Clustering

# PART 1

### 1. LOAD THE DATA

hospital\_data=read.csv("hospitalUSA.csv",header = T)  
head(hospital\_data)

## ZIP HID CITY STATE BEDS RBEDS OUTV ADM SIR SALES  
## 1 919 44604 San Juan PR 386 0 0 12975 4106 4  
## 2 935 5004 San Juan PR 311 0 118065 11309 21049 NA  
## 3 1060 157014 Northampton MA 175 0 114912 7365 5862 1  
## 4 1104 194014 Springfield MA 324 0 95702 10406 13648 57  
## 5 1199 195514 Springfield MA 507 0 108258 22361 15081 7  
## 6 1420 93014 Fitchburg MA 175 25 26428 5619 5701 17  
## HIP KNEE TH TRAUMA REHAB HIP2 KNEE2 FEMUR  
## 1 90 101 0 0 0 101 137 100  
## 2 70 26 1 0 0 66 40 330  
## 3 93 60 0 0 0 97 64 58  
## 4 122 94 0 0 0 152 95 116  
## 5 148 97 1 1 0 166 110 236  
## 6 61 48 1 1 1 57 44 40

# Load the required packages   
library(tidyverse) # data manipulation

## -- Attaching packages ------------------------------------------------------------------- tidyverse 1.3.0 --

## v ggplot2 3.2.1 v purrr 0.3.3  
## v tibble 2.1.3 v dplyr 0.8.3  
## v tidyr 1.0.0 v stringr 1.4.0  
## v readr 1.3.1 v forcats 0.5.0

## -- Conflicts ---------------------------------------------------------------------- tidyverse\_conflicts() --  
## x dplyr::filter() masks stats::filter()  
## x dplyr::lag() masks stats::lag()

library(cluster) # clustering algorithms  
library(factoextra) # clustering algorithms & visualization

## Welcome! Want to learn more? See two factoextra-related books at https://goo.gl/ve3WBa

# Sample 3000 hospitals at random  
dim(hospital\_data)

## [1] 4703 18

hospital\_data = sample\_n(hospital\_data,3000)  
dim(hospital\_data)

## [1] 3000 18

# Exclude the dependent variable and categorical variables  
hospital\_data <- hospital\_data[,-c(1,3,4)]  
colnames(hospital\_data)

## [1] "HID" "BEDS" "RBEDS" "OUTV" "ADM" "SIR" "SALES" "HIP"   
## [9] "KNEE" "TH" "TRAUMA" "REHAB" "HIP2" "KNEE2" "FEMUR"

# Convert the Hospital ID (HID) to the index  
rownames(hospital\_data) <- hospital\_data$HID  
hospital\_data=hospital\_data[,-1] #then drop the HID  
head(hospital\_data)

## BEDS RBEDS OUTV ADM SIR SALES HIP KNEE TH TRAUMA REHAB HIP2 KNEE2  
## 12042 425 0 260111 16236 12695 NA 132 84 1 0 0 140 125  
## 348593 79 0 10950 1768 2867 23 15 0 0 0 0 11 0  
## 62073 74 0 3242 1045 739 1 2 9 0 0 0 6 4  
## 135063 836 35 147309 28504 21635 62 344 377 0 1 1 412 376  
## 214044 449 0 128960 17205 10331 280 138 94 1 1 0 121 103  
## 103536 116 0 0 5415 4426 NA 25 2 0 0 0 29 6  
## FEMUR  
## 12042 143  
## 348593 29  
## 62073 7  
## 135063 282  
## 214044 92  
## 103536 46

### 2. TRANSFORMATION

# Transform the data through scalling  
hospital\_data<-scale(hospital\_data)  
head(hospital\_data)

## BEDS RBEDS OUTV ADM SIR SALES  
## 12042 1.3609389 -0.3449574 2.1772375 1.4235912 1.54410966 NA  
## 348593 -0.6543810 -0.3449574 -0.3802857 -0.7432698 -0.40410043 -0.4350562  
## 62073 -0.6835041 -0.3449574 -0.4594048 -0.8515529 -0.82593509 -0.5396399  
## 135063 3.7548594 1.4407125 1.0193768 3.2609599 3.31629101 -0.2496577  
## 214044 1.5007299 -0.3449574 0.8310327 1.5687176 1.07549258 0.7866720  
## 103536 -0.4388699 -0.3449574 -0.4926824 -0.1970614 -0.09505896 NA  
## HIP KNEE TH TRAUMA REHAB HIP2  
## 12042 1.1856469 0.6577627 1.6370974 -0.3796271 -0.4731972 1.2526164  
## 348593 -0.5252363 -0.6417967 -0.6106336 -0.3796271 -0.4731972 -0.5892076  
## 62073 -0.7153344 -0.5025582 -0.6106336 -0.3796271 -0.4731972 -0.6605961  
## 135063 4.2857088 5.1907499 -0.6106336 2.6332861 2.1125796 5.1361524  
## 214044 1.2733845 0.8124722 1.6370974 2.6332861 -0.4731972 0.9813400  
## 103536 -0.3790069 -0.6108548 -0.6106336 -0.3796271 -0.4731972 -0.3322089  
## KNEE2 FEMUR  
## 12042 1.3204987 1.85310275  
## 348593 -0.6640279 -0.40382511  
## 62073 -0.6005230 -0.83937259  
## 135063 5.3054280 4.60497092  
## 214044 0.9712220 0.84342450  
## 103536 -0.5687706 -0.06726569

### 3. DIMENSION REDUCTION

Use the factor method to summarize the demographic variables and the operation variables and come out with a final reduced list of factor variables (perhaps 3 or 4). Use the rotated factors in order to find a good interpretation of the factors and try to make a good story

#### Factor Analysis

Factor analysis can only be used to reduce continuous variables of the dataset. Therefore, we will be removing categorical variables

* Removing the dependent and categorical variables As mentioned above, factor analysis works in an unsupervised setup only for the numerical variables, therefore, we will get rid of the categorical and the dependent variable.

df=hospital\_data[,-6] #remove SALES variable  
colnames(df)

