## TP2

### You~ZUO

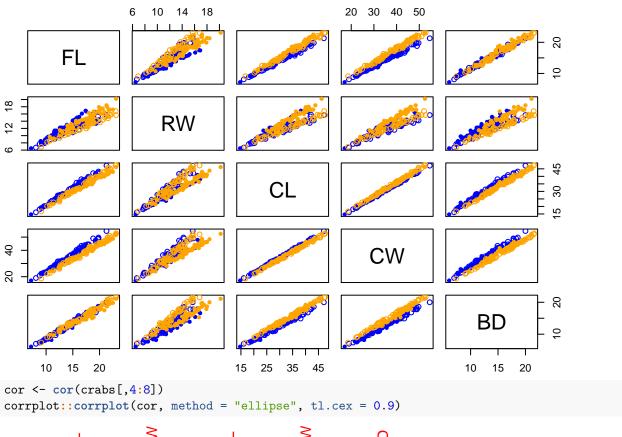
2019/9/23

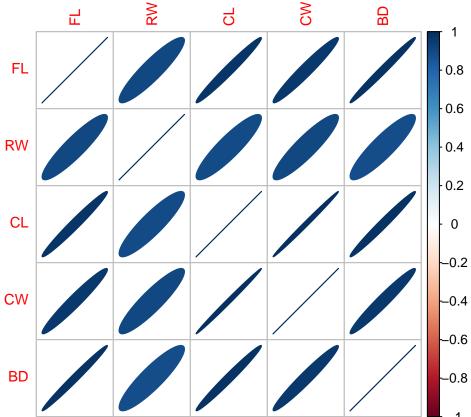
#### exo1

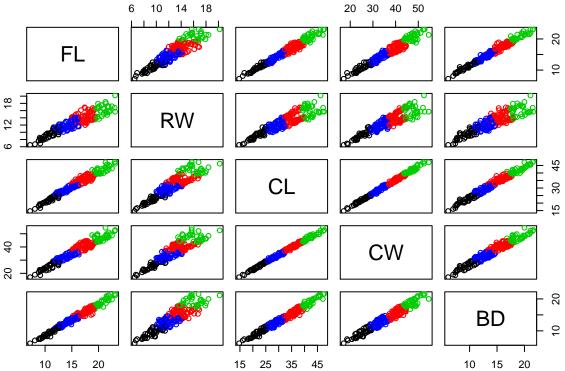
```
library(mclust)
## Package 'mclust' version 5.4.3
## Type 'citation("mclust")' for citing this R package in publications.
library(nnet)
data("iris")
head(iris)
     Sepal.Length Sepal.Width Petal.Length Petal.Width Species
                                                     0.2 setosa
## 1
              5.1
                           3.5
                                         1.4
## 2
              4.9
                           3.0
                                                     0.2 setosa
                                         1.4
## 3
              4.7
                           3.2
                                         1.3
                                                     0.2 setosa
## 4
              4.6
                           3.1
                                         1.5
                                                     0.2 setosa
## 5
                           3.6
                                         1.4
                                                     0.2 setosa
              5.0
## 6
              5.4
                           3.9
                                         1.7
                                                     0.4 setosa
C <- class.ind(cl = iris$Species)</pre>
X <- matrix(iris[,-5])</pre>
mu_T <- sapply(iris[,1:4], mean)</pre>
n_k <- sapply(1:3, function(i){</pre>
 sum(C[,i])
mu_k <- t(as.matrix(C)) %*% as.matrix(iris[,1:4]) / n_k</pre>
```

#### exo4

```
library(MASS)
data(crabs)
help(crabs)
pairs(x = crabs[,4:8], col = c("blue", "orange")[crabs$sp], pch = c(20,21)[crabs$sex])
```

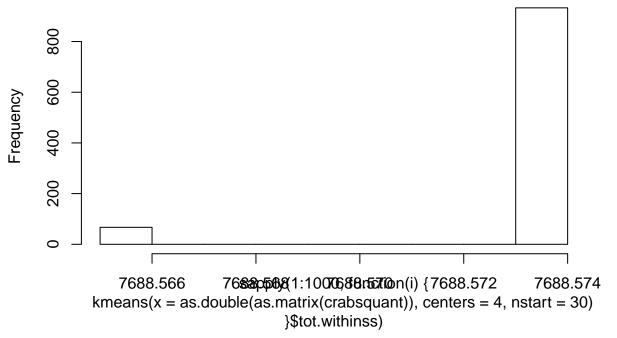






crabsquant <- crabs[,4:8]
hist(sapply(1:1000, function(i){kmeans(x = as.double(as.matrix(crabsquant)), centers = 4, nstart = 30)}</pre>

# Histogram of sapply(1:1000, function(i) { kmeans(x = as.double(as.matrix(crabsquant)), centers = 4, nstart = }\$tot.withinss)



```
crabsquant2 <- crabsquant[,-3]/crabsquant$CL
names(crabsquant2) <- paste(names(crabsquant[,-3]),"/CL")

kmeans(crabsquant2, 4, nstart = 30)$cluster -> cluster
natural.classes <- paste(crabs$sex, crabs$sp, sep = "-")
table(cluster, natural.classes)</pre>
```

```
##
         natural.classes
## cluster F-B F-O M-B M-O
##
        1
            0
                0
                     0
##
                0
                   40
##
        3
            0 50
                    0
                        6
##
        4 50
                0
                   10
```