Y2", "X3", "Y3", "X4", "Y4",
  "X5", "Y5", "X6", "Y6", "X7", "Y7", "X8", "Y8", "X9", "Y9", "X11", "Y11",
  "X12", "Y12")]
res<-MFA(Cocktail.MFA, group=c(2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2), type=c("c",
  "c", "c", "c", "c", "c", "c", "c", "c", "c", "c"), ncp=5,
  name.group=c("Gc1", "Gc2", "Gc3", "Gc4", "Gc5", "Gc6", "Gc7", "Gc8", "Gc9",
  "Gc10", "Gc11"), num.group.sup=c(), graph=FALSE)
plot.MFA(res, axes=c(1, 2), choix="group", lab.grpe=TRUE)
plot.MFA(res, axes=c(1, 2), choix="axes", habillage="group")
plot.MFA(res, axes=c(1, 2), choix="var", lab.var=TRUE, habillage="group",
  lim.cos2.var=0)
plot.MFA(res, axes=c(1, 2), choix="ind", lab.ind.moy=TRUE, lab.par=TRUE,
  habillage="group")
remove(Cocktail.MFA)

# Classification of the juices #
res.hcpc=HCPC(res, nb.clust=-1)

# Panelist tablecloth #
results = pmfa(Cocktail[,c("X5", "Y5")],Cocktail[,c("X1", "Y1", "X2", "Y2",
  "X3", "Y3", "X4", "Y4", "X6", "Y6", "X7", "Y7", "X8", "Y8", "X9", "Y9",
  "X11", "Y11", "X12", "Y12", "Acidity", "Pleasant", "Pineapple", "Banana",
  "Lemon", "classic", "Sweet", "Bland", "Fruity", "Unusual", "Liquid",
  "Heavy", "Soft", "Mango", "Nectar", "Orange", "Grapefruit", "Passion",
  "Spicy", "Syrupy", "Sugar", "Thick", "Banana.acidity", "Banane.lemon",
  "Banane.orange", "lime", "Orange.acidity", "Orange.lemon", "Orange.blend",
  "original.flavour", "tropical.flavour", "pleasant.sugar", "Acidity...",
  "Extremely.acid", "Sugar...")], coord=c(1,2), lim = c(60,40), graph.mfa=1,
  graph.ind=1,dilat=TRUE)results = pmfa(Cocktail[,c("X1", "Y1", "X2", "Y2", "X3", "Y3", "X4", "Y4",
  "X5", "Y5", "X6", "Y6", "X7", "Y7", "X8", "Y8", "X9", "Y9", "X11", "Y11",
  "X12", "Y12")],Cocktail[,c("Acidity", "Pleasant", "Pineapple", "Banana",
  "Lemon", "classic", "Sweet", "Bland", "Fruity", "Unusual", "Liquid",
  "Heavy", "Soft", "Mango", "Nectar", "Orange", "Grapefruit", "Passion",
  "Spicy", "Syrupy", "Sugar", "Thick", "Banana.acidity", "Banane.lemon",
  "Banane.orange", "lime", "Orange.acidity", "Orange.lemon", "Orange.blend",
  "original.flavour", "tropical.flavour", "pleasant.sugar", "Acidity...",
  "Extremely.acid", "Sugar...")], coord=c(1,2), lim = c(60,40), graph.mfa=1,
  graph.ind=1,dilat=TRUE)
results = pmfa(Cocktail[,c("X1", "Y1", "X2", "Y2", "X3", "Y3", "X4", "Y4",
  "X5", "Y5", "X6", "Y6", "X7", "Y7", "X8", "Y8", "X9", "Y9", "X11", "Y11",
  "X12", "Y12")],Cocktail[,c("Acidity", "Pleasant", "Pineapple", "Banana",
  "Lemon", "classic", "Sweet", "Bland", "Fruity", "Unusual", "Liquid",
  "Heavy", "Soft", "Mango", "Nectar", "Orange", "Grapefruit", "Passion",
