Clustering

Group 10 (Umar, Cory, Caroline, Benji)

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Source: https://www.kaggle.com/datasets/sulianova/cardiovascular-disease-dataset

This is a dataset based off of 70,000 records of patient data (Heart Related). Columns (13): ID, Age, Height(cm), Weight(kg), Gender, Systolic Blood Pressure (AP_HIGH), Diastolic Blood Pressure (AP LOW), Cholesterol, Glucose, Smoking, Alcohol Intake, Physical Activity, Presence or Absence of cardiovascular disease.

The .csv file needed to be edited a bit in Microsoft Excel before using it in R. I just performed a split column delimiter function around semicolons, to divide the singular column that existed into 13. Each row had 13 variables in 1 column separated by semicolons, the function I ran split it up into 13 columns, making a 70,000 x 13 table.

https://www.heart.org/en/health-topics/high-blood-pressure/understanding-blood-pressure-readings

Visit the website above to better understand Systolic and Diastolic Blood Pressure

Cleaning Data

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.1.3
```

```
library(flexclust)
```

```
## Warning: package 'flexclust' was built under R version 4.1.3

## Loading required package: grid

## Loading required package: lattice

## Loading required package: modeltools

## Loading required package: stats4
```

```
library(mclust)
```

```
## Warning: package 'mclust' was built under R version 4.1.3

## Package 'mclust' version 5.4.10
## Type 'citation("mclust")' for citing this R package in publications.
```

```r
# Read in .csv file
heart <- read.csv("cardio_train.csv")


# Clean out any rows that have an unrealistic blood pressure (AP_HIGH & AP_LOW)
# They looked to be input errors by the person who made the data set
s <- subset(heart, AP_HIGH > 50)

s1 <- subset(s, AP_HIGH < 200)

s2 <- subset(s1, AP_LOW > 25)

s3 <- subset(s2, AP_LOW < 200)


# Removing little people(4'10") and Giants(7'3"), values are in cm
s4 <- subset(s3, HEIGHT > 147)

s5 <- subset(s4, HEIGHT < 220)


# Removing anyone below 90 lbs and above 375 lbs, the values are in kg
s6 <- subset(s5, WEIGHT > 40)

h1 <- subset(s6, WEIGHT < 180)

# AGE is in days so to get years i just divide by 365
h1$AGE <- (h1$AGE / 365)

# Removing people under 40
h <- subset(h1, AGE > 39)

# Checking for any NA values
# There is none
colSums(is.na(h))
```

```
##                ID               AGE            GENDER            HEIGHT
##                 0                 0                 0                 0
##            WEIGHT           AP_HIGH            AP_LOW       CHOLESTEROL
##                 0                 0                 0                 0
##           GLUCOSE             SMOKE           ALCOHOL PHYSICAL_ACTIVITY
##                 0                 0                 0                 0
##    CARDIO_DISEASE
##                 0
```

```r
# Everything that should be factored is factored
h$GENDER <- factor(h$GENDER)
h$CHOLESTEROL <- factor(h$CHOLESTEROL)
h$GLUCOSE <- factor(h$GLUCOSE)
h$SMOKE <- factor(h$SMOKE)
h$ALCOHOL <- factor(h$ALCOHOL)
h$PHYSICAL_ACTIVITY <- factor(h$PHYSICAL_ACTIVITY)
h$CARDIO_DISEASE <- factor(h$CARDIO_DISEASE)
```

```r
# There is now 67,685 rows

str(h)
```

```
## 'data.frame':    67685 obs. of  13 variables:
##  $ ID                : int  0 1 2 3 4 8 9 12 13 14 ...
##  $ AGE               : num  50.4 55.4 51.7 48.3 47.9 ...
##  $ GENDER            : Factor w/ 2 levels "1","2": 2 1 1 2 1 1 1 2 1 1 ...
##  $ HEIGHT            : int  168 156 165 169 156 151 157 178 158 164 ...
##  $ WEIGHT            : num  62 85 64 82 56 67 93 95 71 68 ...
##  $ AP_HIGH           : int  110 140 130 150 100 120 130 130 110 110 ...
##  $ AP_LOW            : int  80 90 70 100 60 80 80 90 70 60 ...
##  $ CHOLESTEROL       : Factor w/ 3 levels "1","2","3": 1 3 3 1 1 2 3 3 1 1 ...
##  $ GLUCOSE           : Factor w/ 3 levels "1","2","3": 1 1 1 1 1 2 1 3 1 1 ...
##  $ SMOKE             : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ ALCOHOL           : Factor w/ 2 levels "0","1": 1 1 1 1 1 1 1 1 1 1 ...
##  $ PHYSICAL_ACTIVITY: Factor w/ 2 levels "0","1": 2 2 1 2 1 1 2 2 2 1 ...
##  $ CARDIO_DISEASE    : Factor w/ 2 levels "0","1": 1 2 2 2 1 1 1 2 1 1 ...
```

Kmean Clusters

Determining how many numbers of clusters to use for the data

```r
# Function for finding optimal number of clusters

hplot <- function(data, nc = 15, seed = 2354)
{
  hss <- (nrow(h) - 1) * sum(apply(h, 2, var))
  for (i in 2:nc)
  {
    set.seed(seed)
    hss[i] <- sum(kmeans(h, centers = i)$withinss)
  }
  plot(1:nc, hss, type = "b", xlab = "Number of Clusters",
       ylab = "Within groups sum of squares")
}

# Show graph

hplot(h)
```

```
## Warning: Quick-TRANSfer stage steps exceeded maximum (= 3384250)

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```
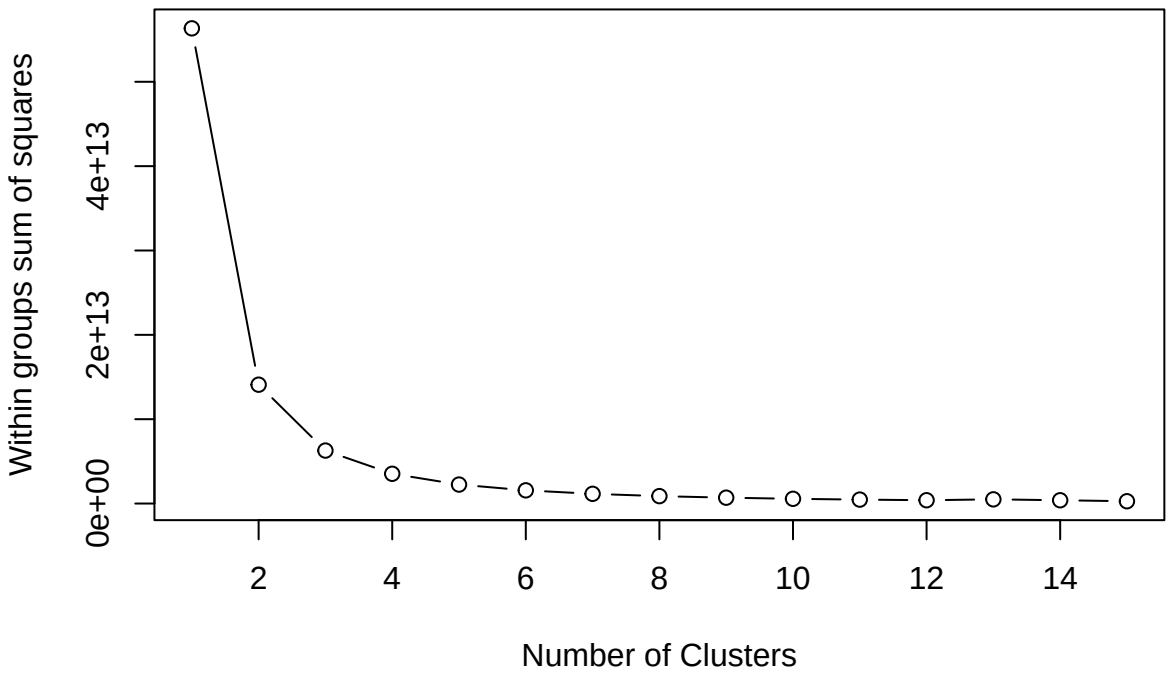




```
cat("Looking at the graph, three seems to be the optimal number of clusters.\n
That's where the 'elbow' is.")
```

```
## Looking at the graph, three seems to be the optimal number of clusters.
##
## That's where the 'elbow' is.
```

Making the kmean clusters based off of 3 clusters

```
# Set unique and repeatable random variable

set.seed(2354)

# Clustering off of Systolic and Diastolic blood pressure

heartCluster <- kmeans(h[, 6:7], 3, nstart = 20)

# Data is too large to show the summary for

cat("K-means clustering with 3 clusters of sizes 12542, 18119, 37024

Cluster means:
   AP_HIGH   AP_LOW
1 106.5830 70.24629
2 148.3140 90.72096
```

```
3 122.4537 80.46778

Clustering vector:

[ reached getOption('max.print') -- omitted 66685 entries ]

Within cluster sum of squares by cluster:
[1] 1330107 3536136 1932918
 (between_SS / total_SS =  71.9 %)

Available components:

[1] 'cluster'      'centers'      'totss'        'withinss'
[5] 'tot.withinss' 'betweenss'    'size'         'iter'
[9] 'ifault'   ")
```

```
## K-means clustering with 3 clusters of sizes 12542, 18119, 37024
##
## Cluster means:
##    AP_HIGH   AP_LOW
## 1 106.5830 70.24629
## 2 148.3140 90.72096
## 3 122.4537 80.46778
##
## Clustering vector:
##
## [ reached getOption('max.print') -- omitted 66685 entries ]
##
## Within cluster sum of squares by cluster:
## [1] 1330107 3536136 1932918
##  (between_SS / total_SS =  71.9 %)
##
## Available components:
##
## [1] 'cluster'      'centers'      'totss'        'withinss'
## [5] 'tot.withinss' 'betweenss'    'size'         'iter'
## [9] 'ifault'
```

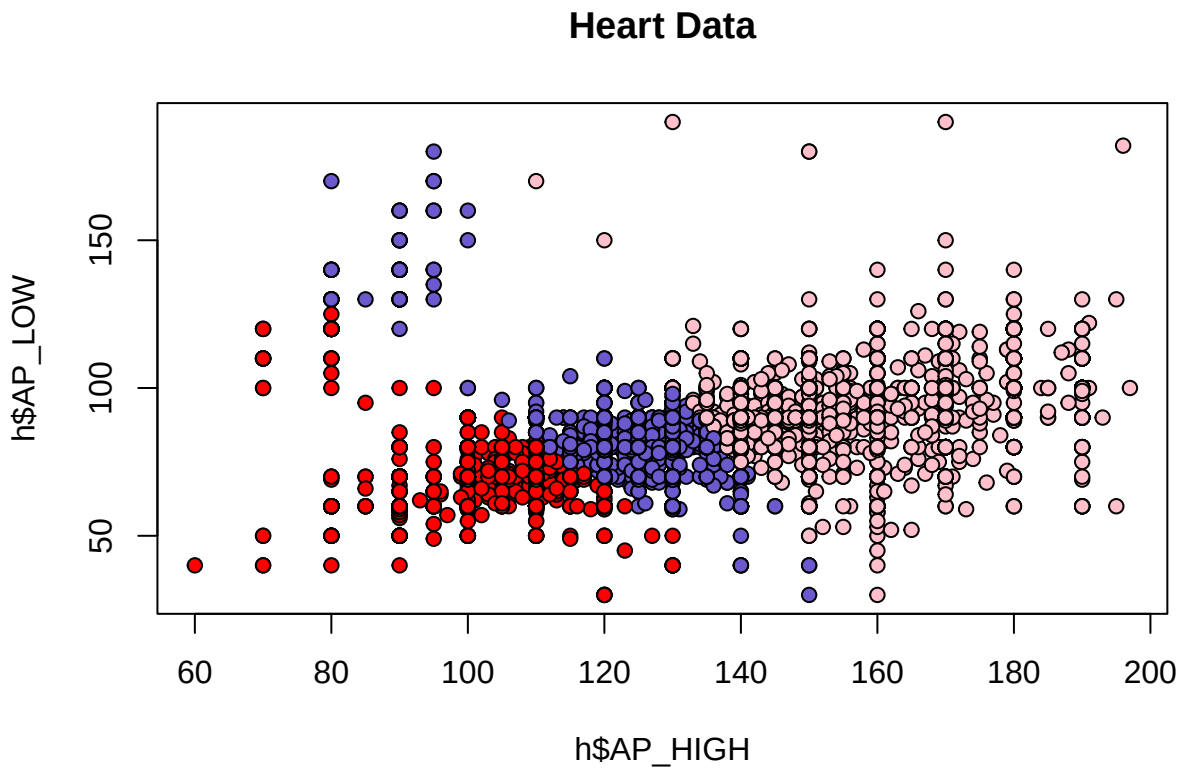
Looking at clusters through the lens of having heart disease

```
# Comparing the cluster and the presence of heart disease
# A '1' on the x-axis means they have heart disease

table(heartCluster$cluster, h$CARDIO_DISEASE)
```

```
##
##         0     1
##   1  9621  2921
##   2  2976 15143
##   3 21662 15362
```

Displaying clusters on scatter plot

```
# Plotting the clusters on a scatter plot

plot(h$AP_HIGH, h$AP_LOW, pch = 21, bg = c("red", "pink", "slateblue")
     [unclass(heartCluster$cluster)], main = "Heart Data")
```



Hierarchical Clustering

```
# Removing any categorical data and ID's

hrt <- subset(h, select = -c(ID, GENDER, CHOLESTEROL, GLUCOSE, SMOKE, ALCOHOL,
                             PHYSICAL_ACTIVITY, CARDIO_DISEASE))

# Limiting data points to 50 for the sake of the visibility of the table

hrt <- hrt[1:50,]

# Displaying new table

head(hrt)
```

```
##        AGE HEIGHT WEIGHT AP_HIGH AP_LOW
## 1 50.39178    168     62     110     80
## 2 55.41918    156     85     140     90
```

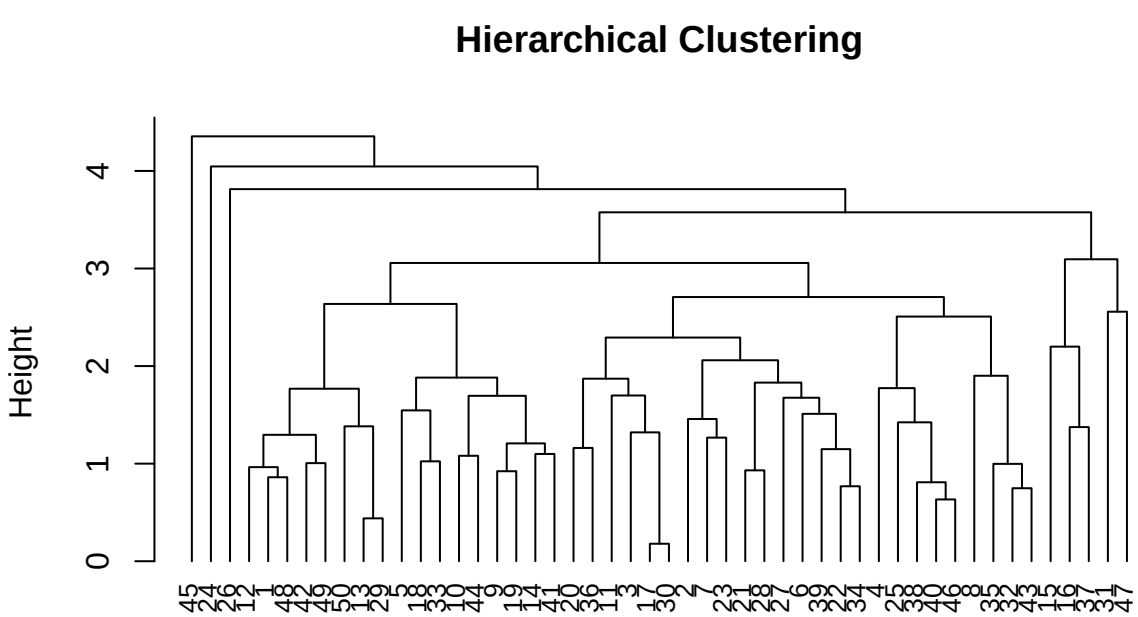
```
## 3 51.66301    165     64     130     70
## 4 48.28219    169     82     150    100
## 5 47.87397    156     56     100     60
## 6 60.03836    151     67     120     80
```

```r
# Scaling the data

hrt.scaled <- scale(hrt)

head(hrt.scaled)
```

```
##          AGE     HEIGHT     WEIGHT    AP_HIGH      AP_LOW
## 1 -0.2993365  0.5634783 -0.7089041 -1.1066532  0.04066093
## 2  0.4338026 -1.0619399  0.8588646  1.0352563  1.05718406
## 3 -0.1139542  0.1571238 -0.5725764  0.3212864 -0.97586221
## 4 -0.6069752  0.6989298  0.6543730  1.7492261  2.07370719
## 5 -0.6665053 -1.0619399 -1.1178873 -1.8206231 -1.99238534
## 6  1.1074115 -1.7391974 -0.3680848 -0.3926834  0.04066093
```

Displaying Hierarchical Graph (Dendogram)

```r
# Finding the distances between each data point

di <- dist(hrt.scaled)

fit.average <- hclust(di, method = "average")

plot(fit.average, hang = -1, cex = .8, main = "Hierarchical Clustering")
```



Cutting data

```
# Learning more about the data through cutting

# SIDENOTE: Hierarchical Clustering isn't the easiest to understand, but is good
# for learning more about your data

for (c in 3:11)
{
  cluster_cut <- cutree(fit.average, c)
  table_cut <- table(cluster_cut, hrt$AP_LOW)
  print(table_cut)
  ri <- randIndex(table_cut)
  print(paste("cut=", c, "Rand Index = ", ri))
}
```

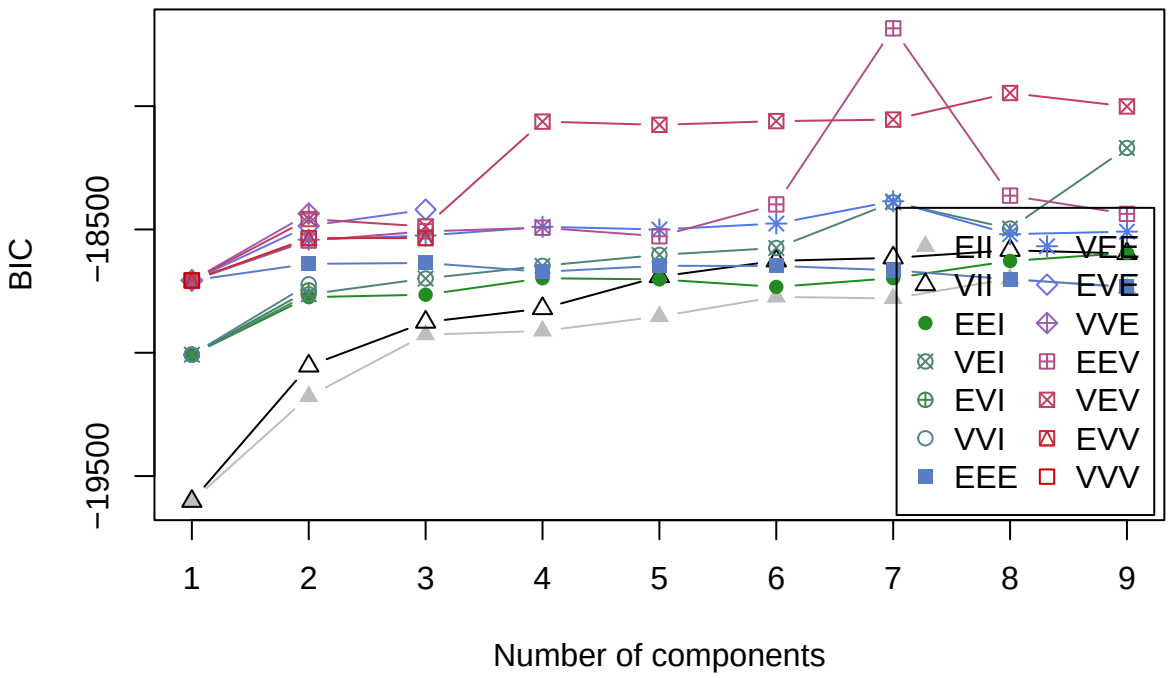
```
##
## cluster_cut 60 70 80 85 90 100
##           1  3 11 18  2 12   2
##           2  1  0  0  0  0   0
##           3  0  0  1  0  0   0
## [1] "cut= 3 Rand Index =  0.00629370629370629"
##
## cluster_cut 60 70 80 85 90 100
##           1  3 11 18  2 12   1
##           2  1  0  0  0  0   0
```

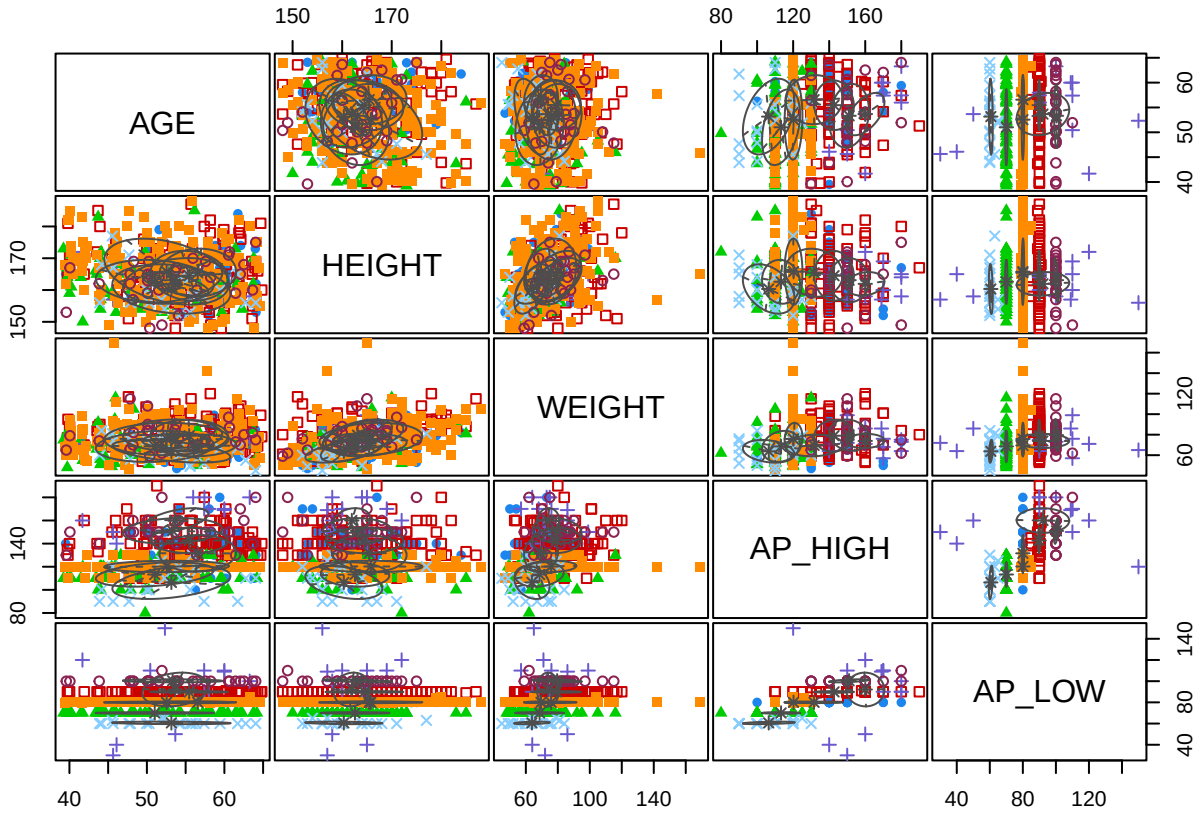
```
##           3  0  0  0  0  0   1
##           4  0  0  1  0  0   0
## [1] "cut= 4 Rand Index =  0.0311563810665069"
##
## cluster_cut 60 70 80 85 90 100
##           1  3 11 15  2 10   1
##           2  0  0  3  0  2   0
##           3  1  0  0  0  0   0
##           4  0  0  0  0  0   1
##           5  0  0  1  0  0   0
## [1] "cut= 5 Rand Index =  -0.000822481151473578"
##
## cluster_cut 60 70 80 85 90 100
##           1  3 11 15  2 10   1
##           2  0  0  2  0  1   0
##           3  1  0  0  0  0   0
##           4  0  0  0  0  0   1
##           5  0  0  1  0  1   0
##           6  0  0  1  0  0   0
## [1] "cut= 6 Rand Index =  -0.00495526496902962"
##
## cluster_cut 60 70 80 85 90 100
##           1  3  7  7  0  0   0
##           2  0  4  8  2 10   1
##           3  0  0  2  0  1   0
##           4  1  0  0  0  0   0
##           5  0  0  0  0  0   1
##           6  0  0  1  0  1   0
##           7  0  0  1  0  0   0
## [1] "cut= 7 Rand Index =  0.0695719844357977"
##
## cluster_cut 60 70 80 85 90 100
##           1  3  7  7  0  0   0
##           2  0  4  8  2  2   0
##           3  0  0  0  0  8   1
##           4  0  0  2  0  1   0
##           5  1  0  0  0  0   0
##           6  0  0  0  0  0   1
##           7  0  0  1  0  1   0
##           8  0  0  1  0  0   0
## [1] "cut= 8 Rand Index =  0.166334841628959"
##
## cluster_cut 60 70 80 85 90 100
##           1  0  1  7  0  0   0
##           2  0  4  8  2  2   0
##           3  0  0  0  0  8   1
##           4  3  6  0  0  0   0
##           5  0  0  2  0  1   0
##           6  1  0  0  0  0   0
##           7  0  0  0  0  0   1
##           8  0  0  1  0  1   0
##           9  0  0  1  0  0   0
## [1] "cut= 9 Rand Index =  0.237241379310345"
##
```

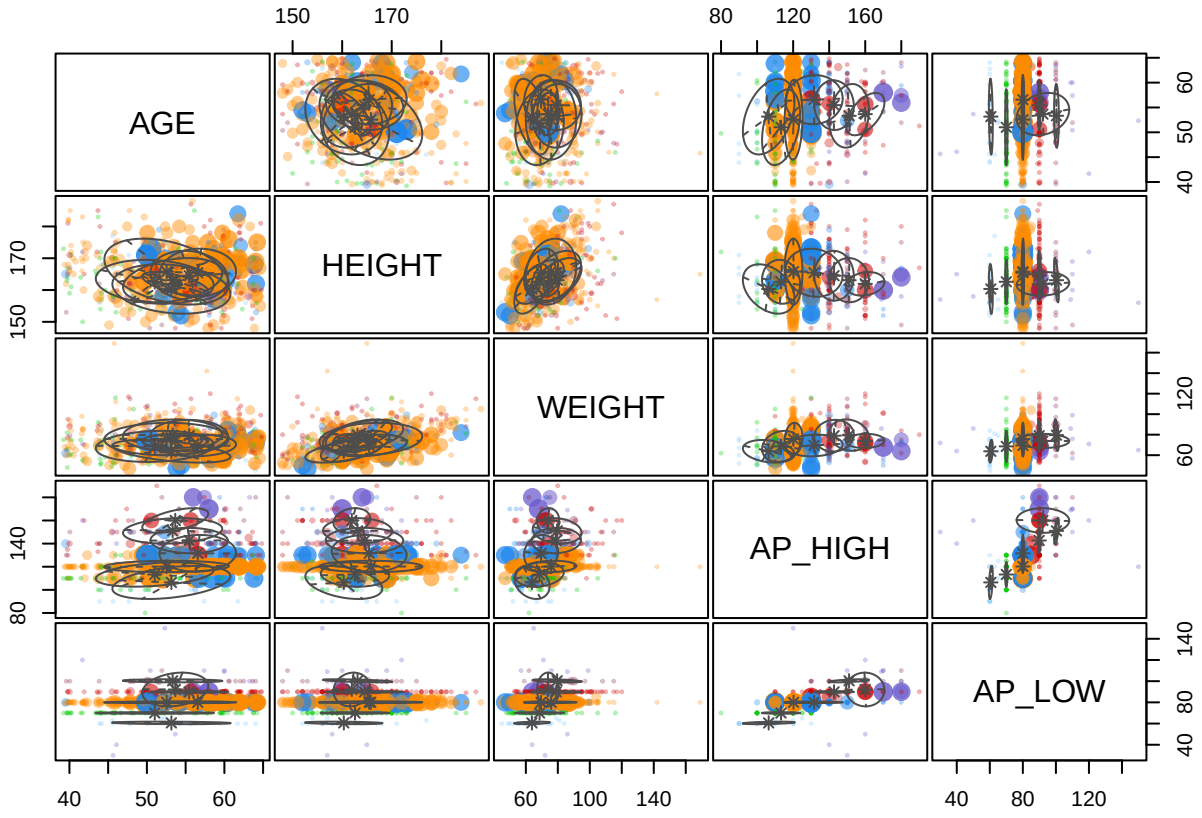
```
## cluster_cut 60 70 80 85 90 100
##           1   0  1  7  0  0   0
##           2   0  4  8  2  2   0
##           3   0  0  0  0  8   1
##           4   3  6  0  0  0   0
##           5   0  0  2  0  1   0
##           6   1  0  0  0  0   0
##           7   0  0  0  0  0   1
##           8   0  0  1  0  0   0
##           9   0  0  1  0  0   0
##           10  0  0  0  0  1   0
## [1] "cut= 10 Rand Index =  0.238717632552404"
##
## cluster_cut 60 70 80 85 90 100
##           1   0  1  7  0  0   0
##           2   0  4  8  2  2   0
##           3   0  0  0  0  4   1
##           4   3  6  0  0  0   0
##           5   0  0  0  0  4   0
##           6   0  0  2  0  1   0
##           7   1  0  0  0  0   0
##           8   0  0  0  0  0   1
##           9   0  0  1  0  0   0
##           10  0  0  1  0  0   0
##           11  0  0  0  0  1   0
## [1] "cut= 11 Rand Index =  0.189734513274336"
```

