Data Visualisation – Lab 7 Clustering

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Ques. Plotting K-Means for European Protein Consumption

Code:

url =

'http://www.biz.uiowa.edu/faculty/jledolter/DataMining/protein.csv' food<-read.csv(url)

head(food)

set.seed(1234)

grp<-kmeans(food[,c(2:10)],centers=3,nstart=10)</pre>

grp

list of cluster assignments

o=order(grp\$cluster)

data.frame(food\$Country[o],grp\$cluster[o])

grpProtein <- kmeans(food[2:10], centers=3, nstart=10)</pre>

o=order(grpProtein\$cluster)

data.frame(food\$Country[o],grpProtein\$cluster[o])

fviz_cluster()

clusplot(food[3:10], grpProtein\$cluster, main='2D

representation of the Cluster solution', color=TRUE,

shade=TRUE, labels=3, lines=0)

foodagg=agnes(food,diss=FALSE,metric="euclidian")

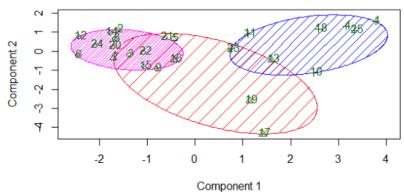
plot(foodagg, main='Dendrogram') ## dendrogram

groups <- cutree(foodagg, k=4) # cut tree into 3 clusters

rect.hclust(foodagg, k=4, border="green")

Screenshot:

2D representation of the Cluster solution



These two components explain 66.74 % of the point variability.

Optimization Screenshots:

