M4_L3_RomilShah

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Read Data and additional packages

```
require(ggplot2)
```

```
## Loading required package: ggplot2
```

```
## Warning: package 'ggplot2' was built under R version 3.2.5
```

```
require(mclust)
```

```
## Loading required package: mclust
```

```
## Warning: package 'mclust' was built under R version 3.2.5
```

```
## Package 'mclust' version 5.2
```

```
## Type 'citation("mclust")' for citing this R package in publications.
```

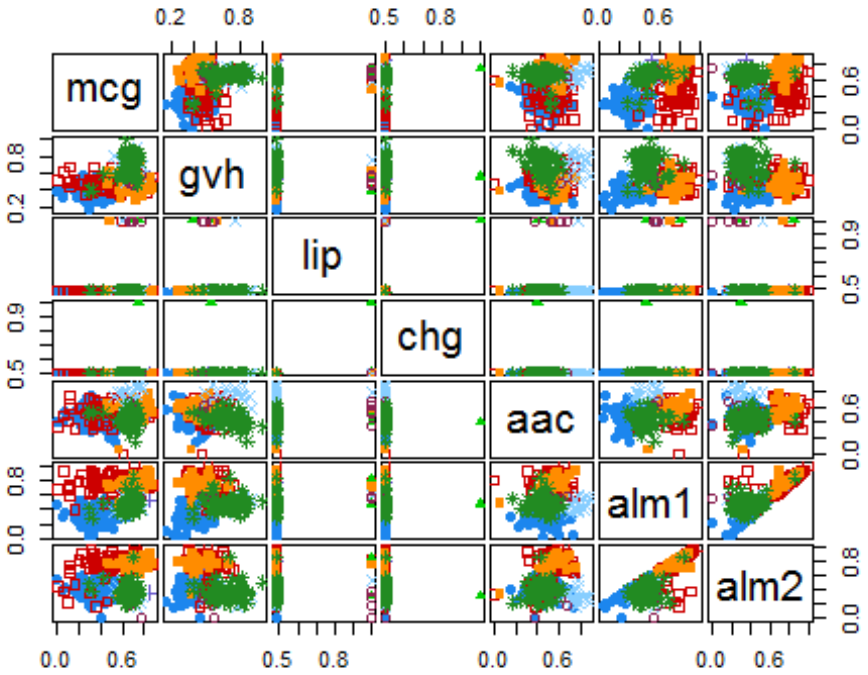
```
dataframe <-
read.table("C:/Users/rams1/Desktop/DSCS6030/Module_04/ecoli.data")
colnames(dataframe) <-
c("SeqNames","mcg","gvh","lip","chg","aac","alm1","alm2","Class")
ecoli <- dataframe[2:8]
class = dataframe$Class
table(class)
```

```
## class
##  cp  im imL imS imU  om omL  pp
## 143  77   2   2  35  20   5  52
```

```
head(ecoli)
```

```
##    mcg  gvh  lip chg  aac alm1 alm2
## 1 0.49 0.29 0.48 0.5 0.56 0.24 0.35
## 2 0.07 0.40 0.48 0.5 0.54 0.35 0.44
## 3 0.56 0.40 0.48 0.5 0.49 0.37 0.46
## 4 0.59 0.49 0.48 0.5 0.52 0.45 0.36
## 5 0.23 0.32 0.48 0.5 0.55 0.25 0.35
## 6 0.67 0.39 0.48 0.5 0.36 0.38 0.46
```

```
# cluster Pairs
clPairs(ecoli,class)
```



