# Assignment 12.1

a. Perform ANOVA test on the discriminant analysis scores of nuclear localization signals of both nuclear and non-nuclear proteins by class variables (Target).
b. Which class is significantly different from others?

```
#1. Title: Protein Localization Sites


#2. Creator and Maintainer:
        # Kenta Nakai
             ##Osaka, University
         ##nakai@imcb.osaka-u.ac.jp
            # http://www.imcb.osaka-u.ac.jp/nakai/psort.html
   #Donor: Paul Horton (paulh@cs.berkeley.edu)
   #Date:  September, 1996
   #See also: ecoli database

#3. Past Usage.
#Reference: "A Probablistic Classification System for Predicting the Cellular
#           Localization Sites of Proteins", Paul Horton & Kenta Nakai,
 #          Intelligent Systems in Molecular Biology, 109-115.
#      St. Louis, USA 1996.
#Results: 55% for Yeast data with an ad hoc structured
    # probability model. Also similar accuracy for Binary Decision Tree and
#    Bayesian Classifier methods applied by the same authors in
    # unpublished results.

#Predicted Attribute: Localization site of protein. ( non-numeric ).


#4. The references below describe a predecessor to this dataset and its
#development. They also give results (not cross-validated) for classification
#by a rule-based expert system with that version of the dataset.

#Reference: "Expert Sytem for Predicting Protein Localization Sites in
#           Gram-Negative Bacteria", Kenta Nakai & Minoru Kanehisa,
     #      PROTEINS: Structure, Function, and Genetics 11:95-110, 1991.
```

```
#Reference: "A Knowledge Base for Predicting Protein Localization Sites in
#      Eukaryotic Cells", Kenta Nakai & Minoru Kanehisa,
#      Genomics 14:897-911, 1992.


#5. Number of Instances:  1484 for the Yeast dataset.

#6. Number of Attributes.
 #        for Yeast dataset:   9 ( 8 predictive, 1 name )

#7. Attribute Information.
#  1.  Sequence Name: Accession number for the SWISS-PROT database
#  2.  mcg: McGeoch's method for signal sequence recognition.
#  3.  gvh: von Heijne's method for signal sequence recognition.
#  4.  alm: Score of the ALOM membrane spanning region prediction program.
 # 5.  mit: Score of discriminant analysis of the amino acid content of
#      the N-terminal region (20 residues long) of mitochondrial and
     #      non-mitochondrial proteins.
  # 6.  erl: Presence of "HDEL" substring (thought to act as a signal for
    #   retention in the endoplasmic reticulum lumen). Binary attribute.
#  7.  pox: Peroxisomal targeting signal in the C-terminus.
 # 8.  vac: Score of discriminant analysis of the amino acid content of
     #      vacuolar and extracellular proteins.
#  9.  nuc: Score of discriminant analysis of nuclear localization signals
#      of nuclear and non-nuclear proteins.


#8. Missing Attribute Values: None.


#9. Class Distribution. The class is the localization site. Please see Nakai
&
#              Kanehisa referenced above for more details.
#  CYT (cytosolic or cytoskeletal)                    463
 # NUC (nuclear)                                      429
#  MIT (mitochondrial)                                244
 # ME3 (membrane protein, no N-terminal signal)       163
 # ME2 (membrane protein, uncleaved signal)            51
 # ME1 (membrane protein, cleaved signal)              44
  #EXC (extracellular)                                 37
 # VAC (vacuolar)                                      30
  #POX (peroxisomal)                                   20
  #ERL (endoplasmic reticulum lumen)                    5


yeast <- read.table("C:/Sourav/R/yeast.txt", quote="\"", comment.char="")
```

```
View(yeast)
summary(yeast)
```

```
##           V1             V2               V3               V4
##  EF1A_YEAST:   2   Min.   :0.1100   Min.   :0.1300   Min.   :0.21
##  H3_YEAST  :   2   1st Qu.:0.4100   1st Qu.:0.4200   1st Qu.:0.46
##  H4_YEAST  :   2   Median :0.4900   Median :0.4900   Median :0.51
##  IF4A_YEAST:   2   Mean   :0.5001   Mean   :0.4999   Mean   :0.50
##  MAT2_YEAST:   2   3rd Qu.:0.5800   3rd Qu.:0.5700   3rd Qu.:0.55
##  MTC_YEAST :   2   Max.   :1.0000   Max.   :1.0000   Max.   :1.00
##  (Other)    1472
##        V5               V6               V7               V8
##  Min.   :0.0000   Min.   :0.5000   Min.   :0.0000   Min.   :0.0000
##  1st Qu.:0.1700   1st Qu.:0.5000   1st Qu.:0.0000   1st Qu.:0.4800
##  Median :0.2200   Median :0.5000   Median :0.0000   Median :0.5100
##  Mean   :0.2612   Mean   :0.5047   Mean   :0.0075   Mean   :0.4999
##  3rd Qu.:0.3200   3rd Qu.:0.5000   3rd Qu.:0.0000   3rd Qu.:0.5300
##  Max.   :1.0000   Max.   :1.0000   Max.   :0.8300   Max.   :0.7300
##
##        V9              V10
##  Min.   :0.0000   CYT     463
##  1st Qu.:0.2200   NUC     429
##  Median :0.2200   MIT     244
##  Mean   :0.2762   ME3     163
##  3rd Qu.:0.3000   ME2    : 51
##  Max.   :1.0000   ME1    : 44
##                   (Other): 90
```

```
dim(yeast)
```

```
## [1] 1484   10
```

```
str(yeast)
```

```
## 'data.frame':    1484 obs. of  10 variables:
##  $ V1 : Factor w/ 1462 levels "6P2K_YEAST","6PGD_YEAST",..: 33 34 35 3 5 4
6 101 7 8 ...
##  $ V2 : num  0.58 0.43 0.64 0.58 0.42 0.51 0.5 0.48 0.55 0.4 ...
##  $ V3 : num  0.61 0.67 0.62 0.44 0.44 0.4 0.54 0.45 0.5 0.39 ...
##  $ V4 : num  0.47 0.48 0.49 0.57 0.48 0.56 0.48 0.59 0.66 0.6 ...
##  $ V5 : num  0.13 0.27 0.15 0.13 0.54 0.17 0.65 0.2 0.36 0.15 ...
##  $ V6 : num  0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 ...
##  $ V7 : num  0 0 0 0 0 0.5 0 0 0 0 ...
##  $ V8 : num  0.48 0.53 0.53 0.54 0.48 0.49 0.53 0.58 0.49 0.58 ...
##  $ V9 : num  0.22 0.22 0.22 0.22 0.22 0.22 0.22 0.34 0.22 0.3 ...
##  $ V10: Factor w/ 10 levels "CYT","ERL","EXC",..: 7 7 7 8 7 1 7 8 7 1 ...
```

