Project

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```
## Data Processing
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.0.2
```

```
## -- Attaching packages ---------------------------------------------------------------------------
```

```
## v ggplot2 3.3.2     v purrr   0.3.4
## v tibble  3.0.1     v dplyr   1.0.2
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.0
```

```
## Warning: package 'ggplot2' was built under R version 4.0.2
```

```
## Warning: package 'tidyr' was built under R version 4.0.2
```

```
## Warning: package 'readr' was built under R version 4.0.2
```

```
## Warning: package 'dplyr' was built under R version 4.0.2
```

```
## Warning: package 'stringr' was built under R version 4.0.2
```

```
## Warning: package 'forcats' was built under R version 4.0.2
```

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

```
library(dplyr)
library(MASS)
```

```
## Warning: package 'MASS' was built under R version 4.0.2
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```
library(leaps)
```

```
## Warning: package 'leaps' was built under R version 4.0.2
```

```
setwd("/Users/maxryoo/Documents/MSDS/STAT6021/Project2")
data <- read.csv("data/insurance.csv")
head(data)
```

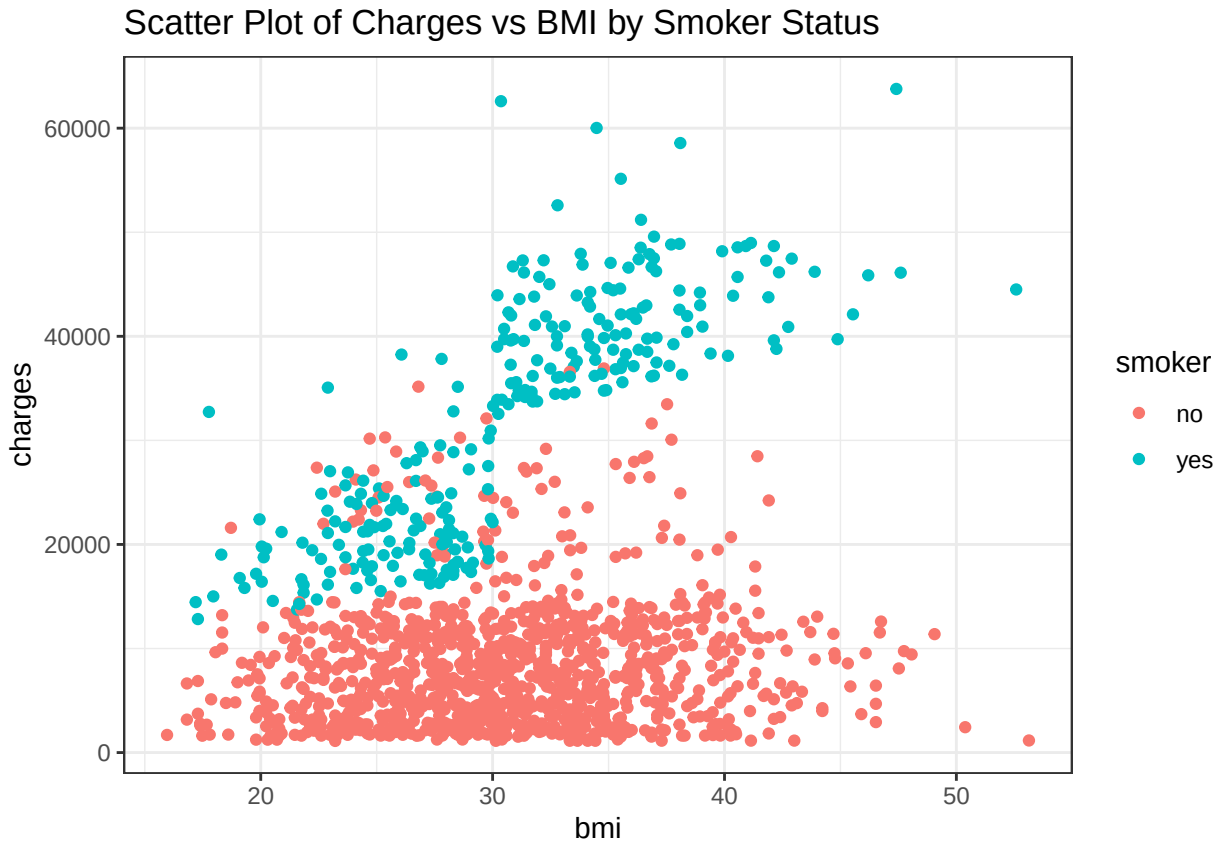
```
##   age    sex    bmi children smoker    region   charges
## 1  19 female 27.900        0    yes southwest 16884.924
```

```
## 2  18   male 33.770        1     no southeast  1725.552
## 3  28   male 33.000        3     no southeast  4449.462
## 4  33   male 22.705        0     no northwest 21984.471
## 5  32   male 28.880        0     no northwest  3866.855
## 6  31 female 25.740        0     no southeast  3756.622
```

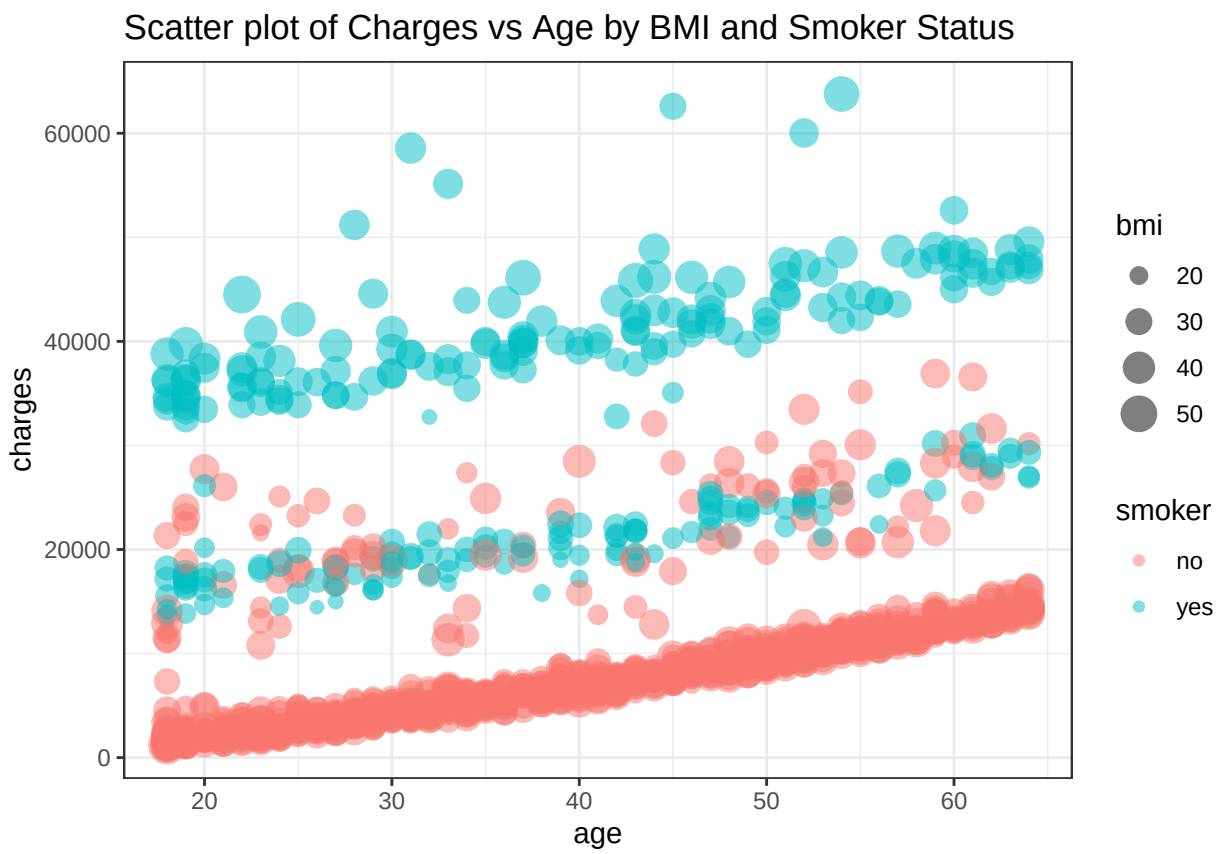
```
data$significant.charge = as.factor(data$charges > median(data$charges))
head(data)
```

```
##   age    sex    bmi children smoker    region   charges significant.charge
## 1  19 female 27.900        0    yes southwest 16884.924               TRUE
## 2  18   male 33.770        1     no southeast  1725.552              FALSE
## 3  28   male 33.000        3     no southeast  4449.462              FALSE
## 4  33   male 22.705        0     no northwest 21984.471               TRUE
## 5  32   male 28.880        0     no northwest  3866.855              FALSE
## 6  31 female 25.740        0     no southeast  3756.622              FALSE
```

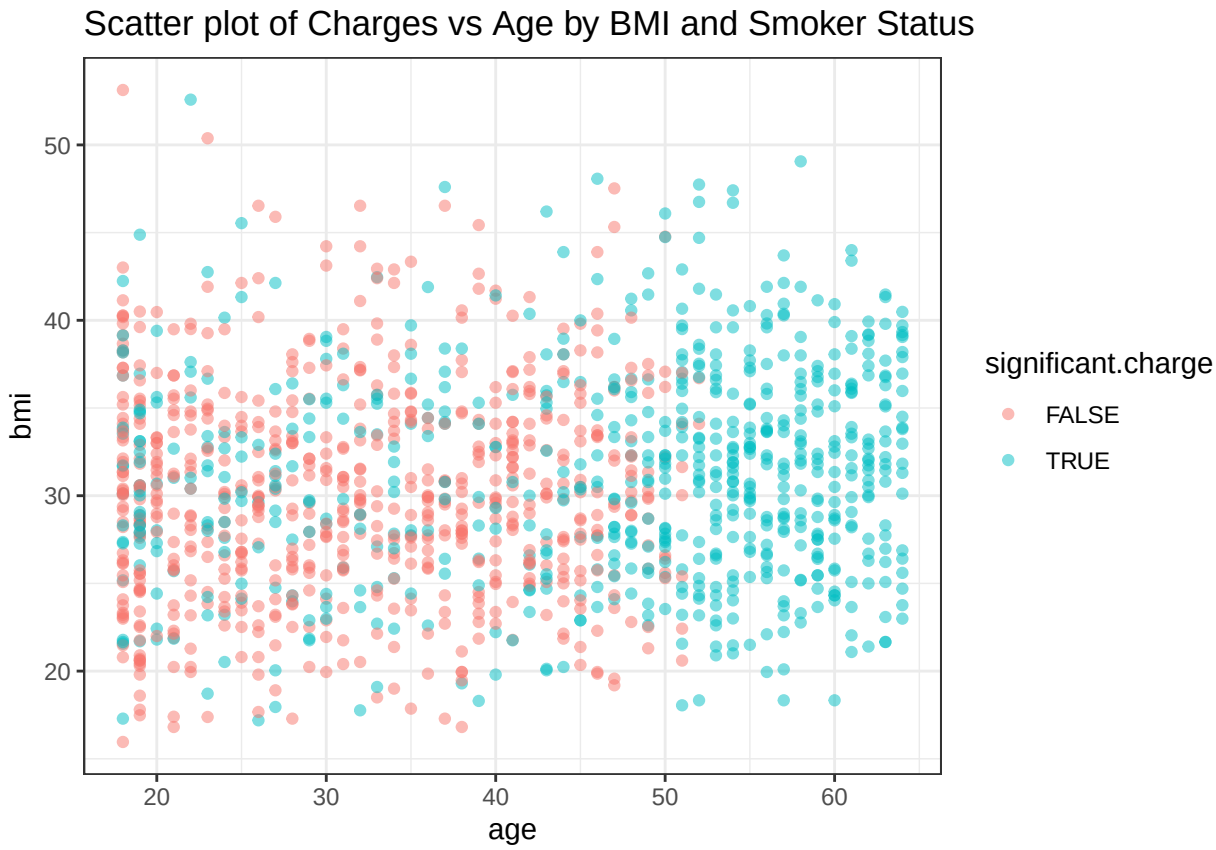
```
ggplot(aes(x=bmi, y=charges, color=smoker), data=data) +
  labs(title="Scatter Plot of Charges vs BMI by Smoker Status") +
  theme_bw() +
  geom_point()
```



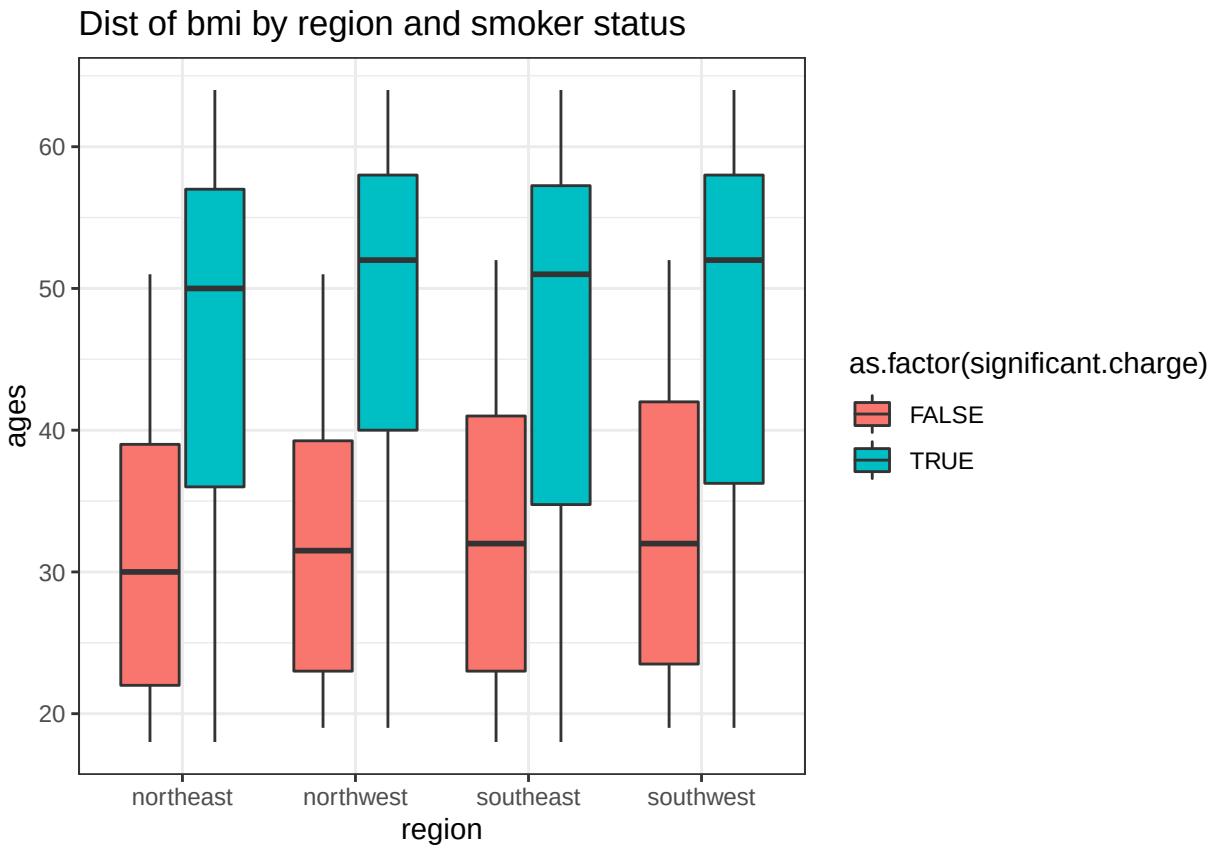

