Predicting Health Insurance Costs

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Dependencies

```
library(NbClust)
library(mclust)
```

```
## Warning: package 'mclust' was built under R version 4.2.3
```

```
## Package 'mclust' version 6.0.0
## Type 'citation("mclust")' for citing this R package in publications.
```

```
library(flexclust)
```

```
## Warning: package 'flexclust' was built under R version 4.2.3
```

```
## Loading required package: grid
```

```
## Loading required package: lattice
```

```
## Loading required package: modeltools
```

```
## Loading required package: stats4
```

```
library(cluster)
library(fpc)
```

```
## Warning: package 'fpc' was built under R version 4.2.3
```

Data Preparation

Import data and remove missing rows.

```
insurance <- read.csv("insurance.csv")
insurance <- na.omit(insurance)
insurance$age <- as.numeric(insurance$age)
insurance$bmi <- as.numeric(insurance$bmi)
```

Linear Regression Models

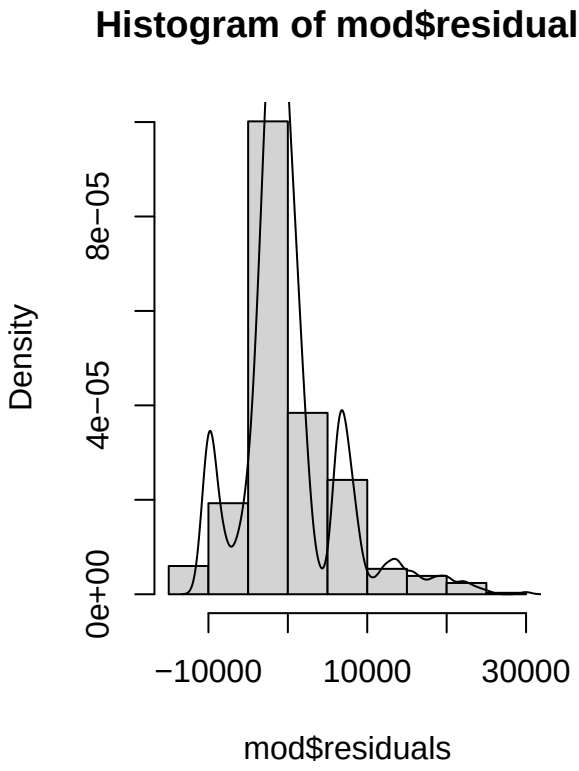
```r
mod<-lm(charges~., data=insurance)
summary(mod)
```

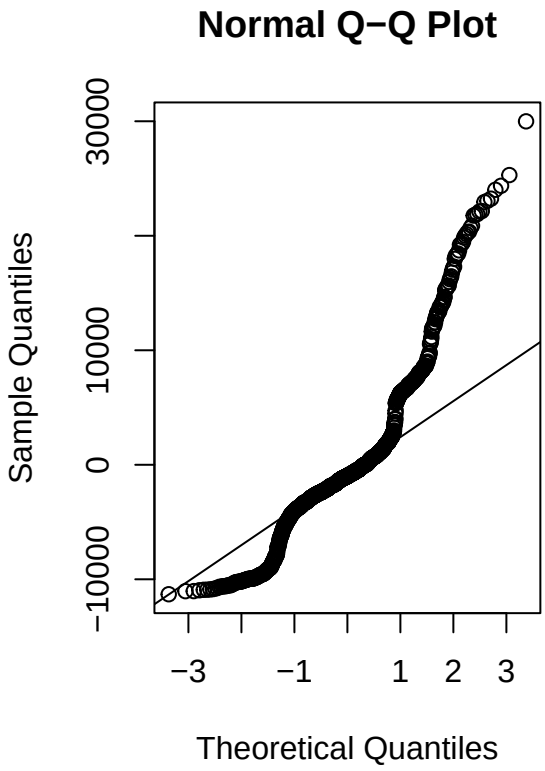
```
##
## Call:
## lm(formula = charges ~ ., data = insurance)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11304.9  -2848.1   -982.1   1393.9  29992.8
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -11938.5      987.8 -12.086  < 2e-16 ***
## age                256.9       11.9  21.587  < 2e-16 ***
## sexmale           -131.3      332.9  -0.394 0.693348
## bmi                339.2       28.6  11.860  < 2e-16 ***
## children           475.5      137.8   3.451 0.000577 ***
## smokeryes        23848.5      413.1  57.723  < 2e-16 ***
## regionnorthwest   -353.0      476.3  -0.741 0.458769
## regionsoutheast  -1035.0      478.7  -2.162 0.030782 *
## regionsouthwest   -960.0      477.9  -2.009 0.044765 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6062 on 1329 degrees of freedom
## Multiple R-squared:  0.7509, Adjusted R-squared:  0.7494
## F-statistic: 500.8 on 8 and 1329 DF,  p-value: < 2.2e-16
```