  "Spicy", "Syrupy", "Sugar", "Thick", "Banana.acidity", "Banane.lemon",
  "Banane.orange", "lime", "Orange.acidity", "Orange.lemon", "Orange.blend",
  "original.flavour", "tropical.flavour", "pleasant.sugar", "Acidity...",
  "Extremely.acid", "Sugar...")], coord=c(1,2), lim = c(60,40), graph.mfa=1,
  graph.ind=1,dilat=TRUE)
```

III. SENSORY PROFILE DATA SET

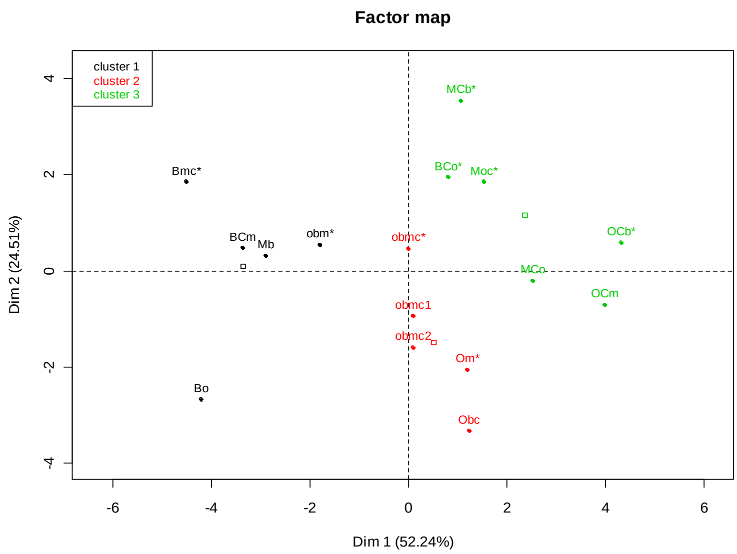
1. Data set

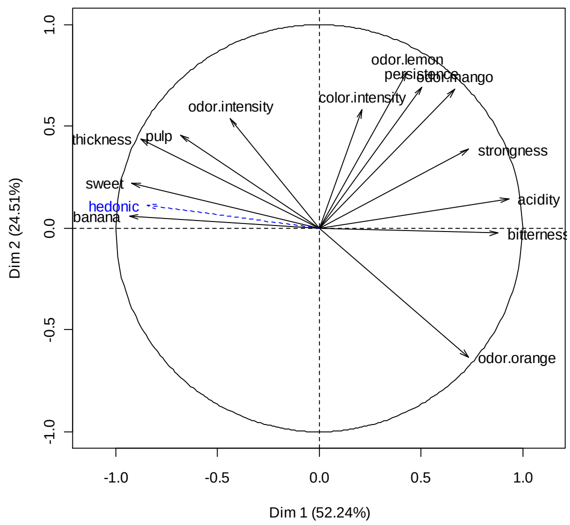
The sensory descriptions are obtained from **11 trained panellists**. Each panellist tastes 16 fruit juices. These juices are made of banana, mango, lemon, and/or orange juices in different proportions. **13 descriptors** have been evaluated on a 10-point scale during **2 sessions**: colour intensity, olfactory intensity, first taste, sweetness, sourness, bitterness, orange flavor, banana flavor, mango flavor, lemon flavor, taste persistence, pulpiness and thickness.

JUICES	Panelists	Color intensity	Olfactory intensity		Persistence	Pulpiness	Thickness
Mb	1 ⋮ 11	5 ⋮ 3	3 ⋮ 7		3 ⋮ 6	1 ⋮ 1	10 ⋮ 8
⋮				…			
BCm	1 ⋮ 11	2 ⋮ 4	7 ⋮ 4		7 ⋮ 6	1 ⋮ 1	8 ⋮ 6

2. *Results*

In each session, panellists taste **all** the juices. The followings analysis is based on the average data table for each taster which allows a multi-dimensional point of view of the products' space. The *panellipse* function from **SensoMineR** is also used. Although there are some missing values, the panelist function estimates them before performing PCA.





The **scaled** Principal Component Analysis (PCA) on the Products*Descriptors matrix reveals that the first two principal components account for **76.7%** of the total variance (PC_1: 52.2%, PC_2: 24.5%).

Axis 1 has an eigenvalue of 6.8 (3.2 for the second axis). It compares juices *Bmc** and *Bo* **(Both contain a lot of banana juice)** to juices *OCb** and *OCm** **(Both with more citrus fruits juices)**. This axis could be characterized by the opposition between **bitterness and sourness** versus **sweetness** and **taste of banana**. We remark that variable **Hedonic** (Illustrative variable) strongly correlates with **Sweet** and **Banana.** Therefore we can conclude that panelists prefer sweet and banana flavored juices.

Axis 2 contrasts juices **with** mango juice *(MCb*)* against juices **without** mango juice (Obc). It is possible that citrus juice flavor is very strong and whites-out the others.

The **HCPC** function (Hierarchical Classification on Principle Components) from **FactoMineR** is launched in order to perform a hierarchical classification on the principal components of the PCA above. We only use the first two PCA axis.