```
ggplot(aes(x=age,y=charges, color=smoker, size=bmi), data=data) +
  labs(title="Scatter plot of Charges vs Age by BMI and Smoker Status") +
  theme_bw() +
  geom_point(alpha=0.5)
```



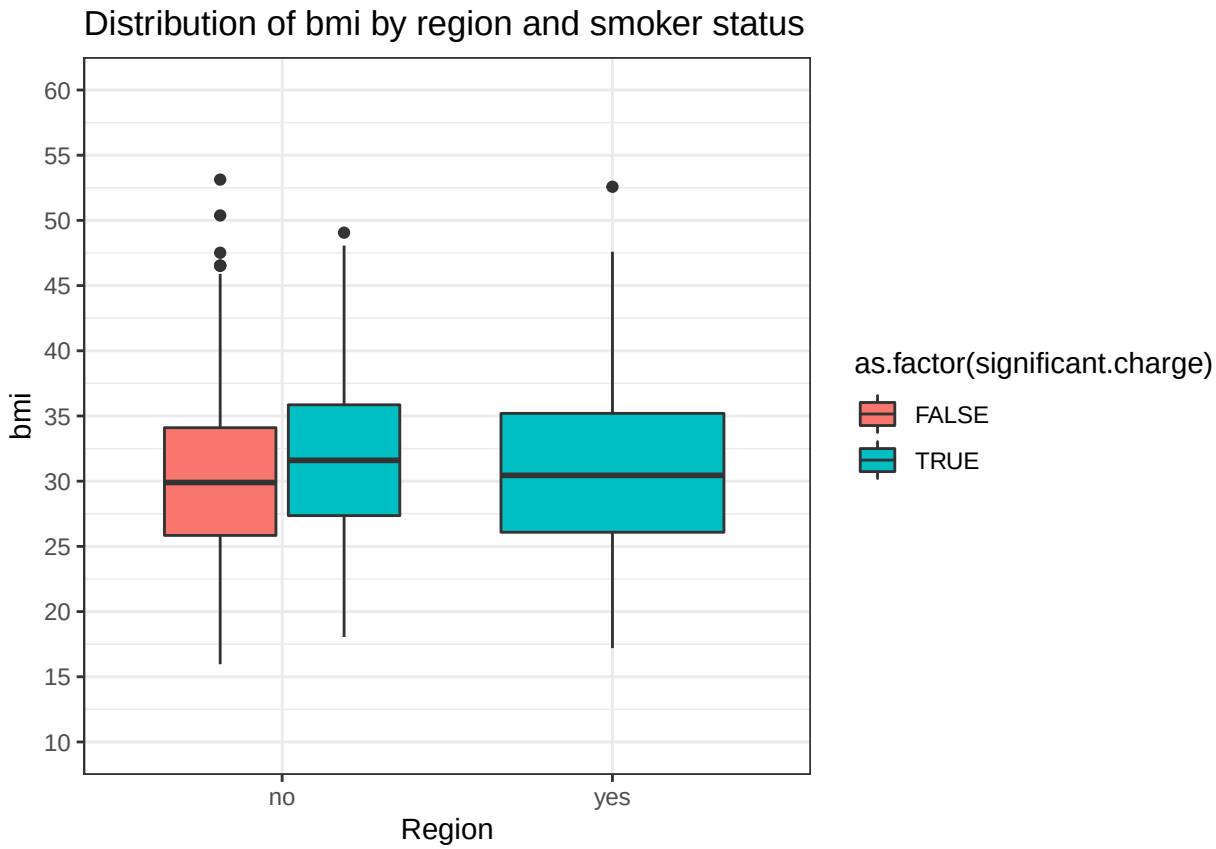

```
ggplot(aes(x=age,y=bmi, color=significant.charge), data=data) +
  labs(title="Scatter plot of Charges vs Age by BMI and Smoker Status") +
  theme_bw() +
  geom_point(alpha=0.5)
```




```
ggplot(data, aes(x=region, y=age, fill=as.factor(significant.charge)))+
  geom_boxplot() +
  theme_bw() +
  labs(x="region", y="ages", title="Dist of bmi by region and smoker status")
```

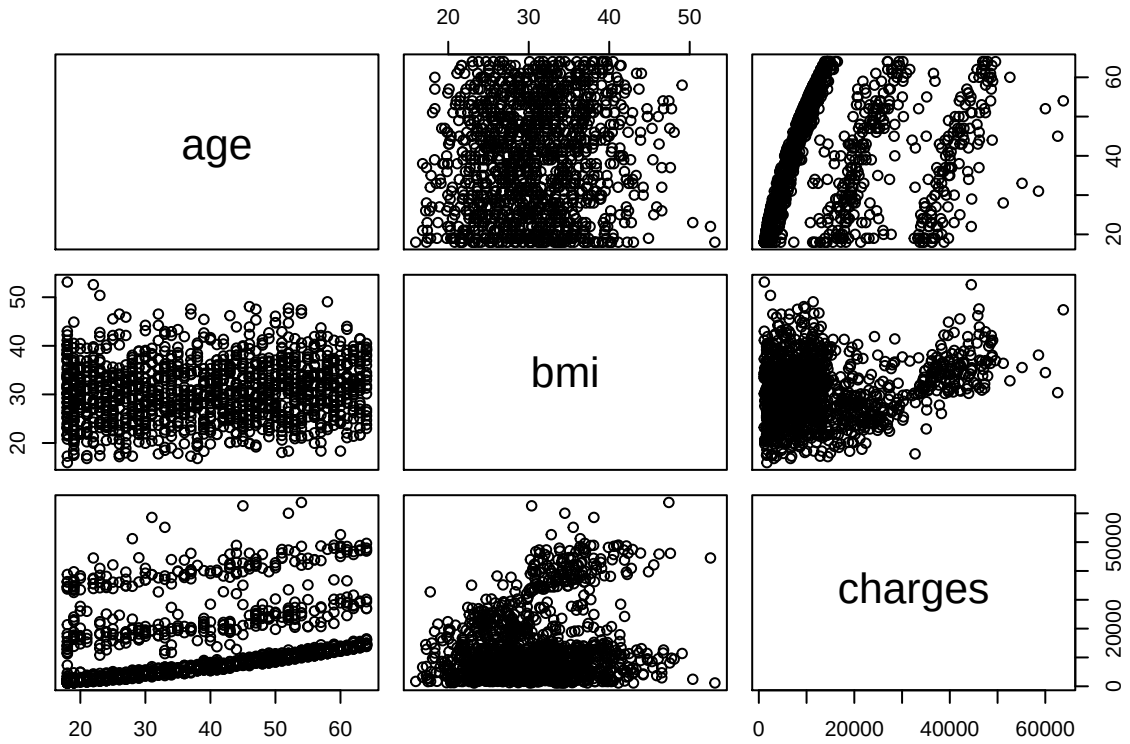



```
ggplot(data, aes(x=smoker, y=bmi, fill=as.factor(significant.charge)))+
  geom_boxplot() +
  theme_bw() +
  labs(x="Region", y="bmi", title="Distribution of bmi by region and smoker status") +  scale_y_continu
```



Correlation

```
pairs(data[c("age", "bmi", "charges")])
```




```
round(cor(data[c("age", "bmi", "charges")]),4)
```

```
##             age    bmi charges
## age     1.0000 0.1093  0.2990
## bmi     0.1093 1.0000  0.1983
## charges 0.2990 0.1983  1.0000
```

All possible regressions and pull based on adjusted R square, mallow, and BIC

```
no_class_predictor = data[1:7]
allreg2 <- regsubsets(charges ~., data=no_class_predictor, nbest=2)
summary(allreg2)
```

```
## Subset selection object
## Call: regsubsets.formula(charges ~ ., data = no_class_predictor, nbest = 2)
## 8 Variables  (and intercept)
##                  Forced in Forced out
## age                  FALSE      FALSE
## sexmale              FALSE      FALSE
## bmi                  FALSE      FALSE
## children             FALSE      FALSE
## smokeryes            FALSE      FALSE
## regionnorthwest      FALSE      FALSE
## regionsoutheast      FALSE      FALSE
## regionsouthwest      FALSE      FALSE
## 2 subsets of each size up to 8
## Selection Algorithm: exhaustive
##          age sexmale bmi children smokeryes regionnorthwest regionsoutheast
## 1  ( 1 ) " " " "     " " " " "      "*"       " "              " "
## 1  ( 2 ) "*" " "     " " " " "      " "       " "              " "
```

```
## 2  ( 1 ) "*" " "     " " " "      "*"       " "             " "
## 2  ( 2 ) " " " "     "*" " "      "*"       " "             " "
## 3  ( 1 ) "*" " "     "*" " "      "*"       " "             " "
## 3  ( 2 ) "*" " "     " " "*"      "*"       " "             " "
## 4  ( 1 ) "*" " "     "*" "*"      "*"       " "             " "
## 4  ( 2 ) "*" " "     "*" " "      "*"       " "             "*"
## 5  ( 1 ) "*" " "     "*" "*"      "*"       " "             "*"
## 5  ( 2 ) "*" " "     "*" "*"      "*"       " "             " "
## 6  ( 1 ) "*" " "     "*" "*"      "*"       " "             "*"
## 6  ( 2 ) "*" "*"     "*" "*"      "*"       " "             "*"
## 7  ( 1 ) "*" " "     "*" "*"      "*"       "*"             "*"
## 7  ( 2 ) "*" "*"     "*" "*"      "*"       " "             "*"
## 8  ( 1 ) "*" "*"     "*" "*"      "*"       "*"             "*"
##          regionsouthwest
## 1  ( 1 ) " "
## 1  ( 2 ) " "
## 2  ( 1 ) " "
## 2  ( 2 ) " "
## 3  ( 1 ) " "
## 3  ( 2 ) " "
## 4  ( 1 ) " "
## 4  ( 2 ) " "
## 5  ( 1 ) " "
## 5  ( 2 ) "*"
## 6  ( 1 ) "*"
## 6  ( 2 ) " "
## 7  ( 1 ) "*"
## 7  ( 2 ) "*"
## 8  ( 1 ) "*"
```

Best for Adjusted R square

```
coef(allreg2, which.max(summary(allreg2)$adjr2))
```

```
##     (Intercept)             age             bmi        children       smokeryes
##     -12165.3824        257.0064        338.6413        471.5441      23843.8749
## regionsoutheast regionsouthwest
##       -858.4696       -782.7452
```

Best for Mallows