## [1] "BEDS" "RBEDS" "OUTV" "ADM" "SIR" "HIP" "KNEE" "TH"   
## [9] "TRAUMA" "REHAB" "HIP2" "KNEE2" "FEMUR"

# Create a matrix out of the data frame  
Factor1 = subset(df)  
class(Factor1)

## [1] "matrix"

head(Factor1)

## BEDS RBEDS OUTV ADM SIR HIP  
## 12042 1.3609389 -0.3449574 2.1772375 1.4235912 1.54410966 1.1856469  
## 348593 -0.6543810 -0.3449574 -0.3802857 -0.7432698 -0.40410043 -0.5252363  
## 62073 -0.6835041 -0.3449574 -0.4594048 -0.8515529 -0.82593509 -0.7153344  
## 135063 3.7548594 1.4407125 1.0193768 3.2609599 3.31629101 4.2857088  
## 214044 1.5007299 -0.3449574 0.8310327 1.5687176 1.07549258 1.2733845  
## 103536 -0.4388699 -0.3449574 -0.4926824 -0.1970614 -0.09505896 -0.3790069  
## KNEE TH TRAUMA REHAB HIP2 KNEE2  
## 12042 0.6577627 1.6370974 -0.3796271 -0.4731972 1.2526164 1.3204987  
## 348593 -0.6417967 -0.6106336 -0.3796271 -0.4731972 -0.5892076 -0.6640279  
## 62073 -0.5025582 -0.6106336 -0.3796271 -0.4731972 -0.6605961 -0.6005230  
## 135063 5.1907499 -0.6106336 2.6332861 2.1125796 5.1361524 5.3054280  
## 214044 0.8124722 1.6370974 2.6332861 -0.4731972 0.9813400 0.9712220  
## 103536 -0.6108548 -0.6106336 -0.3796271 -0.4731972 -0.3322089 -0.5687706  
## FEMUR  
## 12042 1.85310275  
## 348593 -0.40382511  
## 62073 -0.83937259  
## 135063 4.60497092  
## 214044 0.84342450  
## 103536 -0.06726569

# Creating Correlation Matrix for the above dataset  
# This will give us an idea of the variables that are highly correlated to each other.  
corrm<- cor(Factor1)  
corrm

## BEDS RBEDS OUTV ADM SIR HIP  
## BEDS 1.0000000 0.110960695 0.438887403 0.89659485 0.79190237 0.583960917  
## RBEDS 0.1109607 1.000000000 -0.003721587 0.01243735 -0.02645928 0.001525624  
## OUTV 0.4388874 -0.003721587 1.000000000 0.44803187 0.35396418 0.194154639  
## ADM 0.8965949 0.012437349 0.448031869 1.00000000 0.87239542 0.647694010  
## SIR 0.7919024 -0.026459276 0.353964179 0.87239542 1.00000000 0.673471966  
## HIP 0.5839609 0.001525624 0.194154639 0.64769401 0.67347197 1.000000000  
## KNEE 0.5131743 0.008733660 0.163715661 0.57051326 0.62797498 0.907787724  
## TH 0.5557170 0.104143102 0.293094236 0.53069767 0.46070663 0.319229049  
## TRAUMA 0.4279584 0.026459080 0.256693820 0.48442316 0.41098091 0.286319409  
## REHAB 0.1926882 0.728993001 0.051088831 0.13275304 0.11097776 0.119205040  
## HIP2 0.5920893 0.001924356 0.192402678 0.65727536 0.68210579 0.970150315  
## KNEE2 0.5304357 0.005790647 0.155049667 0.58742270 0.64698709 0.886574245  
## FEMUR 0.7134768 -0.028525534 0.241497649 0.80345839 0.77425902 0.756739357  
## KNEE TH TRAUMA REHAB HIP2 KNEE2  
## BEDS 0.51317431 0.5557170 0.42795842 0.19268822 0.592089303 0.530435698  
## RBEDS 0.00873366 0.1041431 0.02645908 0.72899300 0.001924356 0.005790647  
## OUTV 0.16371566 0.2930942 0.25669382 0.05108883 0.192402678 0.155049667  
## ADM 0.57051326 0.5306977 0.48442316 0.13275304 0.657275358 0.587422701  
## SIR 0.62797498 0.4607066 0.41098091 0.11097776 0.682105792 0.646987091  
## HIP 0.90778772 0.3192290 0.28631941 0.11920504 0.970150315 0.886574245  
## KNEE 1.00000000 0.2871889 0.25459050 0.11893655 0.888538845 0.953507956  
## TH 0.28718888 1.0000000 0.30780963 0.17026500 0.325823909 0.289652532  
## TRAUMA 0.25459050 0.3078096 1.00000000 0.11904554 0.279976887 0.245851623  
## REHAB 0.11893655 0.1702650 0.11904554 1.00000000 0.120224223 0.117981226  
## HIP2 0.88853884 0.3258239 0.27997689 0.12022422 1.000000000 0.904953197  
## KNEE2 0.95350796 0.2896525 0.24585162 0.11798123 0.904953197 1.000000000  
## FEMUR 0.65747046 0.3817256 0.43441924 0.12197505 0.779706444 0.700431591  
## FEMUR  
## BEDS 0.71347676  
## RBEDS -0.02852553  
## OUTV 0.24149765  
## ADM 0.80345839  
## SIR 0.77425902  
## HIP 0.75673936  
## KNEE 0.65747046  
## TH 0.38172561  
## TRAUMA 0.43441924  
## REHAB 0.12197505  
## HIP2 0.77970644  
## KNEE2 0.70043159  
## FEMUR 1.00000000

#### Finding Eigen Values

We will now find the eigenvalues to decide the number of factors that will correctly group the features on the level of their similarity allowing us to manually select features from each of these groups.

eigen(corrm)$values

## [1] 6.73073342 1.78358851 1.53454609 0.75250428 0.68048942 0.55840732  
## [7] 0.27357727 0.23273020 0.17684169 0.13288798 0.07350926 0.05269135  
## [13] 0.01749321

Coming up with other useful values such as cumulative eigenvalue, percentage variance and cumulative percentage variance.

eigen\_values <- mutate(data.frame(eigen(corrm)$values),  
 cum\_sum\_eigen=cumsum(eigen.corrm..values),  
 pct\_var=eigen.corrm..values/sum(eigen.corrm..values),  
 cum\_pct\_var=cum\_sum\_eigen/sum(eigen.corrm..values))  
eigen\_values

