Running PAM with Distance Functions

> B<- matrix( c(0,1,2,1,0,4,2,4,0), nrow=3, ncol=3)

> D <-as.dist(B)

> require("cluster")

> r<-pam(D,2)

> r$medoids

[1] 1 3

> a<-c(0,1,-0.5,0.5)

> b<-c(-1,0,0,0.5)

> c<-c(0.5,0,-0.5,0)

> d<-data.frame(a,b,c)

> d

a b c

1 0.0 -1.0 0.5

2 1.0 0.0 0.0

3 -0.5 0.0 -0.5

4 0.5 0.5 0.0

[1] 1 3

> createD(d,c(1,1,1))

1 2 3

2 2.5

3 2.5 2.0

4 2.5 1.0 2.0

>

> DD<-createD(iris[1:4], c(1,1,1,1))

> p<-pam(DD,5)

> p

Medoids:

ID

[1,] 8 8

[2,] 64 64

[3,] 148 148

[4,] 70 70

[5,] 103 103

Clustering vector:

[1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

[38] 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 3 4 2 2 2 4 2 4 4 2 4 2 4 2 2 4 2 4 2 2 2 2

[75] 2 2 2 3 2 4 4 4 4 2 2 2 2 2 4 4 4 2 4 4 4 4 2 2 4 4 5 3 5 3 3 5 4 5 5 5 3

[112] 3 3 3 3 3 3 5 5 2 5 2 5 3 5 5 2 2 3 5 5 5 3 2 2 5 3 3 2 5 3 3 3 5 5 3 3 3

[149] 3 3

Objective function:

build swap

0.9100000 0.8673333

> p<-pam(iris[1:4],5)

> p

Medoids:

ID Sepal.Length Sepal.Width Petal.Length Petal.Width

[1,] 8 5.0 3.4 1.5 0.2

[2,] 64 6.1 2.9 4.7 1.4

[3,] 70 5.6 2.5 3.9 1.1

[4,] 113 6.8 3.0 5.5 2.1

[5,] 106 7.6 3.0 6.6 2.1

Clustering vector:

[1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

[38] 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 3 2 2 2 3 2 3 3 2 3 2 3 2 2 3 2 3 2 3 2 2

[75] 2 2 2 4 2 3 3 3 3 2 2 2 2 2 3 3 3 2 3 3 3 3 3 2 3 3 4 2 4 4 4 5 3 5 4 5 4

[112] 4 4 2 2 4 4 5 5 2 4 2 5 2 4 4 2 2 4 4 5 5 4 2 2 5 4 4 2 4 4 4 2 4 4 4 2 4

[149] 4 2

Objective function:

build swap

0.5520959 0.5272835

>