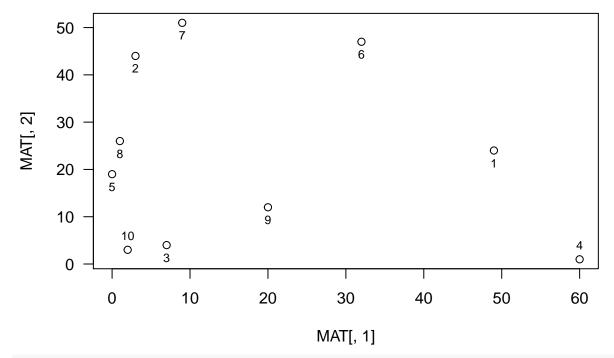
# CLUSTER EN R GUEVARA.R

#### rogerguevara

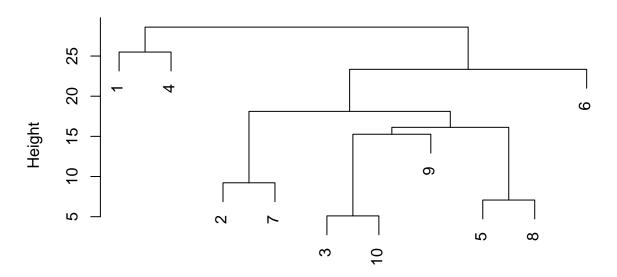
Tue May 14 14:37:36 2019

```
library(vegan)
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.4-6
library(cluster)
?agnes
?hclust
?diana
?mona
?kmeans
?fanny
?dist
?vegdist
?betadiver
?daisy
####
#MAT <- matrix(rnegbin(20, theta=0.4), 10,2)
MAT \leftarrow matrix(c(49,3,7,60,0,32,9,1,20,2,24,44,4,1,19,47,51,26,12,3), 10, 2)
plot(MAT[,1], MAT[,2], las=1)
POS <- rep(1, 10)
POS[(MAT[,2] < 4)] <- 3
text(MAT[,1], MAT[,2], 1:10, pos=POS, cex=0.75)
```



AGNESs <- agnes(MAT, method = "single")
plot(AGNESs, which=2)

## Dendrogram of agnes(x = MAT, method = "single")

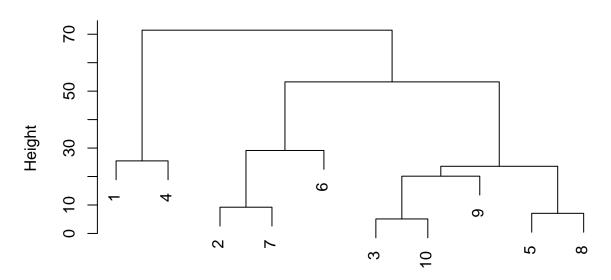


MAT
Agglomerative Coefficient = 0.54



```
## 3 46.518813 40.199502
## 4 25.495098 71.400280 53.084838
## 5 49.254441 25.179357 16.552945 62.641839
## 6 28.600699 29.154759 49.739320 53.851648 42.520583
## 7 48.259714 9.219544 47.042534 71.421285 33.241540 23.345235
## 8 48.041649 18.110770 22.803509 64.078077 7.071068 37.443290 26.248809
## 9 31.384710 36.235342 15.264338 41.484937 21.189620 37.000000 40.521599
## 10 51.478151 41.012193 5.099020 58.034473 16.124515 53.254108 48.507731
##
             8
                       9
## 2
## 3
## 4
## 5
## 6
## 7
## 8
## 9 23.600847
## 10 23.021729 20.124612
AGNESs$height
## [1] 25.495098 28.600699 9.219544 18.110770 5.099020 15.264338 16.124515
## [8] 7.071068 23.345235
AGNESc <- agnes(MAT, method = "complete")
AGNESc$height
## [1] 25.495098 71.421285 9.219544 29.154759 53.254108 5.099020 20.124612
## [8] 23.600847 7.071068
AGNESc$order
## [1] 1 4 2 7 6 3 10 9 5 8
plot(AGNESc, which=2)
```

