High Diminsional Statistics-Sheet 5-Exercise 4

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Consider the orange juice dataset X, called "jusdorange.csv". The dataset contains 7 characteristics of the orange juice, on which we want to perform a principal component analysis.

Prepare

First of all we import the dataset:

```r
path <- "/home/hamed/Documents/datasets/jusdorange.csv"
data <- read.table(path, sep=";", header=T)
#data

url <- "https://hastie.su.domains/ElemStatLearn/datasets/prostate.data"
df <- read.table(url, sep = '\t', header = TRUE)

#drops <- c("Conditionnement","Origine", "Produit")
#df <- data[ , !(names(data) %in% drops)]
X <- data[,sapply(data, is.numeric)]
X
```

```
##   Intensité.odeur Typicité.odeur Caractère.pulpeux Intensité.goût
## 1            2.82           2.53              1.66           3.46
## 2            2.76           2.82              1.91           3.23
## 3            2.83           2.88              4.00           3.45
## 4            2.76           2.59              1.66           3.37
## 5            3.20           3.02              3.69           3.12
## 6            3.07           2.73              3.34           3.54
##   Caractère.acide Caractère.amer Caractère.sucré Glucose Fructose Saccharose
## 1            3.15           2.97            2.60   25.32    27.36      36.45
## 2            2.55           2.08            3.32   17.33    20.00      44.15
## 3            2.42           1.76            3.38   23.65    25.65      52.12
## 4            3.05           2.56            2.80   32.42    34.54      22.92
## 5            2.33           1.97            3.34   22.70    25.32      45.80
## 6            3.31           2.63            2.90   27.16    29.48      38.94
##   Pouvoir.sucrant   pH Titre Acide.citrique Vitamine.C
## 1           89.95 3.59 13.98           0.84      43.44
## 2           82.55 3.89 11.14           0.67      32.70
## 3          102.22 3.85 11.51           0.69      37.00
## 4           90.71 3.60 15.75           0.95      36.60
## 5           94.87 3.82 11.80           0.71      39.50
## 6           96.51 3.68 12.21           0.74      27.00
```

Question 1

Build the centered vector Y starting from X. Compute its covariance matrix Σ and the eigenvectors and eigenvalues of Σ. What do they represent in the principal component analysis?

We create Y by centering X, i.e., subtract mean of each variable (column) from its observations (rows). We then construct covariance matrix of Y and computes its eigenvalues and eigenvectors.

```
# center with 'sapply()'
Y <- sapply(X, function(x) as.numeric(x) - mean(x))

Sigma <- cov(Y)

#Sigma
#summary(Sigma)

e <- eigen(Sigma)

# eigenvalues
eigvals <- e$values

# eigenvectors
eigvecs <- e$vectors

eigvals
```

```
##  [1]  1.400532e+02  5.813757e+01  3.243695e+01  3.091913e-01  1.345573e-01
##  [6]  1.046674e-14  7.409821e-15  1.398509e-15  8.719297e-17 -2.214281e-18
## [11] -1.453968e-17 -1.895423e-17 -5.913880e-17 -4.022990e-16 -7.692731e-16
```

```
#sort(eigvals, decreasing=TRUE)
```

The eigenvectors and eigenvalues of a covariance (or correlation) matrix represent the "core" of a PCA: The eigenvectors (principal components) determine the directions of the new feature space, and the eigenvalues determine their magnitude. In other words, eigenvectors manifest the direction of spread of our data.

Question 2

Compute the variance represented by the first axis. How many principal components do we need to explain at least the 90% of the total variance of the dataset?

In order to determine how many PCA componentes are required, we need to measure the propoertion of variance for each component. In other words, each component explains some part of variability in data, with the first component explains the most (as it is corresponded to the biggest eigen value of Σ) ahd the last has the least contribution.
As we need 90% of the total variance, we can derive the cumulative sum proportion of variance for all components and determine the component at which this sum reaches 90 percent. All components prior to that component with that component are required to explain the 90% proportion.

The fact that first components contribute the most, results in having least number of components required for the explainability we require (90% in this case).