```
coef(allreg2, which.min(summary(allreg2)$cp))
```

```
##     (Intercept)             age             bmi        children       smokeryes
##     -12165.3824        257.0064        338.6413        471.5441      23843.8749
## regionsoutheast regionsouthwest
##       -858.4696       -782.7452
```

Best for BIC

```
coef(allreg2, which.min(summary(allreg2)$bic))
```

```
## (Intercept)         age         bmi    children   smokeryes
## -12102.7694    257.8495    321.8514    473.5023  23811.3998
```

Forward Selection

```
##intercept only model
regnull <- lm(charges~1, data=no_class_predictor)
##model with all predictors
regfull <- lm(charges ~ . , data=no_class_predictor)
```

Forward Selection

```
step(regnull, scope=list(lower=regnull, upper=regfull), direction="forward")
```

```
## Start:  AIC=25160.18
## charges ~ 1
##
##             Df  Sum of Sq        RSS   AIC
## + smoker     1 1.2152e+11 7.4554e+10 23868
## + age        1 1.7530e+10 1.7854e+11 25037
## + bmi        1 7.7134e+09 1.8836e+11 25108
## + children   1 9.0660e+08 1.9517e+11 25156
## + region     3 1.3008e+09 1.9477e+11 25157
## + sex        1 6.4359e+08 1.9543e+11 25158
## <none>                    1.9607e+11 25160
##
## Step:  AIC=23868.38
## charges ~ smoker
##
##             Df  Sum of Sq        RSS   AIC
## + age        1 1.9928e+10 5.4626e+10 23454
## + bmi        1 7.4856e+09 6.7069e+10 23729
## + children   1 7.5272e+08 7.3802e+10 23857
## <none>                    7.4554e+10 23868
## + sex        1 1.4213e+06 7.4553e+10 23870
## + region     3 1.0752e+08 7.4447e+10 23872
##
## Step:  AIC=23454.24
## charges ~ smoker + age
##
##             Df  Sum of Sq        RSS   AIC
## + bmi        1 5112896646 4.9513e+10 23325
## + children   1  459283727 5.4167e+10 23445
## <none>                    5.4626e+10 23454
## + sex        1    2225509 5.4624e+10 23456
## + region     3  138426748 5.4488e+10 23457
##
## Step:  AIC=23324.76
## charges ~ smoker + age + bmi
##
##             Df Sum of Sq        RSS   AIC
## + children   1 434769398 4.9078e+10 23315
## + region     3 232012208 4.9281e+10 23324
## <none>                   4.9513e+10 23325
## + sex        1   3942912 4.9509e+10 23327
##
## Step:  AIC=23314.96
## charges ~ smoker + age + bmi + children
```

```
##
##          Df Sum of Sq        RSS   AIC
## + region  3 233200844 4.8845e+10 23315
## <none>                4.9078e+10 23315
## + sex     1   5486063 4.9073e+10 23317
##
## Step:  AIC=23314.58
## charges ~ smoker + age + bmi + children + region
##
##        Df Sum of Sq        RSS   AIC
## <none>              4.8845e+10 23315
## + sex   1   5716429 4.8840e+10 23316
```

```
##
## Call:
## lm(formula = charges ~ smoker + age + bmi + children + region,
##     data = no_class_predictor)
##
## Coefficients:
##     (Intercept)        smokeryes              age              bmi
##        -11990.3          23836.3            257.0            338.7
##        children  regionnorthwest  regionsoutheast  regionsouthwest
##           474.6           -352.2          -1034.4           -959.4
```

```
(Intercept)             age             bmi        children       smokeryes regionsoutheast
-12165.3824        257.0064        338.6413        471.5441      23843.8749       -858.4696
```

regionsouthwest -782.7452

Backwards

```
step(regfull, scope=list(lower=regnull, upper=regfull), direction="backward")
```

```
## Start:  AIC=23316.43
## charges ~ age + sex + bmi + children + smoker + region
##
##            Df  Sum of Sq        RSS   AIC
## - sex       1 5.7164e+06 4.8845e+10 23315
## <none>                   4.8840e+10 23316
## - region    3 2.3343e+08 4.9073e+10 23317
## - children  1 4.3755e+08 4.9277e+10 23326
## - bmi       1 5.1692e+09 5.4009e+10 23449
## - age       1 1.7124e+10 6.5964e+10 23717
## - smoker    1 1.2245e+11 1.7129e+11 24993
##
## Step:  AIC=23314.58
## charges ~ age + bmi + children + smoker + region
##
##            Df  Sum of Sq        RSS   AIC
## <none>                   4.8845e+10 23315
## - region    3 2.3320e+08 4.9078e+10 23315
## - children  1 4.3596e+08 4.9281e+10 23324
## - bmi       1 5.1645e+09 5.4010e+10 23447
## - age       1 1.7151e+10 6.5996e+10 23715
## - smoker    1 1.2301e+11 1.7186e+11 24996
```

```
##
## Call:
## lm(formula = charges ~ age + bmi + children + smoker + region,
##     data = no_class_predictor)
##
## Coefficients:
##     (Intercept)              age              bmi         children
##        -11990.3            257.0            338.7            474.6
##       smokeryes  regionnorthwest  regionsoutheast  regionsouthwest
##         23836.3           -352.2          -1034.4           -959.4
```

Based on forward and backward

We get the same model for forward and backward

Let's first make a multiple linear regression model with all the predictors.

```
mlr_full = lm(charges ~  age + bmi + children + smoker + region, data=data)
summary(mlr_full)
```

```
##
## Call:
## lm(formula = charges ~ age + bmi + children + smoker + region,
##     data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11367.2  -2835.4   -979.7   1361.9  29935.5
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -11990.27     978.76 -12.250  < 2e-16 ***
## age                256.97      11.89  21.610  < 2e-16 ***
## bmi                338.66      28.56  11.858  < 2e-16 ***
## children           474.57     137.74   3.445 0.000588 ***
## smokeryes        23836.30     411.86  57.875  < 2e-16 ***
## regionnorthwest   -352.18     476.12  -0.740 0.459618
## regionsoutheast  -1034.36     478.54  -2.162 0.030834 *
## regionsouthwest   -959.37     477.78  -2.008 0.044846 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6060 on 1330 degrees of freedom
## Multiple R-squared:  0.7509, Adjusted R-squared:  0.7496
## F-statistic: 572.7 on 7 and 1330 DF,  p-value: < 2.2e-16
```

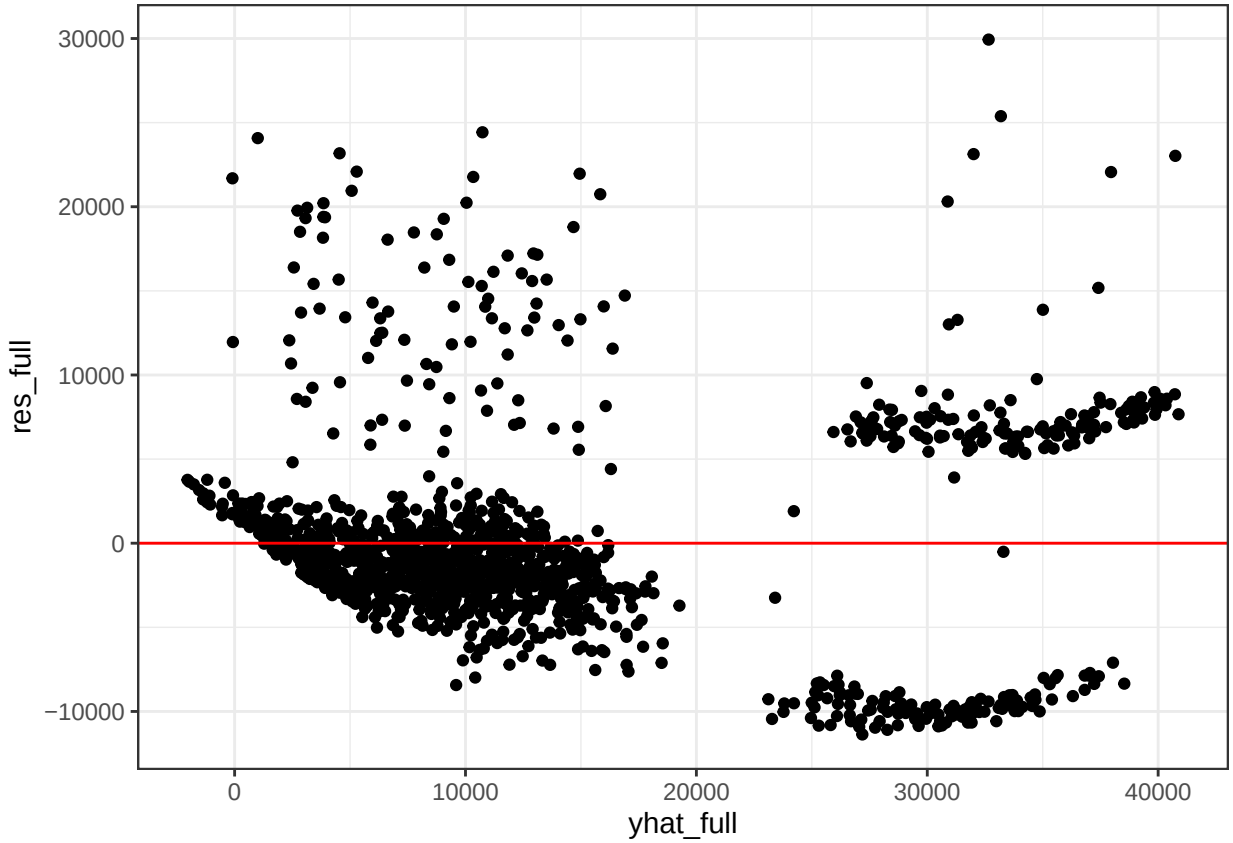
The full regression is as follows.

$$\hat{y} = -11938.5 + 256.9\text{age} - 131.3I_1 + 339.2\text{bmi} + 475.5\text{children} + 23848.5I_2 - 353.0I_3 - 1035.0I_4 - 960.0I_5$$

I_1 indicates whether the sex of the client is male. The value will be 0 for females. I_2 indicates whether that a client smokes. The value will be 0 for non smokers. I_3 indicates that the client is in the northwest region. I_4 indicates that the client is located in the southeast. I_5 indicates that the client is located inthe southwest. If the client is in the northeast I_3, I_4, I_5 will be zero, since this is the reference class.

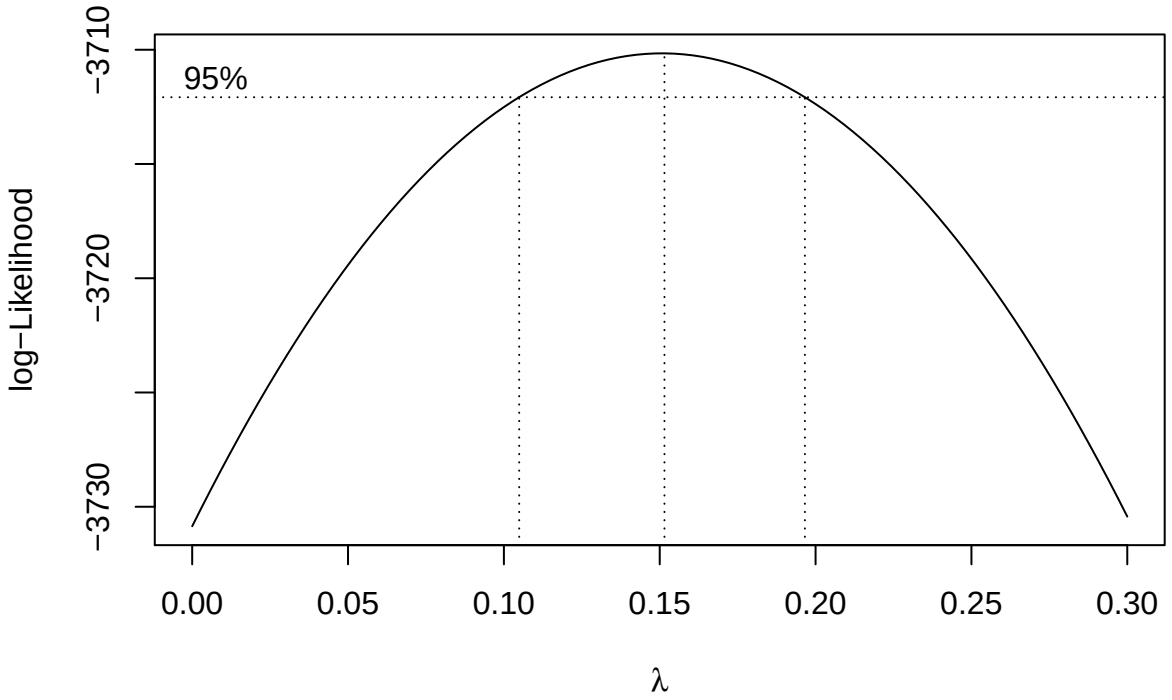
Assumption Check of Full Model

```
yhat_full <- mlr_full$fitted.values
res_full <- mlr_full$residuals
data %>%
  ggplot(aes(yhat_full, res_full)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



The residuals are obviously not evenly scattered, which then we can utilize the boxcox method to give us information about transformation.