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.
2.1 --
```

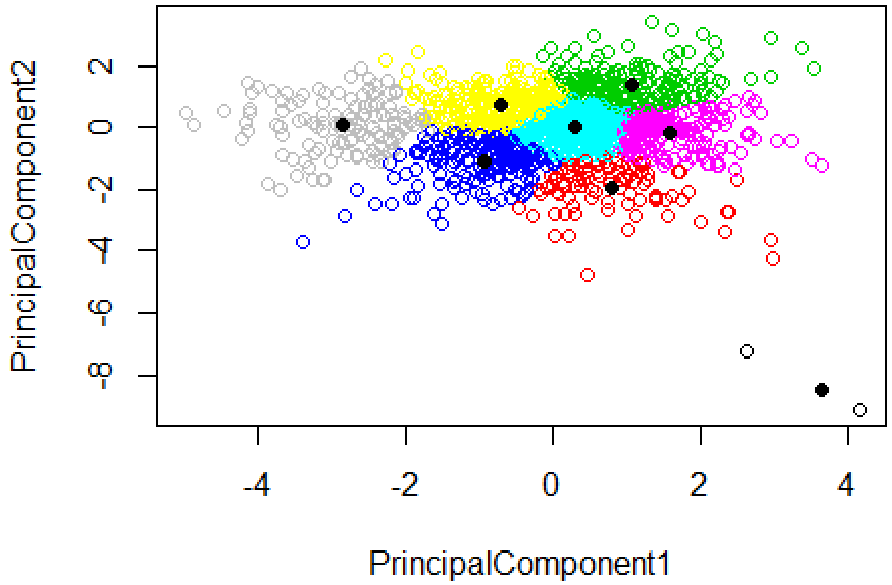
```
## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0

## -- Conflicts ------------------------------------------ tidyverse_conflict
s() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()

yeast <- read.table('https://archive.ics.uci.edu/ml/machine-learning-database
s/yeast/yeast.data', stringsAsFactors = FALSE)
l <- readLines('https://archive.ics.uci.edu/ml/machine-learning-databases/yea
st/yeast.names')
l <- l[(grep('^7', l) + 1):(grep('^8', l) - 1)]
l <- l[grep('\\d\\..*:', l)]
names(yeast) <- make.names(c(sub('.*\\d\\.\\s+(.*):.*', '\\1', l), 'class'))
str(yeast)

## 'data.frame':    1484 obs. of  10 variables:
##  $ Sequence.Name: chr  "ADT1_YEAST" "ADT2_YEAST" "ADT3_YEAST" "AAR2_YEAST"
...
##  $ mcg          : num  0.58 0.43 0.64 0.58 0.42 0.51 0.5 0.48 0.55 0.4 ...
##  $ gvh          : num  0.61 0.67 0.62 0.44 0.44 0.4 0.54 0.45 0.5 0.39 ...
##  $ alm          : num  0.47 0.48 0.49 0.57 0.48 0.56 0.48 0.59 0.66 0.6 ..
.
##  $ mit          : num  0.13 0.27 0.15 0.13 0.54 0.17 0.65 0.2 0.36 0.15 ..
.
##  $ erl          : num  0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 0.5 ...
##  $ pox          : num  0 0 0 0 0 0.5 0 0 0 0 ...
##  $ vac          : num  0.48 0.53 0.53 0.54 0.48 0.49 0.53 0.58 0.49 0.58 .
..
##  $ nuc          : num  0.22 0.22 0.22 0.22 0.22 0.22 0.22 0.34 0.22 0.3 ..
.
##  $ class        : chr  "MIT" "MIT" "MIT" "NUC" ...

pca <- princomp(yeast[, 2:9], cor=T) # principal components analysis using co
rrelation matrix
pc.comp <- pca$scores
PrincipalComponent1 <- -1*pc.comp[,1] # principal component 1 scores (negated
for convenience)
PrincipalComponent2 <- -1*pc.comp[,2] # principal component 2 scores (negated
for convenience)
clustering.data <- cbind(PrincipalComponent1, PrincipalComponent2)
# K-Mean Clustering
set.seed(100)
km <- kmeans(clustering.data, 8, iter.max = 30, nstart=30)
km