Using the PCA model which is defined by applying `prcomp` function on our dataset, we will compute proportion of variance using the two methods, one is just by observing values provided by the summary of the model, and another to compute them, as they are normalized standard deviation.

```
## method1: PCA model
pca <- prcomp(Y, center = FALSE, scale = TRUE)
summary(pca)
```

```
## Importance of components:
##                           PC1    PC2    PC3     PC4    PC5       PC6
## Standard deviation     2.9828 1.6074 1.2685 1.00585 0.9479 1.717e-15
## Proportion of Variance 0.5931 0.1722 0.1073 0.06745 0.0599 0.000e+00
## Cumulative Proportion  0.5931 0.7654 0.8727 0.94010 1.0000 1.000e+00
```

```
##
PoV <- pca$sdev^2/sum(pca$sdev^2)
label_percent()(PoV)
```

```
## [1] "59.31%" "17.23%" "10.73%" "6.74%"  "5.99%"  "0.00%"
```

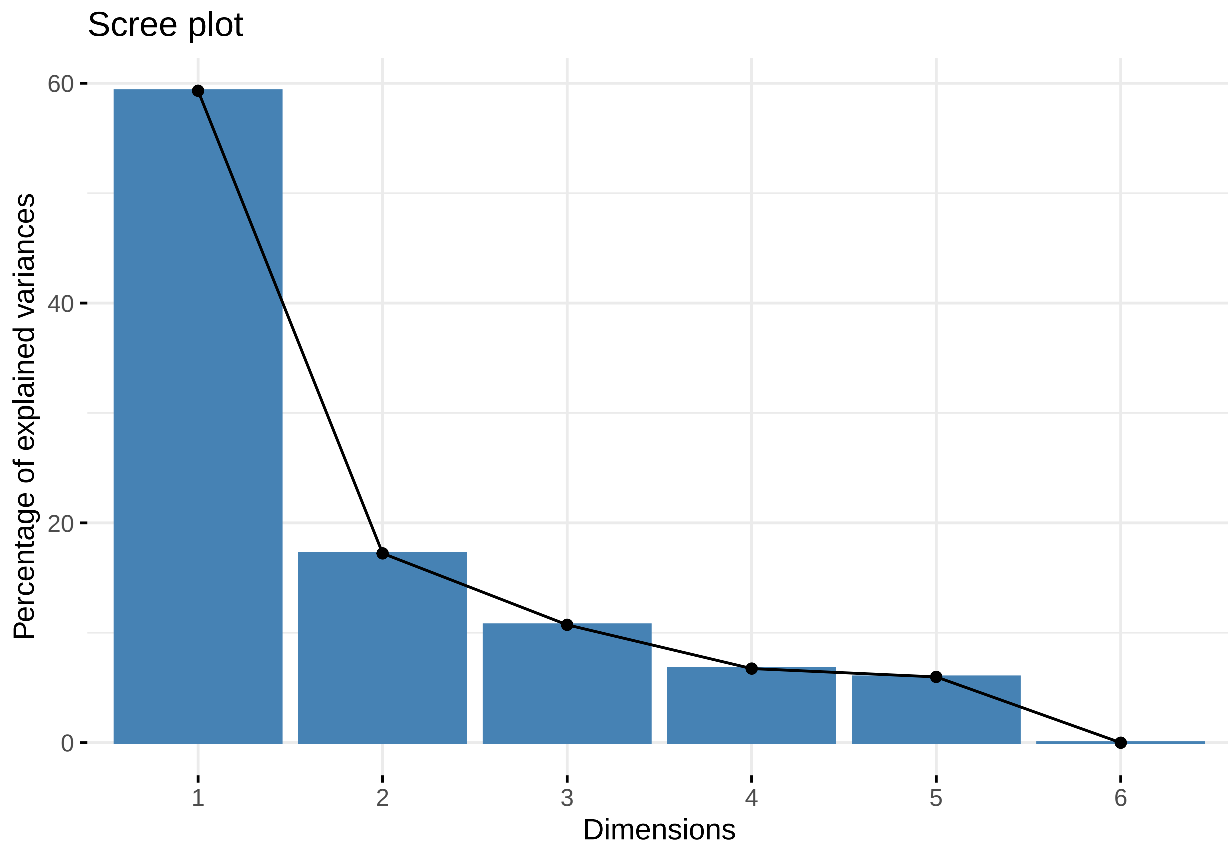
In the summary of our PCA model, we can see that the cumulative variance is equal to 94, therefore reaches 90% at PC4 (4th principal component). However, at PC3 it is also very close to 90%. If we choose to be stringent, then we should choose 4th component.

For the purpose of illustration, I plotted both proportion of variance and cummulative proportion of variance, which validates the statement I made about nubmer of components required.