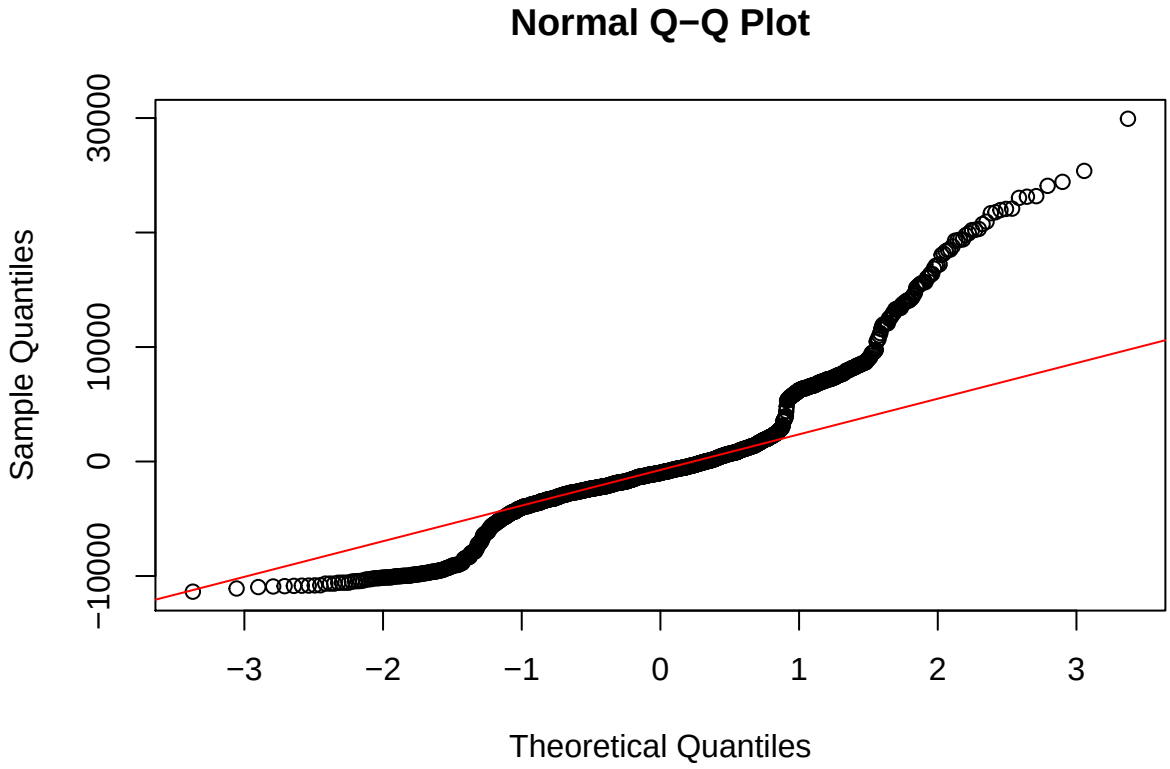
```
boxcox(mlr_full, lambda=seq(0,0.3, 0.01))
```



From the boxcox we can try a lambda value of 0.15 for transformation.

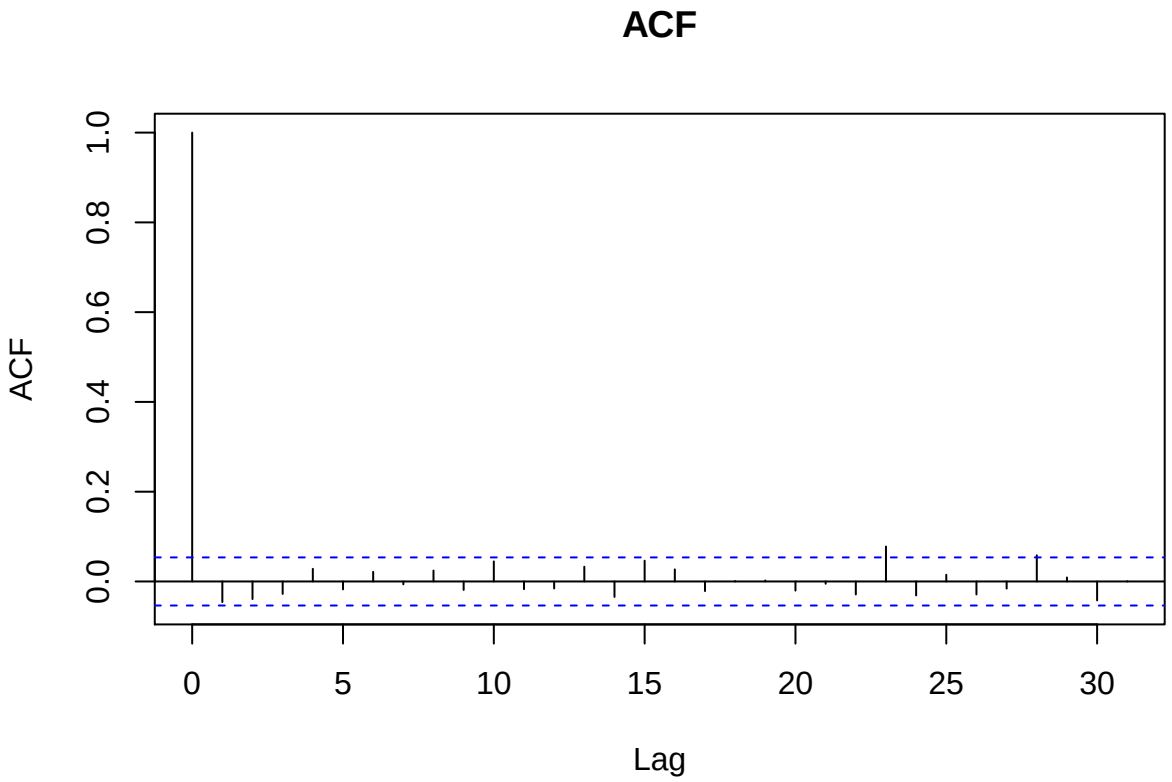
QQPlot

```
{
  qqnorm(mlr_full$residuals)
  qqline(mlr_full$residuals, col="red")
}
```



ACF

```
acf(mlr_full$residuals, main="ACF")
```



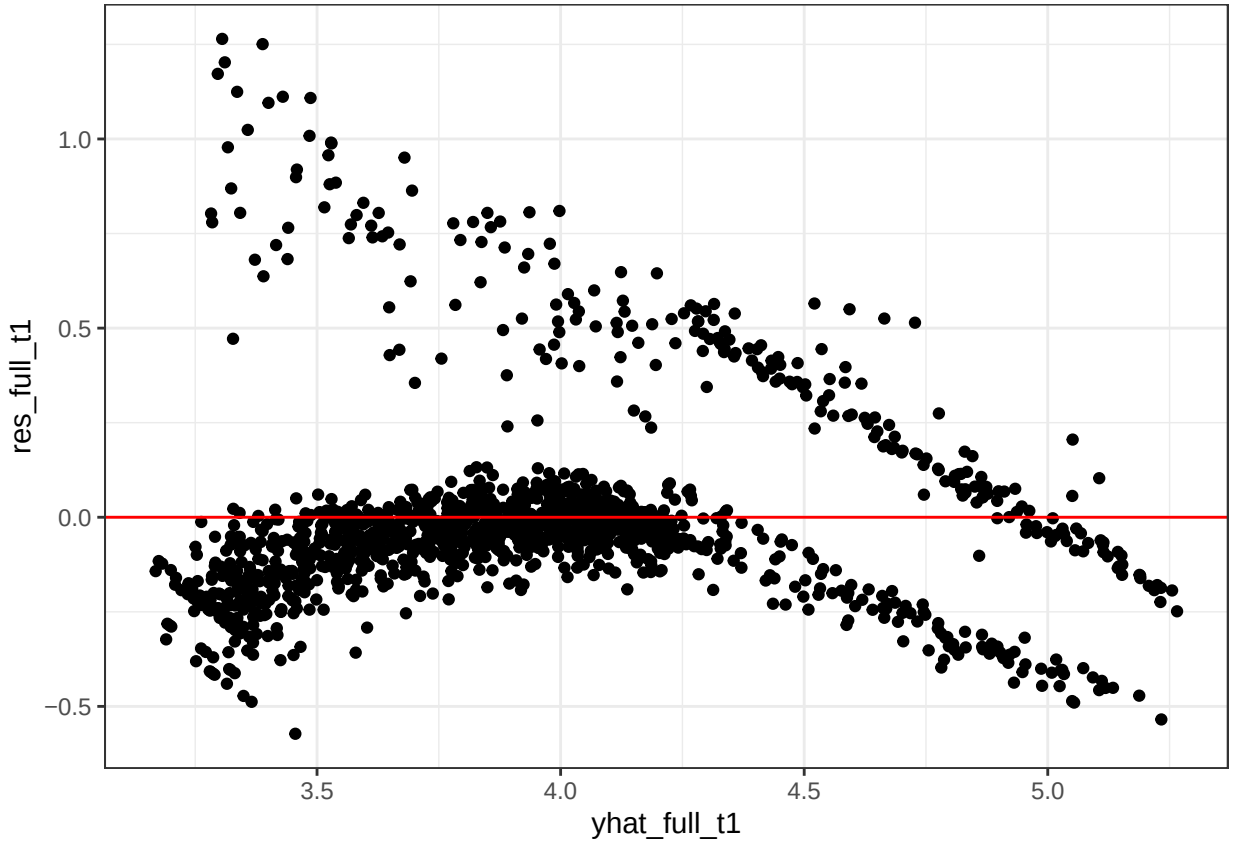

```
first_transformation_full <- data
first_transformation_full$charges <- first_transformation_full$charges^0.15
mlr_transform_first <- lm(charges ~ age + bmi + children + smoker + region, data=first_transformation_fu
summary(mlr_transform_first)
```

```
##
## Call:
## lm(formula = charges ~ age + bmi + children + smoker + region,
##     data = first_transformation_full)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.57232 -0.12513 -0.04165  0.03000  1.26454
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.7239709  0.0416239  65.443  < 2e-16 ***
## age              0.0191744  0.0005057  37.916  < 2e-16 ***
## bmi              0.0088624  0.0012145   7.297 5.04e-13 ***
## children         0.0524721  0.0058577   8.958  < 2e-16 ***
## smokeryes        0.9560821  0.0175151  54.586  < 2e-16 ***
## regionnorthwest -0.0345277  0.0202480  -1.705   0.0884 .
## regionsoutheast -0.0845268  0.0203508  -4.153 3.48e-05 ***
## regionsouthwest -0.0708940  0.0203185  -3.489   0.0005 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 0.2577 on 1330 degrees of freedom
## Multiple R-squared:  0.7754, Adjusted R-squared:  0.7742
## F-statistic: 655.9 on 7 and 1330 DF,  p-value: < 2.2e-16
```