## K-means clustering with 8 clusters of sizes 3, 110, 192, 191, 399, 199, 26
0, 130
```

```
##
## Cluster means:
##   PrincipalComponent1 PrincipalComponent2
## 1           3.6562743         -8.49636811
## 2           0.8085402         -1.96932237
## 3           1.0686111          1.39771690
## 4          -0.9430200         -1.09237604
## 5           0.2882285          0.01334731
## 6           1.6051406         -0.17329450
## 7          -0.7214210          0.76632446
## 8          -2.8601651          0.09471085
##
## Clustering vector:
##    [1] 7 7 7 5 2 5 4 3 2 3 6 6 5 4 4 5 3 5 6 4 5 5 8 5 7 4 7 5 4 8 7 4 3 5
##   [35] 8 4 8 3 4 4 8 8 8 7 6 6 4 5 7 3 5 3 5 5 4 4 7 5 5 4 5 6 5 3 7 7 3 5
##   [69] 5 8 5 7 4 4 2 2 4 4 2 4 4 4 4 2 8 7 3 8 5 5 6 5 6 3 7 5 4 8 8 4 5 3
##  [103] 2 6 6 7 3 5 7 5 5 7 6 5 3 2 4 2 2 6 8 4 4 4 7 4 6 4 5 6 5 5 2 4 5 3
##  [137] 3 5 6 6 6 4 4 5 5 3 5 5 3 5 5 3 5 5 7 3 6 4 5 8 6 6 5 3 7 3 5 5 3 3
##  [171] 6 7 5 6 4 5 6 5 6 2 6 5 5 4 7 5 5 3 7 3 8 8 5 4 4 4 4 8 8 5 7 6 5 4
##  [205] 7 8 2 4 2 2 4 4 4 5 7 5 8 5 8 8 7 7 5 2 2 7 2 6 8 2 5 6 3 8 8 6 6 6
##  [239] 5 5 5 5 5 6 3 5 7 6 7 3 5 7 6 5 7 2 6 6 6 5 6 6 7 7 6 4 6 5 7 7 6 5
##  [273] 7 5 6 5 8 5 5 6 7 8 3 5 5 3 7 8 7 4 7 7 8 7 7 7 5 6 3 7 7 7 7 3 8 8
##  [307] 3 5 7 7 6 7 7 7 3 7 3 3 8 7 7 6 8 3 7 8 8 5 5 2 3 4 7 8 5 6 7 3 7 2
##  [341] 7 5 5 4 7 5 8 6 5 3 3 6 4 3 3 5 5 6 5 5 3 5 5 8 6 5 7 3 3 3 5 5 6 5
##  [375] 5 5 3 7 7 6 5 6 5 3 3 5 5 7 5 5 4 6 7 2 6 7 3 5 3 4 6 6 2 7 5 3 6 6
##  [409] 2 2 7 3 7 5 7 8 6 5 6 5 5 5 3 3 8 2 7 6 4 4 5 7 4 2 7 5 5 6 6 4 6 5
##  [443] 7 7 3 7 5 7 7 3 5 4 4 5 4 4 5 4 4 4 5 4 5 2 5 5 6 5 7 3 8 4 7 7 7 2
##  [477] 3 7 5 5 3 5 8 8 7 7 6 6 8 6 7 8 8 4 4 8 8 3 6 7 4 2 6 4 5 8 8 7 4 5
##  [511] 5 8 8 8 8 6 7 2 3 6 4 4 3 3 7 3 5 5 4 5 5 3 5 3 5 4 4 3 7 5 6 3 6 6
##  [545] 3 6 5 4 4 4 3 8 5 2 6 5 7 7 7 4 4 7 5 6 5 4 4 7 8 7 5 6 7 5 5 7 7 6
##  [579] 2 4 8 2 4 5 5 3 6 5 7 4 7 5 5 8 8 8 4 7 4 7 3 4 2 2 5 2 5 2 2 4 6 4
##  [613] 5 2 5 2 2 4 4 4 2 5 2 4 4 2 4 4 5 4 4 4 7 7 8 5 6 4 3 7 7 4 4 6 3 5
##  [647] 7 5 4 4 5 4 2 5 5 5 6 6 5 7 5 2 7 4 8 7 5 4 6 5 4 6 2 6 5 4 8 7 7 4
##  [681] 4 3 3 6 6 7 7 5 3 5 6 3 3 6 6 4 3 6 8 3 5 4 3 4 4 7 6 8 8 3 8 7 4 5
##  [715] 2 5 3 3 3 8 6 6 5 7 5 5 5 4 5 5 7 4 4 5 5 5 5 7 5 8 3 4 3 6 4 8 5 5
##  [749] 8 7 6 5 5 5 4 4 5 6 5 5 4 5 5 5 7 2 6 5 3 5 3 2 8 8 5 8 6 8 7 7 3 6
##  [783] 3 2 4 3 4 4 4 4 5 8 7 3 3 7 8 8 3 7 3 7 5 5 6 7 3 6 7 5 7 2 5 7 4 5
##  [817] 6 7 7 8 4 4 4 7 5 5 2 6 2 5 8 5 6 5 6 6 5 5 3 6 6 3 5 3 5 5 3 5 5 4
##  [851] 4 5 8 5 6 3 2 6 5 4 5 5 7 5 5 4 7 5 5 7 6 4 3 5 6 6 5 3 5 5 5 3 3 5
##  [885] 5 6 5 7 5 5 3 3 7 4 5 5 5 4 5 5 6 4 6 6 7 7 3 6 6 5 5 5 5 7 6 4 4 3
##  [919] 2 5 4 5 7 4 5 5 2 2 6 6 5 2 2 2 2 2 2 6 7 6 5 5 5 5 3 5 6 6 6 5 5 2
##  [953] 2 5 6 3 6 6 3 3 3 6 2 2 2 2 7 7 5 5 5 5 5 2 2 2 2 4 4 4 6 6 5 6 2 2
##  [987] 2 2 1 1 1 5 5 2 6 5 7 7 7 7 8 5 5 7 4 6 2 2 6 6 5 6 6 6 4 4 5 5 5 5
## [1021] 5 4 2 3 4 4 6 6 7 2 6 6 2 7 5 6 8 5 3 8 5 7 4 5 4 4 4 4 5 7 8 7 6 3
## [1055] 7 5 3 7 7 7 7 5 5 5 7 5 8 7 7 3 7 3 5 7 6 5 8 7 6 3 5 3 5 4 8 8 7 4
## [1089] 7 7 2 5 5 5 2 5 3 3 3 5 3 5 7 2 3 3 5 8 7 6 5 5 3 7 6 7 3 5 4 3 3 5
## [1123] 3 3 5 2 2 6 7 4 7 7 2 6 5 6 2 2 5 7 5 5 4 4 5 7 3 5 6 3 5 7 5 4 3 3
## [1157] 7 6 5 7 7 2 5 6 5 6 5 3 5 5 3 7 5 5 5 5 5 5 6 4 5 3 2 5 3 8 5 5 8 5
## [1191] 3 7 2 7 3 8 6 7 7 2 6 7 5 5 3 7 7 8 8 4 5 6 5 3 5 5 6 6 6 4 6 5 3 3
## [1225] 5 8 3 7 3 7 5 7 7 5 5 5 5 4 5 4 5 6 7 7 5 5 8 5 7 7 5 3 3 5 4 6 6 6
## [1259] 6 3 6 6 3 7 7 8 5 8 8 7 7 5 6 5 3 3 5 5 5 6 2 6 2 6 4 5 3 3 7 5 5 7
## [1293] 6 5 7 5 7 4 5 8 5 5 5 5 4 2 6 7 7 5 7 7 7 5 2 7 6 3 3 3 7 6 5 5 5 7
## [1327] 5 2 2 7 5 7 7 5 5 8 6 8 5 7 5 4 2 7 3 5 7 5 6 4 4 7 5 5 8 7 8 6 8 3
## [1361] 7 7 7 8 8 7 5 5 5 8 3 5 5 4 6 3 3 7 6 4 7 3 3 3 3 7 8 6 5 7 7 7 8 8
## [1395] 7 4 2 4 7 8 7 3 8 7 5 7 5 5 8 5 4 3 7 4 5 3 7 3 5 7 8 7 6 8 8 3 7 5
## [1429] 7 5 3 5 8 7 8 3 8 8 7 8 8 3 8 8 7 7 2 3 3 7 8 6 3 6 4 3 8 5 7 3 4 8
## [1463] 4 3 3 7 3 2 5 5 4 5 7 4 5 4 5 2 2 8 6 7 3 7
## 
## Within cluster sum of squares by cluster:
## [1]   3.998783 113.647111 145.595268 144.310502 126.152899 114.078257
## [7] 127.815144 149.922267
##  (between_SS / total_SS =  79.8 %)
## 
## Available components:
## 
## [1] "cluster"      "centers"      "totss"        "withinss"    
## [5] "tot.withinss" "betweenss"    "size"         "iter"        
## [9] "ifault"
```