Finding residuals and QQ plots for all factors

```r
par(mfrow=c(1,2))
hist(mod$residuals, prob = TRUE)
lines(density(mod$residuals))

qqnorm(y=mod$residuals)
qqline(y=mod$residuals, datax = FALSE)
```





Using only statistically significant factors: age, bmi, children, smoker (yes).

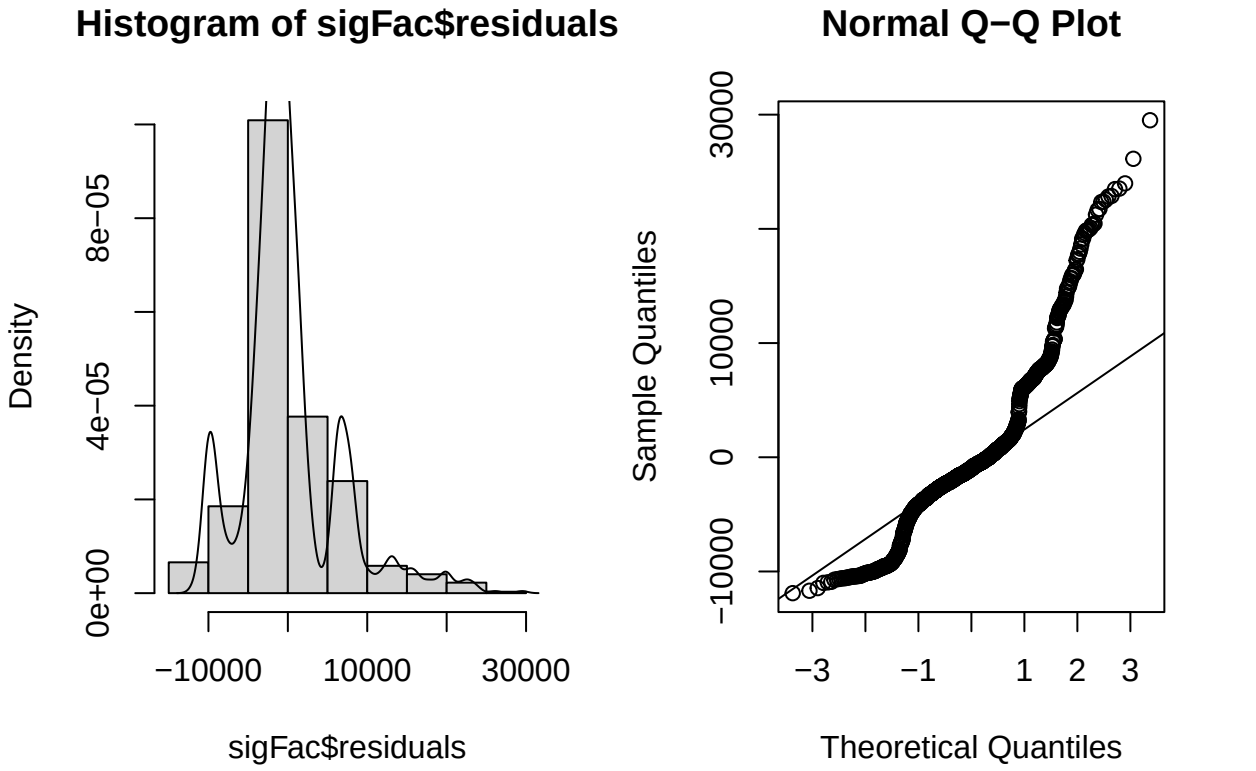
```
sigFac<-lm(charges~age + bmi + children + smoker, data=insurance)
summary(sigFac)
```

```
##
## Call:
## lm(formula = charges ~ age + bmi + children + smoker, data = insurance)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11897.9  -2920.8   -986.6   1392.2  29509.6
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -12102.77     941.98 -12.848  < 2e-16 ***
## age            257.85      11.90  21.675  < 2e-16 ***
## bmi            321.85      27.38  11.756  < 2e-16 ***
## children       473.50     137.79   3.436 0.000608 ***
## smokeryes    23811.40     411.22  57.904  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6068 on 1333 degrees of freedom
## Multiple R-squared:  0.7497, Adjusted R-squared:  0.7489
## F-statistic: 998.1 on 4 and 1333 DF,  p-value: < 2.2e-16
```

