

PROJECT 3 STAT 5474

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PART II

(i) Read the data into R. List the missing rate (in percentage) for each variable.

```
dat <- read.csv("HMEQ.csv")
dim(dat)
```

```
## [1] 5960 13
```

Comment

The dimesion is 5960 rows and 13 variables

```
miss.perc <- function(dat, filename=NULL){
  vnames <- colnames(dat); vnames
  n <- nrow(dat)
  out <- NULL
  for (j in 1: ncol(dat)){
    vname <- colnames(dat)[j]
    x <- as.vector(dat[,j])
    n1 <- sum(is.na(x), na.rm=T)
    n2 <- sum(x=="NA", na.rm=T)
    n3 <- sum(x=="", na.rm=T)
    nmiss <- n1 + n2 + n3
    ncomplete <- n-nmiss
    out <- rbind(out, c(col.number=j, vname=vname,
                        mode=mode(x), n.levels=length(unique(x)),
                        ncomplete=ncomplete, miss.perc=nmiss/n))
  }
  out <- as.data.frame(out)
  row.names(out) <- NULL
  if (!is.null(filename)) write.csv(out, file = filename, row.names=F)
  return(out)
}
miss.perc(dat)
```

##	col.number	vname	mode	n.levels	ncomplete	miss.perc
## 1	1	BAD	numeric	2	5960	0
## 2	2	LOAN	numeric	540	5960	0
## 3	3	MORTDUE	numeric	5054	5442	0.0869127516778524
## 4	4	VALUE	numeric	5382	5848	0.0187919463087248
## 5	5	REASON	character	3	5708	0.0422818791946309
## 6	6	JOB	character	7	5681	0.0468120805369127
## 7	7	YOJ	numeric	100	5445	0.0864093959731544
## 8	8	DEROG	numeric	12	5252	0.118791946308725
## 9	9	DELINQ	numeric	15	5380	0.0973154362416107
## 10	10	CLAGE	numeric	5315	5652	0.0516778523489933
## 11	11	NINQ	numeric	17	5450	0.0855704697986577
## 12	12	CLNO	numeric	63	5738	0.037248322147651
## 13	13	DEBTINC	numeric	4694	4693	0.21258389261745

Comment

From the output we have DEBTINC has the highest percentage of missing values that is 21.258%. The variables “BAD” and “LOAN” have no missing values.

(ii)

(a) Replace missing values for both JOB and REASON with default constant “Unknown”. Output the frequency table after the replacement

```
dat$JOB[dat$JOB==""] <- "Unknown"
dat$REASON[dat$REASON==""] <- "Unknown"

table(dat$JOB)
```

##	Mgr	Office	Other	ProfExe	Sales	Self	Unknown
##	767	948	2388	1276	109	193	279

```
table(dat$REASON)
```

##	DebtCon	HomeImp	Unknown
##	3928	1780	252

Comment

Mgr Office Other ProfExe Sales Self Unknown

767 948 2388 1276 109 193 279

DebtCon HomeImp Unknown

3928 1780 252

From the above tables, we see that the missing values for the variables

“JOB” and “REASON” have been replaced with unknown. We replaced 279 missing ## values with unknow for the variable “JOB” and 252 for the variable “REASON”.

(b)

Perform the (natural) logarithm transformation on the following

variables: LOAN, VALUE, MORTDUE, YOJ, and CLAGE. If a variable has value 0, then try $\log(x+1)$ for the transformation.

```
log.transf <- function(x)
{
  a <- x
  if(sum(a==0, na.rm=TRUE) > 1)
  {
    x <- log(a+1)
  }
  else
  {
    x <- log(a)
  }
  return(x)
}
```

```
dat$LOAN <- log.transf(dat$LOAN)
head(dat$LOAN, 10)
```

```
## [1] 7.003065 7.170120 7.313220 7.313220 7.438384 7.438384 7.495542 7.495542
## [9] 7.600902 7.600902
```

```
dat$VALUE <- log.transf(dat$VALUE)
head(dat$VALUE, 10)
```

```
## [1] 10.571958 11.133128 9.723164 NA 11.626254 10.604603 10.951455
## [8] 10.669746 10.752356 11.038914
```

```
dat$MORTDUE <- log.transf(dat$MORTDUE)
head(dat$MORTDUE, 10)
```

```
## [1] 10.160453 11.157007 9.510445 NA 11.490680 10.327054 10.792387
## [8] 10.257730 10.395130 NA
```

```
dat$Y0J <- log.transf(dat$Y0J)
head(dat$Y0J, 10)
```

```
## [1] 2.442347 2.079442 1.609438 NA 1.386294 2.302585 1.791759 2.484907
## [9] 1.386294 2.833213
```

```
dat$CLAGE <- log.transf(dat$CLAGE)
head(dat$CLAGE, 10)
```

```
## [1] 4.557729 4.810828 5.013742 NA 4.546835 4.629531 4.357990 4.497207
## [9] 5.384189 4.760463
```

(c)

Impute all the remaining values with an appropriate imputation

procedure of your choice

```
library(mice)
```

```
## Registered S3 methods overwritten by 'tibble':
##   method      from
##   format.tbl  pillar
##   print.tbl   pillar
```

```
##
## Attaching package: 'mice'
```

```
## The following object is masked from 'package:stats':
##
##   filter
```

```
## The following objects are masked from 'package:base':
##
##   cbind, rbind
```

```
imputed.dat <- mice(dat, m=1, maxit = 50, method = 'pmm', seed = 500)
```

[illegible]

```
## Warning: Number of logged events: 2
```

```
summary(imputed.dat)
```

```
## Class: mids
## Number of multiple imputations: 1
## Imputation methods:
##      BAD      LOAN MORTDUE  VALUE REASON      JOB      YOJ      DEROG  DELINQ  CLAGE
##      ""      ""      "pmm"  "pmm"      ""      ""      "pmm"  "pmm"  "pmm"  "pmm"
##      NINQ     CLNO DEBTINC
##      "pmm"    "pmm"  "pmm"
## PredictorMatrix:
##      BAD LOAN MORTDUE VALUE REASON JOB YOJ DEROG DELINQ CLAGE NINQ CLNO
## BAD      0   1       1    1      0   0   1   1      1   1   1   1
## LOAN      1   0       1    1      0   0   1   1      1   1   1   1
## MORTDUE   1   1       0    1      0   0   1   1      1   1   1   1
## VALUE     1   1       1    0      0   0   1   1      1   1   1   1
## REASON    1   1       1    1      0   0   1   1      1   1   1   1
## JOB       1   1       1    1      0   0   1   1      1   1   1   1
##      DEBTINC
## BAD              1
## LOAN              1
## MORTDUE           1
## VALUE             1
## REASON            1
## JOB               1
## Number of logged events: 2
##   it im dep      meth   out
## 1  0  0      constant REASON
## 2  0  0      constant   JOB
```

```
dat.complete <- complete(imputed.dat, 1)
dat <- as.data.frame(dat.complete)
```

(iii) Distance Matrix

```
dat0 <- model.matrix(~.-1, data = dat.complete)
dim(dat0)
```

```
## [1] 5960 20
```

```
dat.1 <- as.data.frame(dat0)
```

Removing BAD because it's our outcome

```
dat.1 <- dat.1[, -1]
names(dat.1)
```

```
## [1] "LOAN" "MORTDUE" "VALUE" "REASONDebtCon"
```

```
## [5] "REASONHomeImp" "REASONUnknown" "JOBOffice" "JOBOther"
## [9] "JOBProfExe" "JOBSales" "JOBSelf" "JOBUnknown"
## [13] "YOJ" "DEROG" "DELINQ" "CLAGE"
## [17] "NINQ" "CLNO" "DEBTINC"
```

```
library(cluster)
library(gower)
Dist. <- daisy(dat.1, metric = "gower")
```

```
## Warning in daisy(dat.1, metric = "gower"): binary variable(s) 4, 5, 6, 7, 8, 9,
## 10, 11, 12 treated as interval scaled
```

```
summary(Dist.)
```

```
## 17757820 dissimilarities, summarized :
##      Min.   1st Qu.   Median     Mean   3rd Qu.     Max.
## 0.0002954 0.1315000 0.1708100 0.1778700 0.2454400 0.4550600
## Metric : mixed ; Types = I, I, I, I, I, I, I, I, I, I, I, I, I, I, I, I, I, I
## Number of objects : 5960
```

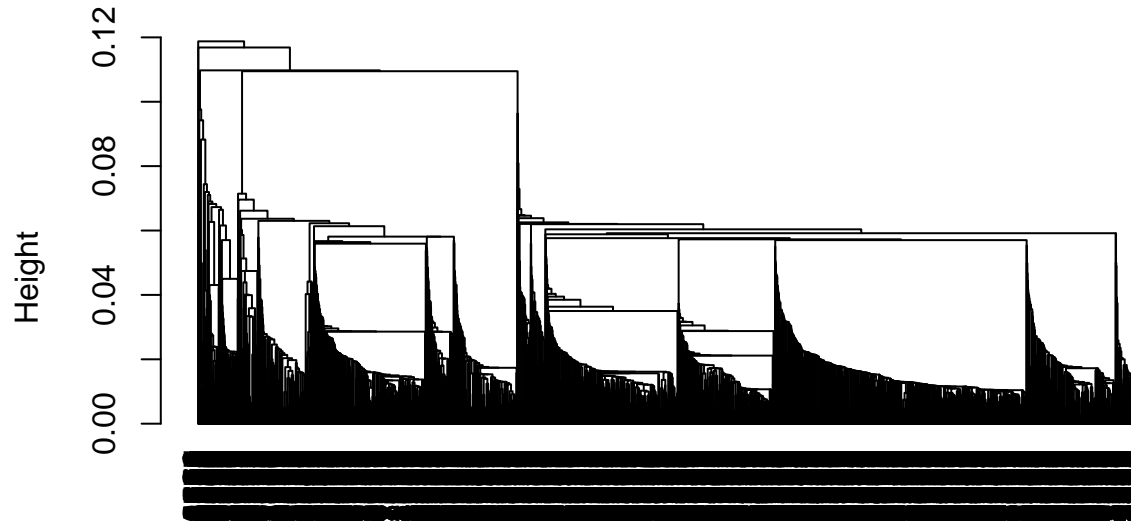
(iv) CLUSTER ANALYSIS

METHOD 1 : Hierarchial Clustering

First, we determine which of the hierarchial method to use.

```
library(cluster)
fit.single <- hclust(Dist., method="single")
fit.average <- hclust(Dist., method="average")
fit.complete <- hclust(Dist., method="complete")
plot(fit.single, hang = -0.5)
```

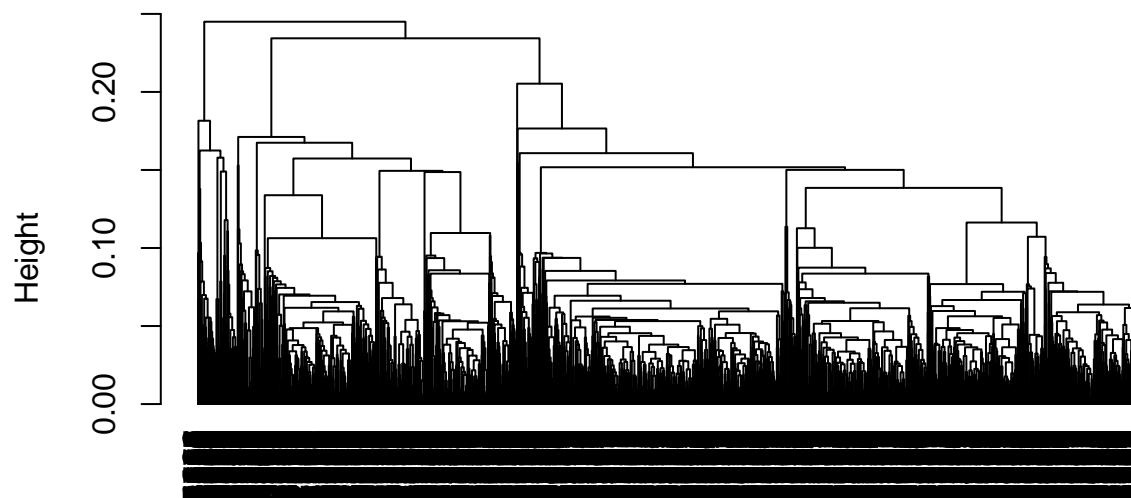
Cluster Dendrogram



Dist.
hclust (*, "single")