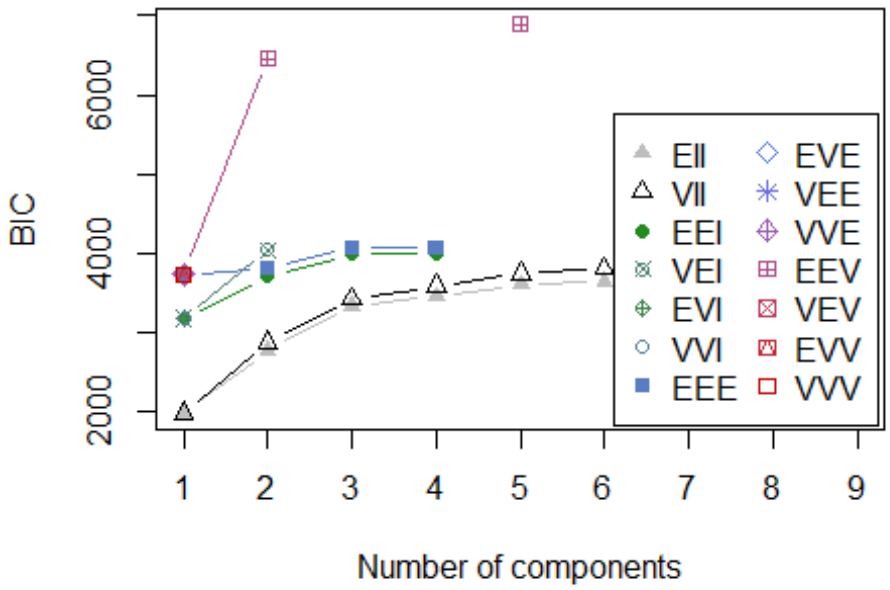
Expectation Maximization Clustering

Obtaining the EM Model

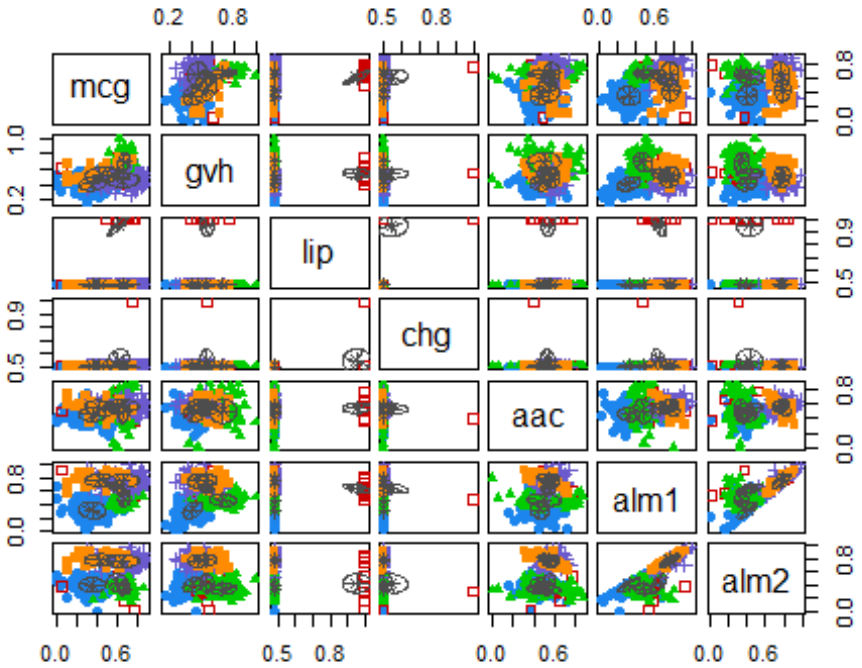
```
mod1<-Mclust(ecoli)
mod1

## 'Mclust' model object:
##  best model: ellipsoidal, equal volume and shape (EEV) with 5 components

summary(mod1)

## ----------------------------------------------------
## Gaussian finite mixture model fitted by EM algorithm
## ----------------------------------------------------
##
## Mclust EEV (ellipsoidal, equal volume and shape) model with 5 components:
##
##  log.likelihood   n  df     BIC      ICL
##        3882.357 336 151 6886.33 6841.295
##
## Clustering table:
##   1   2   3   4   5
## 147  11  75  75  28
```