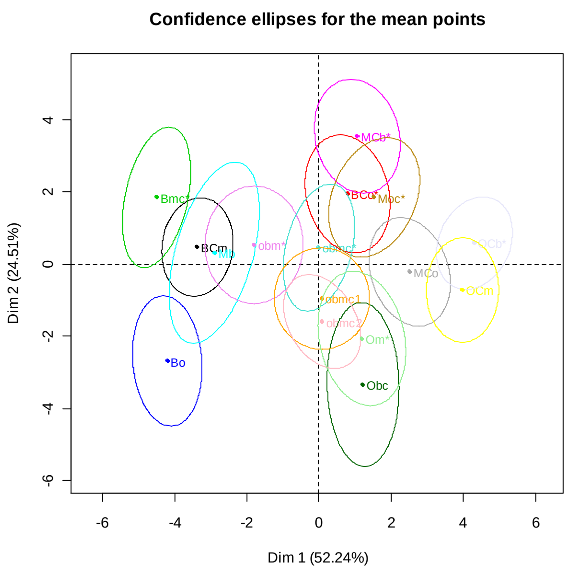
There are **3 juice clusters** that are emphasized *(Juices are colored by cluster in the factor map on the previous page)*:

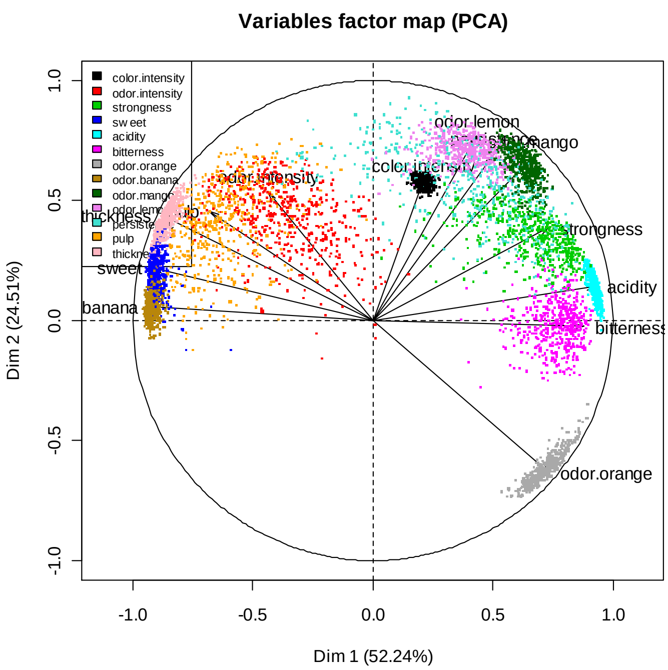
- Mb, BCm, Bmc*, obm* and Bo (Black colored)
- obmc1, obmc2, obmc*, Om* and Obc (Red colored)
- Moc*, OCb*, BCo*, MCo, MCb and OCm (Green colored).

The hedonic descriptor (Global appreciation of each juice) shows that black colored juices are preferred by the panelists, especially *Bmc**, *Bo* and *BCm (Contribution to axis 1: 18.6, 16.3% and 10.4%)*. On the opposite side, *OCm* and *Ocb** are disliked.

Finally, we constructed confidence ellipses for each product. We generate virtual panels using bootstrap techniques in order to display the **confidence ellipses** around the 16 beverages. Thus, it reveals the uncertainty of the positions of each juice. The dataset has been re-sampled 500 times.
Confidence ellipses contain 95% of the simulated data. Products are **not distinguishable from** one another. It is not possible to distinguish the more similar juices, nevertheless, **differences are perceived** by the panellists. *(e.g: BCm and OCm)*

Similarly, to get an impression of the **variables' variability**, the same procedure is carried out. 500 variable projections are shown on the variables factor map plot.
As we can see from this figure, some attributes are very **stable** (Color intensity, sour, mango aroma) while others are more spread out (Odor intensity particularly)





3. Characterization of the products

We chose a different way to characterize our juices; indeed, we will **not** use the CA method, otherwise correlations between juices and variables.
The table below allows us to compare all the juices using the 13 descriptors.

Ajusted mean

	sweet	odor.banana	hedonic	thickness	pulp	odor.intensity	color.intensity	odor.lemon	persistence	odor.mango	odor.orange	strongness	bitterness	acidity
Bmc*	8.333	8.167	6.042	7.5	2.708	6.042	7.625	4.583	6.208	3.125	2.5	5.542	1.625	2.792
Bo	7.083	8	5.75	6.208	2.167	5.583	2.792	2.042	5.292	1.708	4.542	5.625	1.458	3.25
BCm	7.208	7.542	5.833	7.083	2.583	6.167	2.083	3.708	6	3.292	3.208	6.083	1.792	4.375
Mb	7.75	5.208	6.167	6.75	2.208	5.458	3.417	4.417	6.125	3.542	3.25	5.875	1.542	3.292
obm*	7.208	4.417	6.917	5.792	2.333	5	7.875	4.75	6.167	4.125	4.333	5.708	1.5	3.542
obmc*	6.083	3.167	5.292	5.333	2.417	5.25	8.208	4.667	6.167	4.375	5.542	4.845	1.958	5.042
obmc2	6.167	3.667	5.167	5	2.458	4.167	3.125	4	6.208	3.833	6.042	5.458	2.125	5.583