Residual Plots

```
par(mfrow=c(1,2))
hist(sigFac$residuals, prob = TRUE)
lines(density(sigFac$residuals))

qqnorm(y=sigFac$residuals)
qqline(y=sigFac$residuals, datax = FALSE)
```



Testing Correlation With Clustering Our previous model stated that age, bmi, children, smoker (yes) were all significant factors. We are now going to perform a clustering model to see if this still holds true.

```
seed.val<-1234

insurance.scaled <- scale(insurance[1] + insurance[3])
for(i in 1:ncol(insurance.scaled)){
print(max(insurance.scaled[ , i]))
}
```

```
## [1] 2.336639
```

```
RNGversion("4.1.2")
set.seed(seed.val)


clusterInsurance <- kmeans(insurance.scaled, 2, nstart = 25)
```

```
clusterInsurance$size
```

```
## [1] 657 681
```

```
clusterInsurance$tot.withinss
```

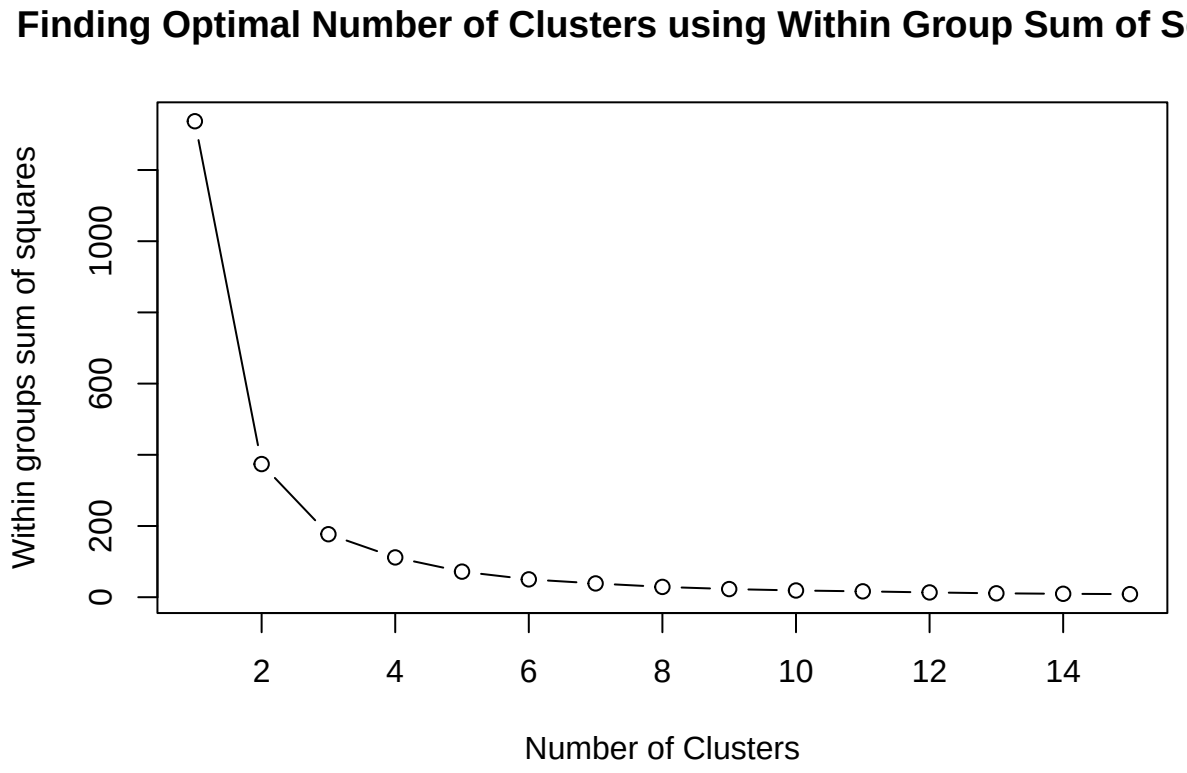
```
## [1] 374.0375
```

```
clusterInsurance$betweenss
```