## eigen.corrm..values cum\_sum\_eigen pct\_var cum\_pct\_var  
## 1 6.73073342 6.730733 0.517748725 0.5177487  
## 2 1.78358851 8.514322 0.137199116 0.6549478  
## 3 1.53454609 10.048868 0.118042007 0.7729898  
## 4 0.75250428 10.801372 0.057884945 0.8308748  
## 5 0.68048942 11.481862 0.052345340 0.8832201  
## 6 0.55840732 12.040269 0.042954409 0.9261745  
## 7 0.27357727 12.313846 0.021044405 0.9472189  
## 8 0.23273020 12.546577 0.017902323 0.9651213  
## 9 0.17684169 12.723418 0.013603207 0.9787245  
## 10 0.13288798 12.856306 0.010222152 0.9889466  
## 11 0.07350926 12.929815 0.005654559 0.9946012  
## 12 0.05269135 12.982507 0.004053181 0.9986544  
## 13 0.01749321 13.000000 0.001345632 1.0000000

Clearly, the four factors explain approximately 78% of the variance. Therefore, the number of factors will be equal to 4 in our case.

# Reducing Variable using Factor Analysis  
# Using FA to perform factor analysis.  
require(psych)

## Loading required package: psych

##   
## Attaching package: 'psych'

## The following objects are masked from 'package:ggplot2':  
##   
## %+%, alpha

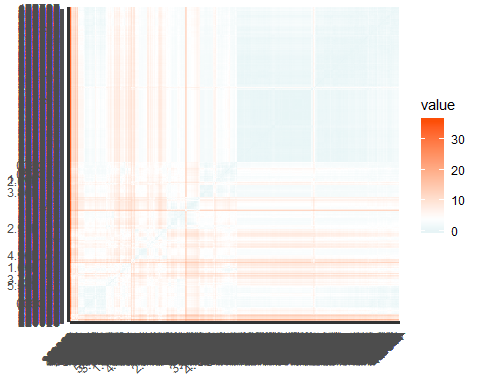
FA<-fa(r=corrm, 4, rotate="varimax", fm="ml")  
FA\_SORT<-fa.sort(FA)  
  
# Grouping variables.  
load1 = FA\_SORT$loadings  
load1

##   
## Loadings:  
## ML1 ML3 ML2 ML4   
## KNEE 0.938 0.253 -0.222  
## KNEE2 0.916 0.275 -0.102  
## HIP2 0.911 0.333 0.232  
## HIP 0.909 0.328 0.137  
## ADM 0.374 0.912   
## BEDS 0.326 0.844 0.119   
## SIR 0.467 0.764   
## FEMUR 0.577 0.632 0.191  
## TH 0.163 0.518 0.109   
## TRAUMA 0.138 0.475   
## OUTV 0.473   
## RBEDS 0.991   
## REHAB 0.104 0.738   
##   
## ML1 ML3 ML2 ML4  
## SS loadings 4.226 3.614 1.558 0.174  
## Proportion Var 0.325 0.278 0.120 0.013  
## Cumulative Var 0.325 0.603 0.723 0.736

### MARKET SEGMENTATION

* (i). K-means clustering

# visualize the distance matrix   
distance <- get\_dist(df)  
fviz\_dist(distance, gradient = list(low = "#00AFBB", mid = "white", high = "#FC4E07"))

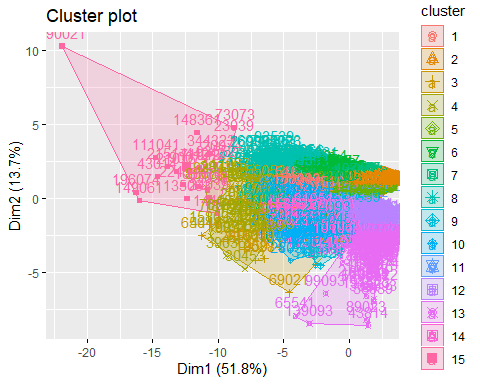


# Here will group the data into fifteen clusters   
k2 <- kmeans(df, centers = 15, nstart = 25)  
str(k2)

## List of 9  
## $ cluster : Named int [1:3000] 1 2 2 15 10 7 7 2 2 6 ...  
## ..- attr(\*, "names")= chr [1:3000] "12042" "348593" "62073" "135063" ...  
## $ centers : num [1:15, 1:13] 0.99172 -0.70955 2.65321 2.88026 -0.00334 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:15] "1" "2" "3" "4" ...  
## .. ..$ : chr [1:13] "BEDS" "RBEDS" "OUTV" "ADM" ...  
## $ totss : num 38987  
## $ withinss : num [1:15] 512 386 653 969 469 ...  
## $ tot.withinss: num 9747  
## $ betweenss : num 29240  
## $ size : int [1:15] 131 995 22 58 221 223 502 102 55 150 ...  
## $ iter : int 7  
## $ ifault : int 0  
## - attr(\*, "class")= chr "kmeans"

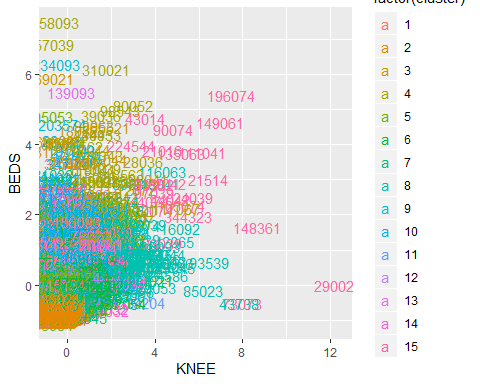
We can also view our results by using fviz\_cluster. This provides a nice illustration of the clusters. If there are more than two dimensions (variables) fviz\_cluster will perform principal component analysis (PCA) and plot the data points according to the first two principal components that explain the majority of the variance.

fviz\_cluster(k2, data = df)



Alternatively, you can use standard pairwise scatter plots to illustrate the clusters compared to the original variables.

df %>%  
 as\_tibble() %>%  
 mutate(cluster = k2$cluster,  
 hospitals = row.names(df)) %>%  
 ggplot(aes(KNEE, BEDS, color = factor(cluster), label = hospitals)) +  
 geom\_text()



