

Classifying spectrometric curves

- **Statistical aim**

We recall that for each unit i (among 215 pieces of finely chopped meat), we observe one spectrometric curve (\mathbf{x}_i) which corresponds to the absorbance measured at 100 wavelengths (i.e. $\mathbf{x}_i = (\chi_i(\lambda_1), \dots, \chi_i(\lambda_{100}))$). The first 100 columns of the file “npfda-spectrometric.dat” contain the observed curves $\{\mathbf{x}_i\}_{i=1, \dots, 215}$. It is worth noting that the reponse (fat content) is completely ignored for this classification analysis.

- **R/S+ commandlines:**

- **Entering spectrometric data**

```
SPECDAT <- as.matrix(read.table("npfda-spectrometric.dat"))
attributes(SPECDAT)$dimnames[[1]] <- character(0)
SPECURVES <- SPECDAT[,1:100]           # sample of curves
```

- **Automatical classification: the following commandline allows to get directly the groups:**

```
spec.classif <- classif.npfda(SPECURVES, 2, 20, c(0,1),
                             semimetric="deriv", threshold=0.05, nb.bw=100,
                             nss=0, mspg=10, centrality="mean")
```

Remark: `nss=0` means that the criterion HI is used instead of SHI whereas `centrality="mean"` implies that HI is based on differences between mean and modal curves.

- **Loading the groups**

```
Group1 <- spec.classif$Partition[[1]]
Group21 <- spec.classif$Partition[[2]]
Group22 <- spec.classif$Partition[[3]]
```

Remark: `spec.classif$Labels` contains the history of the splitting procedure namely ‘1’, ‘21’ and ‘22’.

- **Plotting terminal leaves: Group1, Group21 and Group22**

- **Computing the second derivatives of the spectrometric curves**

```
SPEC2D2 <- t(approx.spline.deriv(SPECURVES, 2, 20,
                                c(0,1))$APPROX)
```

- **Loading the modal curve for each group**

```
MODAL.CURVES <- spec.classif$MODES
```

- **Computing the second derivatives of the modal curves**

```
MODAL.CURVESD2 <- t(approx.spline.deriv(
                    MODAL.CURVES, 2, 20, c(0,1))$APPROX)
```

- **Displaying groups: original data, second derivatives and corresponding modal curves**

The following R/S+ commandlines allow to build Figure 1:

```
x <- seq(850, 1050, length=100)
##
# GROUP1
#####
par(mfrow=c(3,3))
plot(x,SPECURVES[Group1[1],],ylim=range(SPECURVES), type="l",
      xlab="Wavelengths",ylab="Absorbances", main="GROUP 1")
for(i in Group1[-1]){
  par(new=T)
  plot(x,SPECURVES[i,],ylim=range(SPECURVES), type="l",
        xlab="", ylab="", axes=F)
}
plot(x,SPEC2D2[Group1[1],],ylim=range(SPEC2D2), type="l",
      xlab="Wavelengths", ylab="Absorbances",
      main="GROUP 1: second derivatives")
for(i in Group1[-1]){
  par(new=T)
  plot(x,SPEC2D2[i,],ylim=range(SPEC2D2), type="l",
        xlab="",ylab="", axes=F)
}
plot(x, MODAL.CURVESD2[1,], ylim=range(SPEC2D2), type="l",
      xlab="Wavelengths", ylab="Absorbances",
      main="GROUP 1: modal curve")
##
```

```

# GROUP21
#####
plot(x,SPECURVES[Group21[1],],ylim=range(SPECURVES), type="l",
      xlab="Wavelengths",ylab="Absorbances", main="GROUP 21")
for(i in Group21[-1]){
  par(new=T)
  plot(x,SPECURVES[i,],ylim=range(SPECURVES), type="l",
        xlab="", ylab="", axes=F)
}
plot(x,SPEC2D[Group21[1],],ylim=range(SPEC2D), type="l",
      xlab="Wavelengths", ylab="Absorbances",
      main="GROUP 21: second derivatives")
for(i in Group21[-1]){
  par(new=T)
  plot(x,SPEC2D[i,],ylim=range(SPEC2D), type="l", xlab="",
        ylab="", axes=F)
}
plot(x, MODAL.CURVESD2[2,], ylim=range(SPEC2D), type="l",
      xlab="Wavelengths", ylab="Absorbances",
      main="GROUP 21: modal curve")
##
# GROUP22
#####
plot(x,SPECURVES[Group22[1],],ylim=range(SPECURVES), type="l",
      xlab="Wavelengths",ylab="Absorbances", main="GROUP 22")
for(i in Group22[-1]){
  par(new=T)
  plot(x,SPECURVES[i,],ylim=range(SPECURVES), type="l",
        xlab="", ylab="", axes=F)
}
plot(x,SPEC2D[Group22[1],],ylim=range(SPEC2D), type="l",
      xlab="Wavelengths", ylab="Absorbances",
      main="GROUP 22: second derivatives")
for(i in Group22[-1]){
  par(new=T)
  plot(x,SPEC2D[i,],ylim=range(SPEC2D), type="l", xlab="",
        ylab="", axes=F)
}