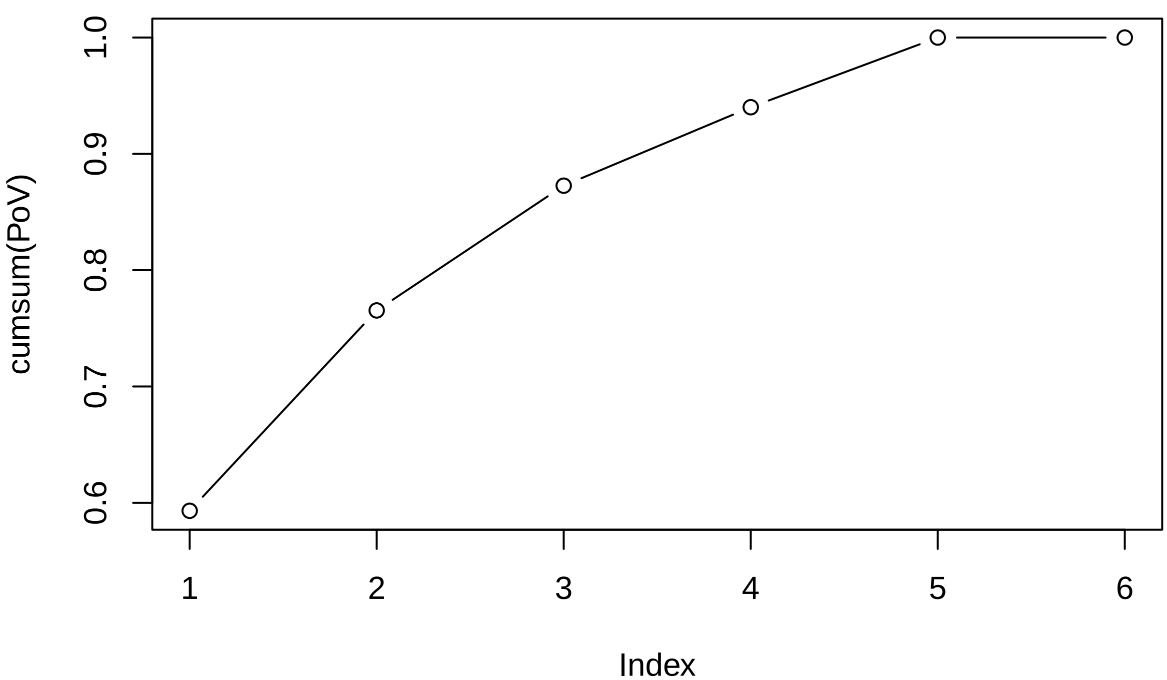
```
# compute PCA
get_eig(pca)
```

```
##         eigenvalue variance.percent cumulative.variance.percent
## Dim.1 8.897003e+00     5.931335e+01                    59.31335
## Dim.2 2.583801e+00     1.722534e+01                    76.53869
## Dim.3 1.609019e+00     1.072679e+01                    87.26548
## Dim.4 1.011732e+00     6.744883e+00                    94.01036
## Dim.5 8.984454e-01     5.989636e+00                   100.00000
## Dim.6 2.948015e-30     1.965343e-29                   100.00000
```

```
fviz_eig(pca)
```