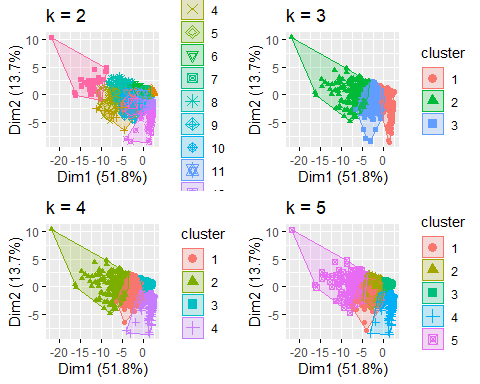
Because the number of clusters (k) must be set before we start the algorithm, it is often advantageous to use several different values of k and examine the differences in the results. We can execute the same process for 3, 4, and 5 clusters, and the results are shown in the figure:

k3 <- kmeans(df, centers = 3, nstart = 25)  
k4 <- kmeans(df, centers = 4, nstart = 25)  
k5 <- kmeans(df, centers = 5, nstart = 25)  
  
# plots to compare  
p1 <- fviz\_cluster(k2, geom = "point", data = df) + ggtitle("k = 2")  
p2 <- fviz\_cluster(k3, geom = "point", data = df) + ggtitle("k = 3")  
p3 <- fviz\_cluster(k4, geom = "point", data = df) + ggtitle("k = 4")  
p4 <- fviz\_cluster(k5, geom = "point", data = df) + ggtitle("k = 5")  
  
library(gridExtra)

##   
## Attaching package: 'gridExtra'

## The following object is masked from 'package:dplyr':  
##   
## combine

grid.arrange(p1, p2, p3, p4, nrow = 2)



Although this visual assessment tells us where true dilineations occur(or do not occur) between clusters,it does not tell us what the optimal number of clusters is.

#### Determining Optimal Clusters

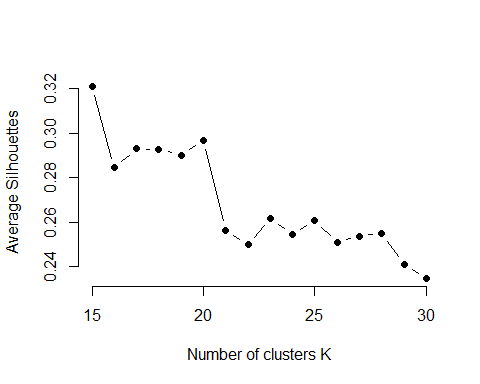
As you may recall the analyst specifies the number of clusters to use;preferably the analyst would like to use the optimal number of clusters. To aid the analyst,the following explains the three most popular methods for determining the optimal clusters, which includes:

#### Average Silhouette Method

In short, the average silhouette approach measures the quality of a clustering. That is, it determines how well each object lies within its cluster. A high average silhouette width indicates a good clustering. The average silhouette method computes the average silhouette of observations for different values of k. The optimal number of clusters k is the one that maximizes the average silhouette over a range of possible values for k.2

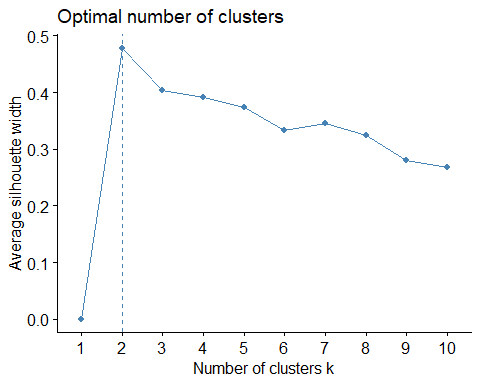
* We can use the silhouette function in the cluster package to compuate the average silhouette width. The following code computes this approach for 1-15 clusters. The results show that 2 clusters maximize the average silhouette values with 4 clusters coming in as second optimal number of clusters. function to compute average silhouette for k clusters

avg\_sil <- function(k) {  
 km.res <- kmeans(df, centers = k, nstart = 25)  
 ss <- silhouette(km.res$cluster, dist(df))  
 mean(ss[, 3])  
}  
  
  
# Compute and plot wss for k = 15 to k = 30  
k.values <- 15:30  
  
# extract avg silhouette for 2-15 clusters  
avg\_sil\_values <- map\_dbl(k.values, avg\_sil)  
  
plot(k.values, avg\_sil\_values,  
 type = "b", pch = 19, frame = FALSE,   
 xlab = "Number of clusters K",  
 ylab = "Average Silhouettes")



Similar to the elbow method, this process to compute the “average silhoutte method” has been wrapped up in a single function (fviz\_nbclust):

fviz\_nbclust(df, kmeans, method = "silhouette")

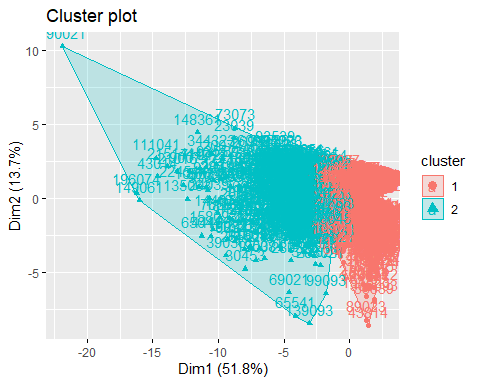


# Now will group the data into four clusters since thats optimal k  
k3 <- kmeans(df, centers = 2, nstart = 25)  
str(k3)

## List of 9  
## $ cluster : Named int [1:3000] 2 1 1 2 2 1 1 1 1 1 ...  
## ..- attr(\*, "names")= chr [1:3000] "12042" "348593" "62073" "135063" ...  
## $ centers : num [1:2, 1:13] -0.3702 1.2947 -0.0383 0.134 -0.1735 ...  
## ..- attr(\*, "dimnames")=List of 2  
## .. ..$ : chr [1:2] "1" "2"  
## .. ..$ : chr [1:13] "BEDS" "RBEDS" "OUTV" "ADM" ...  
## $ totss : num 38987  
## $ withinss : num [1:2] 11347 14218  
## $ tot.withinss: num 25565  
## $ betweenss : num 13422  
## $ size : int [1:2] 2333 667  
## $ iter : int 1  
## $ ifault : int 0  
## - attr(\*, "class")= chr "kmeans"

We can also view our results by using fviz\_cluster. This provides a nice illustration of the clusters. If there are more than two dimensions (variables) fviz\_cluster will perform principal component analysis (PCA) and plot the data points according to the first two principal components that explain the majority of the variance.

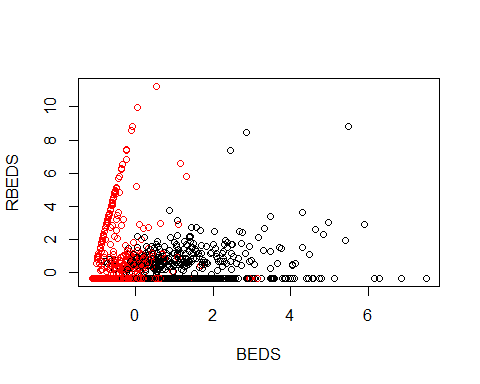
fviz\_cluster(k3, data = df)



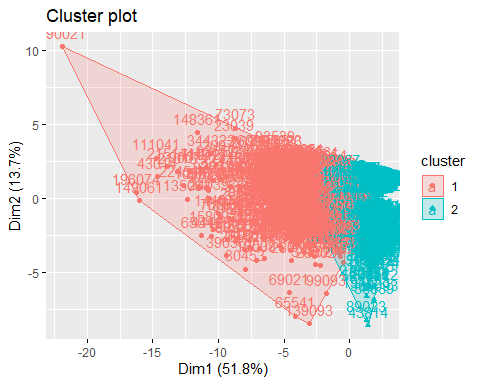
# Partitioning Around Medoids (PAM)  
#execute the pam algorithm with the dataset created for the example  
result <- pam(df, 2, FALSE, "euclidean")  
  
#print the results data in the screen  
summary(result)

## Medoids:  
## ID BEDS RBEDS OUTV ADM SIR HIP  
## 36084 2238 1.1221293 -0.3449574 0.0513485 0.7397450 1.0439739 0.9078112  
## 4074 824 -0.6019594 -0.3449574 -0.3018133 -0.4563119 -0.6170001 -0.4959904  
## KNEE TH TRAUMA REHAB HIP2 KNEE2  
## 36084 0.7351175 1.6370974 -0.3796271 -0.4731972 1.0241731 0.8442123  
## 4074 -0.4561454 -0.6106336 -0.3796271 -0.4731972 -0.5035414 -0.4893895  
## FEMUR  
## 36084 0.7444364  
## 4074 -0.5424084  
## Clustering vector:  
## 12042 348593 62073 135063 214044 103536 147023 3561   
## 1 2 2 1 1 2 2 2   
## 33254 117014 135021 139963 64462 23066 284593 46034   
## 2 1 2 2 2 2 2 2   
## 17551 231874 733339 196045 373593 178243 161074 245544   
## 2 2 2 2 2 2 2 2   
## 906973 94563 11588 311023 9012 405721 9639 313043   
## 2 2 2 2 2 2 2 2   
## 6088 49539 69021 253043 43532 55538 135514 76553   
## 2 1 1 2 2 1 2 2   
## 2016 265023 11067 7388 50493 23041 79039 47532   
## 1 2 2 1 2 2 2 2   
## 116043 11034 166044 104023 35012 17311 229044 1672   
## 2 2 2 1 2 2 1 2   
## 98539 144042 77767 211993 291174 45081 388993 533021   
## 2 2 2 2 2 2 2 1   
## 10539 80073 62072 150074 56671 48139 94039 21093   
## 2 1 2 2 2 1 1 2   
## 139063 111041 10531 97038 44162 166045 57239 29082   
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## 51686 214574 99439 3035 126061 37837 2063 121023   
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## 37051 340023 9552 55343 92043 81093 164044 362174   
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## 9293 67561 64893 169545 24061 45034 105874 225043   
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## 355023 63071 29004 11674 22066 188044 111036 33353   
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## 488521 209043 208074 5.50E+24 130721 28067 5091 58032   
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## 389093 44493 91053 44022 20454 28063 57038 64032   
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## 75034 489021 120062 35034 1084 73084 26033 179544   
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## 33743 53039 92084 172374 38095 49052 6504 60037   
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## 136042 7567 143021 21722 51967 337293 7095 88534   
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## 21571 80054 47554 26839 73042 67093 273093 205545   
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## 376574 118021 1582 231041 35035 85054 29562 11031   
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## 927574 32093 191043 163093 536 7072 90067 167044   
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## 92051 125114 118093 12033 115334 41081 3034 332023   
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## 2.91E+95 59063 141042 131093 239021 326723 63574 418021   
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## 28011 239044 121034 24437 110239 39141 82766 11041   
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## 130043 41052 22012 44604 51072 46574 99236 73036   
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## 173041 64538 117893 138541 18563 59753 254023 94584   
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## 318093 316043 5038 56639 32036 85073 44011 184045   
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## 197021 19065 150045 68035 029A04 54092 365074 83073   
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## 202593 99093 74551 136536 379974 12041 46036 86051   
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## 6552 143042 152822 24039 101043 341574 61032 26044   
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## 16766 131063 4534 151543 191023 81252 269093 312374   
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## 240274 111839 138044 303574 33067 21092 12593 978072   
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## 61551 73022 2504 6351 277023 21191 90074 39061   
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## 45038 88022 1962 51052 348523 16554 45016 19763   
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## 77539 181074 202045 911193 30939 115052 102552 116134   
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## 46067 546021 93693 283074 117593 29053 29095 40038   
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## 9022 240044 15023 44539 298543 80063 187023 41016   
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## 236044 33593 14034 78023 529521 4592 180041 67539   
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## 191593 180141 91584 13023 356593 189041 227093 67034   
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## 945593 19095 211061 225041 191041 22593 12034 5011   
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## 283093 145074 41972 29452 234093 55052 118045 137641   
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## 28042 333793 64574 89536 57039 177061 153014 118091   
## 2 2 2 2 1 2 1 2   
## 35472 49771 211593 81051 910063 5034 19091 192793   
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## 196974 31074 41165 307438 223021 273043 380021 61292   
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## 45072 265521 129136 213021 246244 18367 33084 73074   
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## 151041 86053 4071 109352 156093 136021 6086 5053   
## 1 2 2 2 1 2 2 2   
## 386593 227593 158561 22539 97045 24972 37004 23974   
## 2 2 1 1 1 2 2 2   
## Objective function:  
## build swap   
## 2.376369 2.354030   
##   
## Numerical information per cluster:  
## size max\_diss av\_diss diameter separation  
## [1,] 861 30.39395 4.076859 35.85149 0.372815  
## [2,] 2139 11.94174 1.660549 15.09580 0.372815  
##   
## Isolated clusters:  
## L-clusters: character(0)  
## L\*-clusters: character(0)  
##   
## Silhouette plot information:  
## cluster neighbor sil\_width  
## 114044 1 2 0.3236163418  
## 489021 1 2 0.3232157307  
## 429021 1 2 0.3212124210  
## 355023 1 2 0.3190291250  
## 28041 1 2 0.3179181620  
## 295043 1 2 0.3167842608  
## 298043 1 2 0.3154395351  
## 54092 1 2 0.3138191066  
## 73038 1 2 0.3137301115  
## 54543 1 2 0.3137119073  
## 55052 1 2 0.3119554188  
## 104042 1 2 0.3109832178  
## 15015 1 2 0.3108201225  
## 103039 1 2 0.3107716201  
## 43011 1 2 0.3107664187  
## 104052 1 2 0.3100070765  
## 5585 1 2 0.3100014058  
## 433021 1 2 0.3099809099  
## 111021 1 2 0.3095624933  
## 51086 1 2 0.3081552977  
## 263023 1 2 0.3076455502  
## 116045 1 2 0.3074024234  
## 68022 1 2 0.3070365204  
## 190023 1 2 0.3066121286  
## 13039 1 2 0.3062280782  
## 18038 1 2 0.3061115153  
## 84143 1 2 0.3058621480  
## 78044 1 2 0.3054030639  
## 40544 1 2 0.3049011136  
## 80544 1 2 0.3044300960  
## 262043 1 2 0.3032397224  
## 41016 1 2 0.3026994240  
## 25016 1 2 0.3024787076  
## 241343 1 2 0.3020687455  
## 487021 1 2 0.3004599316  
## 116563 1 2 0.3003715682  
## 235093 1 2 0.3001038857  
## 28036 1 2 0.3000320305  
## 92134 1 2 0.2998101796  
## 195074 1 2 0.2977685936  
## 112023 1 2 0.2970735941  
## 38095 1 2 0.2969139836  
## 245021 1 2 0.2968318090  
## 76023 1 2 0.2966424265  
## 230093 1 2 0.2961741343  
## 81561 1 2 0.2951030220  
## 278593 1 2 0.2948705456  
## 118041 1 2 0.2945303581  
## 106052 1 2 0.2936672635  
## 273093 1 2 0.2927232837  
## 26087 1 2 0.2924818563  
## 117067 1 2 0.2922376218  
## 119041 1 2 0.2920733788  
## 118536 1 2 0.2916135754  
## 218041 1 2 0.2913975304  
## 166043 1 2 0.2911074950  
## 51053 1 2 0.2899243089  
## 91023 1 2 0.2897064126  
## 93063 1 2 0.2893898658  
## 26023 1 2 0.2886353148  
## 110039 1 2 0.2865545075  
## 104041 1 2 0.2864231022  
## 154044 1 2 0.2860530382  
## 6552 1 2 0.2834409714  
## 12072 1 2 0.2828088364  
## 71066 1 2 0.2820544002  
## 39039 1 2 0.2819168879  
## 113044 1 2 0.2815930195  
## 14584 1 2 0.2812287917  
## 10016 1 2 0.2810752884  
## 92022 1 2 0.2810581205  
## 278043 1 2 0.2808580255  
## 144074 1 2 0.2786788132  
## 53039 1 2 0.2785913544  
## 80052 1 2 0.2781550001  
## 121043 1 2 0.2774633932  
## 72066 1 2 0.2762829716  
## 342074 1 2 0.2762792728  
## 93552 1 2 0.2755856772  
## 339093 1 2 0.2754134830  
## 81252 1 2 0.2738039400  
## 51052 1 2 0.2734897392  
## 297023 1 2 0.2733756531  
## 68045 1 2 0.2730341299  
## 102574 1 2 0.2727507223  
## 117393 1 2 0.2722471555  
## 72873 1 2 0.2718083050  
## 123522 1 2 0.2711653536  
## 41872 1 2 0.2708736107  
## 224093 1 2 0.2708252998  
## 95061 1 2 0.2695686040  
## 6988 1 2 0.2691268518  
## 10531 1 2 0.2689470616  
## 64536 1 2 0.2687944317  
## 5011 1 2 0.2686988287  
## 103844 1 2 0.2682750349  
## 44042 1 2 0.2682692300  
## 71042 1 2 0.2682376279  
## 2016 1 2 0.2676788413  
## 84061 1 2 0.2664314049  
## 4082 1 2 0.2663571961  
## 163423 1 2 0.2654736180  
## 129093 1 2 0.2645347167  
## 158561 1 2 0.2642393018  
## 98543 1 2 0.2636130701  
## 41061 1 2 0.2634218434  
## 312274 1 2 0.2633076473  
## 155044 1 2 0.2627533344  
## 116063 1 2 0.2622045914  
## 92041 1 2 0.2619724214  
## 44036 1 2 0.2611585102  
## 1021 1 2 0.2610288269  
## 81093 1 2 0.2603166702  
## 189023 1 2 0.2593517042  
## 160044 1 2 0.2593491974  
## 130042 1 2 0.2593366661  
## 087F61 1 2 0.2593014914  
## 44493 1 2 0.2580219088  
## 90074 1 2 0.2577601943  
## 61037 1 2 0.2576401074  
## 3.70E+94 1 2 0.2572317348  
## 1.00E+24 1 2 0.2569985307  
## 45045 1 2 0.2569274685  
## 206021 1 2 0.2560395879  
## 251023 1 2 0.2552133281  
## 39036 1 2 0.2551869814  
## 96053 1 2 0.2550069099  
## 2023 1 2 0.2543256426  
## 21016 1 2 0.2542778592  
## 20074 1 2 0.2540758378  
## 224544 1 2 0.2534597214  
## 39552 1 2 0.2524426014  
## 76074 1 2 0.2523559961  
## 310021 1 2 0.2517969668  
## 200074 1 2 0.2514872418  
## 26037 1 2 0.2513501006  
## 38084 1 2 0.2509338045  
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## 82572 1 2 0.2491286736  
## 160636 1 2 0.2490693112  
## 12042 1 2 0.2481062052  
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## 78023 1 2 0.2466311066  
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## 169043 1 2 0.2457720386  
## 102061 1 2 0.2455192503  
## 5082 1 2 0.2451987101  
## 208545 1 2 0.2450659174  
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## 97045 1 2 0.2429057201  
## 81332 1 2 0.2424000985  
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## 77538 1 2 0.2416992440  
## 30453 1 2 0.2415043550  
## 214044 1 2 0.2407394433  
## 3037 1 2 0.2407183454  
## 346023 1 2 0.2388225187  
## 102738 1 2 0.2385884846  
## 344323 1 2 0.2385069717  
## 319143 1 2 0.2373519706  
## 37551 1 2 0.2370216787  
## 182014 1 2 0.2368230594  
## 97039 1 2 0.2364856392  
## 120041 1 2 0.2357098830  
## 365074 1 2 0.2354710834  
## 29087 1 2 0.2353141293  
## 12033 1 2 0.2348834254  
## 16092 1 2 0.2333385697  
## 168536 1 2 0.2325169785  
## 105074 1 2 0.2321696897  
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## 192043 1 2 0.2312229689  
## 46652 1 2 0.2302650345  
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## 9074 1 2 0.2238688013  
## 85044 1 2 0.2235478338  
## 106091 1 2 0.2235245723  
## 3839 1 2 0.2232027017  
## 29041 1 2 0.2231306017  
## 21071 1 2 0.2227609164  
## 54041 1 2 0.2212467232  
## 211593 1 2 0.2212366260  
## 17086 1 2 0.2209233328  
## 161574 1 2 0.2205159443  
## 48838 1 2 0.2204162437  
## 63084 1 2 0.2200229579  
## 115036 1 2 0.2184849023  
## 88793 1 2 0.2172958376  
## 111939 1 2 0.2170410150  
## 474021 1 2 0.2151303882  
## 17062 1 2 0.2146777719  
## 83539 1 2 0.2143886854  
## 40061 1 2 0.2134135565  
## 347021 1 2 0.2125239328  
## 57038 1 2 0.2123526581  
## 189074 1 2 0.2119754708  
## 70553 1 2 0.2102388321  
## 118067 1 2 0.2101400689  
## 37886 1 2 0.2094346557  
## 488521 1 2 0.2083916028  
## 6091 1 2 0.2080979469  
## 40016 1 2 0.2064919437  
## 57552 1 2 0.2046421197  
## 154061 1 2 0.2024431889  
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## 17551 2 1 0.1561032964  
## 121841 2 1 0.1429971528  
## 9084 2 1 0.1173791910  
## 89023 2 1 0.1137060672  
## 103045 2 1 0.1106019975  
## 43814 2 1 0.1051434926  
## 5573 2 1 0.1016803925  
## 60563 2 1 0.1005076922  
## 137574 2 1 0.0334452147  
## 370021 2 1 0.0308946473  
## Average silhouette width per cluster:  
## [1] 0.04573536 0.59030629  
## Average silhouette width of total data set:  
## [1] 0.4340144  
##   
## Available components:  
## [1] "medoids" "id.med" "clustering" "objective" "isolation"   
## [6] "clusinfo" "silinfo" "diss" "call" "data"

#plot a graphic showing the clusters and the medoids of each cluster  
plot(result$data, col = result$clustering)  
points(result$medoids, col = 1:2, pch = 4)



# Compute PAM  
library("cluster")  
pam.res <- pam(df, 2)  
  
# Visualize  
fviz\_cluster(pam.res)



#### ii). Summary statistics for each cluster

clust=data.frame("cluster"=pam.res$clustering)  
clust$cluster=as.factor(clust$cluster)  
  
# Make the index into a column for the clustered\_data  
Hospital\_ID <- rownames(clust)  
clust<- cbind(Hospital\_ID,clust)  
head(clust)

## Hospital\_ID cluster  
## 12042 12042 1  
## 348593 348593 2  
## 62073 62073 2  
## 135063 135063 1  
## 214044 214044 1  
## 103536 103536 2

str(clust)

## 'data.frame': 3000 obs. of 2 variables:  
## $ Hospital\_ID: Factor w/ 3000 levels " 006F61"," 006G61",..: 309 1649 2344 427 1009 86 521 1681 1588 261 ...  
## $ cluster : Factor w/ 2 levels "1","2": 1 2 2 1 1 2 2 2 2 1 ...

# Make the index into a column for the hospital\_data  
Hospital\_ID <- rownames(hospital\_data)  
sales=data.frame("SALES"=hospital\_data[,6])  
sales\_data <- cbind(Hospital\_ID,sales)  
head(sales\_data)

## Hospital\_ID SALES  
## 12042 12042 NA  
## 348593 348593 -0.4350562  
## 62073 62073 -0.5396399  
## 135063 135063 -0.2496577  
## 214044 214044 0.7866720  
## 103536 103536 NA

str(sales\_data)

## 'data.frame': 3000 obs. of 2 variables:  
## $ Hospital\_ID: Factor w/ 3000 levels " 006F61"," 006G61",..: 309 1649 2344 427 1009 86 521 1681 1588 261 ...  
## $ SALES : num NA -0.435 -0.54 -0.25 0.787 ...

new\_df = merge(x=sales\_data,y=clust,by='Hospital\_ID')  
head(new\_df)

## Hospital\_ID SALES cluster  
## 1 006F61 -0.5206247 2  
## 2 006G61 NA 1  
## 3 009A74 NA 2  
## 4 011A71 NA 2  
## 5 011A72 -0.4445638 2  
## 6 015A63 NA 2

str(new\_df)