```
km$cluster
```

```
##    [1] 7 7 7 5 2 5 4 3 2 3 6 6 5 4 4 5 3 5 6 4 5 5 8 5 7 4 7 5 4 8 7 4 3 5
##   [35] 8 4 8 3 4 4 8 8 8 7 6 6 4 5 7 3 5 3 5 5 4 4 7 5 5 4 5 6 5 3 7 7 3 5
##   [69] 5 8 5 7 4 4 2 2 4 4 2 4 4 4 4 2 8 7 3 8 5 5 6 5 6 3 7 5 4 8 8 4 5 3
##  [103] 2 6 6 7 3 5 7 5 5 7 6 5 3 2 4 2 2 6 8 4 4 4 7 4 6 4 5 6 5 5 2 4 5 3
##  [137] 3 5 6 6 6 4 4 5 5 3 5 5 3 5 5 3 5 5 7 3 6 4 5 8 6 6 5 3 7 3 5 5 3 3
##  [171] 6 7 5 6 4 5 6 5 6 2 6 5 5 4 7 5 5 3 7 3 8 8 5 4 4 4 4 8 8 5 7 6 5 4
##  [205] 7 8 2 4 2 2 4 4 4 5 7 5 8 5 8 8 7 7 5 2 2 7 2 6 8 2 5 6 3 8 8 6 6 6
##  [239] 5 5 5 5 5 6 3 5 7 6 7 3 5 7 6 5 7 2 6 6 6 5 6 6 7 7 6 4 6 5 7 7 6 5
##  [273] 7 5 6 5 8 5 5 6 7 8 3 5 5 3 7 8 7 4 7 7 8 7 7 7 5 6 3 7 7 7 7 3 8 8
##  [307] 3 5 7 7 6 7 7 7 3 7 3 3 8 7 7 6 8 3 7 8 8 5 5 2 3 4 7 8 5 6 7 3 7 2
##  [341] 7 5 5 4 7 5 8 6 5 3 3 6 4 3 3 5 5 6 5 5 3 5 5 8 6 5 7 3 3 3 5 5 6 5
##  [375] 5 5 3 7 7 6 5 6 5 3 3 5 5 7 5 5 4 6 7 2 6 7 3 5 3 4 6 6 2 7 5 3 6 6
##  [409] 2 2 7 3 7 5 7 8 6 5 6 5 5 5 3 3 8 2 7 6 4 4 5 7 4 2 7 5 5 6 6 4 6 5
##  [443] 7 7 3 7 5 7 7 3 5 4 4 5 4 4 5 4 4 4 5 4 5 2 5 5 6 5 7 3 8 4 7 7 7 2
##  [477] 3 7 5 5 3 5 8 8 7 7 6 6 8 6 7 8 8 4 4 8 8 3 6 7 4 2 6 4 5 8 8 7 4 5
##  [511] 5 8 8 8 8 6 7 2 3 6 4 4 3 3 7 3 5 5 4 5 5 3 5 3 5 4 4 3 7 5 6 3 6 6
##  [545] 3 6 5 4 4 4 3 8 5 2 6 5 7 7 7 4 4 7 5 6 5 4 4 7 8 7 5 6 7 5 5 7 7 6
##  [579] 2 4 8 2 4 5 5 3 6 5 7 4 7 5 5 8 8 8 4 7 4 7 3 4 2 2 5 2 5 2 2 4 6 4
##  [613] 5 2 5 2 2 4 4 4 2 5 2 4 4 2 4 4 5 4 4 4 7 7 8 5 6 4 3 7 7 4 4 6 3 5
##  [647] 7 5 4 4 5 4 2 5 5 5 6 6 5 7 5 2 7 4 8 7 5 4 6 5 4 6 2 6 5 4 8 7 7 4
##  [681] 4 3 3 6 6 7 7 5 3 5 6 3 3 6 6 4 3 6 8 3 5 4 3 4 4 7 6 8 8 3 8 7 4 5
##  [715] 2 5 3 3 3 8 6 6 5 7 5 5 5 4 5 5 7 4 4 5 5 5 5 7 5 8 3 4 3 6 4 8 5 5
##  [749] 8 7 6 5 5 5 4 4 5 6 5 5 4 5 5 5 7 2 6 5 3 5 3 2 8 8 5 8 6 8 7 7 3 6
##  [783] 3 2 4 3 4 4 4 4 5 8 7 3 3 7 8 8 3 7 3 7 5 5 6 7 3 6 7 5 7 2 5 7 4 5
##  [817] 6 7 7 8 4 4 4 7 5 5 2 6 2 5 8 5 6 5 6 6 5 5 3 6 6 3 5 3 5 5 3 5 5 4
##  [851] 4 5 8 5 6 3 2 6 5 4 5 5 7 5 5 4 7 5 5 7 6 4 3 5 6 6 5 3 5 5 5 3 3 5
##  [885] 5 6 5 7 5 5 3 3 7 4 5 5 5 4 5 5 6 4 6 6 7 7 3 6 6 5 5 5 5 7 6 4 4 3
##  [919] 2 5 4 5 7 4 5 5 2 2 6 6 5 2 2 2 2 2 2 6 7 6 5 5 5 5 3 5 6 6 6 5 5 2
##  [953] 2 5 6 3 6 6 3 3 3 6 2 2 2 2 7 7 5 5 5 5 5 2 2 2 2 4 4 4 6 6 5 6 2 2
##  [987] 2 2 1 1 1 5 5 2 6 5 7 7 7 7 8 5 5 7 4 6 2 2 6 6 5 6 6 6 4 4 5 5 5 5
## [1021] 5 4 2 3 4 4 6 6 7 2 6 6 2 7 5 6 8 5 3 8 5 7 4 5 4 4 4 4 5 7 8 7 6 3
## [1055] 7 5 3 7 7 7 7 5 5 5 7 5 8 7 7 3 7 3 5 7 6 5 8 7 6 3 5 3 5 4 8 8 7 4
## [1089] 7 7 2 5 5 5 2 5 3 3 3 5 3 5 7 2 3 3 5 8 7 6 5 5 3 7 6 7 3 5 4 3 3 5
## [1123] 3 3 5 2 2 6 7 4 7 7 2 6 5 6 2 2 5 7 5 5 4 4 5 7 3 5 6 3 5 7 5 4 3 3
## [1157] 7 6 5 7 7 2 5 6 5 6 5 3 5 5 3 7 5 5 5 5 5 5 6 4 5 3 2 5 3 8 5 5 8 5
## [1191] 3 7 2 7 3 8 6 7 7 2 6 7 5 5 3 7 7 8 8 4 5 6 5 3 5 5 6 6 6 4 6 5 3 3
## [1225] 5 8 3 7 3 7 5 7 7 5 5 5 5 4 5 4 5 6 7 7 5 5 8 5 7 7 5 3 3 5 4 6 6 6
## [1259] 6 3 6 6 3 7 7 8 5 8 8 7 7 5 6 5 3 3 5 5 5 6 2 6 2 6 4 5 3 3 7 5 5 7
## [1293] 6 5 7 5 7 4 5 8 5 5 5 5 4 2 6 7 7 5 7 7 7 5 2 7 6 3 3 3 7 6 5 5 5 7
## [1327] 5 2 2 7 5 7 7 5 5 8 6 8 5 7 5 4 2 7 3 5 7 5 6 4 4 7 5 5 8 7 8 6 8 3
## [1361] 7 7 7 8 8 7 5 5 5 8 3 5 5 4 6 3 3 7 6 4 7 3 3 3 3 7 8 6 5 7 7 7 8 8
## [1395] 7 4 2 4 7 8 7 3 8 7 5 7 5 5 8 5 4 3 7 4 5 3 7 3 5 7 8 7 6 8 8 3 7 5
## [1429] 7 5 3 5 8 7 8 3 8 8 7 8 8 3 8 8 7 7 2 3 3 7 8 6 3 6 4 3 8 5 7 3 4 8
## [1463] 4 3 3 7 3 2 5 5 4 5 7 4 5 4 5 2 2 8 6 7 3 7
```

```
plot(PrincipalComponent1, PrincipalComponent2, col=km$cluster)
points(km$centers, pch=16)
```



```
names(yeast)<- c("SequenceName", "mcg", "gvh", "alm", "mit", "erl", "pox", "v
ac", "nuc", "LocalizationSite")
aggregate(yeast[, 2:9],by=list(km$cluster),mean)
```

```
##   Group.1       mcg       gvh       alm       mit       erl         pox
## 1       1 0.3766667 0.2133333 0.9300000 0.7966667 0.5000000 0.000000000
## 2       2 0.4693636 0.4452727 0.5797273 0.3632727 0.5000000 0.004545455
## 3       3 0.3833333 0.4115104 0.4686458 0.1800000 0.5052083 0.000000000
## 4       4 0.5817277 0.5768063 0.5130366 0.4321466 0.5026178 0.004345550
## 5       5 0.4792231 0.4787719 0.5196992 0.2337343 0.5000000 0.012080201
## 6       6 0.3757286 0.3686935 0.5618593 0.2151759 0.5000000 0.004170854
## 7       7 0.5357692 0.5591154 0.4424231 0.2018462 0.5096154 0.012769231
## 8       8 0.7648462 0.7179231 0.4101538 0.3045385 0.5230769 0.006384615
##         vac         nuc
## 1 0.1600000 0.006666667
## 2 0.4034545 0.215727273
## 3 0.5272396 0.408750000
## 4 0.4853927 0.240471204
## 5 0.5055138 0.259548872
## 6 0.4818090 0.276532663
## 7 0.5303462 0.273076923
## 8 0.5196923 0.247153846
```