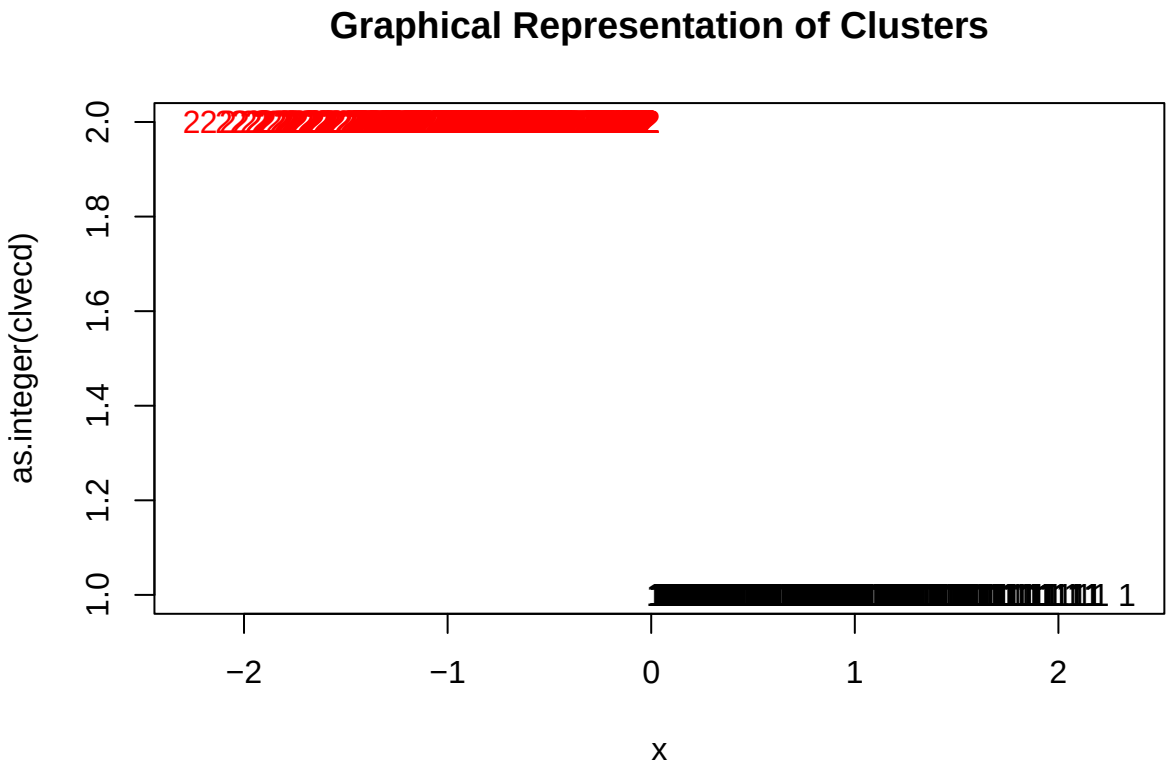
```
## [1] 962.9625
```

```
wssplot <- function(data, nc=15, seed=1234){
               wss <- (nrow(data)-1)*sum(apply(data,2,var))
               for (i in 2:nc){
                    set.seed(seed)
                    wss[i] <- sum(kmeans(data, centers=i)$withinss)}
                plot(1:nc, wss, main = "Finding Optimal Number of Clusters using Within Group Sum of Sq
                     ylab="Within groups sum of squares")
}

wssplot(insurance.scaled)
```



```
plotcluster(insurance.scaled, clusterInsurance$cluster)
title("Graphical Representation of Clusters")
```



Commented out because of knitting issues. Returned k = 2 as optimal amount of clusters.