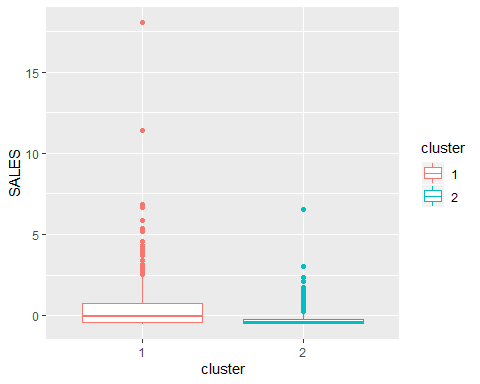
## 'data.frame': 3000 obs. of 3 variables:  
## $ Hospital\_ID: Factor w/ 3000 levels " 006F61"," 006G61",..: 1 2 3 4 5 6 7 8 9 10 ...  
## $ SALES : num -0.521 NA NA NA -0.445 ...  
## $ cluster : Factor w/ 2 levels "1","2": 2 1 2 2 2 2 2 2 1 2 ...

# Box plot of sales by clusters  
# From the box plots cluster 10 had the highest average sales, cluster 14 had the most outliers  
  
attach(new\_df)

## The following object is masked \_by\_ .GlobalEnv:  
##   
## Hospital\_ID

p<-ggplot(new\_df, aes(x=cluster, y=SALES, color=cluster)) +  
 geom\_boxplot()  
p

## Warning: Removed 1280 rows containing non-finite values (stat\_boxplot).



# PART 2

# Data preparation  
  
hospital\_data=as.data.frame(hospital\_data)  
dim(hospital\_data)

## [1] 3000 14

sum(is.na(hospital\_data)) #how many missing values

## [1] 1280

hospitals=na.omit(hospital\_data)#remove missing values  
dim(hospitals)

## [1] 1720 14

#Split the data into train and test data  
smp\_size <- floor(0.80 \* nrow(hospitals))  
train\_ind <- sample(seq\_len(nrow(hospitals)), size = smp\_size)  
train.set <- hospitals[train\_ind, ]  
validation.set <- hospitals[-train\_ind, ]

### Decision tree model

Thus model will be used predict the sales using the independent variables (operational and demographic)

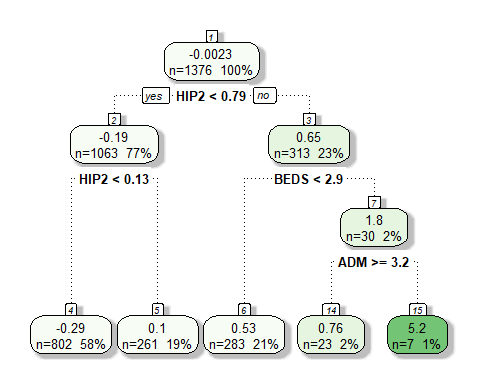
library(rpart)  
mytree <- rpart(  
 SALES ~ .,   
 data = train.set)  
mytree

## n= 1376   
##   
## node), split, n, deviance, yval  
## \* denotes terminal node  
##   
## 1) root 1376 1365.42400 -0.00225944   
## 2) HIP2< 0.788591 1063 334.56940 -0.19447690   
## 4) HIP2< 0.1318165 802 166.64450 -0.29142250 \*  
## 5) HIP2>=0.1318165 261 137.22600 0.10341710 \*  
## 3) HIP2>=0.788591 313 858.19380 0.65054300   
## 6) BEDS< 2.863692 283 421.77380 0.53055440 \*  
## 7) BEDS>=2.863692 30 393.91020 1.78243600   
## 14) ADM>=3.188247 23 73.42777 0.75504880 \*  
## 15) ADM< 3.188247 7 216.43790 5.15813600 \*

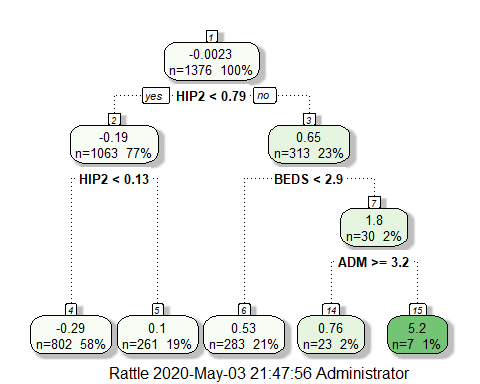
library(rattle)

## Rattle: A free graphical interface for data science with R.  
## Version 5.3.0 Copyright (c) 2006-2018 Togaware Pty Ltd.  
## Type 'rattle()' to shake, rattle, and roll your data.

library(rpart.plot)  
library(RColorBrewer)  
  
# plot mytree  
fancyRpartPlot(mytree, caption = NULL)



# Full-grown tree with 6 splits using different variables (Not running the line below - do it to see the tree)  
fancyRpartPlot(mytree)



# As always, predict and evaluate on the test set, here the predicted vales of transformed sales is compared with actual validation test data and the mean squared error is calculated to check the error of our prediction, the smaller the better.   
test.pred.rtree <- predict(mytree,validation.set)   
  
RMSE.rtree <- sqrt(mean((test.pred.rtree-validation.set$SALES)^2))  
RMSE.rtree

## [1] 0.7926431

#Mean absolute error  
MAE.rtree <- mean(abs(test.pred.rtree-validation.set$SALES))  
MAE.rtree

## [1] 0.4762711

# Now that we have a full-grown tree, let’s see if it’s possible to prune it…  
  
# Check cross-validation results (xerror column)  
printcp(mytree)

##   
## Regression tree:  
## rpart(formula = SALES ~ ., data = train.set)  
##   
## Variables actually used in tree construction:  
## [1] ADM BEDS HIP2  
##   
## Root node error: 1365.4/1376 = 0.99231  
##   
## n= 1376   
##   
## CP nsplit rel error xerror xstd  
## 1 0.126452 0 1.00000 1.00111 0.25342  
## 2 0.053666 1 0.87355 0.89584 0.23517  
## 3 0.022483 3 0.76622 0.93729 0.23676  
## 4 0.010000 4 0.74373 0.94176 0.23990