Plots for EM produces following plots

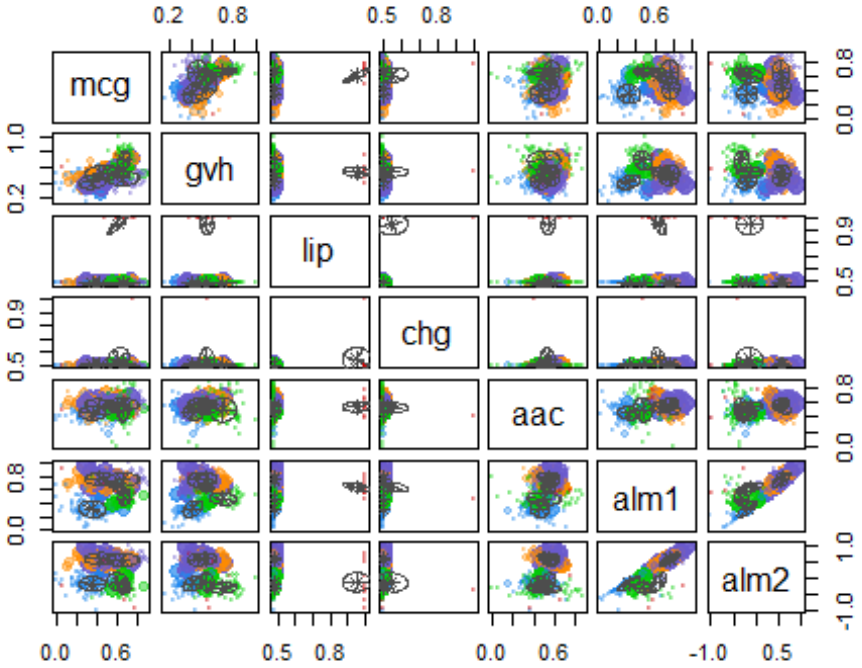
```
# BIC
plot(mod1,what="BIC")
```



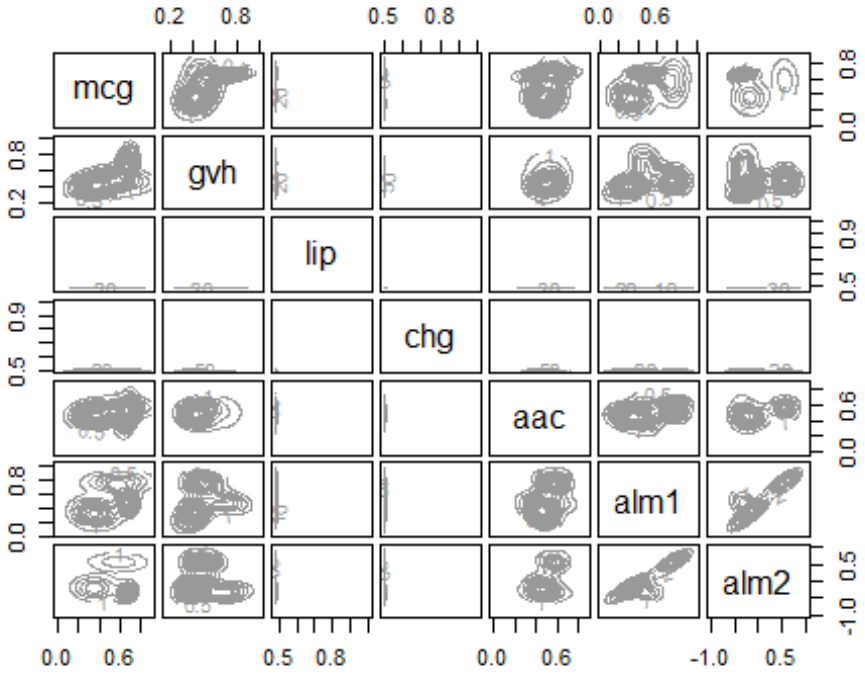

```
# Classification
plot(mod1, what = "classification")
```




```
# Uncertainty
plot(mod1, what = "uncertainty")
```



```
# Density
plot(mod1, what = "density")
```




```
# Only BIC for EM initialized by model based clustering
BIC = mclustBIC(ecoli)
summary(BIC)
```

```
## Best BIC values:
##             EEV,5     EEV,2     EEE,3
## BIC      6886.33 6461.3391  4068.066
## BIC diff    0.00 -424.9909 -2818.264
```

Answers:

Answers to the questions:

A(1)

The data consists of various relations between the clusters. The EM model was chosen such that the clustering by EM algorithm assigns the different clusters tothe data. As we have about 7 classes, it becomes easier to cluster the data such that the E step estimates the data of the Ecoli database and the M step will maximize the cluster allotment based on minimum error and maximum aposteriori.

A(2)

EM clustering is very similar to the clustering by k-means or PAM or hierarchical. But the major difference is that the overlap of the gaussians can be possible in EM which is not possible in -means. Thus the clustering gaussians can overlap so that the data is ordered into proper clusters which is not possible in k-means.