```
table(km$cluster, yeast$LocalizationSite)
```

```
##    
##     CYT ERL EXC ME1 ME2 ME3 MIT NUC POX VAC
##   1   3   0   0   0   0   0   0   0   0   0
##   2  48   0   2   0   0   0  32  26   1   1
##   3  45   0   0   0   4  49   3  88   0   3
##   4  36   0  12   1   3   2 113  21   1   2
##   5 179   0   1   0   0  25  48 130  10   6
##   6  76   0   0   0   0   3  11 105   1   3
##   7  73   0   0   0  14  78  23  57   5  10
##   8   3   5  20  43  30   6  14   2   2   5
```

```
#Spectral Clustering
library(kknn)
```

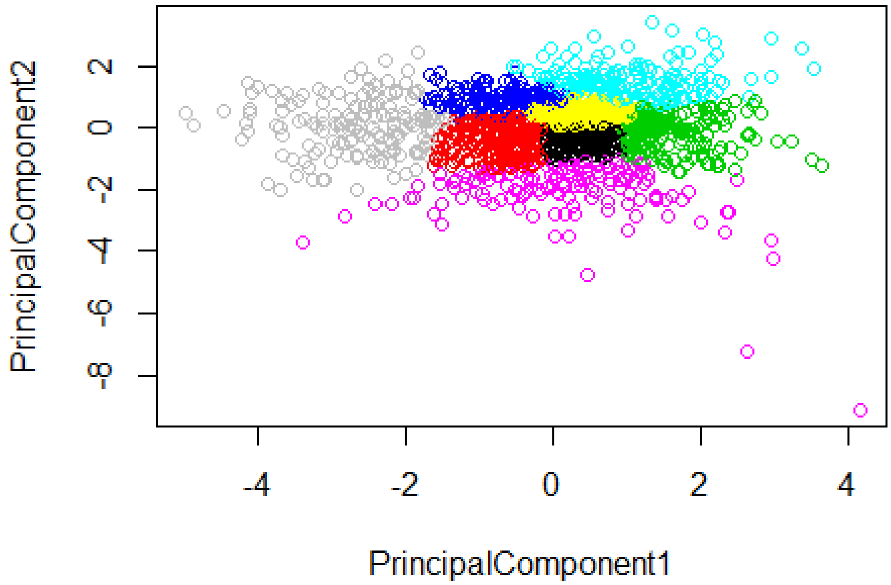
```
## Warning: package 'kknn' was built under R version 3.5.1
```

```
cl   <- specClust(clustering.data, centers=8, nn=50, iter.max=100)
cl
```

```
## K-means clustering with 8 clusters of sizes 186, 219, 195, 156, 172, 161,
235, 160
## 
```