## Dendrogram of agnes(x = MAT, method = "complete")



MAT Agglomerative Coefficient = 0.8

```
AGNESa <- agnes(MAT, method = "average")
AGNESa$height

## [1] 25.495098 51.855956 9.219544 26.249997 38.417112 5.099020 17.694475

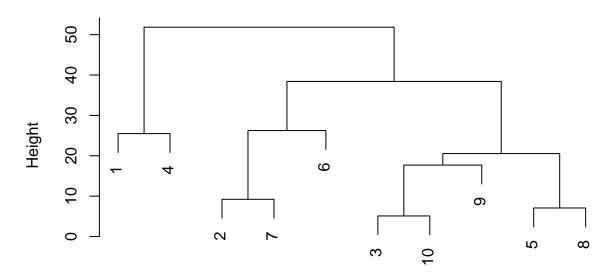
## [8] 20.548861 7.071068

AGNESa$order

## [1] 1 4 2 7 6 3 10 9 5 8

plot(AGNESa, which=2)
```

## Dendrogram of agnes(x = MAT, method = "average")



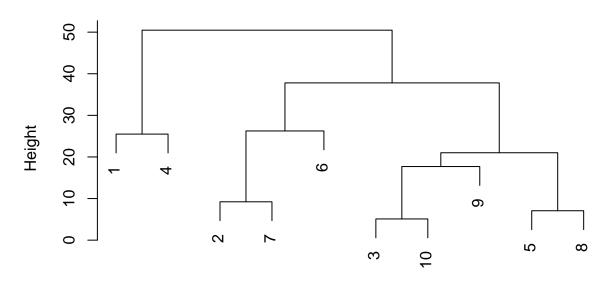
MAT
Agglomerative Coefficient = 0.73

```
AGNESwa <- agnes(MAT, method = "weighted")
AGNESwa$order

## [1] 1 4 2 7 6 3 10 9 5 8

plot(AGNESwa, which=2)
```

### Dendrogram of agnes(x = MAT, method = "weighted")



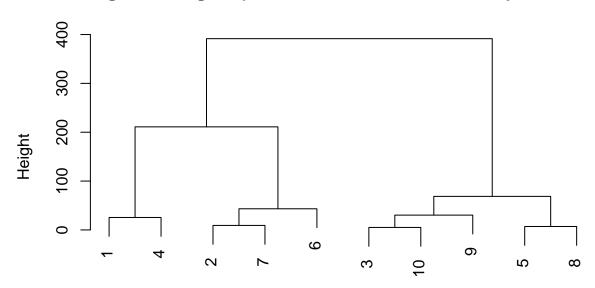
MAT
Agglomerative Coefficient = 0.73

```
AGNESwa$height
## [1] 25.495098 50.474344 9.219544 26.249997 37.802473 5.099020 17.694475
## [8] 21.010454 7.071068
dist(MAT)
##
                        2
                                  3
                                                      5
                                                                6
                                                                          7
## 2 50.159745
## 3 46.518813 40.199502
## 4 25.495098 71.400280 53.084838
## 5 49.254441 25.179357 16.552945 62.641839
## 6 28.600699 29.154759 49.739320 53.851648 42.520583
## 7 48.259714 9.219544 47.042534 71.421285 33.241540 23.345235
## 8 48.041649 18.110770 22.803509 64.078077 7.071068 37.443290 26.248809
     31.384710 36.235342 15.264338 41.484937 21.189620 37.000000 40.521599
## 10 51.478151 41.012193 5.099020 58.034473 16.124515 53.254108 48.507731
##
              8
## 2
## 3
## 4
## 5
## 6
## 7
## 8
## 9 23.600847
## 10 23.021729 20.124612
AGNESf <- agnes(MAT, method = "flexible",par.method=1)
AGNESf$height
```

```
## [1] 25.495098 210.983638   9.219544  43.280450 391.523796  5.099020
## [7] 30.289930  68.663061   7.071068

AGNESf$order
## [1] 1 4 2 7 6 3 10 9 5 8
plot(AGNESf, which=2)
```

