```
library(vegan)

###NON-HIERARCHICAL CLASSIFICATION-----------------------------------
#k-means with climatic data only
clust.env <- kmeans(env.tab.s[,c(9,12)], centers= 3, iter.max = 100)
clust.env

plot(env.tab.s[,c(9,12)], col = clust.env$cluster, pch=16)
points(clust.env$centers, pch = 8, cex = 2, col="blue")

#k-means with all environmental data
clust.env <- cascadeKM(env.tab.s, inf.gr = 2, sup.gr = 10, criterion =
"ssi")
clust.env
plot(clust.env)#show optimal number of clusters based on ssi

plot(coord, pch=16, col=clust.env$partition[,1])

#k-means with species data
#transform data using Hellinger transformation
spe.hel <- decostand(spe, "hellinger")
clust.k <- cascadeKM(spe.hel, inf.gr = 2, sup.gr = 10, iter = 100,
criterion = "ssi")
plot(clust.k)

plot(coord, pch=16, col=clust.k$partition[,4])

my.cols <- c("blue", "red", "green", "yellow", "orange")
plot(coord, pch=16, col=my.cols[clust.k$partition[,4]])

##HIERARCHICAL CLASSIFICATION---------------------------------------
#single linkage
clust.single <- hclust(beta.b, method='single')
plot (clust.single, main = 'Single linkage')
```

```
#complete linkage
clust.complete <- hclust(beta.b, method='complete')
plot (clust.complete, main = 'Complete linkage')

#average linkage
clust.upgma <- hclust(beta.b, method='average')
plot (clust.upgma, main = 'UPGMA')

#is matrix Euclidean?
#install.packages("ade4")
library(ade4)

is.euclid(beta.b)
is.euclid(envdist)

#transform to Euclidean
beta.bc <- cailliez(beta.b, cor.zero = FALSE)
is.euclid(beta.bc)

#what is the constant?
(beta.bc - beta.b)[1]
plot(beta.bc, beta.b)

#ward clustering
clust.ward <- hclust(beta.bc, method='ward.D2')
plot(clust.ward)

###NUMBER OF CLUSTERS---------------------------------------
#for ward clustering
plot(clust.ward)
rect.hclust (clust.ward, k = 3, border="red")
rect.hclust (clust.ward, k = 5, border="blue")
```

```
cl.ward <- cutree(clust.ward, k=5)

plot(coord, pch=16, col=my.cols[cl.ward])


#for upgma clustering

cl.upgma <- cutree(clust.upgma, k=5)

plot(forest$X, forest$Y, pch=16, col=my.cols[cl.upgma])



###MANTEL-OPTIMAL NUMBER OF CLUSTERS ACCORDING TO BORCARD ET AL. 2011-----------------------------------------------------------------

#define function grpdist

grpdist <- function(X)

{

  require(cluster)

  gr <- as.data.frame(as.factor(X))

  distgr <- daisy(gr)

  distgr

}


#define object kt where the results of Mantel correlations will be stored

kt <- data.frame(k=1:10, r=0)

kt


#calculate Mantel correlations

for (i in 2:10)

{

  gr <- cutree(clust.ward, k=i) #here paste hclust object

  distgr <- grpdist(gr)

  mt <- cor(beta.b, distgr, method="pearson") #here paste dissimilarity matrix and distgr matrix

  kt[i,2] <- mt

}
```

```
kt

k.best <- which.max(kt$r)


#plot optimal number of clusters

plot(kt$k, kt$r, type="h", main="Mantel-optimal number of clusters",
xlab="k (number of clusters)",

     ylab="Pearson's correlation", las=1, cex.axis=1.2, cex.lab=1.2,
cex.main=1.4)

axis(1, k.best, paste("optimum", k.best, sep="\n"), col="red",

     font=2, col.axis="red")

points(k.best, max(kt$r), pch=16, col="red", cex=1.2)
```