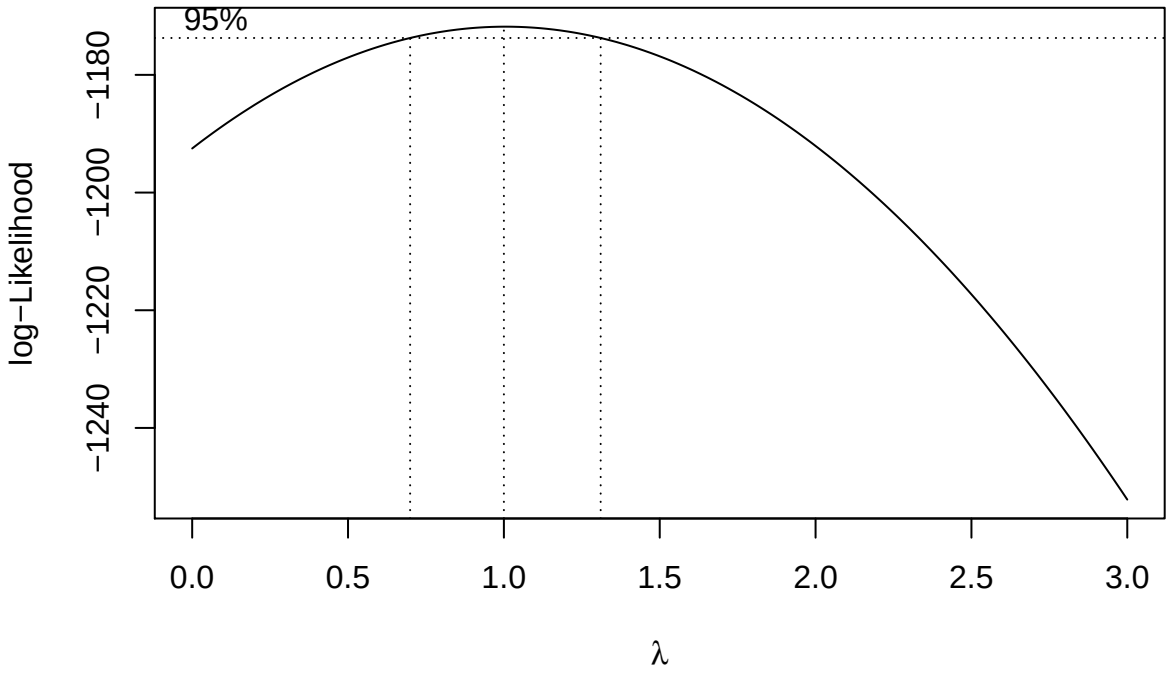
Residual Plot of the transformed model.

```
yhat_full_t1 <- mlr_transform_first$fitted.values
res_full_t1 <- mlr_transform_first$residuals
data %>%
  ggplot(aes(yhat_full_t1, res_full_t1)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



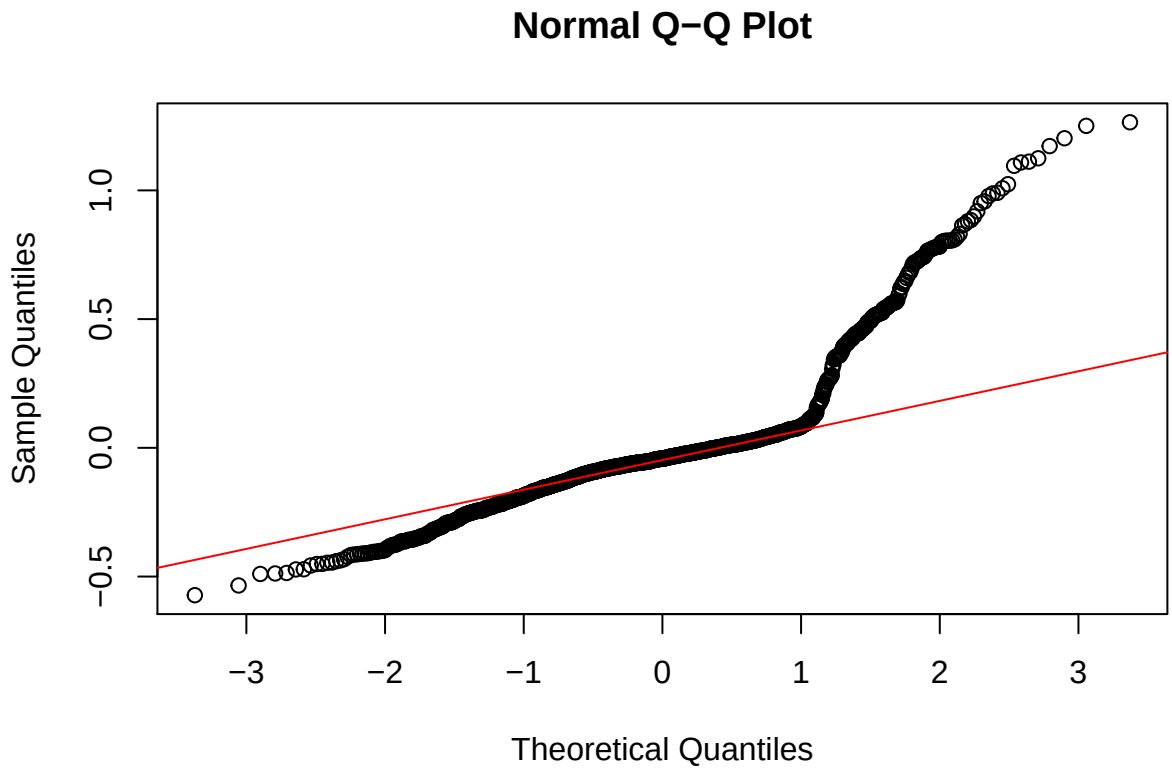
Violation in constant variance

```
boxcox(mlr_transform_first, lambda=seq(0,3, 0.01))
```



QQPLOT

```
{
  qqnorm(mlr_transform_first$residuals)
  qqline(mlr_transform_first$residuals, col="red")
}
```



Externally Studentized Residuals

```
res<-mlr_transform_first$residuals
standard.res<-res/summary(mlr_transform_first)$sigma
student.res <- rstandard(mlr_transform_first)
ext.student.res<-rstudent(mlr_transform_first)
res.frame<-data.frame(res,standard.res, student.res,ext.student.res)
```

Outlier Detection

```
summary(mlr_transform_first)
```

```
##
## Call:
## lm(formula = charges ~ age + bmi + children + smoker + region,
##     data = first_transformation_full)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.57232 -0.12513 -0.04165  0.03000  1.26454
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.7239709  0.0416239  65.443  < 2e-16 ***
## age              0.0191744  0.0005057  37.916  < 2e-16 ***
## bmi              0.0088624  0.0012145   7.297 5.04e-13 ***
## children         0.0524721  0.0058577   8.958  < 2e-16 ***
## smokeryes        0.9560821  0.0175151  54.586  < 2e-16 ***
## regionnorthwest -0.0345277  0.0202480  -1.705   0.0884 .
## regionsoutheast -0.0845268  0.0203508  -4.153 3.48e-05 ***
## regionsouthwest -0.0708940  0.0203185  -3.489   0.0005 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2577 on 1330 degrees of freedom
## Multiple R-squared:  0.7754, Adjusted R-squared:  0.7742
## F-statistic: 655.9 on 7 and 1330 DF,  p-value: < 2.2e-16
```

```
n = dim(data)[1]
p = 8
crit<-qt(1-0.05/(2*n), n-p-1)
ext.student.res[abs(ext.student.res)>crit]
```

```
##      103      220      431      517      527     1020     1028     1040
## 4.406092 4.965919 4.716688 4.906189 4.354028 4.341191 4.598196 4.289690
```

Possible Leverages

```
lev<-lm.influence(mlr_transform_first)$hat
##identify high leverage points
lev[lev>2*p/n]
```

```
##         33        167        414        426        439        495        641
## 0.01288482 0.01378652 0.01283465 0.01323416 0.01501336 0.01209154 0.01430552
```

```
##        861        985       1048       1086       1131       1246       1273
## 0.01313806 0.01316421 0.01538367 0.01718913 0.01325871 0.01242249 0.01266884
##       1318
## 0.01483116
```

Influential Observations

```
COOKS<-cooks.distance(mlr_transform_first)
COOKS[COOKS>qf(0.5,p,n-p)]
```

```
## named numeric(0)
```

DFFITs

```
DFFITS<-dffits(mlr_transform_first)
DFFITS[abs(DFFITS)>2*sqrt(p/n)]
```

```
##          4         10         31         35         58         63         93
##  0.2614931  0.1819451  0.1716066  0.1925629  0.1562565  0.1580639 -0.2026735
##         99        103        104        116        141        144        162
## -0.1710392  0.3304758 -0.1802906  0.1671294  0.2596225  0.1842272  0.1951450
##        220        224        243        245        260        263        264
##  0.3976236  0.1918318  0.2149013 -0.1682505  0.1762766 -0.1823450  0.1931683
##        290        292        302        306        307        322        341
##  0.1839115  0.1980673 -0.1897982  0.1974357  0.2272869  0.3157972  0.2798323
##        355        356        378        388        398        420        430
##  0.2639221  0.1993921  0.1589216  0.1882289  0.2661634 -0.1618457  0.2200216
##        431        443        469        475        476        492        504
##  0.3569007 -0.1681355  0.2513915 -0.1710679 -0.1601466  0.1762699  0.1759623
##        517        521        526        527        534        540        555
##  0.3336860  0.1715211  0.2213937  0.3195535  0.1735929  0.1831383  0.2760641
##        578        584        600        619        624        638        662
##  0.1862508  0.2311363  0.1872154  0.1802149  0.1741776  0.2142287  0.1554201
##        665        689        755        760        804        807        820
## -0.1699229  0.2046203  0.2377304  0.1960007  0.2176502  0.2473289  0.1930009
##        855        859        877        891        912        937        958
## -0.1655747  0.2167721  0.1744460 -0.1672555  0.1694201  0.1948270  0.1724181
##        960        984        988       1004       1009       1013       1020
##  0.1779760  0.1813215  0.1842179  0.1578416  0.2709168  0.1957965  0.3182986
##       1028       1040       1048       1081       1086       1094       1105
##  0.3836793  0.3121348  0.2174214  0.2784995 -0.2057463  0.1553807  0.1967031
##       1121       1124       1135       1140       1143       1157       1158
##  0.1588416  0.2021021  0.2422537  0.1991262  0.2347513  0.2202891  0.2179828
##       1163       1190       1196       1197       1207       1212       1216
##  0.1933110  0.2211726  0.2957771  0.1763085  0.1817089  0.1697490  0.2556803
##       1266       1289       1292       1301       1314       1316       1318
## -0.1710438  0.1668444  0.1921438  0.1601948  0.1630070  0.1886844 -0.2749287
##       1319       1322       1329       1332
##  0.1773834 -0.1699762  0.2865060  0.1788383
```

DFBETAs

```
##dfbetas
DFBETAS<-dfbetas(mlr_transform_first)
DFBETAS[abs(DFBETAS[,1])>2/sqrt(n),1]
```

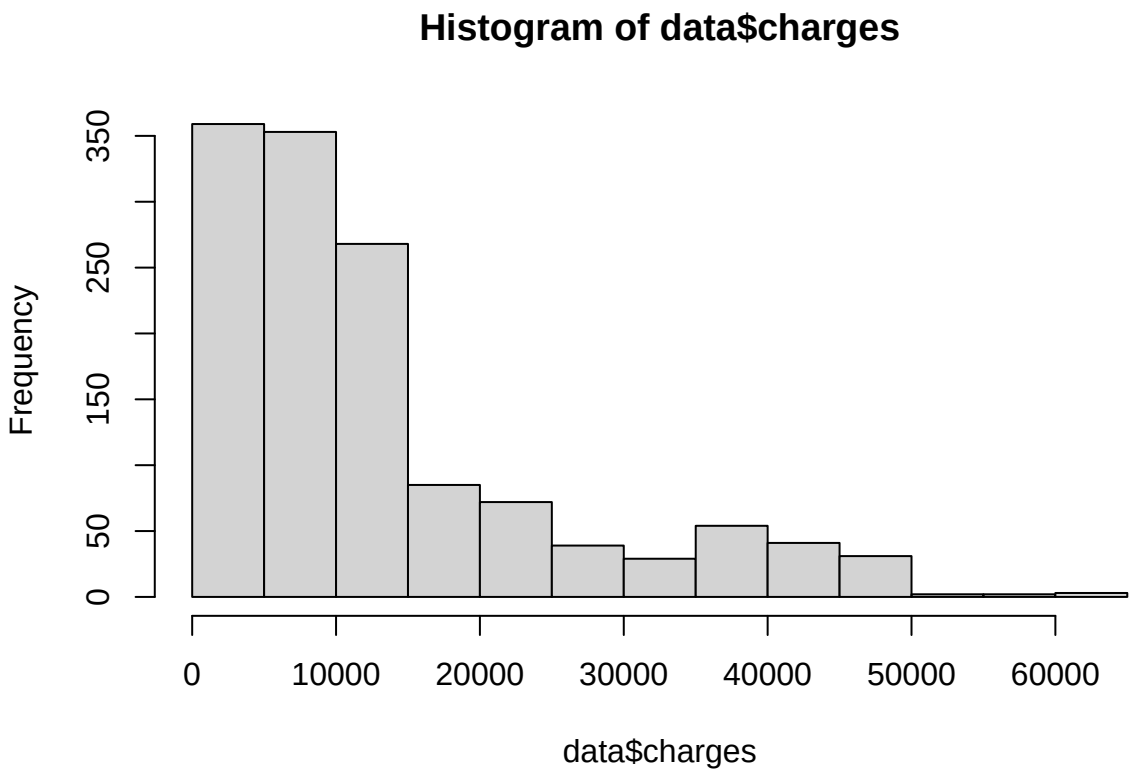
```
##           4          99         103         141         173         220
##  0.12441926 -0.06582735  0.15663115  0.17609881 -0.05543226  0.26675833
##         228         292         293         307         322         341
## -0.06863251  0.08617261 -0.06042304  0.06596842  0.07080797  0.10787059
##         381         398         412         413         428         469
## -0.05600351  0.10152995 -0.05989988 -0.05869406  0.07186825  0.18307584
##         521         526         584         585         600         682
##  0.05737413  0.05485404  0.13915511 -0.06370821 -0.10525102 -0.06465315
##         689         807         848         859         897         941
##  0.06241119 -0.13690408  0.07042443  0.05765956 -0.06242929 -0.07313631
##         958         960         965         984        1009        1028
##  0.05829767 -0.08584503 -0.07397664  0.07042485  0.17153096  0.25600077
##        1040        1048        1081        1101        1124        1143
##  0.09096234 -0.11368282  0.18296476 -0.05933970  0.05518460  0.08042317
##        1157        1158        1190        1192        1196        1207
## -0.06595512  0.10033177  0.08217259  0.07727122  0.05784004 -0.07831504
##        1213        1224        1252        1259        1316        1318
## -0.05479425  0.07050695 -0.06578023 -0.08472433  0.10534725  0.12222103
##        1329
##  0.19218460
```