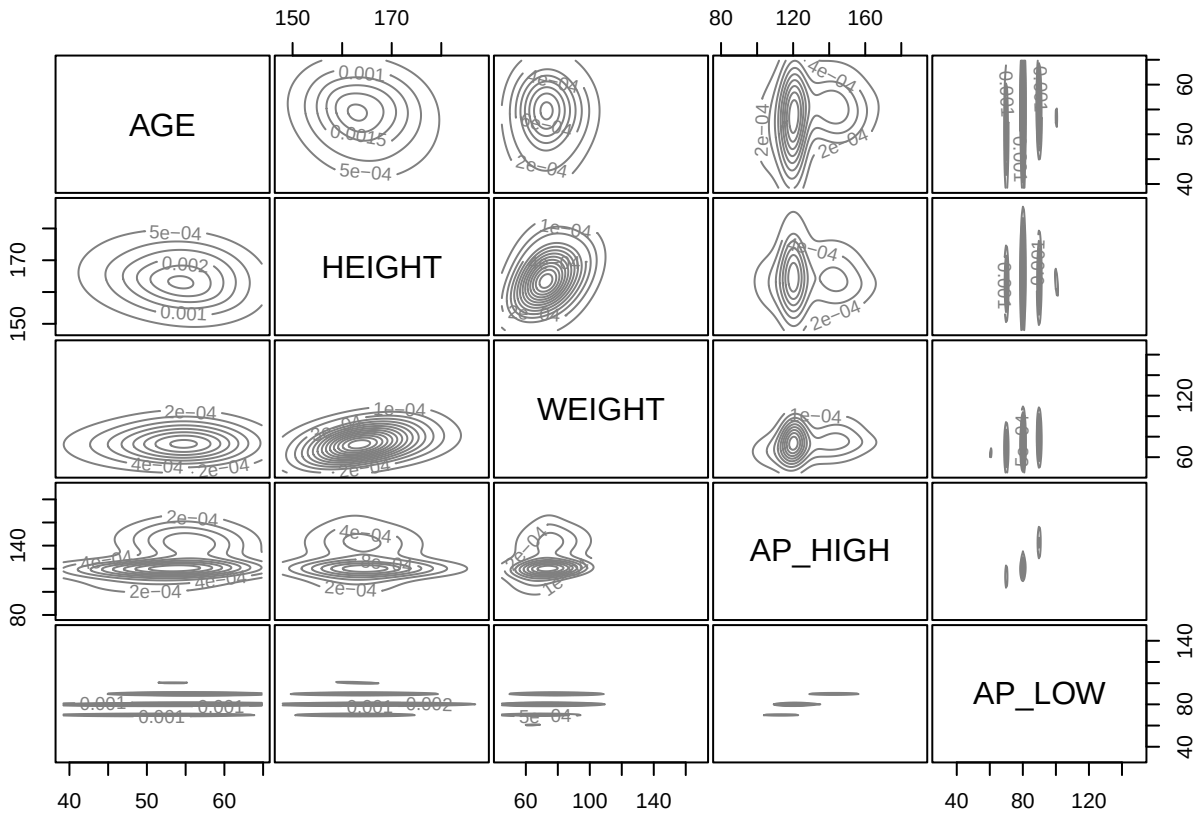
Model Based

```
# Shrink data set to 500 for the sake of the algorithms

hhrt <- subset(h[1:500,], select = -c(ID, GENDER, CHOLESTEROL, GLUCOSE, SMOKE, ALCOHOL,
                              PHYSICAL_ACTIVITY, CARDIO_DISEASE))

fitt <- Mclust(hhrt)

# Plot results

plot(fitt)
```


BIC
−18500
−19500
1
2
3
4
5
6
7
8
9
Number of components
EII
VII
EEI
VEI
EVI
VVI
EEE
VEE
EVE
VVE
EEV
VEV
EVV
VVV


AGE
HEIGHT
WEIGHT
AP_HIGH
AP_LOW
150
170
80
120
160
40
50
60
150
170
60
120
80
140
40
50
60
60
100
140
40
80
120
40
50
60
80
140


AGE
HEIGHT
WEIGHT
AP_HIGH
AP_LOW
150
170
80
120
160
40
50
60
150
170
60
120
80
140
40
80
140
40
50
60
60
100
140
40
80
120




```
# Display the best model

summary(fitt)
```

```
## ----------------------------------------------------
## Gaussian finite mixture model fitted by EM algorithm
## ----------------------------------------------------
##
## Mclust EEV (ellipsoidal, equal volume and shape) model with 7 components:
##
##  log-likelihood   n  df       BIC       ICL
##       -8481.832 500 116 -17684.56 -17765.93
##
## Clustering table:
##   1   2   3   4   5   6   7
##  50 113  76  13 198  21  29
```

```
cat("The first one is the BIC graph, it suggests EEV with 7 groups, based on the
\nhighest BIC value and the number of components it intersects with. The summary
\nof the model also suggests the same thing. Classification, uncertainty, and
\ndensity all have a very similar looking graphs. They just show correlation
\non a scatterplot matrix. Unsurprisingly, age and height seem to have very
\nlittle correlation, due to the age range of the data (40 - 65), and systolic
\nand diastolic blood pressure have the most correlation.")
```

```
## The first one is the BIC graph, it suggests EEV with 7 groups, based on the
##
## highest BIC value and the number of components it intersects with. The summary
##
## of the model also suggests the same thing. Classification, uncertainty, and
##
## density all have a very similar looking graphs. They just show correlation
##
## on a scatterplot matrix. Unsurprisingly, age and height seem to have very
##
## little correlation, due to the age range of the data (40 - 65), and systolic
##
## and diastolic blood pressure have the most correlation.
```