```

```
plot(x, MODAL.CURVESD2[3,], ylim=range(SPECD2), type="l",  
      xlab="Wavelengths", ylab="Absorbances",  
      main="GROUP 22: modal curve")
```

- Displaying the splitting score behavior along the procedure

The following commandlines allow to perform Figure 2:

```
Splitting.score <- spec.classif$$Sc  
Split.names <- c(paste("GROUPS","\n","1 & 2"),  
                 paste("GROUPS", "\n","21 & 22"))  
par(mfrow=c(1,1))  
barplot(Splitting.score, names=Split.names, main="Splitting scores",  
        ylab="Percentages")  
abline(h=0.05, lwd=3)
```

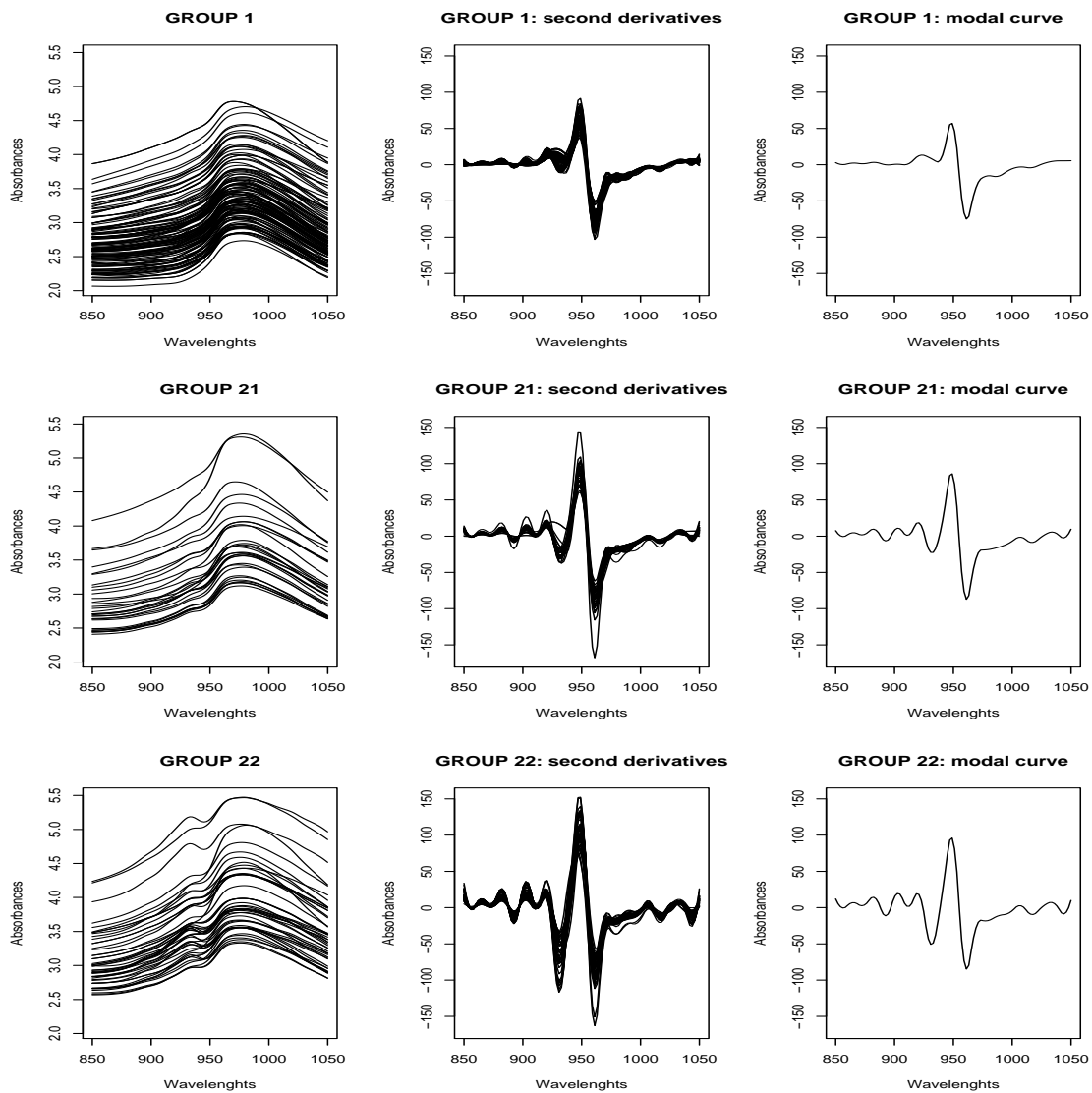


Figure 1: For each group: left column displays the original spectrometric curves, middle column plots their second derivatives and right column displays the corresponding functional mode

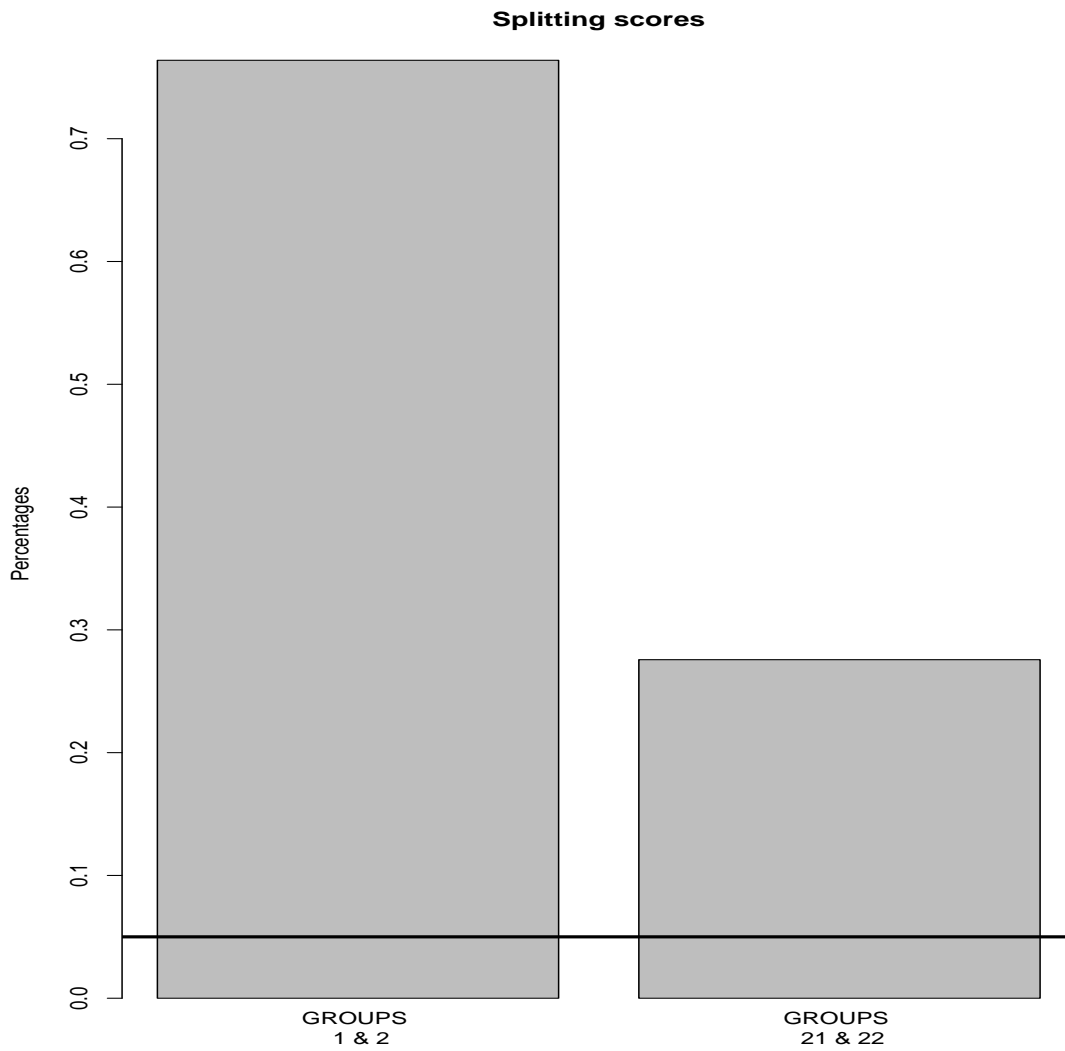


Figure 2: Behavior of splitting score for the spectrometric data; the horizontal line corresponds to the threshold of splitting score