```
DFBETAS[abs(DFBETAS[,1])>2/sqrt(n),2]
```

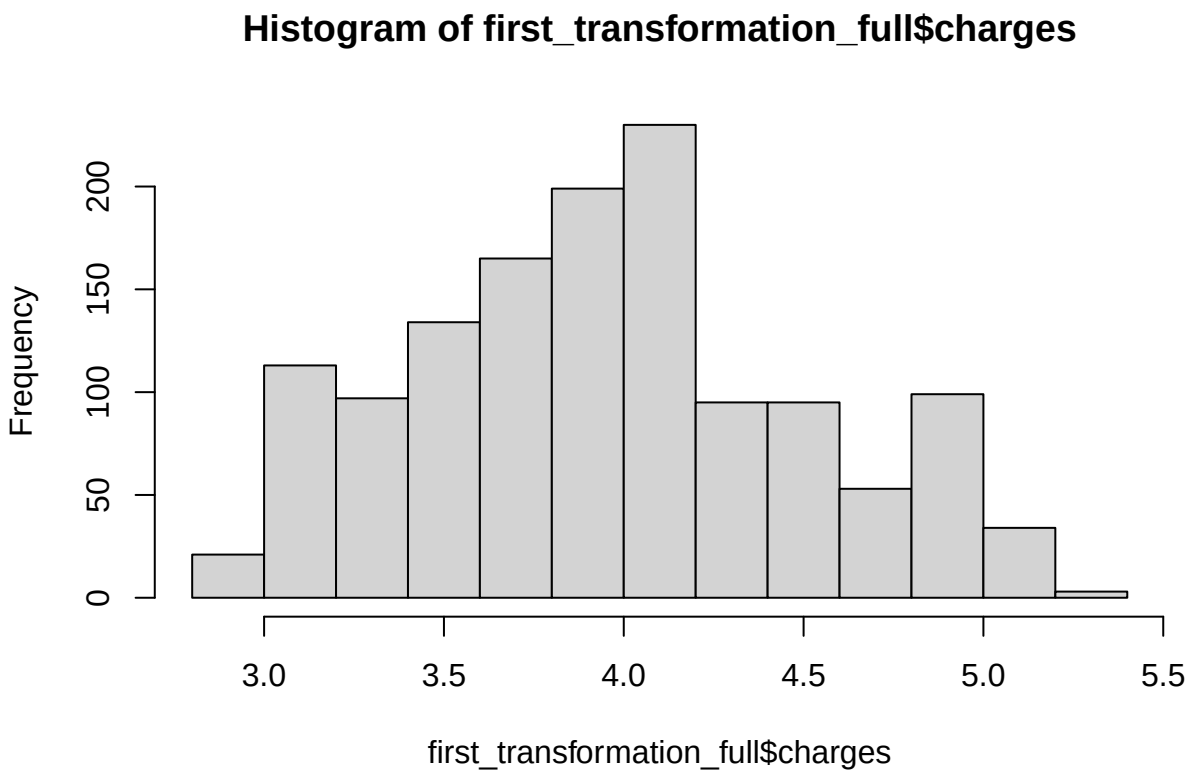
```
##           4          99         103         141         173         220
## -0.029396407 -0.068726116 -0.183842780 -0.029277874  0.021229822 -0.115611883
##         228         292         293         307         322         341
##  0.055078337 -0.067210760 -0.047013970 -0.075667150 -0.099555308 -0.112107259
##         381         398         412         413         428         469
##  0.015898325 -0.127829365 -0.021269352  0.017137523 -0.075702692 -0.076611336
##         521         526         584         585         600         682
##  0.058500408 -0.124464498 -0.027805682  0.038375307  0.049433622  0.037692685
##         689         807         848         859         897         941
##  0.055528817 -0.016032765  0.057471335 -0.095245933 -0.018681572  0.044141719
##         958         960         965         984        1009        1028
## -0.076360885  0.034181327  0.038093620 -0.072429067 -0.104270844 -0.116672873
##        1040        1048        1081        1101        1124        1143
## -0.170506313 -0.074493689 -0.113560876  0.007166292 -0.081548217  0.092591189
##        1157        1158        1190        1192        1196        1207
## -0.091512791 -0.088514924 -0.094762280  0.011711403 -0.147609177  0.088163815
##        1213        1224        1252        1259        1316        1318
##  0.029798927 -0.047495332  0.036847545  0.043859317 -0.110546668  0.115809805
##        1329
## -0.120326885
```

Why is this happening? Is there some weird behavior in the response variable?

```
hist(data$charges)
```




```r
hist(first_transformation_full$charges)
```



Trial of other predictors to fullfill the linearity assumption.

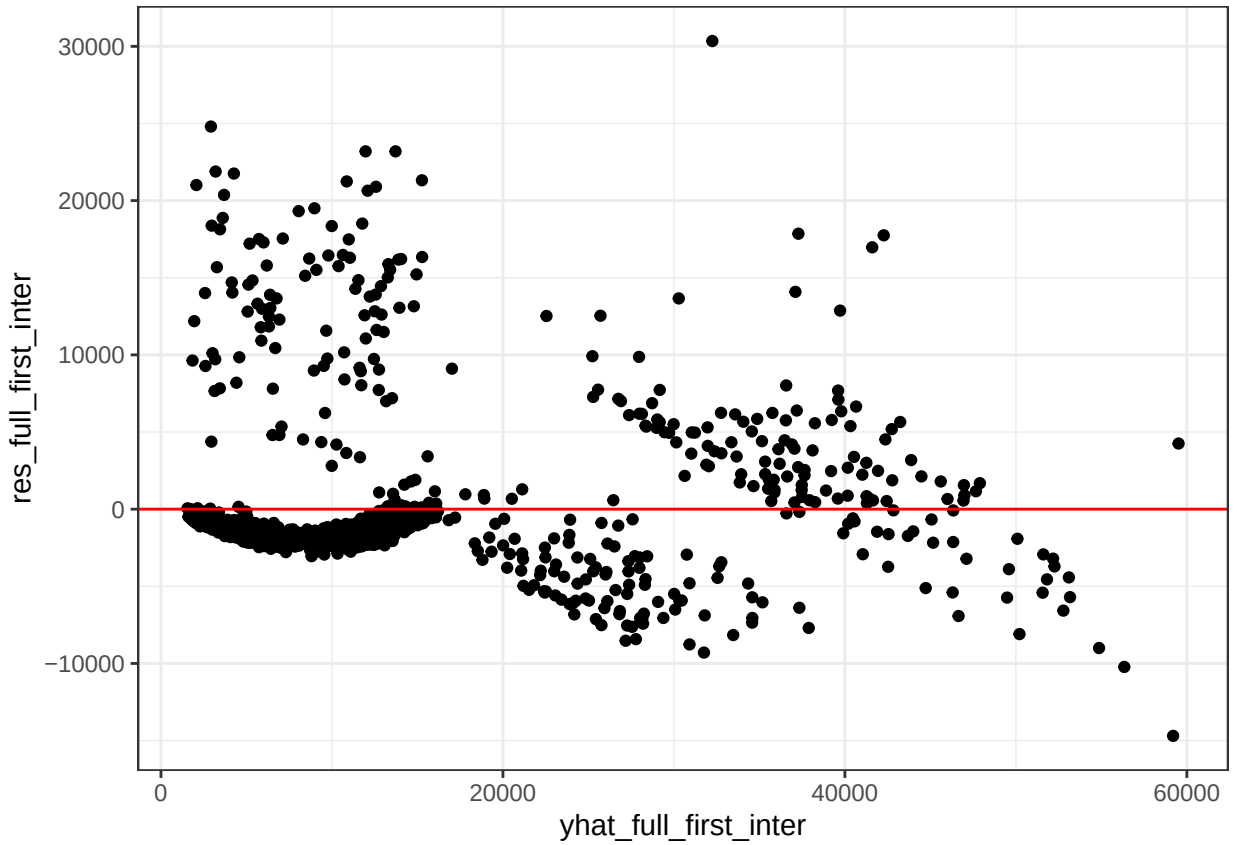
Maybe we can add some interaction terms to the model to see if we can fix the linearity assumption.

```r
interaction_age_bmi_with_smoker = lm(charges ~  age*smoker + bmi*smoker + children  + region, data=data)
summary(interaction_age_bmi_with_smoker)
```

```
##
## Call:
## lm(formula = charges ~ age * smoker + bmi * smoker + children +
##     region, data = data)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14695.2  -1918.6  -1316.2   -480.3  30345.6
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -2469.101    870.166  -2.838  0.00462 **
## age                264.558     10.672  24.791  < 2e-16 ***
## smokeryes        -20223.654   1831.889 -11.040  < 2e-16 ***
## bmi                 22.444     25.679   0.874  0.38228
## children           512.956    110.331   4.649 3.66e-06 ***
## regionnorthwest   -581.232    381.383  -1.524  0.12774
## regionsoutheast  -1205.652    383.462  -3.144  0.00170 **
## regionsouthwest  -1228.623    382.837  -3.209  0.00136 **
## age:smokeryes       -2.542     23.711  -0.107  0.91464
## smokeryes:bmi     1438.525     52.793  27.249  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4853 on 1328 degrees of freedom
## Multiple R-squared:  0.8405, Adjusted R-squared:  0.8394
## F-statistic: 777.5 on 9 and 1328 DF,  p-value: < 2.2e-16
```

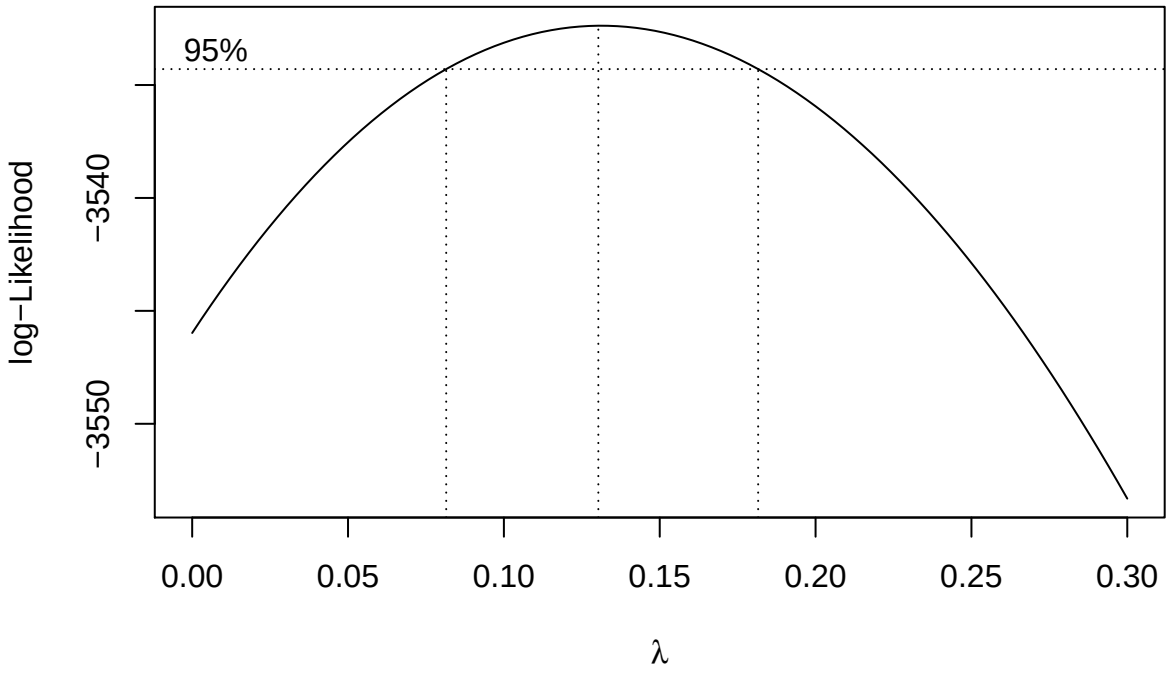
Residual Plot

```r
yhat_full_first_inter <- interaction_age_bmi_with_smoker$fitted.values
res_full_first_inter <- interaction_age_bmi_with_smoker$residuals
data %>%
  ggplot(aes(yhat_full_first_inter, res_full_first_inter)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



This residual plot is a little better, lets see if we can transform the response with this new equation.

```
boxcox(interaction_age_bmi_with_smoker, lambda=seq(0,0.3, 0.01))
```