obmc1	6.083	3.5	4.875	4.75	2.458	4.708	3.458	4.375	6.375	3.375	5.792	5.833	2.042	5.5
Om*	5.75	1.625	5.208	4.167	5.75	4.708	8.167	3.583	5.625	4.208	6.708	5.856	2.083	5.125
BCo*	5	4.917	4.125	6.167	2.417	5.542	7.875	4.25	6.417	5.792	3.958	6.667	2.125	7.5
MCb*	6.208	2.958	4.583	6.083	2.542	5.583	7.958	6.25	6.792	5.958	3.75	6.958	2	7.083
Moc*	6.042	2.25	5.292	4.958	2	5.542	8.583	5.5	6.833	5.125	4.917	6.292	2.042	6.583
Obc	4.667	3.083	3.708	4.042	1.792	4.708	3.458	2.833	5.833	2.875	7.292	5.958	2.125	6.208
MCo	4.917	1.667	3.792	4.042	1.667	5.292	3.5	5.875	5.875	4.583	5.625	7.25	1.917	7.708
OCm	4.208	1.167	3.25	3.333	1.583	5.5	3.5	4.583	6.667	4.583	7.5	7	2.292	8.333
OCb*	4.542	1.542	3.167	3.667	1.75	4.792	7.792	5	6.75	5.25	6.125	7.292	2.458	8.333

White: marks **borderline**; Pink: marks **down on the borderline**; Blue: marks **across the borderline**.

First, we notice that the most preferred juice is *obm* (Best Appreciation mark: 6.91)*. This juice is more sugary (7,17) and flashier than the others. Furthermore, its bitterness, sourness, and orange flavor are **less prominent**. It has no lemon juice and is made of 46,7% orange juice, 26,7% mango juice, 26,7% banana juice.

Contrary to *obm**, *OCb** is the **liked the least**. (Appreciation mark: 316). It is very **sour, watery** and **sugarless** because of its amount of citrus fruit juices. Although it is not made with mango juice, panelists noticed a **strong mango favor**.

Thus, we can characterize each products as we did with *obm** and *OCb**.

In general, the panelists' performances were good. They managed **to discriminate** between the juices (Table below). The flavor persistence was not a **discriminating descriptor**.

Panel performance (sorted by product P-value)

	Juice	Panelist	Juice:Panelist	median
color.intensity	2.083e-72	1.744e-05	2.017e-06	2.017e-06
acidity	3.323e-39	3.462e-24	0.4694	3.462e-24
odor.banana	1.018e-34	4.557e-07	0.009051	4.557e-07
thickness	2.625e-25	2.17e-22	0.04572	2.17e-22
odor.orange	2.041e-22	7.577e-17	0.02383	7.577e-17
sweet	1.665e-20	4.119e-19	0.007344	4.119e-19
hedonic	1.659e-14	6.155e-15	0.03871	1.659e-14
odor.mango	1.798e-11	0.1308	1	0.1308
odor.lemon	3.452e-07	0.01308	0.9988	0.01308
strongness	1.231e-05	2.692e-18	0.9064	1.231e-05
pulp	0.0001766	1.793e-48	0.9324	0.0001766
bitterness	0.002443	1.393e-51	0.5387	0.002443
odor.intensity	0.04493	1.53e-09	0.2295	0.04493
persistence	0.1318	6.118e-17	0.1131	0.1131

4. *R-code*

The data set is named "*Experts profil*" and can be downloaded from [AGROCAMPUS OUEST] website.