## Dendrogram of agnes(x = MAT, method = "flexible", par.method = 1



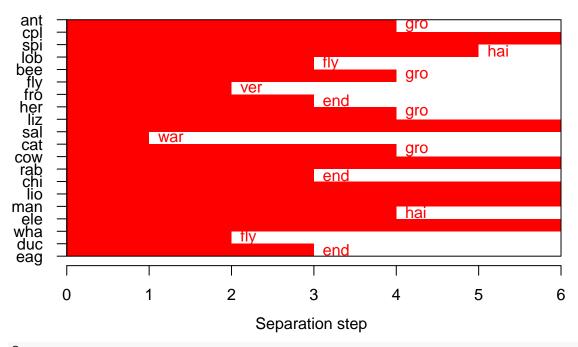
MAT
Agglomerative Coefficient = 0.96

```
ma <- mona(animals)</pre>
## mona(x, ..) fit; x of dimension 20x6
## Because of NA's, revised data:
##
       war fly ver end gro hai
## ant
             0
## bee
         0
             1
                 0
                     0
                              1
  cat
                 0
                         0
## cpl
         0
             0
                     0
## chi
         1
                     1
## cow
         1
                              1
## duc
                         0
                              0
   eag
         1
             1
                 1
                     1
                        1
   ele
         1
##
                     1
## fly
## fro
             0
                     1
                              0
## her
         0
             0
                 1
                     0
                         1
                              0
## lio
```

####

```
## liz
             0
                         0
## lob
         0
             0
                 0
                     0
                         0
                             0
## man
                             1
             0
                     0
                         1
## rab
                 1
                             1
         1
## sal
         0
             0
                     0
                         0
                             0
## spi
         0
             0
                 0
                     0
                         0
                             1
## wha
         1
                     1
                             0
## Order of objects:
   [1] ant cpl spi lob bee fly fro her liz sal cat cow rab chi lio man ele
## [18] wha duc eag
## Variable used:
\#\# [1] gro NULL hai fly gro ver end gro NULL war gro NULL end NULL
## [15] NULL hai NULL fly end
## Separation step:
## [1] 4 0 5 3 4 2 3 4 0 1 4 0 3 0 0 4 0 2 3
##
## Available components:
## [1] "data"
                   "hasNA"
                                                                    "order.lab"
                               "order"
                                           "variable" "step"
## [7] "call"
plot(ma)
```

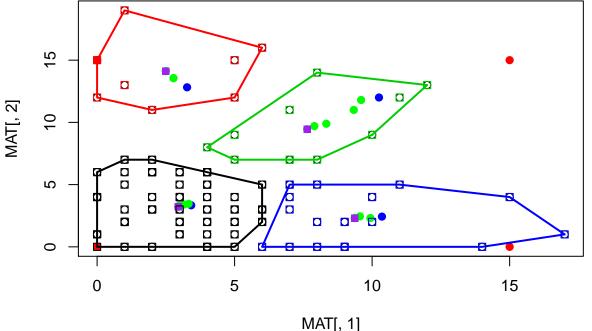
#### Banner of mona(x = animals)



```
?mona
#### K MEANS
MAT <- matrix(sample(rnbinom(200,3, prob=0.4)),100,2)
rownames(MAT) <- paste("S", 1:100, sep="")
colnames(MAT) <- c("A", "B")
###SEMILLAS EN LOS EXTREMOS</pre>
```