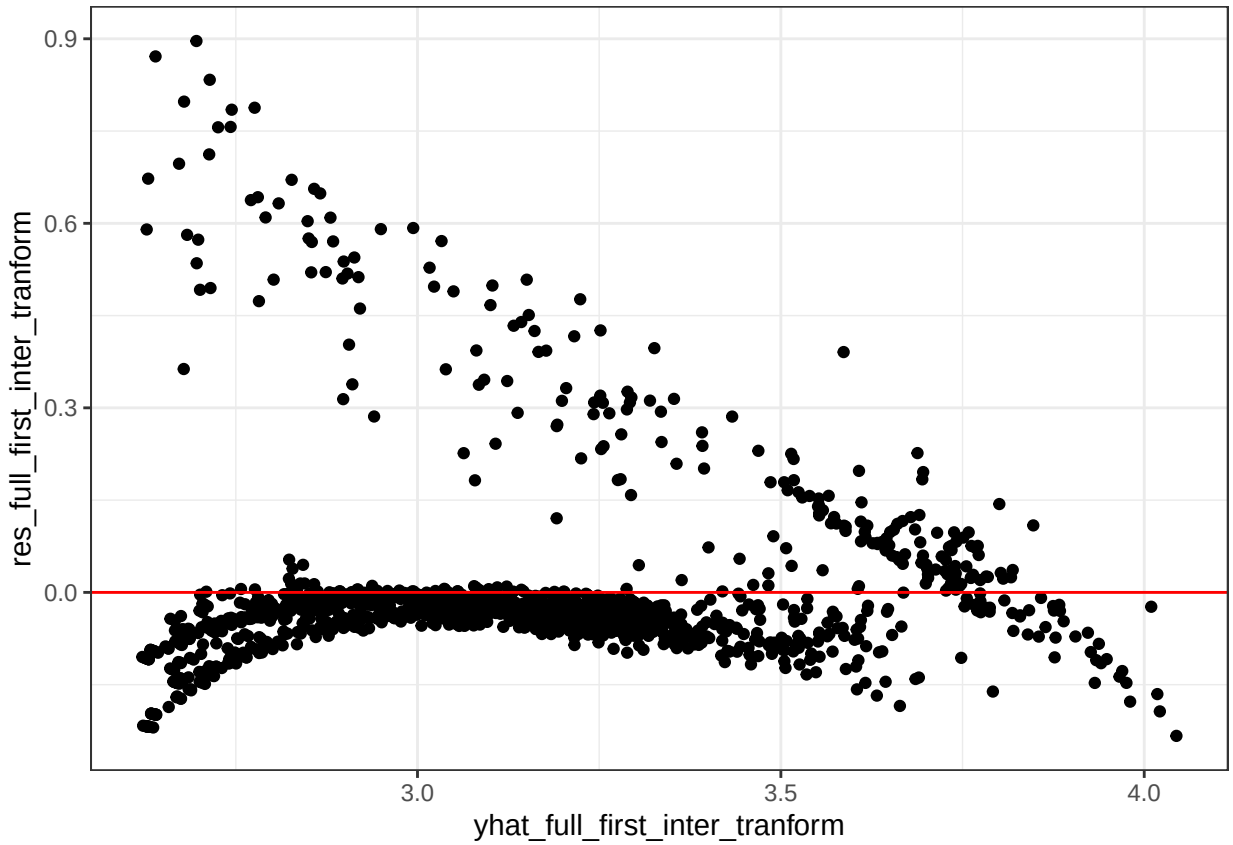
Maybe we can use a lambda value of 0.125

```r
interaction_transform <- data
interaction_transform$charges <- interaction_transform$charges^0.125
mlr_interaction_tranform <- lm(charges ~  age*smoker + bmi*smoker + children  + region, data=interactio
summary(mlr_interaction_tranform)
```

```
##
## Call:
## lm(formula = charges ~ age * smoker + bmi * smoker + children +
##     region, data = interaction_transform)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.23325 -0.05925 -0.03216 -0.00578  0.89638
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      2.3898138  0.0268794  88.909  < 2e-16 ***
## age              0.0152818  0.0003296  46.358  < 2e-16 ***
## smokeryes        0.3867297  0.0565870   6.834 1.25e-11 ***
## bmi              0.0004622  0.0007932   0.583   0.5602
## children         0.0371914  0.0034081  10.913  < 2e-16 ***
## regionnorthwest -0.0243318  0.0117809  -2.065   0.0391 *
## regionsoutheast -0.0531652  0.0118451  -4.488 7.80e-06 ***
## regionsouthwest -0.0559589  0.0118258  -4.732 2.46e-06 ***
## age:smokeryes   -0.0115120  0.0007324 -15.717  < 2e-16 ***
## smokeryes:bmi    0.0223756  0.0016308  13.721  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1499 on 1328 degrees of freedom
## Multiple R-squared:  0.827,  Adjusted R-squared:  0.8259
## F-statistic: 705.6 on 9 and 1328 DF,  p-value: < 2.2e-16
```

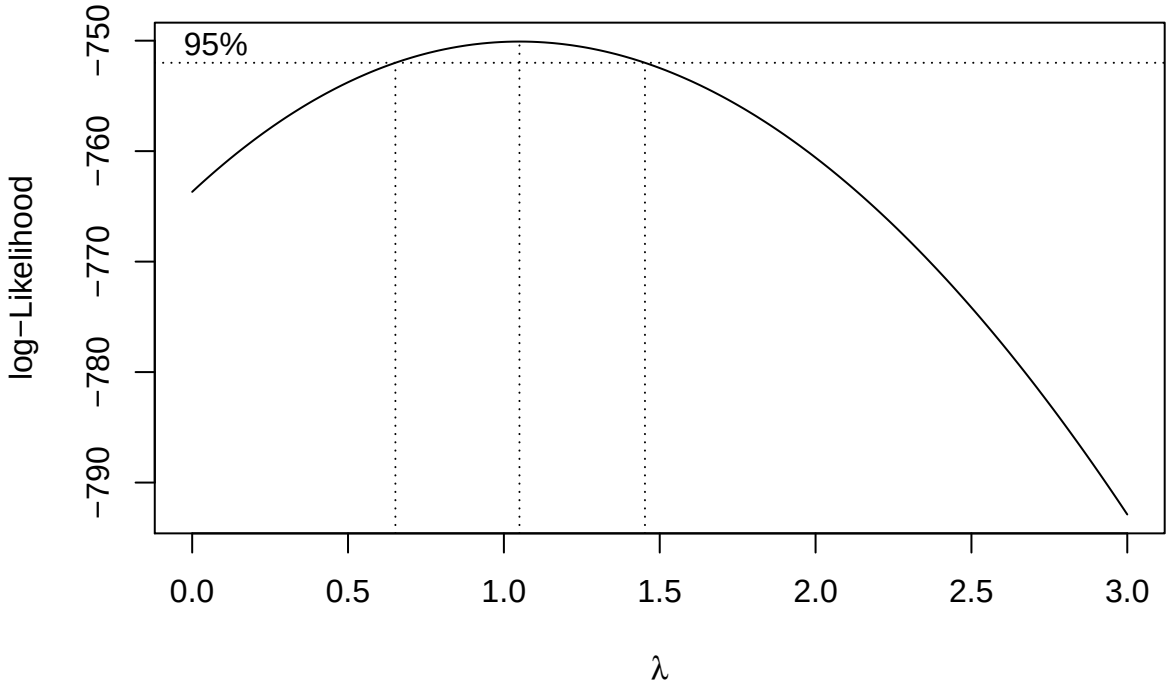
Recheck Residual Plot

```r
yhat_full_first_inter_tranform <- mlr_interaction_tranform$fitted.values
res_full_first_inter_tranform <- mlr_interaction_tranform$residuals
data %>%
  ggplot(aes(yhat_full_first_inter_tranform, res_full_first_inter_tranform)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



Still see the same without adding the interaction terms.

```
boxcox(mlr_interaction_tranform, lambda=seq(0,3, 0.01))
```



Still no luck. We retried this many times, but weren't lucky.

Partial F test of the interaction vs simple model after two transformation of response variable

```
full <- mlr_interaction_tranform
reduced <- lm(charges ~ age + bmi + children + smoker + region, data=interaction_transform)
anova(reduced, full)
```

```
## Analysis of Variance Table
##
## Model 1: charges ~ age + bmi + children + smoker + region
## Model 2: charges ~ age * smoker + bmi * smoker + children + region
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1   1330 38.959
## 2   1328 29.842  2    9.1174 202.87 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can't drop the interaction terms.

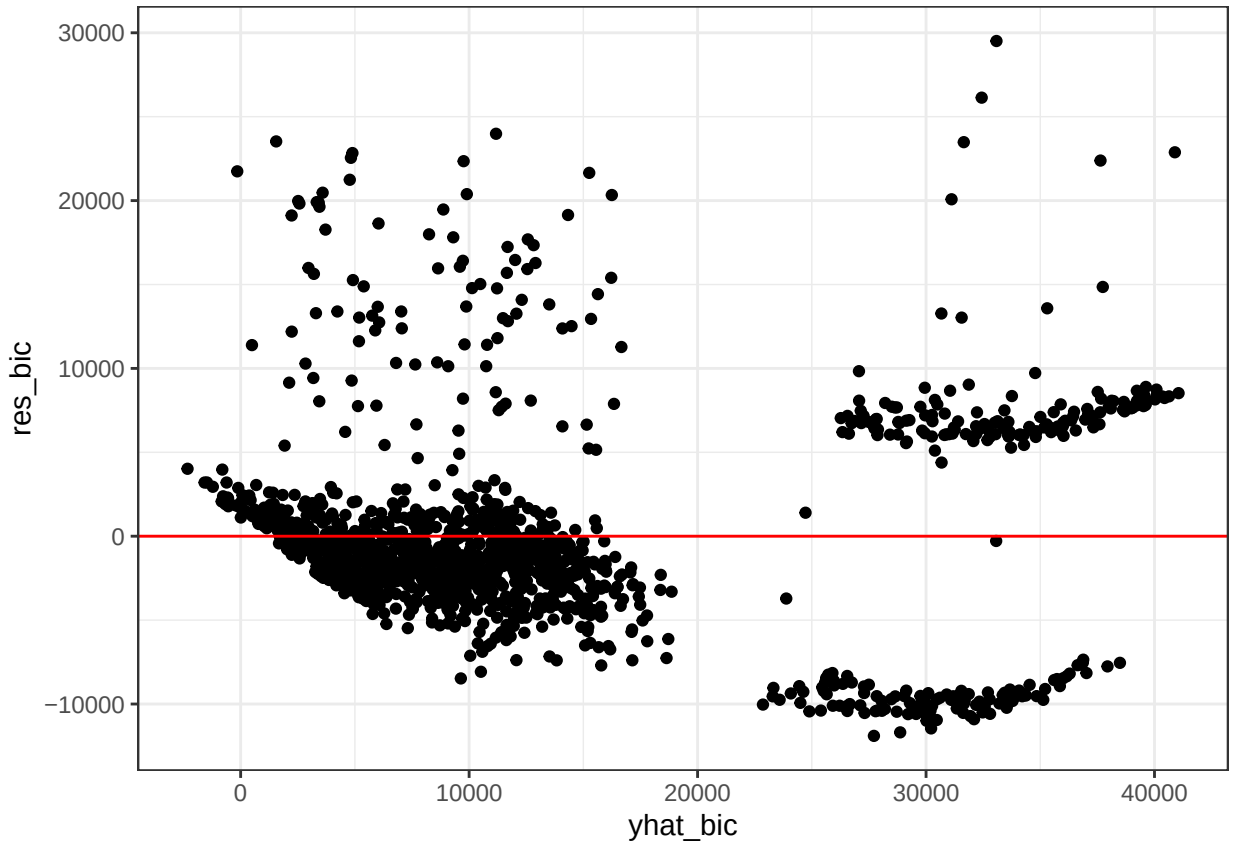
BIC Model selection model might be better

```
bic_selection_model = lm(charges ~  age + bmi + children  + smoker, data=data)
summary(bic_selection_model)
```

```
##
## Call:
## lm(formula = charges ~ age + bmi + children + smoker, data = data)
##
## 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
```