#nc <- NbClust(insurance.scaled, min.nc=2, max.nc=15, method="kmeans")

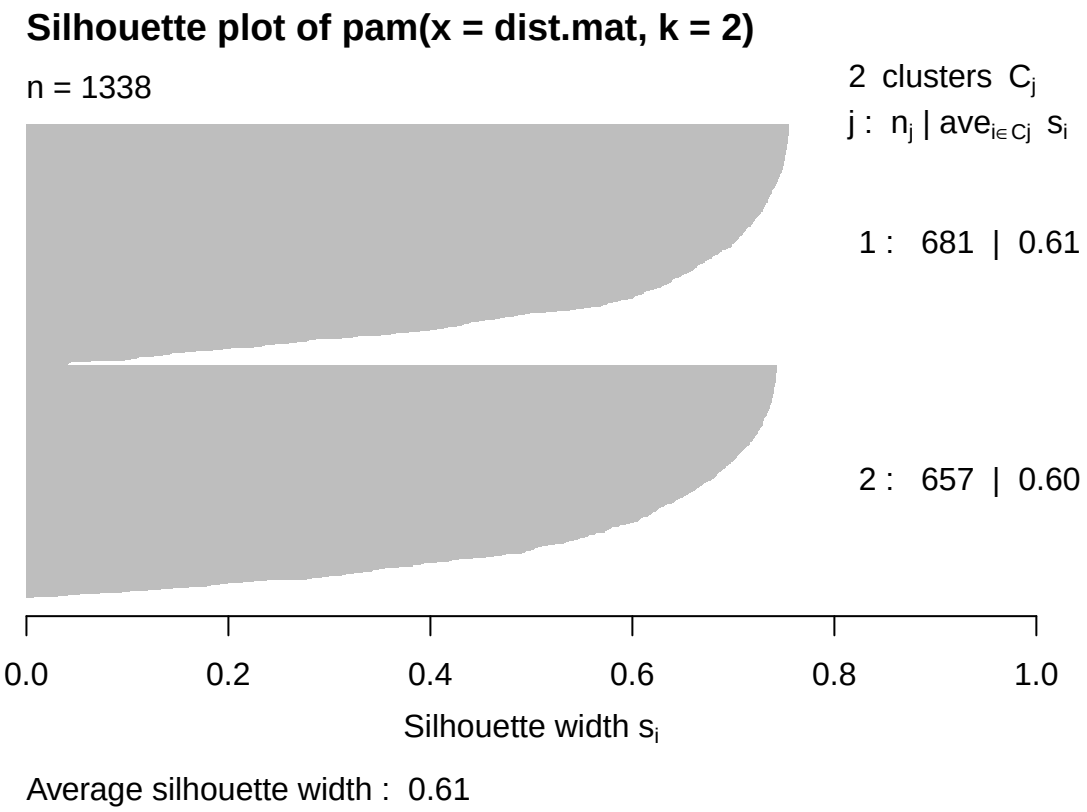
#table(nc$Best.n[1,])

Optimal number of clusters using PAM

```
dist.mat<-daisy(insurance.scaled,  metric="euclidean")
pk <- pamk(dist.mat, krange=2:15, usepam=TRUE, diss=TRUE)
pk$nc
```

```
## [1] 2
```

```
fit.pam = pam(dist.mat,2)
plot(fit.pam)
```




```
jpeg("MYPLOT.jpg")
plot(fit.pam)
dev.off()
```

```
## pdf
##   2
```

Chi-Squared Test

```
cont.table <- table(insurance$charges, clusterInsurance$cluster)
print(chisq.test(cont.table))
```

```
## Warning in chisq.test(cont.table): Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  cont.table
## X-squared = 1338, df = 1336, p-value = 0.4794
```

How different are the clusters?

```
randIndex(cont.table)
```

```
##          ARI
## 2.237909e-06
```