```
library(SensoMineR)

######## ####################################################################################
#DATA FILE

classique <- read.table("Experts.csv", header=TRUE, sep=";", na.strings="", dec=",")
names(classique) #nom des variables
#Supprime les variables non utilisées (commentaires) et renomme les variables (libellés anglais)
classique<-classique[,-23]
classique<-classique[,-21]
classique<-classique[,-18]
classique<-classique[,-8]
classique<-classique[,-6]
names(classique)[1]="Session"
names(classique)[2]="Panelist"
names(classique)[3]="Rank"
names(classique)[4]="Juice"
names(classique)[5]="color.intensity"
names(classique)[6]="odor.intensity"
```

```
names(classique)[7]="strongness"
names(classique)[8]="sweet"
names(classique)[9]="acidity"
names(classique)[10]="bitterness"
names(classique)[11]="odor.orange"
names(classique)[12]="odor.banana"
names(classique)[13]="odor.mango"
names(classique)[14]="odor.lemon"
names(classique)[15]="persistence"
names(classique)[16]="pulp"
names(classique)[17]="thickness"
names(classique)[18]="hedonic"

for(i in 1:3) classique[,i]<-as.factor(classique[,i]) #transforme en facteur

#Pour voir si données équilibrées
table(classique$Session,classique$Panelist) #chaque juge a goûté les 16 produits
table(classique$Session,classique$Juice)  #chaque produit a été testé aux 2 séances
table(classique$Panelist,classique$Juice) #chaque juge a goûté 2 fois chaque produit

numSummary(classique, statistics=c("mean", "sd")) #statistiques descriptives


#Boîte à moustaches pour chacun des descripteurs
boxprod(classique[,c("Session", "Panelist", "Rank", "Juice", "color.intensity", "odor.intensity", "strongness", "sweet",
"acidity", "bitterness",
  "odor.orange", "odor.banana", "odor.mango", "odor.lemon", "persistence", "pulp", "thickness",
"hedonic")],firstvar=5,col.p=4,numr=2,numc=1)