```
## Cluster means:
##         [,1]         [,2]         [,3]        [,4]        [,5]        [,6]
## 1 -0.3808008 -0.010307326 -0.335345170 -0.34971429 -0.12569821  0.12122808
## 2 -0.3859207 -0.356402209  0.001120503 -0.18897403  0.15872031  0.42663259
## 3 -0.3490415  0.263465580 -0.365421550  0.18599020 -0.39027381 -0.23528531
## 4 -0.3706620  0.009057016  0.499097988 -0.08118804  0.25164079 -0.49508121
## 5 -0.3261405  0.473393062  0.201756081  0.43978983  0.28173634  0.29245070
## 6 -0.3113686 -0.308406853 -0.445304695  0.27223211  0.38520253 -0.27321926
## 7 -0.3971609  0.303283449  0.099096132 -0.38195357 -0.03938998 -0.02858538
## 8 -0.3253228 -0.481735595  0.380420920  0.30376846 -0.43922822  0.00971019
##         [,7]       [,8]
## 1  0.2889526  0.51087588
## 2  0.1959341 -0.34792688
## 3  0.1942592 -0.29581023
## 4  0.2549182 -0.02314869
## 5  0.1178271  0.14336792
## 6 -0.3357884 -0.03074654
## 7 -0.5215953 -0.04244720
## 8 -0.1457893  0.17068547
## 
## Clustering vector:
##    [1] 2 2 4 7 6 1 2 7 6 5 7 3 1 2 2 7 5 7 3 2 7 7 8 7 4 2 4 1 2 8 4 6 5 1
##   [35] 8 8 8 7 2 2 8 8 8 4 3 3 6 1 8 5 7 5 1 1 2 2 2 2 1 6 1 3 7 7 4 4 5 7
##   [69] 7 8 7 4 6 6 6 6 2 2 6 6 1 2 2 6 8 5 5 8 1 1 3 7 3 5 2 1 8 8 8 6 2 7
##  [103] 6 3 1 4 7 1 4 7 1 7 5 1 5 6 6 6 6 3 8 2 2 2 4 2 3 2 1 3 2 1 6 2 7 7
##  [137] 5 7 3 3 3 2 2 1 7 5 1 7 5 1 7 5 7 7 4 3 3 8 1 8 3 3 7 5 4 5 7 7 7 5
##  [171] 3 2 2 3 2 1 3 1 3 6 3 1 1 2 2 7 7 5 2 5 8 8 7 2 2 6 6 8 8 7 2 3 2 6
##  [205] 4 8 6 6 6 6 6 2 8 2 4 7 8 1 8 8 4 4 2 6 6 4 6 3 8 6 7 1 5 8 8 1 3 3
##  [239] 1 1 7 1 1 3 5 1 2 3 4 5 1 4 3 1 4 6 3 3 3 7 3 3 2 4 3 2 3 7 4 4 3 1
##  [273] 5 2 3 1 8 7 2 3 5 8 5 2 2 5 8 8 4 2 4 4 8 4 8 4 7 3 7 4 4 2 5 5 8 8
##  [307] 5 7 2 4 3 2 2 2 5 2 5 5 8 2 4 3 8 5 4 8 8 7 1 6 5 8 4 8 2 3 2 5 4 6
##  [341] 4 7 1 2 4 1 8 3 1 5 7 3 2 5 5 7 7 3 1 1 5 1 1 8 3 7 4 5 5 7 7 7 3 7
##  [375] 7 7 5 4 4 3 2 3 1 5 5 1 1 7 7 1 2 3 4 6 3 4 5 7 5 2 3 3 6 4 7 5 3 3
##  [409] 6 6 4 5 4 7 4 8 3 1 3 1 7 7 5 5 8 6 4 3 2 2 7 4 2 6 4 1 1 3 3 2 3 1
##  [443] 7 7 5 4 7 4 4 5 1 2 6 1 2 2 7 2 6 6 1 2 7 6 7 1 3 1 4 5 8 2 4 4 4 6
##  [477] 5 4 1 1 5 7 8 8 8 4 3 3 8 3 4 8 8 6 2 8 8 7 3 7 2 6 3 6 3 8 8 4 6 7
##  [511] 1 8 8 8 8 3 7 6 5 3 6 2 3 7 4 5 2 7 6 7 2 5 7 5 7 6 2 5 4 1 3 5 3 3
##  [545] 5 3 1 6 2 8 7 8 7 6 3 7 2 4 2 6 2 8 7 3 2 2 2 4 8 4 2 1 4 1 7 2 2 3
##  [579] 6 8 8 6 2 1 7 5 3 7 4 2 4 1 1 8 8 8 2 7 6 2 5 2 6 6 1 6 1 6 6 2 3 6
##  [613] 1 6 1 6 6 2 2 2 6 1 6 6 6 6 2 6 1 2 2 2 2 2 8 2 3 2 5 2 2 6 2 3 7 7
##  [647] 2 1 6 2 1 2 6 1 7 7 3 3 7 4 7 6 4 2 8 4 1 6 3 1 2 7 1 3 7 2 8 4 2 2
##  [681] 2 5 5 3 3 5 4 7 5 7 3 5 5 3 3 8 5 3 8 5 7 8 7 2 6 2 3 8 8 5 8 4 6 1
##  [715] 6 7 5 5 5 8 3 3 1 2 2 1 1 6 1 7 4 2 6 7 1 7 1 4 7 8 5 2 5 3 2 8 7 7
##  [749] 8 7 3 2 1 2 8 6 1 3 1 2 6 1 7 2 5 6 3 1 4 7 5 6 8 8 7 8 3 8 4 4 5 3
##  [783] 5 6 2 5 6 6 6 6 2 8 4 5 5 7 8 8 5 5 7 4 7 7 3 7 7 3 4 1 4 6 1 8 2 7
##  [817] 3 2 8 8 2 2 2 2 1 1 6 3 6 7 8 7 3 1 3 3 7 1 7 3 3 5 1 5 1 7 7 1 2 2
##  [851] 2 1 8 1 3 5 6 3 7 2 2 7 4 1 7 2 2 1 2 2 3 2 5 1 3 3 7 5 1 1 1 5 5 1
##  [885] 2 3 1 2 1 1 5 5 5 2 7 7 1 2 1 1 3 2 3 3 7 4 5 3 3 1 7 1 1 4 3 2 2 5
##  [919] 6 1 2 1 5 2 1 1 6 3 3 3 1 6 6 6 6 6 6 1 4 3 7 7 1 7 7 2 3 3 3 1 1 6
##  [953] 6 7 3 5 3 3 7 5 5 3 6 6 6 6 4 4 1 7 7 1 1 6 6 6 6 6 2 2 3 3 2 1 6 6
##  [987] 6 6 6 6 6 1 1 6 3 1 4 4 4 8 8 7 2 4 2 3 6 6 3 3 1 3 3 3 1 1 1 1 1 1
## [1021] 1 2 6 5 2 2 3 3 7 6 3 3 6 4 1 3 8 2 5 8 7 5 2 7 6 6 8 2 7 4 8 4 3 5
## [1055] 7 7 7 4 4 4 4 7 1 7 4 7 8 4 8 7 4 5 2 4 3 7 8 8 3 5 1 5 7 2 8 8 4 2
## [1089] 7 8 6 1 1 2 6 1 5 5 5 7 7 7 4 6 5 5 7 8 4 3 7 7 5 4 3 4 5 2 2 5 5 7
## [1123] 5 7 1 6 6 3 4 2 4 4 6 3 1 3 6 6 7 4 1 7 2 6 7 7 5 7 3 5 1 4 2 2 7 5
## [1157] 7 7 7 4 2 6 7 3 7 3 1 5 1 7 5 4 7 7 1 7 7 7 3 2 7 5 6 7 5 8 7 7 8 1
## [1191] 5 4 6 4 5 8 3 4 2 6 3 4 7 7 3 4 8 8 8 8 1 3 2 5 7 7 3 3 3 2 3 7 5 5
## [1225] 7 8 7 2 5 7 1 7 7 7 2 7 1 2 1 2 7 3 7 7 7 7 8 1 4 4 1 5 5 1 2 3 3 3
## [1259] 3 7 3 3 5 4 4 8 1 8 8 2 2 7 3 1 5 5 1 2 1 3 6 3 3 3 2 1 5 5 2 7 7 2
## [1293] 3 7 4 1 2 2 2 8 1 1 1 7 8 6 3 2 4 2 4 4 4 7 6 4 3 5 5 5 4 3 7 1 7 7
## [1327] 7 6 6 5 1 4 4 7 7 8 3 8 7 2 1 2 6 4 5 7 8 7 3 2 8 7 1 7 8 4 8 3 8 5
## [1361] 4 2 4 8 8 7 7 2 7 8 5 7 1 6 3 5 5 4 3 2 4 5 5 5 5 4 8 3 7 4 4 8 8 8
## [1395] 4 6 6 6 4 8 7 5 8 4 1 4 7 7 8 1 8 5 7 2 7 5 2 5 7 4 8 4 3 8 8 5 4 7
## [1429] 2 1 5 2 8 4 8 5 8 8 4 8 8 5 8 8 2 4 6 5 5 2 8 3 5 3 6 5 8 7 2 5 2 8
## [1463] 6 5 5 4 5 6 7 1 2 7 4 2 1 2 2 6 6 8 3 8 5 2
## 
## Within cluster sum of squares by cluster:
## [1] 45.59679 70.44780 60.00491 36.33080 40.60411 32.00669 74.81030 29.0714
8
##  (between_SS / total_SS =  69.9 %)
## 
## Available components:
## 
##  [1] "cluster"      "centers"      "totss"        "withinss"    
##  [5] "tot.withinss" "betweenss"    "size"         "iter"        
##  [9] "ifault"       "eigenvalue"   "eigenvector"  "data"        
## [13] "indAll"       "indUnique"    "L"            "archetype"   
## [17] "call"
```

```
plot(PrincipalComponent1, PrincipalComponent2, col=cl$cluster)
```



```
table(cl$cluster, yeast$LocalizationSite)
```

```
## 
##     CYT ERL EXC ME1 ME2 ME3 MIT NUC POX VAC
##   1  71   0   1   0   0   3  31  70   9   1
##   2  72   0   2   0   2  11  93  33   2   4
##   3  74   0   0   0   1   3  11 102   1   3
##   4  42   0   0   0  10  55   8  34   2   5
##    5  35   0   0   0   2  50   2  80   0   3
##    6  52   0   7   1   2   0  67  29   2   1
##    7 110   0   0   0   1  29  12  75   2   6
##    8   7   5  25  43  33  12  20   6   2   7
```

```
aggregate(yeast[, 2:9],by=list(cl$cluster),mean)
```

```
##   Group.1       mcg       gvh       alm       mit       erl         pox
## 1       1 0.4755914 0.4774731 0.5415054 0.2611290 0.5000000 0.018763441
## 2       2 0.5599087 0.5620548 0.5038813 0.3309132 0.5022831 0.013652968
## 3       3 0.3738462 0.3676923 0.5625641 0.2140000 0.5000000 0.004256410
## 4       4 0.5244231 0.5530769 0.4301282 0.1937821 0.5096154 0.005320513
## 5       5 0.3816860 0.4130233 0.4589535 0.1778488 0.5087209 0.000000000
## 6       6 0.5042236 0.4885714 0.5668323 0.4272671 0.5000000 0.003105590
## 7       7 0.4680426 0.4667660 0.4985957 0.2000000 0.5000000 0.007063830
## 8       8 0.7473125 0.7039375 0.4175625 0.3013750 0.5218750 0.005187500
##         vac       nuc
## 1 0.4927957 0.2497312
## 2 0.5059817 0.2422831
## 3 0.4819487 0.2754359
## 4 0.5362179 0.2767949
## 5 0.5279651 0.4241860
## 6 0.4114907 0.2188199
## 7 0.5174043 0.2804681
## 8 0.5192500 0.2461250
```

```
#Hierarchical Clustering
d_yeast<- dist(clustering.data)
hclusters <- hclust(d_yeast, method = "average")
clusterCut <- cutree(hclusters, 8)
clusterCut
```