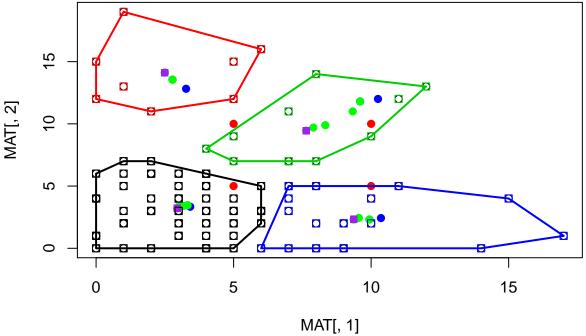
```
plot(MAT[,1], MAT[,2])
points(c(0,0,15,15), c(0,15,15,0), pch = 19, col = "red")
DIST1 <- cbind(sqrt((MAT[,1]-0)^2 + (MAT[,2]-0)^2),
               sqrt((MAT[,1]-0)^2 + (MAT[,2]-15)^2),
               sqrt((MAT[,1]-15)^2 + (MAT[,2]-15)^2),
               sqrt((MAT[,1]-15)^2 + (MAT[,2]-0)^2))
GRUPOS <- numeric()</pre>
for(i in 1:100){
  GRUPOS <- c(GRUPOS, which(DIST1[i,]==min(DIST1[i,])))</pre>
CENTROIDES <- rbind(colMeans(MAT[GRUPOS==1,]),</pre>
                     colMeans (MAT [GRUPOS==2,]),
                     colMeans (MAT [GRUPOS==3,]),
                     colMeans(MAT[GRUPOS==4,]))
points(CENTROIDES[,1], CENTROIDES[,2], col ="blue", pch = 19)
DIST2 <- cbind(sqrt((MAT[,1]-CENTROIDES[1,1])^2 +(MAT[,2]-CENTROIDES[1,2])^2),
               sqrt((MAT[,1]-CENTROIDES[2,1])^2 + (MAT[,2]-CENTROIDES[2,2])^2),
               sqrt((MAT[,1]-CENTROIDES[3,1])^2 + (MAT[,2]-CENTROIDES[3,2])^2),
               sqrt((MAT[,1]-CENTROIDES[4,1])^2 + (MAT[,2]-CENTROIDES[4,2])^2))
GRUPOS2 <- numeric()</pre>
for(i in 1:100){
  GRUPOS2 <- c(GRUPOS2, which(DIST2[i,]==min(DIST2[i,])))</pre>
}
rbind(table(GRUPOS),
     table(GRUPOS2))
##
       1 2 3 4
## [1,] 71 11 4 14
## [2,] 70 9 5 16
sum(GRUPOS2==GRUPOS)
## [1] 96
GRUPOSx2 <- GRUPOS2
GRUPOSx<- sample(GRUPOSx2)</pre>
while(sum(GRUPOSx2==GRUPOSx) != 100){
  GRUPOSx <- GRUPOSx2
  CENTROIDESx <- rbind(colMeans(MAT[GRUPOSx==1,]),</pre>
                        colMeans (MAT [GRUPOSx==2,]),
                        colMeans (MAT [GRUPOSx==3,]),
                        colMeans (MAT [GRUPOSx==4,]))
  points(CENTROIDESx[,1], CENTROIDESx[,2], col ="green", pch = 19)
  DISTx <- cbind(sqrt((MAT[,1]-CENTROIDESx[1,1])^2 +(MAT[,2]-CENTROIDESx[1,2])^2),
                  sqrt((MAT[,1]-CENTROIDESx[2,1])^2 + (MAT[,2]-CENTROIDESx[2,2])^2),
```

```
sqrt((MAT[,1]-CENTROIDESx[3,1])^2 + (MAT[,2]-CENTROIDESx[3,2])^2),
                 sqrt((MAT[,1]-CENTROIDESx[4,1])^2 + (MAT[,2]-CENTROIDESx[4,2])^2))
  GRUPOSx2 <- numeric()</pre>
  for(i in 1:100){
    GRUPOSx2 <- c(GRUPOSx2, which(DISTx[i,]==min(DISTx[i,])))</pre>
  print(rbind(table(GRUPOSx),
              table(GRUPOSx2)))
}
##
         1 2 3 4
## [1,] 70 9 5 16
## [2,] 67 9 6 18
##
         1 2 3 4
## [1,] 67 9 6 18
   [2,] 64 8 9 19
         1 2