#########################################################################################
#   MULTIVARIATE ANALYSIS


##################
#1ère METHODE: ACP via panellipse Menu SensoMineR/CharacterizationProducts/ultidimensional Sensory Profile =
panellipse
##################

r_panellipse=panellipse(classique[,c("Session", "Panelist", "Rank", "Juice", "color.intensity", "odor.intensity",
  "strongness", "sweet", "acidity", "bitterness", "odor.orange", "odor.banana", "odor.mango", "odor.lemon",
  "persistence", "pulp", "thickness")],col.p=4,col.j=2,firstvar=5,alpha=0.05,coord = c(1,2), nbsimul =500,nbchoix =NULL,
  level.search.desc=0.2,scale.unit=1,variability.variable =TRUE,centerbypanelist =TRUE,scalebypanelist=FALSE,
  name.panelist=FALSE)


##################
#2ème METHODE
##################

moyennes=scalebypanelist(classique,firstvar=5,center=FALSE,scale=FALSE,col.p=4,col.j=2)
average=moyennes[1:16,] #seul les moyennes par produit nous intéressent
row.names(average)=average[,2]

#PCA
res_pcamoy=PCA(average[1:16,-(1:2)],quanti.sup=14:14)
#Représentation des jus de fruits sur le plan (1,2)


######################################################
#######################           CAH

#On peut ensuite lancer une CAH automatique sur les résultats de l'ACP.
res.HCPC<-HCPC(res_pcamoy,nb.clust=-1)
res.HCPC


################################################################################
##############          Analyses univariées              #############


#Donne les produits en fonction des descripteurs les plus importants
#Modèle note_descripteur~Juice+Panelist+Juice:Panelist
resdecat=decat(classique[,c("Session", "Panelist", "Rank", "Juice", "color.intensity", "odor.intensity", "strongness",
  "sweet", "acidity", "bitterness", "odor.orange", "odor.banana", "odor.mango", "odor.lemon", "persistence", "pulp",

"thickness","hedonic")],firstvar=5,formul=~Juice+Panelist+Juice:Panelist,proba=0.05,graph=TRUE,col.lower="mistyrose",
  col.upper="lightblue")
resdecat