```
##   [1] 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 2 2 3 2 1 1
##  [35] 2 2 2 1 1 1 2 2 2 1 1 1 4 1 2 1 1 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##  [69] 1 2 1 1 2 1 1 1 1 1 1 1 1 1 1 1 2 3 1 2 1 1 1 1 1 3 1 1 2 2 2 1 1 1
## [103] 1 1 1 1 1 1 2 1 1 1 1 1 3 1 2 1 5 1 2 1 2 1 2 1 1 2 1 1 1 1 1 1 1 1
## [137] 1 1 1 1 1 1 1 1 1 3 1 1 3 1 1 3 1 1 1 1 1 2 1 2 1 1 1 1 1 1 1 1 1 3
## [171] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 1 1 2 1 1 2 2 1 1 1 1 1
## [205] 2 2 1 1 1 1 1 1 2 1 1 1 2 1 2 2 2 1 1 1 1 1 1 1 2 1 1 1 3 2 2 1 1 1
## [239] 1 1 1 1 1 1 3 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
## [273] 3 1 1 1 2 1 1 1 1 2 1 1 1 1 2 2 1 1 1 1 2 1 2 1 1 1 1 1 2 1 1 1 2 2
## [307] 3 1 1 2 1 1 1 1 1 1 1 3 2 1 1 1 2 3 1 2 2 1 1 1 1 2 1 2 1 1 1 1 1 1
## [341] 1 1 1 1 1 1 2 1 1 1 1 1 1 1 3 1 1 1 1 1 3 1 1 2 1 1 1 1 1 1 1 1 1 1
## [375] 1 1 3 1 1 1 1 1 1 3 1 1 1 1 1 1 2 1 1 5 1 2 3 1 1 2 1 1 1 1 1 1 1 1
## [409] 5 5 1 1 1 1 2 2 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1
## [443] 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 2 1 1 1 1 5
## [477] 1 2 1 1 1 1 2 2 2 1 1 1 2 1 1 2 2 1 1 2 2 1 1 1 1 1 1 4 1 2 2 1 4 1
## [511] 1 2 2 2 2 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 3 1 3 1 1 1 1 1 1 1 1 1
## [545] 1 1 1 1 1 2 1 2 1 5 1 1 1 2 1 1 1 2 1 1 1 1 1 2 2 1 1 1 1 1 1 1 1 1
## [579] 1 4 2 1 1 1 1 3 1 1 2 2 1 1 1 2 2 2 1 1 1 1 3 2 1 1 1 1 1 1 1 1 1 1
## [613] 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 2 1 1 2 1 1 1 1 1 1 1 1 1 1 1
##  [647] 1 1 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 2 2 1 1 1
##  [681] 1 3 1 1 1 1 1 1 3 1 1 3 3 1 1 2 1 1 2 1 1 2 1 2 4 1 1 2 2 1 2 2 2 1
##  [715] 1 1 3 3 3 2 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 1 2 3 1 1 1 1 2 1 1
##  [749] 2 1 1 1 1 1 2 1 1 1 1 1 2 1 1 1 3 1 1 1 1 1 3 1 2 2 1 2 1 2 2 1 1 1
##  [783] 3 1 2 1 1 4 4 4 1 2 1 3 1 1 2 2 3 1 1 1 1 1 1 1 1 1 1 1 1 5 1 2 1 1
##  [817] 1 1 2 2 2 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 1 1 1 1 1 3 1 3 1 1 1 1 1 1
##  [851] 1 1 2 1 1 3 1 1 1 2 1 1 2 1 1 1 1 1 1 1 1 1 3 1 1 1 1 1 1 1 1 3 3 1
##  [885] 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 3
##  [919] 1 1 1 1 1 2 1 1 5 1 1 1 1 1 1 1 1 5 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
##  [953] 1 1 1 1 1 1 1 3 3 1 5 5 1 1 1 1 1 1 1 1 1 5 1 1 1 1 2 2 1 1 1 1 1 1
##  [987] 5 5 6 6 6 1 1 1 1 1 1 2 2 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [1021] 1 1 5 3 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 2 1 1 1 1 2 1 2 1 1 1 2 1 1 1
## [1055] 1 1 1 1 1 1 1 1 1 1 1 1 2 1 2 1 1 1 1 1 1 1 2 2 1 3 1 3 1 1 2 2 1 1
## [1089] 1 2 5 1 1 1 1 1 3 1 3 1 1 1 1 1 1 3 1 2 2 7 1 1 1 1 1 1 3 1 1 1 1 1
## [1123] 3 1 1 8 1 1 1 1 1 1 1 1 1 1 5 5 1 1 1 1 2 4 1 1 3 1 1 3 1 1 1 1 1 3
## [1157] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 3 1 1 1 1 1 1 1 1 1 1 3 5 1 1 2 1 1 2 1
## [1191] 1 1 5 1 3 2 1 1 1 1 7 1 1 1 1 1 2 2 2 2 1 1 1 3 1 1 1 1 1 1 1 1 3 3
## [1225] 1 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 1 1 1 1 1 3 1 1 1 1 1
## [1259] 1 1 1 1 1 1 1 2 1 2 2 1 1 1 1 1 3 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [1293] 1 1 2 1 1 1 1 2 1 1 1 1 2 1 1 1 1 1 1 1 1 1 5 1 1 3 1 1 1 1 1 1 1 1
## [1327] 1 5 5 1 1 1 1 1 1 2 1 2 1 1 1 1 1 1 1 1 2 1 1 1 2 1 1 1 2 1 2 1 2 1
## [1361] 1 1 1 2 2 1 1 1 1 2 1 1 1 1 1 3 3 1 1 1 1 1 3 1 1 1 2 1 1 1 1 2 2 2
## [1395] 1 1 1 1 1 2 1 1 2 2 1 1 1 1 2 1 2 1 1 1 1 3 1 1 1 1 2 2 1 2 2 3 1 1
## [1429] 1 1 3 1 2 1 2 3 2 2 1 2 2 1 2 2 1 1 1 3 3 1 2 1 3 1 4 3 2 1 1 3 1 2
## [1463] 1 1 3 1 3 1 1 1 2 1 1 1 1 1 1 5 5 2 1 2 1 1
```

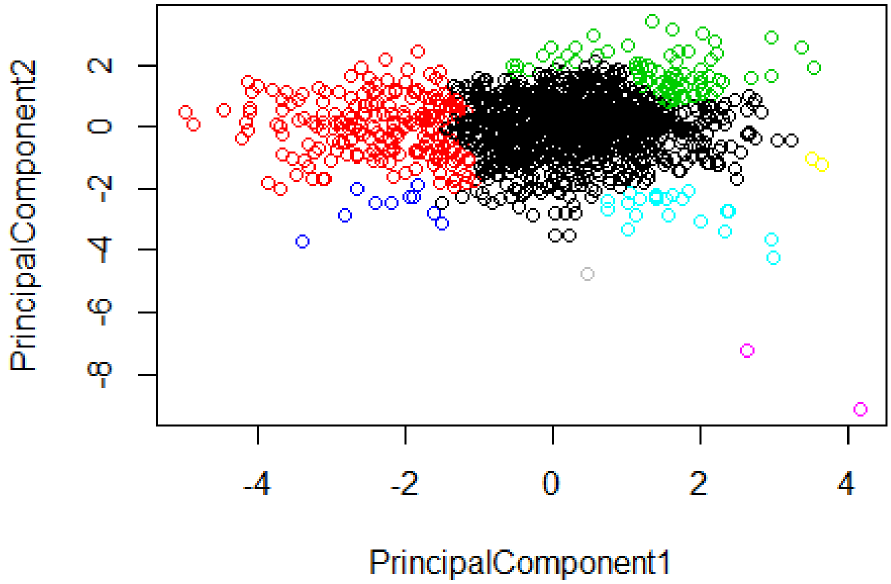
```
table(clusterCut, yeast$LocalizationSite)
```