##
             3 4
## [1,] 64 8 9 19
## [2,] 63 8 10 19
##
         1 2 3 4
## [1,] 63 8 10 19
## [2,] 62 8 11 19
##
         1 2 3 4
## [1,] 62 8 11 19
## [2,] 62 8 11 19
points(CENTROIDESx[,1], CENTROIDESx[,2], col ="purple", pch = 15)
for(i in 1:nrow(CENTROIDESx)){ points(MAT[GRUPOSx2==i, 1], MAT[GRUPOSx2==i, 2], pch=0, col=i)
polygon(MAT[GRUPOSx2==i,][chull(MAT[GRUPOSx2==i,]), ], border=i, lwd=2)
```



```
rbind(table(GRUPOSx),
     table(GRUPOSx2))
         1 2 3 4
## [1,] 62 8 11 19
## [2,] 62 8 11 19
sum(GRUPOSx2==GRUPOSx)
## [1] 100
####SEMILLAS UBICADASS AL CENTRO
plot(MAT[,1], MAT[,2])
points(c(5,5,10,10), c(5,10,10,5), pch = 19, col ="red")
DIST1 <- cbind(sqrt((MAT[,1]-5)^2 + (MAT[,2]-5)^2),
      sqrt((MAT[,1]-5)^2 + (MAT[,2]-10)^2),
      sqrt((MAT[,1]-10)^2 + (MAT[,2]-10)^2),
      sqrt((MAT[,1]-10)^2 + (MAT[,2]-5)^2))
GRUPOS <- numeric()</pre>
for(i in 1:100){
  GRUPOS <- c(GRUPOS, which(DIST1[i,]==min(DIST1[i,])))</pre>
CENTROIDES <- rbind(colMeans(MAT[GRUPOS==1,]),</pre>
      colMeans (MAT [GRUPOS==2,]),
      colMeans(MAT[GRUPOS==3,]),
      colMeans(MAT[GRUPOS==4,]))
points(CENTROIDES[,1], CENTROIDES[,2], col ="blue", pch = 19)
DIST2 <- cbind(sqrt((MAT[,1]-CENTROIDES[1,1])^2 +(MAT[,2]-CENTROIDES[1,2])^2),
               sqrt((MAT[,1]-CENTROIDES[2,1])^2 + (MAT[,2]-CENTROIDES[2,2])^2),
               sqrt((MAT[,1]-CENTROIDES[3,1])^2 + (MAT[,2]-CENTROIDES[3,2])^2),
               sqrt((MAT[,1]-CENTROIDES[4,1])^2 + (MAT[,2]-CENTROIDES[4,2])^2))
GRUPOS2 <- numeric()</pre>
for(i in 1:100){
  GRUPOS2 <- c(GRUPOS2, which(DIST2[i,]==min(DIST2[i,]))[1])</pre>
CENTROIDES <- rbind(colMeans(MAT[GRUPOS2==1,]),
                    colMeans(MAT[GRUPOS2==2,]),
                    colMeans(MAT[GRUPOS2==3,]),
                    colMeans(MAT[GRUPOS2==4,]))
points(CENTROIDES[,1], CENTROIDES[,2], col ="blue", pch = 19)
rbind(table(GRUPOS),
table(GRUPOS2))
        1 2 3 4
##
## [1,] 71 11 4 14
## [2,] 70 9 5 16
sum(GRUPOS2==GRUPOS)
```

```
## [1] 96
GRUPOSx2 <- GRUPOS2
GRUPOSx<- sample(GRUPOSx2)</pre>
while(sum(GRUPOSx2==GRUPOSx) != 100){
  GRUPOSx <- GRUPOSx2
CENTROIDESx <- rbind(colMeans(MAT[GRUPOSx==1,]),</pre>
                    colMeans(MAT[GRUPOSx==2,]),
                    colMeans(MAT[GRUPOSx==3,]),
                    colMeans(MAT[GRUPOSx==4,]))