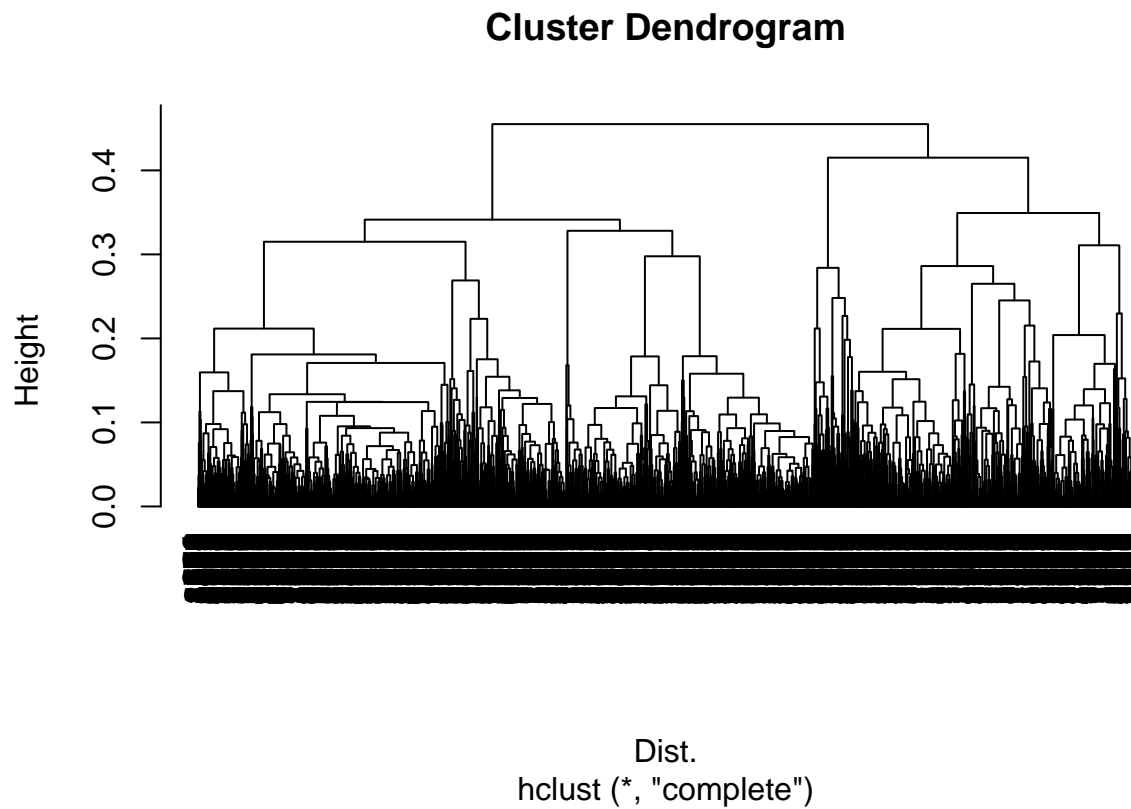
```
plot(fit.average, hang = -0.5)
```

Cluster Dendrogram



Dist.
hclust (*, "average")


```
plot(fit.complete, hang = -0.5)
```

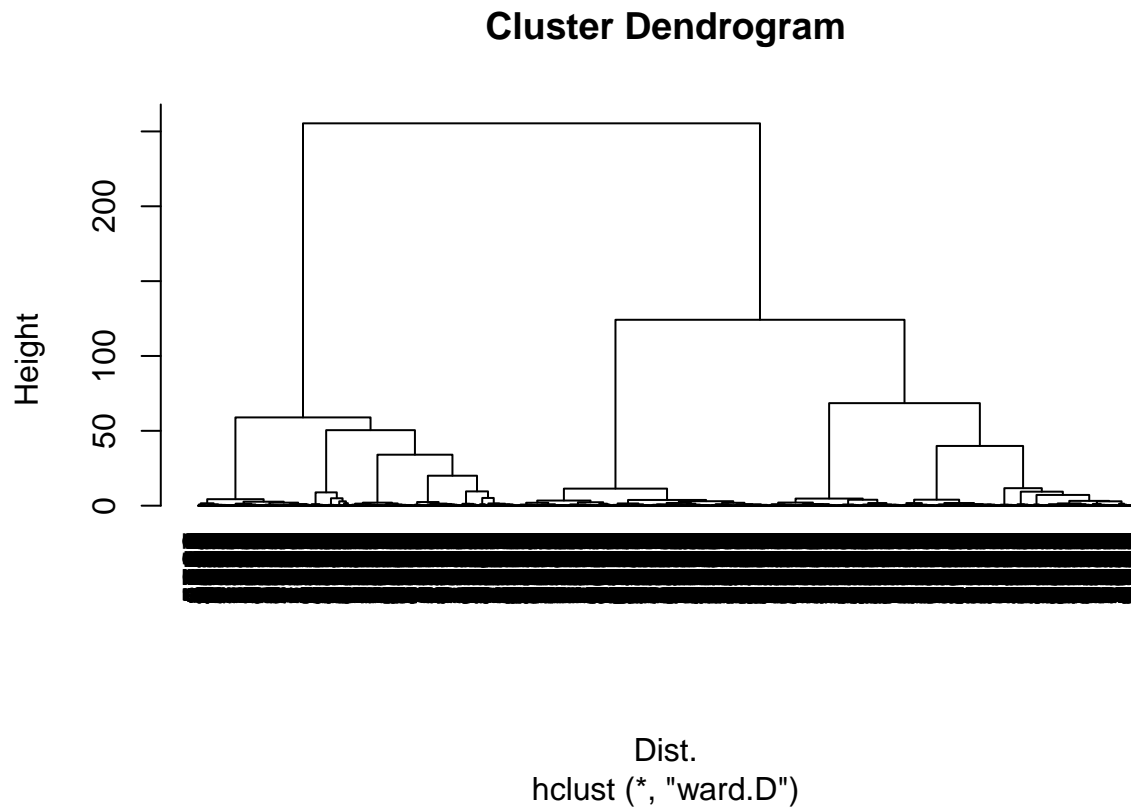


Comment

From the three cluster Dendrogram, we observe that the ward method gives a more clearer dendrogram that the number of clusters can clearly be determined from it.

Using the ward method

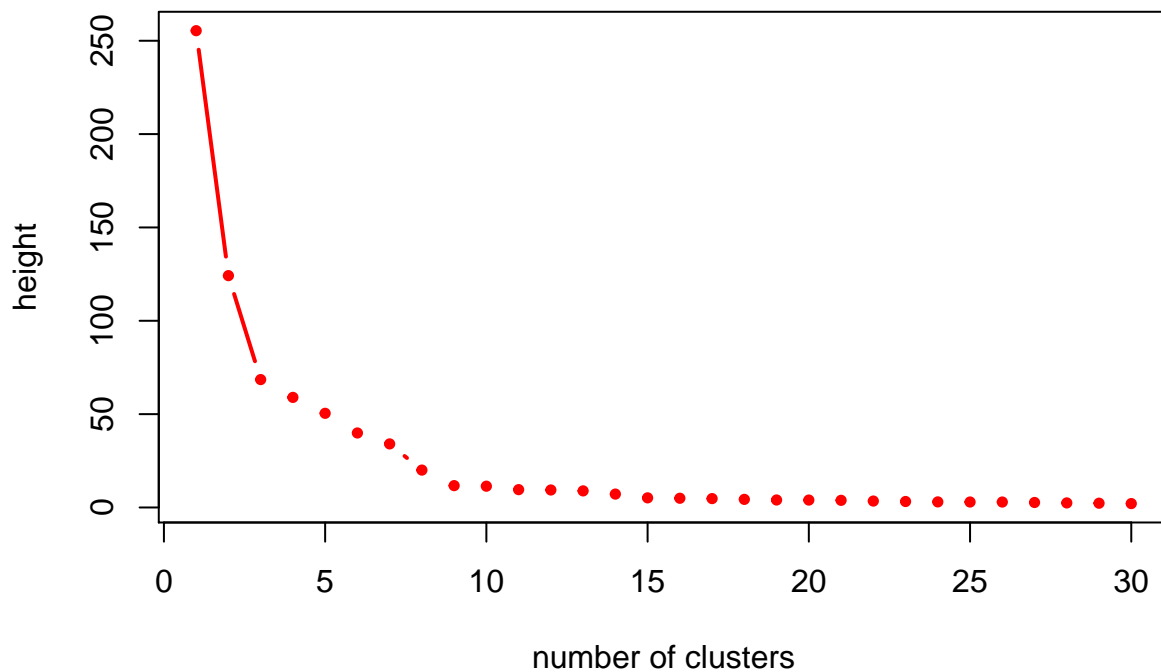
```
fit.ward.d2 <- hclust(Dist., method="ward.D")
plot(fit.ward.d2, hang = -0.5)
```



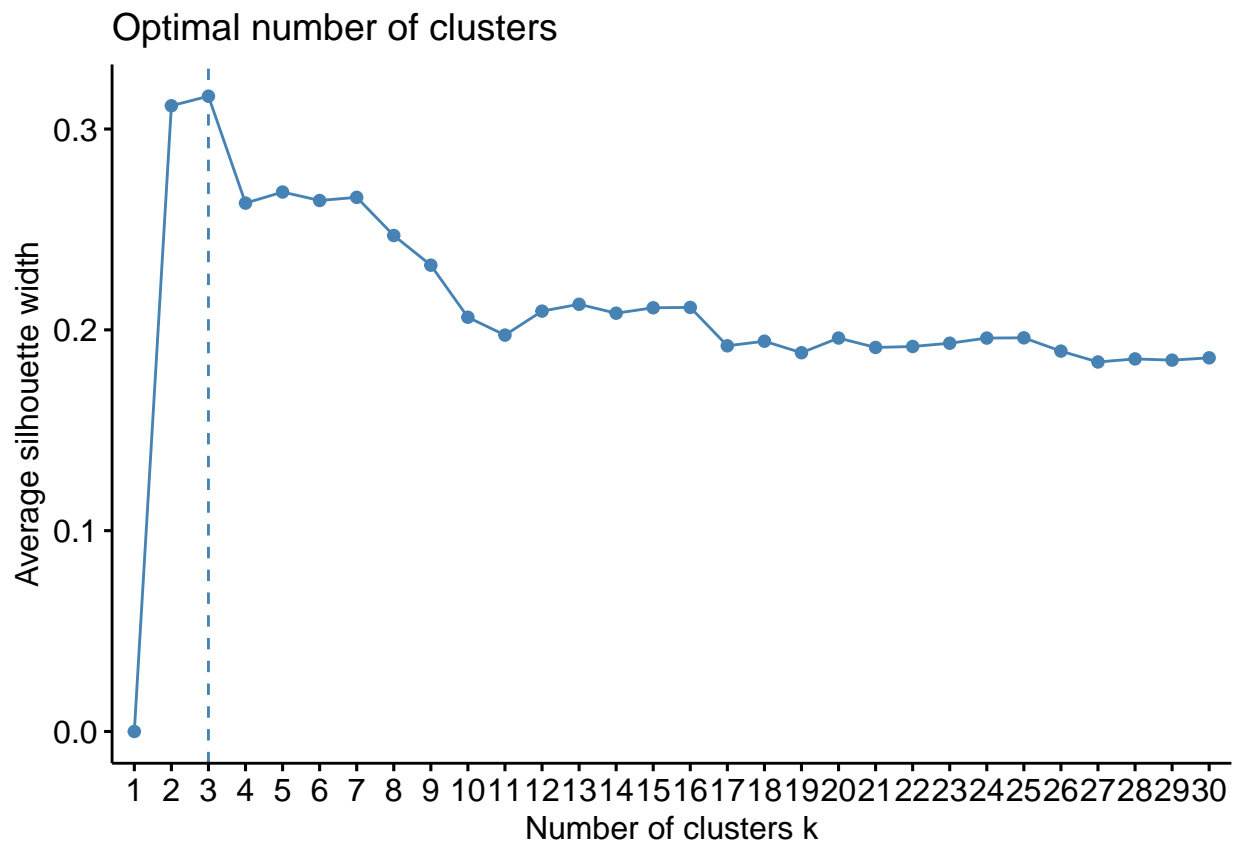
Determine Optimal Cluster

Screeplot of height in hierarchial clustering

```
K.max <- 30
height <- tail(fit.ward.d2$height, n=K.max)
n.cluster <- tail((nrow(dat.1)-1):1, n=K.max)
plot(n.cluster, height, type="b", pch=19, cex=.5, xlab="number of clusters",
      ylab="height", col="red", lwd=2)
```



```
suppressMessages(library(factoextra))
fviz_nbclust(x=dat.1, FUNcluster = hcut, method = c("silhouette"), diss = NULL, k.max = 30)
```



CLUSTER MEMBERSHIPS

```
hclust.groups <- cutree(fit.ward.d2, k=2)
table(hclust.groups)
```

```
## hclust.groups
##      1      2
## 2032 3928
```

Comment

hclust.groups

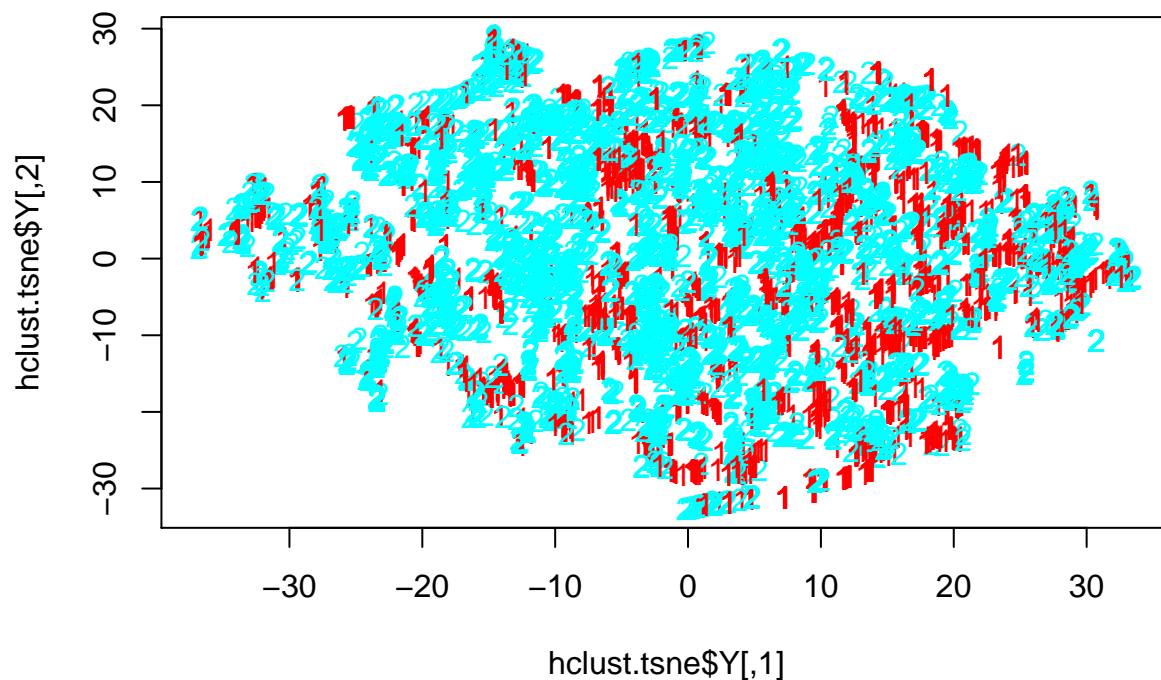
1 2

2032 3928

Plotting the data dat.1

```
library(Rtsne)
colors = rainbow(length(unique(hclust.groups)))
names(colors) = unique(hclust.groups)
hclust.tsne <- Rtsne(dat.1, dims=2, perplexity=30, max_iter=500)
plot(hclust.tsne$Y, t="n", main = "tSNE for Hierarchical Clustering")
text(hclust.tsne$Y, labels = hclust.groups, col = colors[hclust.groups])
```

tSNE for Hierarchical Clustering

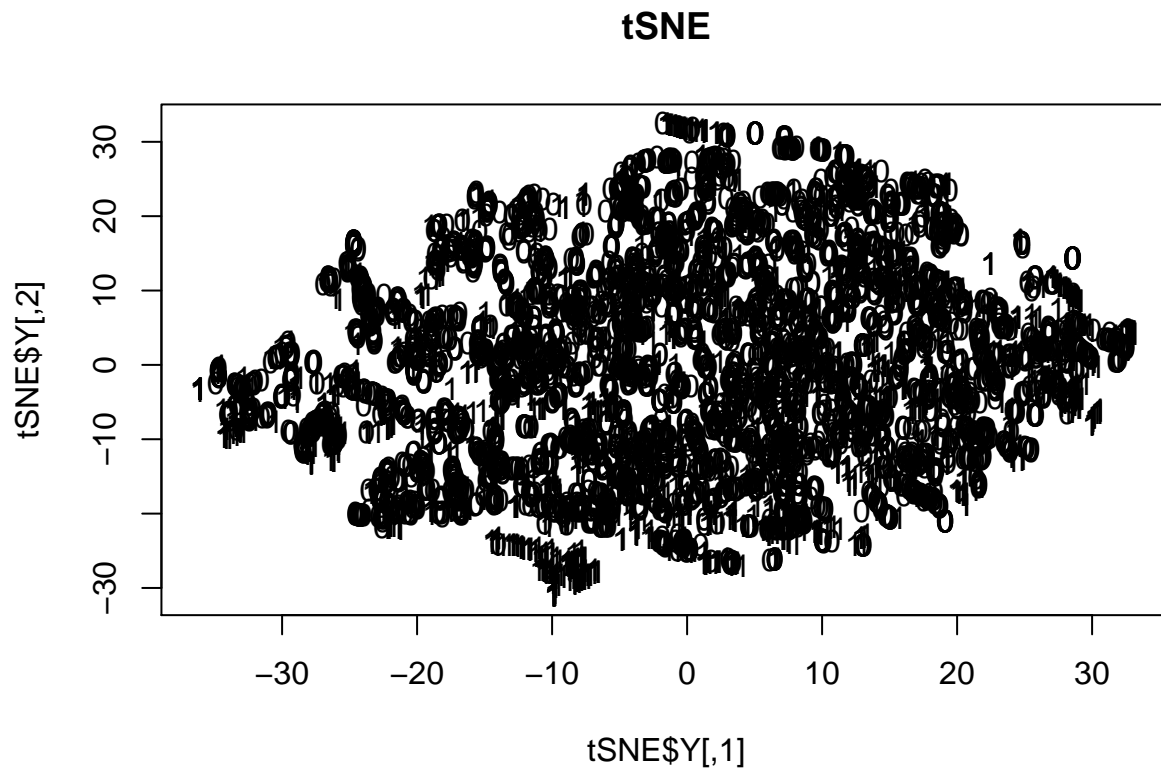


Plot the data using an MDS procedure (e.g., PCA or tSNE). Highlight both the `##` clustering memberships and the BAD value with different color and symbols.

```
BAD <- dat$BAD
BAD <- as.vector(dat$BAD)
dat.2 <- (cbind(dat0,BAD))
dat.2 <- data.frame(dat.2)
library(Rtsne)
tSNE <- Rtsne(dat0, dims=2, perplexity=30, verbose=TRUE, max_iter = 500)
```

```
## Performing PCA
## Read the 5960 x 20 data matrix successfully!
## Using no_dims = 2, perplexity = 30.000000, and theta = 0.500000
## Computing input similarities...
## Building tree...
## Done in 1.41 seconds (sparsity = 0.020005)!
## Learning embedding...
## Iteration 50: error is 91.834635 (50 iterations in 2.17 seconds)
## Iteration 100: error is 77.117264 (50 iterations in 1.58 seconds)
## Iteration 150: error is 73.217206 (50 iterations in 1.31 seconds)
## Iteration 200: error is 72.635922 (50 iterations in 1.31 seconds)
## Iteration 250: error is 72.488880 (50 iterations in 1.37 seconds)
## Iteration 300: error is 2.232922 (50 iterations in 1.58 seconds)
## Iteration 350: error is 1.798011 (50 iterations in 1.51 seconds)
## Iteration 400: error is 1.564351 (50 iterations in 1.53 seconds)
## Iteration 450: error is 1.416048 (50 iterations in 1.44 seconds)
## Iteration 500: error is 1.314290 (50 iterations in 1.47 seconds)
## Fitting performed in 15.27 seconds.
```

```
plot(tSNE$Y, t='n', main="tSNE")
text(tSNE$Y, labels=dat.2$BAD, col=fit.ward.d2$cluster)
```



METHOD 2: K-Means Cluster Analysis

```
library(cluster)
library(Rtsne)
K <- 2
```

```
fit.kmeans <- kmeans(dat0, K)
```

cluster memberships

```
kmeans.groups <- fit.kmeans$cluster
table(kmeans.groups)
```

```
## kmeans.groups
##      1      2
## 3674 2286
```

Comment

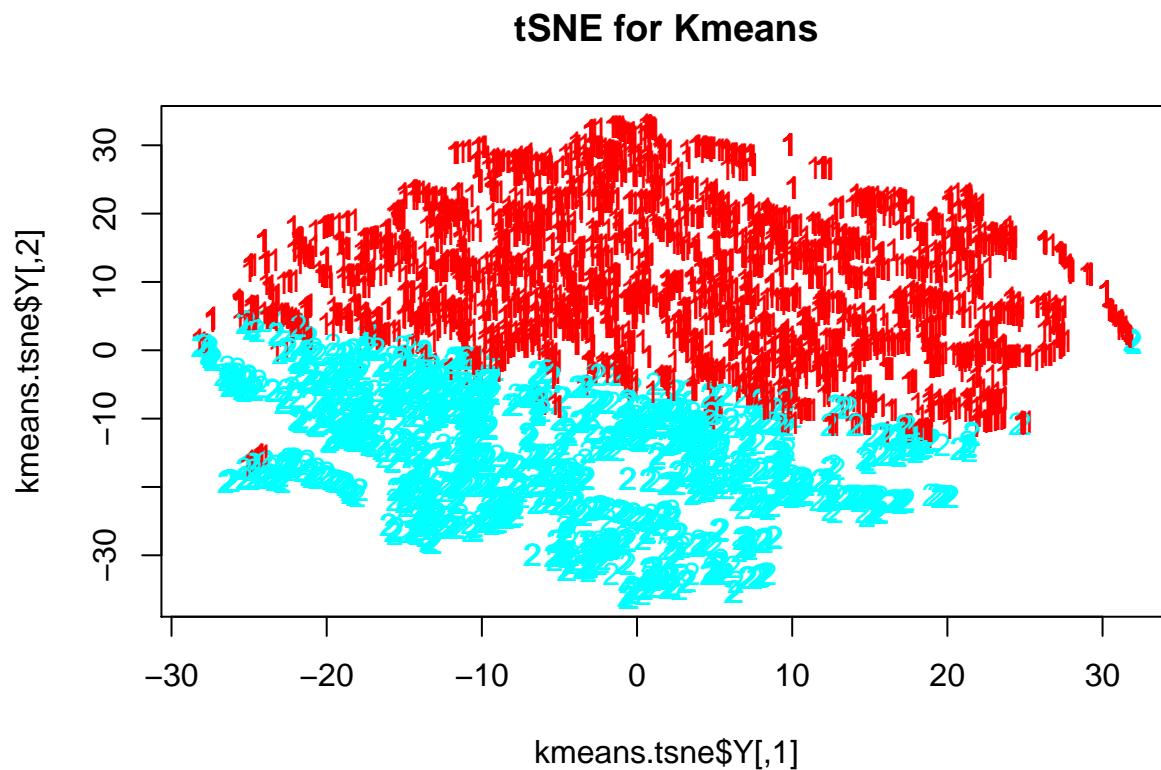
kmeans.groups

1 2

3674 2286

Plotting data

```
library(Rtsne)
colors = rainbow(length(unique(kmeans.groups)))
names(colors) = unique(kmeans.groups)
kmeans.tsne <- Rtsne(dat0, dims=2, perplexity=30, max_iter=500)
plot(kmeans.tsne$Y, t="n", main = "tSNE for Kmeans")
text(kmeans.tsne$Y, labels = kmeans.groups, col = colors[kmeans.groups])
```

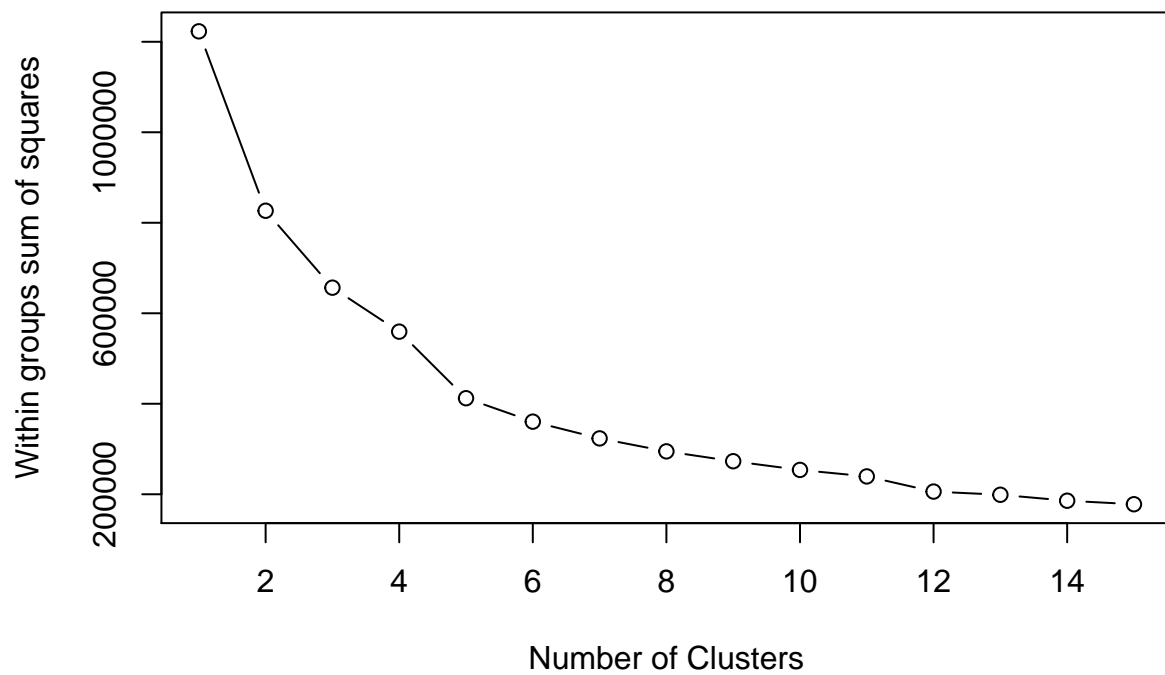


Determine Optimal Cluster

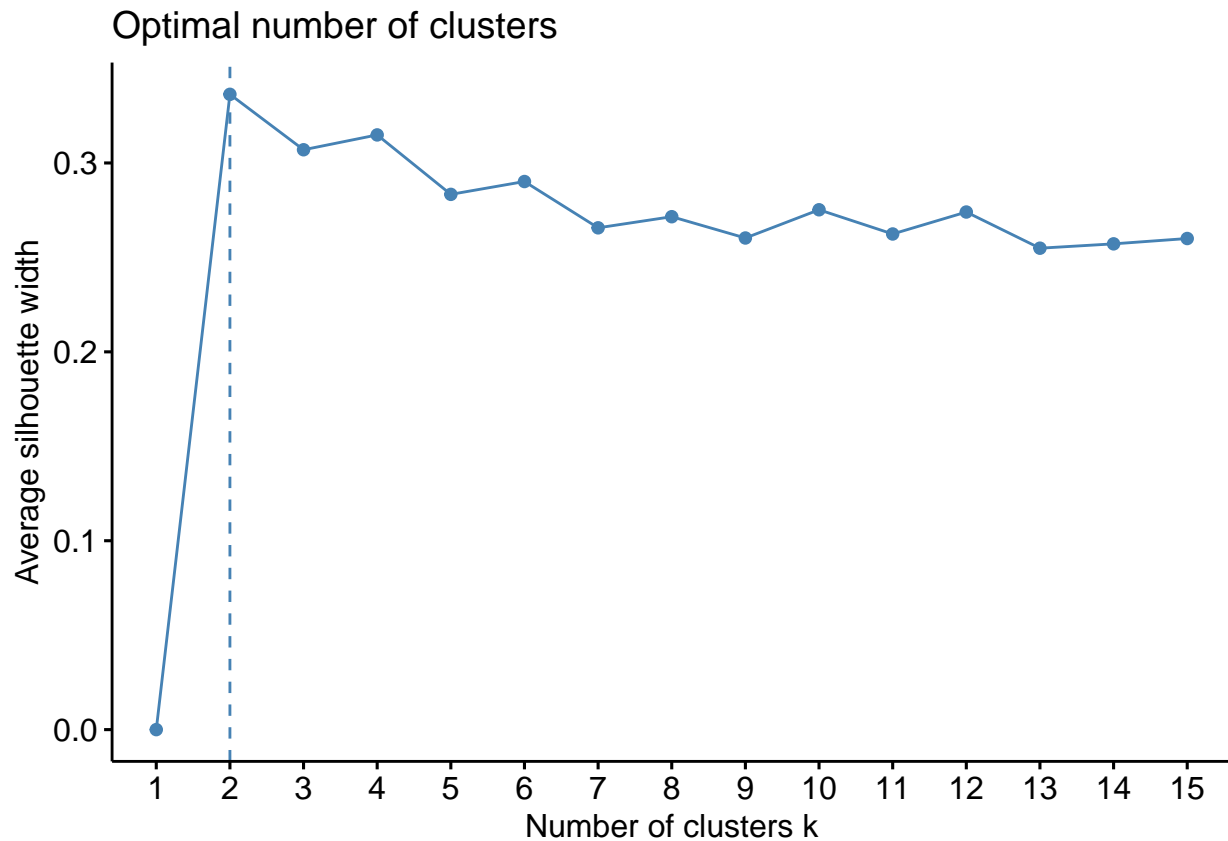
Scree plot of height IN Kmeans clustering

```
wss <- (nrow(dat0)-1)*sum(apply(dat0,2,var))
K.max <- 15
for (K in 2:K.max) wss[K] <- sum(kmeans(dat0, centers=K)$withinss)
```

```
plot(1:K.max, wss, type="b", xlab="Number of Clusters",
     ylab="Within groups sum of squares")
```



```
suppressMessages(library(factoextra))
fviz_nbclust(x=dat0, FUNcluster = kmeans, method = c("silhouette"), diss = NULL, k.max = 15)
```

Comment

We observe from the scree plot that the graph begins to decrease slowly when $K = 2$, which suggest two clusters in the data.

Also, the silhouette method confirms that there are two clusters.

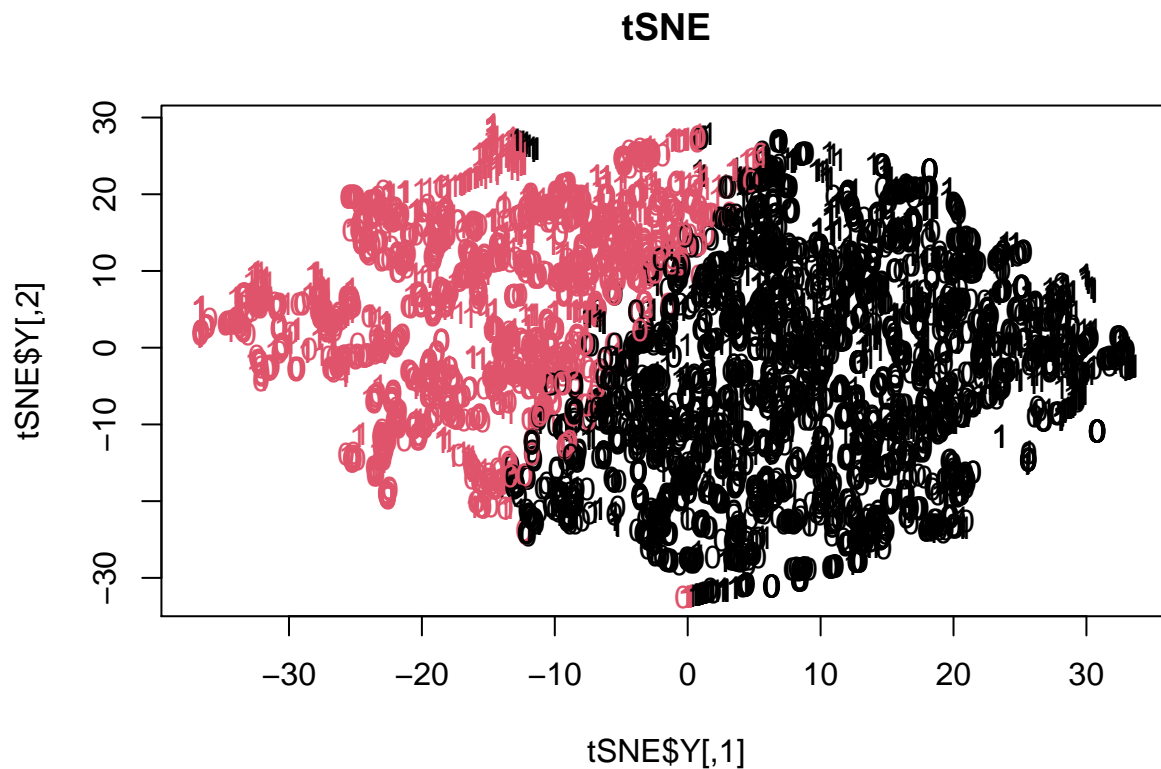
Plot the data using an MDS procedure (e.g., PCA or tSNE). Highlight both the clustering memberships and the BAD value with different color and symbols.

```
BAD <- dat$BAD
BAD <- as.vector(dat$BAD)
dat.3 <- (cbind(dat0,BAD))
dat.3 <- data.frame(dat.3)
library(Rtsne)
tSNE <- Rtsne(dat0, dims=2, perplexity=30, verbose=TRUE, max_iter = 500)
```

```
## Performing PCA
## Read the 5960 x 20 data matrix successfully!
```

```
## Using no_dims = 2, perplexity = 30.000000, and theta = 0.500000
## Computing input similarities...
## Building tree...
## Done in 1.27 seconds (sparsity = 0.020005)!
## Learning embedding...
## Iteration 50: error is 91.830285 (50 iterations in 1.38 seconds)
## Iteration 100: error is 77.372182 (50 iterations in 1.32 seconds)
## Iteration 150: error is 74.179776 (50 iterations in 1.19 seconds)
## Iteration 200: error is 72.922391 (50 iterations in 1.19 seconds)
## Iteration 250: error is 72.584742 (50 iterations in 1.24 seconds)
## Iteration 300: error is 2.219963 (50 iterations in 1.16 seconds)
## Iteration 350: error is 1.789959 (50 iterations in 1.14 seconds)
## Iteration 400: error is 1.559274 (50 iterations in 1.17 seconds)
## Iteration 450: error is 1.411966 (50 iterations in 1.18 seconds)
## Iteration 500: error is 1.311419 (50 iterations in 1.18 seconds)
## Fitting performed in 12.16 seconds.
```

```
plot(tSNE$Y, t='n', main="tSNE")
text(tSNE$Y, labels=dat.3$BAD, col=fit.kmeans$cluster)
```



Comments

We observe from the two graphs of tSNE that the hierarchical clustering better cluster the data into the two clusters than Kmeans.

Comparing Hierarchical Clustering and Kmeans Clustering

```
library(clusteval)
jaccard <- cluster_similarity(hclust.groups, kmeans.groups,
                             similarity = "jaccard")
rand <- cluster_similarity(hclust.groups, kmeans.groups, similarity = "rand")
matrix(c("Jaccard", jaccard, "Rand", rand), byrow = T, ncol = 2)
```

```
##      [,1]      [,2]
## [1,] "Jaccard" "0.366788613397245"
## [2,] "Rand"   "0.500781965353855"
```

Comment

```
[,1] [,2]
```

```
[1,] "Jaccard" "0.366788613397245"
```

```
[2,] "Rand" "0.500781965353855"
```

Comment

We observe that the values are close or fairly similar.

(v)

Post Hoc Analysis

We consider the result from the hierarchical clustering method to perform post hoc analysis. We characterize each cluster, and explore the association of the cluster with the 12 predictors and the outcome 'BAD'.

Performing a t test for the differences in means

```
aggregate(dat[, c(1,2,3,4,7,9,13)], list(hclust.groups), mean, na.rm =T)
```

```
##   Group.1      BAD      LOAN MORTDUE      VALUE      YOJ      DELINQ  DEBTINC
## 1      1 0.2185039 9.461746 10.87125 11.36399 2.015710 0.4768701 33.34093
## 2      2 0.1896640 9.780385 11.01978 11.42175 1.909102 0.4368635 34.77807
```

Comment

We observe that there is a statistically significant

difference in the mean value of DEBTINC: Debt-to-income ratio for the two ## groups. Cluster 2 turns to have high Debt-to-income ratio than Cluster 1.

```
cond1 <- hclust.groups == 1
cond2 <- hclust.groups == 2
var.test(dat$DEBTINC[cond1], dat$DEBTINC[cond2], alternative = "two.sided")
```

```
##
## F test to compare two variances
##
## data: dat$DEBTINC[cond1] and dat$DEBTINC[cond2]
## F = 1.3652, num df = 2031, denom df = 3927, p-value = 4.441e-16
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  1.266178 1.473372
## sample estimates:
## ratio of variances
##           1.36522
```

Comment

F test to compare two variances

data: dat*DEBTINC*[cond1] and dat*DEBTINC*[cond2]

F = 1.3652, num df = 2031, denom df = 3927, p-value = 4.441e-16

alternative hypothesis: true ratio of variances is not equal to 1

95 percent confidence interval:

1.266178 1.473372

sample estimates:

ratio of variances

1.36522

```
t.test(dat$DEBTINC[cond1], dat$DEBTINC[cond2], alternative = "two.sided",
var.equal = T)
```

```
##
## Two Sample t-test
##
## data: dat$DEBTINC[cond1] and dat$DEBTINC[cond2]
## t = -5.4297, df = 5958, p-value = 5.867e-08
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -1.956016 -0.918275
## sample estimates:
## mean of x mean of y
## 33.34093 34.77807
```

Comment

Two Sample t-test

data: $\text{dat}DEBTINC[cond1]$ and $\text{dat}DEBTINC[cond2]$

$t = -5.4297$, $df = 5958$, $p\text{-value} = 5.867e-08$

alternative hypothesis: true difference in means is not equal to 0

95 percent confidence interval:

-1.956016 -0.918275

sample estimates:

mean of x mean of y

33.34093 34.77807

Difference in CLNO

```
dat.4 <- table(dat$CLNO , hclust.groups)
dat.4 <- as.data.frame(dat.4)
dat.4$Var1 <- as.numeric(dat.4$Var1)
dat.4$hclust.groups <- as.numeric(dat.4$hclust.groups)
cond1 <- (dat.4$Var1 <= 21) & (dat.4$hclust.groups == 1)
cond2 <- (dat.4$Var1 <= 21) & (dat.4$hclust.groups == 2)
lessq1 <- sum(dat.4$Freq[cond1])
lessq2 <- sum(dat.4$Freq[cond2])
cond11 <- (dat.4$Var1 > 21) & (dat.4$hclust.groups == 1)
cond22 <- (dat.4$Var1 > 21) & (dat.4$hclust.groups == 2)
grt1 <- sum(dat.4$Freq[cond11])
grt2 <- sum(dat.4$Freq[cond22])
matrix(c("CLNO", "Cluster 1", "Cluster 2", "<= 21", lessq1, lessq2, "> 21", grt1, grt2), byrow = T, ncol
```

```
##      [,1]      [,2]      [,3]
## [1,] "CLNO"    "Cluster 1" "Cluster 2"
## [2,] "<= 21"  "1209"      "1861"
## [3,] "> 21"   "823"       "2067"
```

Comment

```
[1,] [1,] "CLNO" "Cluster 1" "Cluster 2"
[2,] [2,] "<= 21" "1209" "1861"
[3,] [3,] "> 21" "823" "2067"
```

We observe from the table above that 1209 individuals in Cluster 1 have number of credit lines (CLNO) less than or equal to 21, whereas, 2067 individuals in Cluster 2 have number of credit lines (CLNO) greater than 21.

Relationship between Clusters and Predictors

```
table(dat$JOB , hclust.groups)
```

```
##      hclust.groups
##      1      2
## Mgr      195  572
## Office   328  620
## Other    784 1604
## ProfExe  429  847
## Sales     12   97
## Self     120   73
## Unknown  164  115
```

Comment

hclust.groups

1 2

Mgr 195 572

Office 328 620

Other 784 1604

ProfExe 429 847

Sales 12 97

Self 120 73

Unknown 164 115

Comment

We observe that other Jobs are the main reason given by applicants in the applicants in the two clusters.

```
table(dat$REASON , hclust.groups)
```

```
##          hclust.groups
##          1      2
## DebtCon    0 3928
## HomeImp 1780    0
## Unknown  252    0
```

Comment

hclust.groups

1 2

DebtCon 0 3928

HomeImp 1780 0

Unknown 252 0

Comment

Debt consolidation is the main reason for applicants in cluster 2 while

HomeImp is the main reason for applicants in cluster 1.

Association between cluster and the outcome “BAD”

```
table(dat$BAD, hclust.groups)
```

```
##      hclust.groups
##           1      2
## 0 1588 3183
## 1  444  745
```

Comment

hclust.groups

1 2

0 1588 3183

1 444 745

We observe that value 0 has the highest number in both cluster which means when the homeowner repaid the home equity line of credit.