```
## 
## clusterCut CYT ERL EXC ME1 ME2 ME3 MIT NUC POX VAC
##          1 411   0   4   0  14 130 194 358  17  21
##          2  16   5  25  43  36  19  46  10   3   9
##          3  16   0   0   0   0  14   2  49   0   0
##          4   0   0   6   1   1   0   0   2   0   0
##          5  17   0   0   0   0   0   1   8   0   0
##          6   3   0   0   0   0   0   0   0   0   0
##          7   0   0   0   0   0   0   1   1   0   0
##          8   0   0   0   0   0   0   0   1   0   0
```

```
aggregate(yeast[, 2:9],by=list(clusterCut),mean)
```

```
##   Group.1       mcg       gvh       alm       mit       erl         pox
## 1       1 0.4715405 0.4762228 0.5104178 0.2522715 0.5013055 0.008964317
## 2       2 0.7120283 0.6790566 0.4296698 0.3211792 0.5188679 0.003915094
## 3       3 0.3545679 0.3871605 0.4807407 0.1697531 0.5185185 0.000000000
## 4       4 0.7750000 0.7390000 0.5210000 0.4280000 0.5000000 0.000000000
## 5       5 0.4115385 0.4076923 0.5992308 0.3080769 0.5000000 0.000000000
## 6       6 0.3766667 0.2133333 0.9300000 0.7966667 0.5000000 0.000000000
## 7       7 0.2350000 0.1700000 0.7000000 0.3100000 0.5000000 0.000000000
## 8       8 0.6600000 0.4300000 0.5700000 0.6000000 0.5000000 0.000000000
##         vac       nuc
## 1 0.5007659 0.268398607
## 2 0.5205189 0.248867925
## 3 0.5237037 0.497530864
## 4 0.3660000 0.241000000
## 5 0.3219231 0.200384615
## 6 0.1600000 0.006666667
## 7 0.4900000 0.230000000
## 8 0.1900000 0.330000000
```

```
plot(PrincipalComponent1, PrincipalComponent2, col=clusterCut)
```



```
# Show a random sample
set.seed(1234)
dplyr::sample_n(yeast, 10)
```

```
##       SequenceName  mcg  gvh  alm  mit erl  pox  vac  nuc LocalizationSite
## 169     CHS2_YEAST 0.39 0.42 0.38 0.40 0.5    0 0.49 0.47              ME3
## 923     RNA1_YEAST 0.45 0.52 0.50 0.12 0.5    0 0.60 0.22              CYT
## 903     R104_YEAST 0.44 0.33 0.55 0.16 0.5    0 0.49 0.22              NUC
## 924     RN12_YEAST 0.56 0.51 0.32 0.49 0.5    0 0.48 0.22              NUC
## 1275    TOP1_YEAST 0.41 0.42 0.53 0.17 0.5    0 0.48 0.58              NUC
## 948     RPB5_YEAST 0.40 0.30 0.57 0.13 0.5    0 0.46 0.22              NUC
## 15      ACR1_YEAST 0.66 0.55 0.45 0.19 0.5    0 0.46 0.22              MIT
## 344     GAL8_YEAST 0.60 0.60 0.49 0.30 0.5    0 0.53 0.22              NUC
## 984     RL34_YEAST 0.38 0.43 0.53 0.22 0.5    0 0.48 0.11              CYT
## 759     PT91_YEAST 0.59 0.45 0.58 0.21 0.5    0 0.49 0.22              MIT
```

```r
# Show the levels
levels(yeast$group)

## NULL

library(dplyr)
group_by(yeast, SequenceName) %>%
  summarise(
    count = n(),
    mean = mean(nuc, na.rm = TRUE),
    sd = sd(nuc, na.rm = TRUE)
  )

## # A tibble: 1,462 x 4
##    SequenceName count  mean    sd
##    <chr>        <int> <dbl> <dbl>
##  1 6P2K_YEAST       1 0.3     NaN
##  2 6PGD_YEAST       1 0.31    NaN
##  3 AAR2_YEAST       1 0.22    NaN
##  4 AATC_YEAST       1 0.22    NaN
##  5 AATM_YEAST       1 0.22    NaN
##  6 ABC1_YEAST       1 0.22    NaN
##  7 ABF2_YEAST       1 0.22    NaN
##  8 ABP1_YEAST       1 0.3     NaN
##  9 ACE1_YEAST       1 0.27    NaN
## 10 ACE2_YEAST       1 0.290   NaN
## # ... with 1,452 more rows
```

c. Perform ANOVA test on the discriminant analysis scores of nuclear localization signals of both nuclear and non-nuclear proteins by class variables (Target).

d. Which class is significantly different from others?

```r
# Compute the analysis of variance
res.aov<-aov(nuc~ LocalizationSite,data=yeast)
summary(res.aov)

##                    Df Sum Sq Mean Sq F value Pr(>F)
## LocalizationSite    9  1.993 0.22141   22.01 <2e-16 ***
## Residuals        1474 14.825 0.01006
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

res.aov <- aov(nuc ~ vac, data = yeast)
# Summary of the analysis
summary(res.aov)
```

```
##                Df Sum Sq Mean Sq F value   Pr(>F)    
## vac             1  0.135 0.13529   12.02 0.000542 ***
## Residuals    1482 16.682 0.01126                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
res.aov <- aov(nuc ~ pox, data = yeast)
summary(res.aov)
```

```
##                Df Sum Sq Mean Sq F value Pr(>F)
## pox             1  0.021 0.02138   1.887   0.17
## Residuals    1482 16.796 0.01133
```

```
res.aov <- aov(nuc ~ erl, data = yeast)
summary(res.aov)
```

```
##                Df Sum Sq  Mean Sq F value Pr(>F)
## erl             1   0.00 0.000135   0.012  0.913
## Residuals    1482  16.82 0.011348
```

```
res.aov <- aov(nuc ~mit , data = yeast)
summary(res.aov)
```

```
##                Df Sum Sq Mean Sq F value Pr(>F)  
## mit             1   0.05 0.05050   4.463 0.0348 *
## Residuals    1482  16.77 0.01131                 
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
res.aov <- aov(nuc ~alm , data = yeast)
summary(res.aov)
```

```
##                Df Sum Sq  Mean Sq F value Pr(>F)
## alm             1  0.008 0.008171    0.72  0.396
## Residuals    1482 16.809 0.011342
```

```
res.aov <- aov(nuc ~gvh , data = yeast)
summary(res.aov)
```

```
##                Df Sum Sq Mean Sq F value   Pr(>F)    
## gvh             1  0.178 0.17836   15.89 7.05e-05 ***
## Residuals    1482 16.639 0.01123                     
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
res.aov <- aov(nuc ~ mcg, data = yeast)
summary(res.aov)
```

```
##                Df Sum Sq Mean Sq F value   Pr(>F)    
## mcg             1  0.261 0.26085   23.35 1.49e-06 ***
## Residuals    1482 16.557 0.01117
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```