points(CENTROIDESx[,1], CENTROIDESx[,2], col ="green", pch = 19)
DISTx <- cbind(sqrt((MAT[,1]-CENTROIDESx[1,1])^2 +(MAT[,2]-CENTROIDESx[1,2])^2),
               sqrt((MAT[,1]-CENTROIDESx[2,1])^2 + (MAT[,2]-CENTROIDESx[2,2])^2),
               sqrt((MAT[,1]-CENTROIDESx[3,1])^2 + (MAT[,2]-CENTROIDESx[3,2])^2),
               sqrt((MAT[,1]-CENTROIDESx[4,1])^2 + (MAT[,2]-CENTROIDESx[4,2])^2))
GRUPOSx2 <- numeric()</pre>
for(i in 1:100){
  GRUPOSx2 <- c(GRUPOSx2, which(DISTx[i,]==min(DISTx[i,])))</pre>
print(rbind(table(GRUPOSx),
            table(GRUPOSx2)))
         1 2 3 4
## [1,] 70 9 5 16
## [2,] 67 9 6 18
##
         1 2 3 4
## [1,] 67 9 6 18
## [2,] 64 8 9 19
         1 2 3 4
## [1,] 64 8 9 19
## [2,] 63 8 10 19
         1 2 3 4
## [1,] 63 8 10 19
## [2,] 62 8 11 19
         1 2 3 4
##
## [1,] 62 8 11 19
## [2,] 62 8 11 19
points(CENTROIDESx[,1], CENTROIDESx[,2], col ="purple", pch = 15)
for(i in 1:nrow(CENTROIDESx)) {points(MAT[GRUPOSx2==i, 1], MAT[GRUPOSx2==i, 2], pch=0, col=i)
polygon(MAT[GRUPOSx2==i,][chull(MAT[GRUPOSx2==i,]), ], border=i, lwd=2)}
```



```
rbind(table(GRUPOSx),
      table(GRUPOSx2))
         1 2 3 4
##
## [1,] 62 8 11 19
## [2,] 62 8 11 19
sum(GRUPOSx2==GRUPOSx)
## [1] 100
####SEMILLAS POR QUANTILES
plot(MAT[,1], MAT[,2])
quantile(MAT[,1], c(0.25, 0.75))
## 25% 75%
    2
quantile(MAT[,2], c(0.25, 0.75))
## 25% 75%
##
    2 6
points(c(2,2,6.25,6.25), c(2,6,6,2), pch = 19, col ="red")
DIST1 <- cbind(sqrt((MAT[,1]-2)^2 + (MAT[,2]-2)^2),
               sqrt((MAT[,1]-2)^2 + (MAT[,2]-6)^2),
               sqrt((MAT[,1]-6.25)^2 + (MAT[,2]-6)^2),
               sqrt((MAT[,1]-6.25)^2 + (MAT[,2]-2)^2))
GRUPOS <- numeric()</pre>
for(i in 1:100){
  GRUPOS <- c(GRUPOS, which(DIST1[i,]==min(DIST1[i,]))[1])</pre>
}
```

```
CENTROIDES <- rbind(colMeans(MAT[GRUPOS==1,]),</pre>
                    colMeans (MAT [GRUPOS==2,]),
                    colMeans(MAT[GRUPOS==3,]),
                    colMeans (MAT [GRUPOS==4,]))
points(CENTROIDES[,1], CENTROIDES[,2], col ="blue", pch = 19)
DIST2 <- cbind(sqrt((MAT[,1]-CENTROIDES[1,1])^2 +(MAT[,2]-CENTROIDES[1,2])^2),
               sqrt((MAT[,1]-CENTROIDES[2,1])^2 + (MAT[,2]-CENTROIDES[2,2])^2),
               sqrt((MAT[,1]-CENTROIDES[3,1])^2 + (MAT[,2]-CENTROIDES[3,2])^2),
               sqrt((MAT[,1]-CENTROIDES[4,1])^2 + (MAT[,2]-CENTROIDES[4,2])^2))