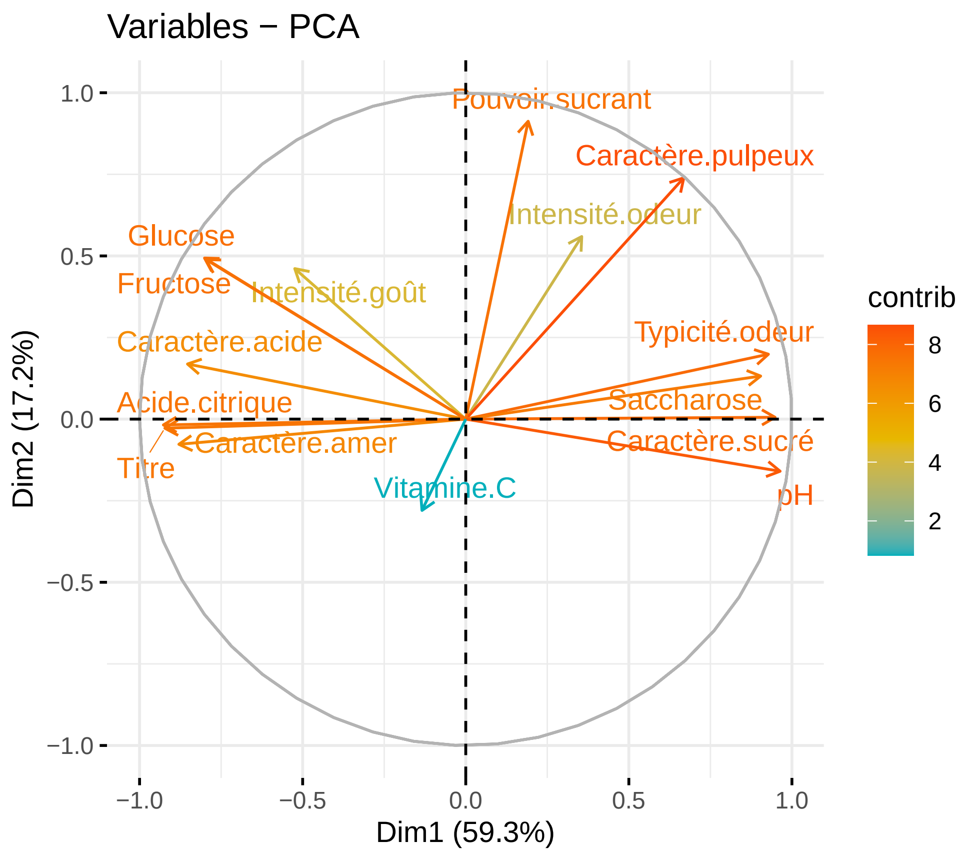



```r
plot(cumsum(PoV), type="b")
```



Graph of variables. Positive correlated variables point to the same side of the plot. Negative correlated variables point to opposite sides of the graph.

```r
fviz_pca_var(pca,
             col.var = "contrib", # Color by contributions to the PC
             gradient.cols = c("#00AFBB", "#E7B800", "#FC4E07"),
             repel = TRUE     # Avoid text overlapping
             )
```

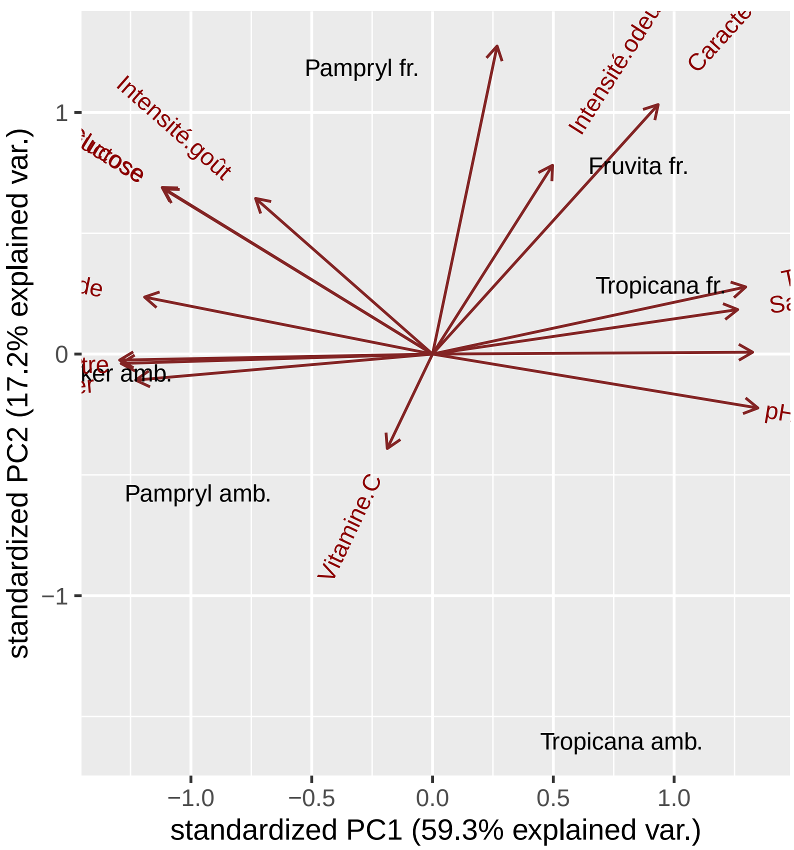



```r
eig.val <- get_eigenvalue(pca)
eig.val
```

```
##         eigenvalue variance.percent cumulative.variance.percent
## Dim.1 8.897003e+00     5.931335e+01                    59.31335
## Dim.2 2.583801e+00     1.722534e+01                    76.53869
## Dim.3 1.609019e+00     1.072679e+01                    87.26548
## Dim.4 1.011732e+00     6.744883e+00                    94.01036
## Dim.5 8.984454e-01     5.989636e+00                   100.00000
## Dim.6 2.948015e-30     1.965343e-29                   100.00000
```

The procedure I pursue is as following:

```r
labels <- data[,1]
rownames(X) <- labels
ggbiplot(pca, labels = labels)
```




```
labels
```

```
## [1] "Pampryl amb."   "Tropicana amb." "Fruvita fr."    "Joker amb."
## [5] "Tropicana fr."  "Pampryl fr."
```

ggbiplot(mtcars.pca,ellipse=TRUE, labels=rownames(mtcars), groups=mtcars.country)