#
respanelperf=panelperf(classique[,c("Session", "Panelist", "Rank", "Juice", "color.intensity", "odor.intensity",
  "strongness", "sweet", "acidity", "bitterness", "odor.orange", "odor.banana", "odor.mango", "odor.lemon",
  "persistence", "pulp", "thickness","hedonic")],firstvar=5,formul=~"Juice+Panelist+Juice:Panelist",random=1)
respanelperf$p.value
coltable(magicsort(respanelperf$p.value, sort.mat = respanelperf$p.value[,1], bycol = FALSE,method = "median"),
  main.title = "Panel performance (sorted by product P-value)")
```

IV. PREFERENTIAL MAPPING

Preference mapping methods are commonly used in the fields of marketing research and research and development in order to explore and understand the structure and tendencies of consumer preferences, to link consumer preference information to other data, and to predict the behaviour of consumers in terms of acceptance of a given product.
This function refers to the method introduced by M. DANZART. A response surface is computed per consumer; then according to a certain threshold, preference zones are delimited and finally superimposed.

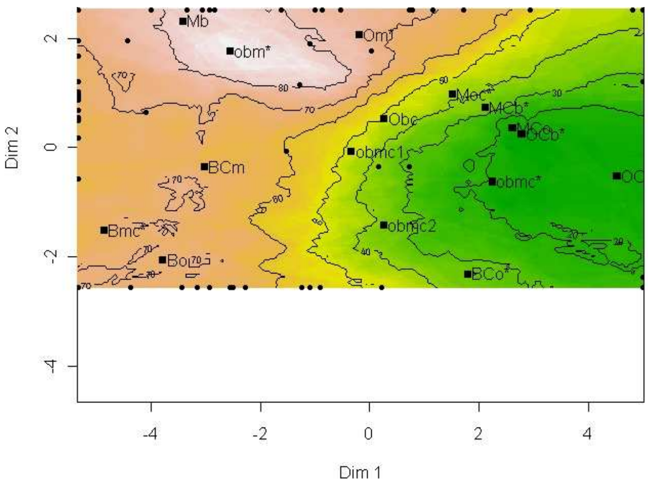
1. *Data set*

In order to perform preference mapping, it is necessary to use a new data set made with the coordinates of the products in the first plan *(Dimensions 1 and 2)* and hedonics marks attributed by each consumers as shown below:

JUICES	Dim_1	Dim_2	C_1	...	C_{100}
BCm	-3.02	-0.36	4	...	6
BCo*	1.80	-2.31	4	...	4
⋮					
Om*	-0.19	2.05	6	...	3

This data frame has the dimension (16,102): each row represents one of the 16 juices.
The two first variables are the **coordinates of the products in the first plan**. They are obtained from the Multiple Factor Analysis (**MFA**) or Principal Component Analysis (**PCA**) which was obtained in the third and the fourth part with a Napping® or Classical profile.

2. ***Napping®*** *profile preference mapping*



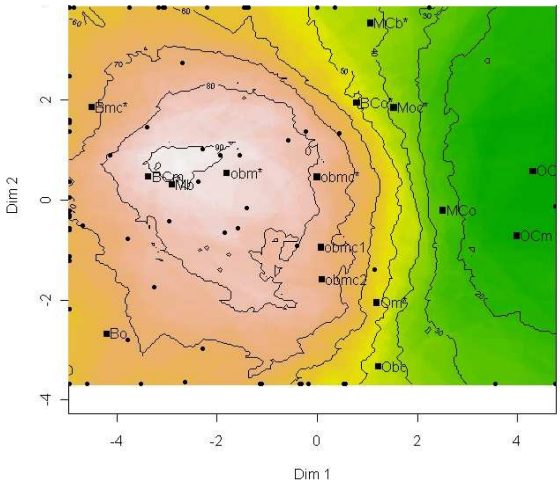
The Napping® preference mapping data set can be downloaded here.

Preference mapping shows a kind of products' appreciation degree.
The opposite **preference map** reveals that 95% of the tasters **liked** *Mb* and *obm**; which means these products have been **marked higher** than the others. At the other hand, *OCm* was disliked by the tasters.

It is important to remark that the **more juices have citrus juice the more they are unappreciated**. Juices with banana juice are the most liked.

3. ***Classical*** *profile preference mapping*

The preference mapping data set for the classical method can be downloaded here.



This **preference mapping** reveals that *Mb, BCm* and *obm** are **the most prefered.**
Like the Napping® preference mapping, juice *OCb** and *OCm* are the less appreciated.

CONCLUSION

In conclusion, the results are **similar** for both methods. Juices *Mb* and *obm** are the most **liked by consumers** and juices OCb* and OCm **the least appreciated by consumers**.
As we said in the first part about the Napping® profile, *Mb* is **sugary, orangey**, **pineapple,** and **acidic** like *obm**. The features of these juices show the consumers' preferences.

This similarity is interesting to notice this similarity. Napping®, contrary to classical analysis, is **not restricted** to several descriptors and is **the quickest method**. Panelists class juices according to their own perceptions.
Napping®, like the classic method, permits to characterize the juices with the taster's own vocabulary which allows a preference mapping to be built.