GRUPOS2 <- numeric()</pre>
for(i in 1:100){
 GRUPOS2 <- c(GRUPOS2, which(DIST2[i,]==min(DIST2[i,])))</pre>
CENTROIDES <- rbind(colMeans(MAT[GRUPOS2==1,]),</pre>
                    colMeans(MAT[GRUPOS2==2,]),
                    colMeans(MAT[GRUPOS2==3,]),
                    colMeans(MAT[GRUPOS2==4,]))
points(CENTROIDES[,1], CENTROIDES[,2], col ="blue", pch = 19)
rbind(table(GRUPOS),
     table(GRUPOS2))
        1 2 3 4
##
## [1,] 34 22 22 22
## [2,] 40 20 17 23
sum(GRUPOS2==GRUPOS)
## [1] 90
GRUPOSx2 <- GRUPOS2
GRUPOSx<- sample(GRUPOSx2)</pre>
while(sum(GRUPOSx2==GRUPOSx) != 100){
  GRUPOSx <- GRUPOSx2
  CENTROIDESx <- rbind(colMeans(MAT[GRUPOSx==1,]),
                        colMeans(MAT[GRUPOSx==2,]),
                        colMeans(MAT[GRUPOSx==3,]),
                        colMeans(MAT[GRUPOSx==4,]))
  points(CENTROIDESx[,1], CENTROIDESx[,2], col ="green", pch = 19)
  DISTx <- cbind(sqrt((MAT[,1]-CENTROIDESx[1,1])^2 +(MAT[,2]-CENTROIDESx[1,2])^2),
                 sqrt((MAT[,1]-CENTROIDESx[2,1])^2 + (MAT[,2]-CENTROIDESx[2,2])^2),
                 sqrt((MAT[,1]-CENTROIDESx[3,1])^2 + (MAT[,2]-CENTROIDESx[3,2])^2),
                 sqrt((MAT[,1]-CENTROIDESx[4,1])^2 + (MAT[,2]-CENTROIDESx[4,2])^2))
  GRUPOSx2 <- numeric()</pre>
  for(i in 1:100){
    GRUPOSx2 <- c(GRUPOSx2, which(DISTx[i,]==min(DISTx[i,])))</pre>
  print(rbind(table(GRUPOSx),
              table(GRUPOSx2)))
```

```
1 2 3 4
## [1,] 40 20 17 23
## [2,] 45 19 12 24
##
        1 2 3 4
## [1,] 45 19 12 24
## [2,] 45 19 12 24
        1 2 3 4
## [1,] 45 19 12 24
## [2,] 45 21 9 25
##
        1 2 3 4
## [1,] 45 21 9 25
## [2,] 45 20 10 25
        1 2 3 4
## [1,] 45 20 10 25
## [2,] 41 23 11 25
##
        1 2 3 4
## [1,] 41 23 11 25
## [2,] 41 24 11 24
##
        1 2 3 4
## [1,] 41 24 11 24
## [2,] 41 23 12 24
        1 2 3 4
## [1,] 41 23 12 24
## [2,] 41 22 13 24
##
        1 2 3 4
## [1,] 41 22 13 24
## [2,] 40 23 13 24
        1 2 3 4
## [1,] 40 23 13 24
## [2,] 39 24 13 24
        1 2 3 4
##
## [1,] 39 24 13 24
## [2,] 39 24 13 24
points(CENTROIDESx[,1], CENTROIDESx[,2], col ="purple", pch = 15)
for(i in 1:nrow(CENTROIDESx)){points(MAT[GRUPOSx2==i, 1], MAT[GRUPOSx2==i, 2], pch=0, col=i)
polygon(MAT[GRUPOSx2==i,][chull(MAT[GRUPOSx2==i,]), ], border =i, lwd=2)}
```

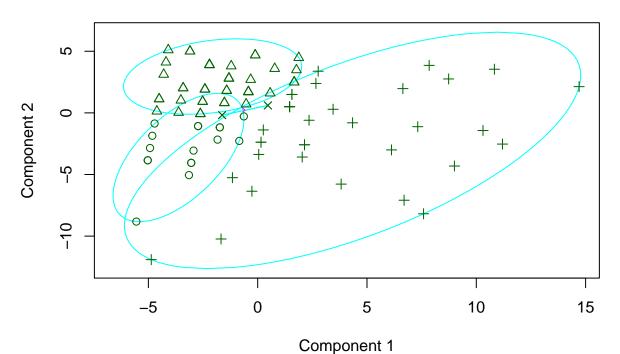
```
MAT[, 1]
```

```
rbind(table(GRUPOSx),
     table(GRUPOSx2))
##
## [1,] 39 24 13 24
## [2,] 39 24 13 24
sum(GRUPOSx2==GRUPOSx)
## [1] 100
sum(dist(MAT[GRUPOSx2==1],))/sum(GRUPOSx2==1)
## [1] 130.1538
sum(dist(MAT[GRUPOSx2==2],))/sum(GRUPOSx2==2)
## [1] 106.6667
sum(dist(MAT[GRUPOSx2==3],))/sum(GRUPOSx2==3)
## [1] 152.9231
sum(dist(MAT[GRUPOSx2==4],))/sum(GRUPOSx2==4)
## [1] 211.125
#Kmeans
plot(MAT[,1], MAT[,2])
quantile(MAT[,1], c(0.25, 0.75))
## 25% 75%
##
    2 7
quantile(MAT[,2], c(0.25, 0.75))
## 25% 75%
##
    2
       6
```

```
NGROUPS <- 4
KMENAS <- kmeans(MAT, centers = NGROUPS, algorithm="L")</pre>
KMENAS$cluster
                S3
##
     S1
          S2
                     S4
                          S5
                                S6
                                     S7
                                           S8
                                                S9
                                                    S10
                                                          S11
                                                               S12
                                                                     S13
                                                                          S14
                                                                                S15
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##
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##
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                                                 1
points(KMENAS$centers[,1], KMENAS$centers[,2], col ="purple", pch = 15)
for(i in 1:NGROUPS) {points(MAT[KMENAS$cluster==i, 1], MAT[KMENAS$cluster==i, 2], pch=0, col=i)
polygon(MAT[KMENAS$cluster==i,][chull(MAT[KMENAS$cluster==i,]), ], border=i, lwd=2)}
      15
                                   10
                                   2
                                                0
                                   0
              0
                                   5
                                                        10
                                                                             15
                                              MAT[, 1]
###MEDIODS
library(cluster)
plot(fanny(MAT, k=4))
```

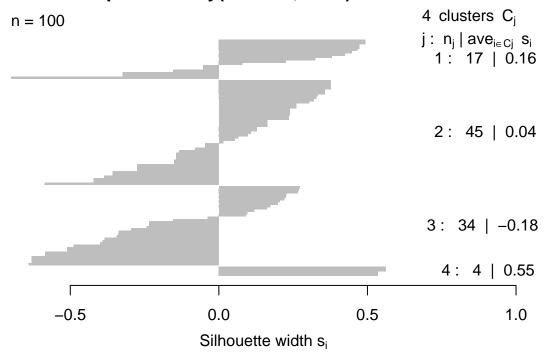
## Warning in fanny(MAT, k = 4): FANNY algorithm has not converged in 'maxit' ## = 500 iterations

### clusplot(fanny(x = MAT, k = 4))



These two components explain 100 % of the point variability.

### Silhouette plot of fanny(x = MAT, k = 4)



Average silhouette width: 0.01