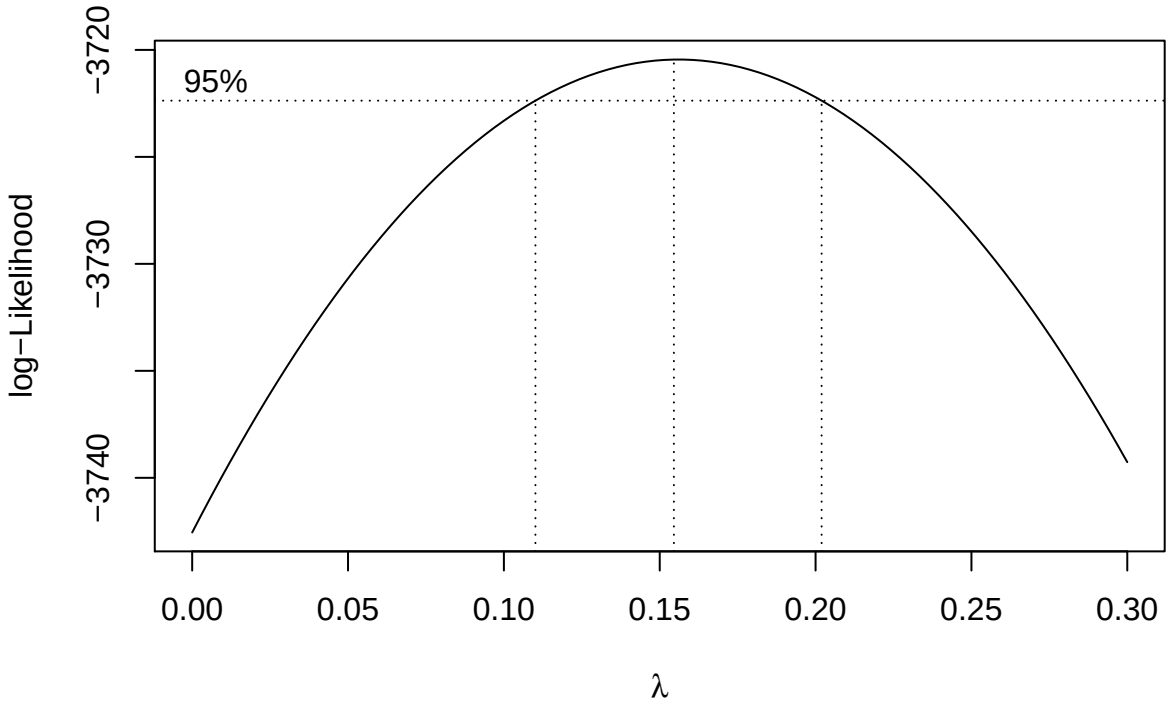
Residual Plot

```
yhat_bic <- bic_selection_model$fitted.values
res_bic <- bic_selection_model$residuals
data %>%
  ggplot(aes(yhat_bic, res_bic)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



We see a similar plot. Transformation?

```
boxcox(bic_selection_model, lambda=seq(0,0.3, 0.01))
```



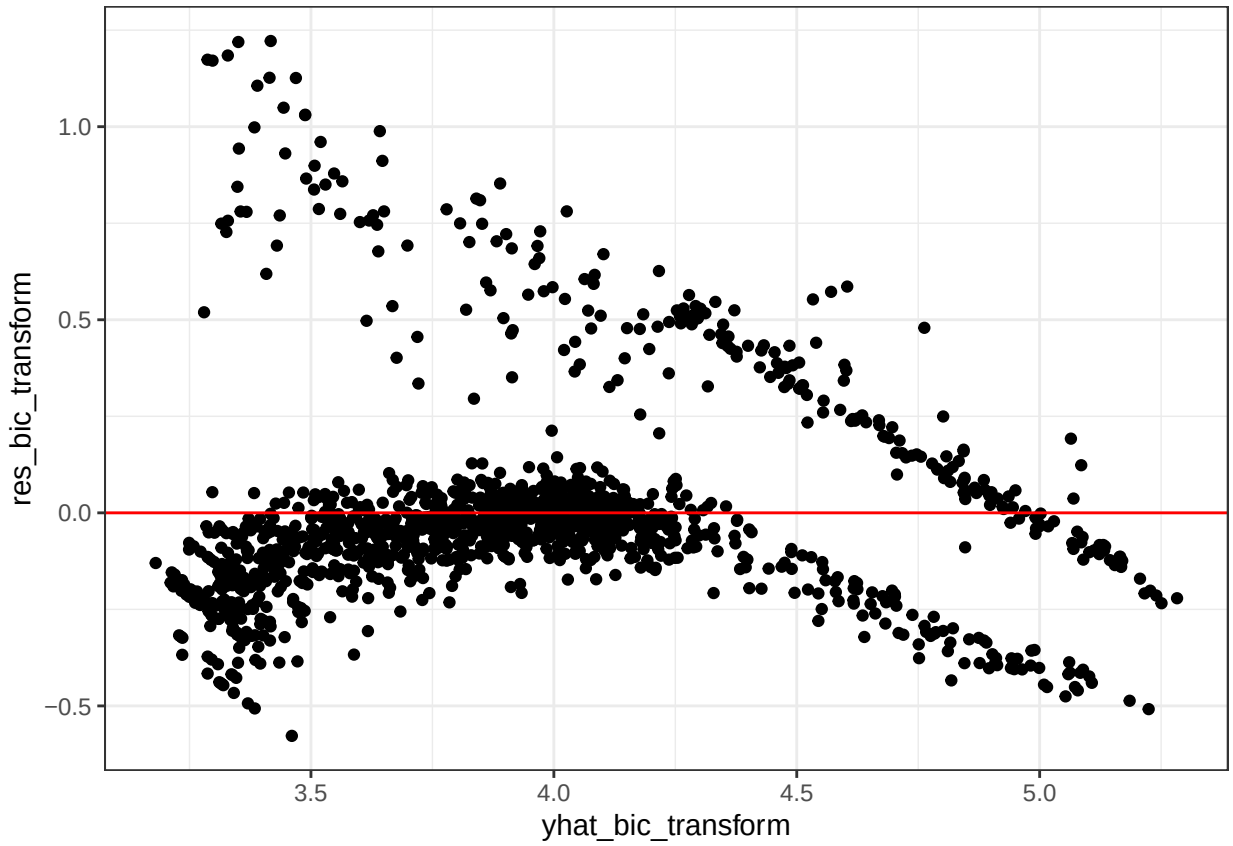
Again lambda of 0.15

```
bic_transform <- data
bic_transform$charges <- bic_transform$charges^(0.15)
bic_selection_model_transform = lm(charges ~  age + bmi + children  + smoker, data=bic_transform)
summary(bic_selection_model_transform)
```

```
##
## Call:
## lm(formula = charges ~ age + bmi + children + smoker, data = bic_transform)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.57755 -0.12028 -0.03776  0.03505  1.22187
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.7136331  0.0402741  67.379  < 2e-16 ***
## age         0.0192458  0.0005086  37.839  < 2e-16 ***
## bmi         0.0075402  0.0011705   6.442 1.65e-10 ***
## children    0.0523899  0.0058912   8.893  < 2e-16 ***
## smokeryes   0.9539751  0.0175815  54.260  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2594 on 1333 degrees of freedom
## Multiple R-squared:  0.7719, Adjusted R-squared:  0.7712
## F-statistic:  1128 on 4 and 1333 DF,  p-value: < 2.2e-16
```

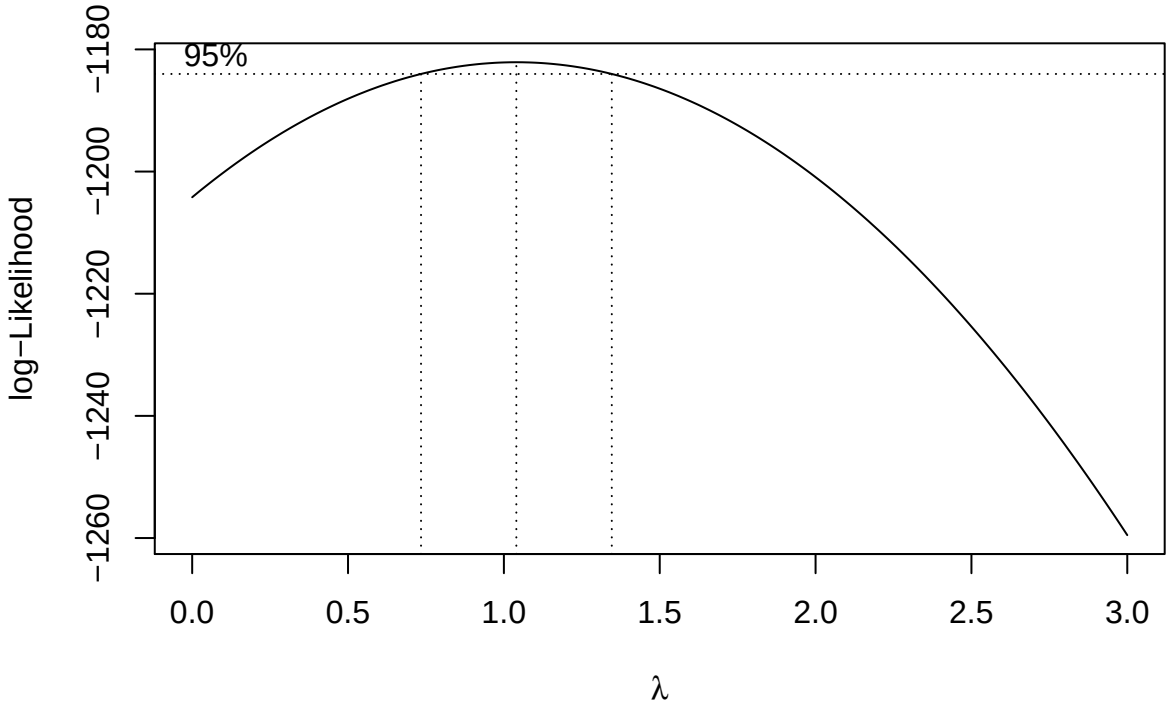
Residual Plot

```
yhat_bic_transform <- bic_selection_model_transform$fitted.values
res_bic_transform <- bic_selection_model_transform$residuals
data %>%
  ggplot(aes(yhat_bic_transform, res_bic_transform)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



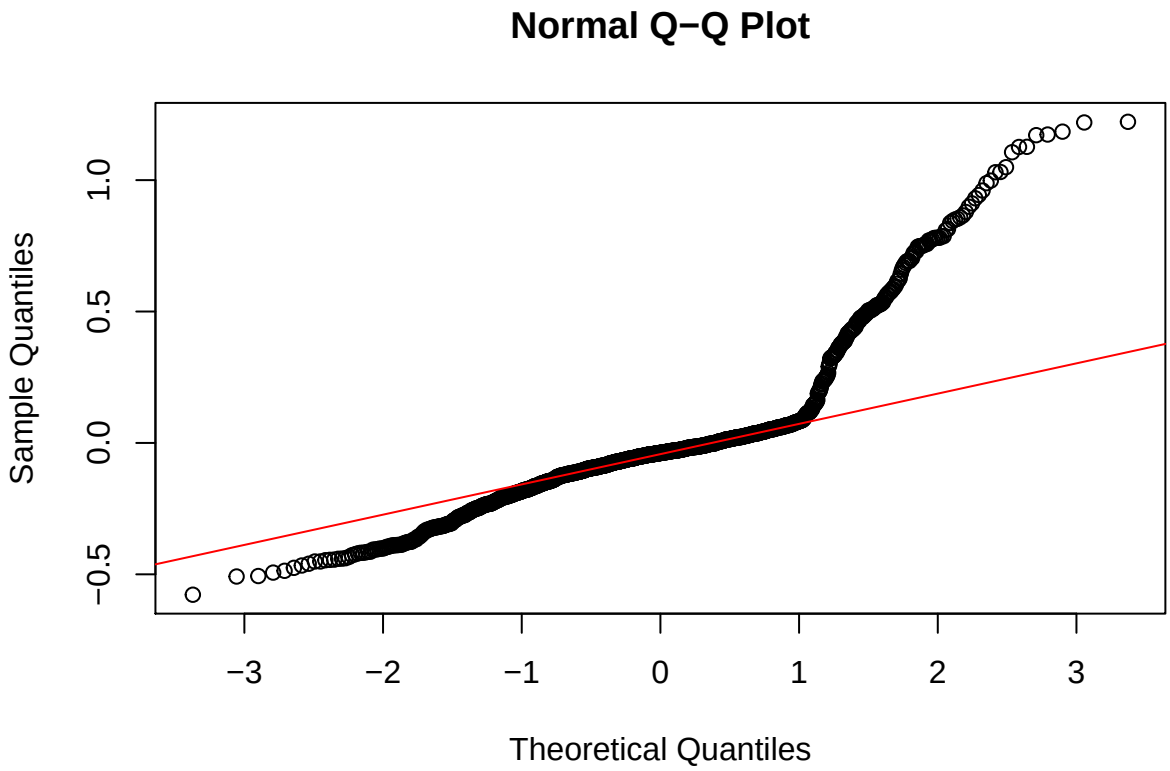
Same Stuff happening.

```
boxcox(bic_selection_model_transform, lambda=seq(0,3, 0.01))
```



QQPlot

```r
{
  qqnorm(bic_selection_model_transform$residuals)
  qqline(bic_selection_model_transform$residuals, col="red")
}
```



Logistic

```r
set.seed(6021) ##for reproducibility
sample<-sample.int(nrow(data), floor(.50*nrow(data)), replace = F)
train<- data[sample, ] ##training data frame
test<-data[-sample, ] ##test data frame
result<-glm(significant.charge ~ age + bmi + children + smoker + region, family="binomial", data=train)
summary(result)
```

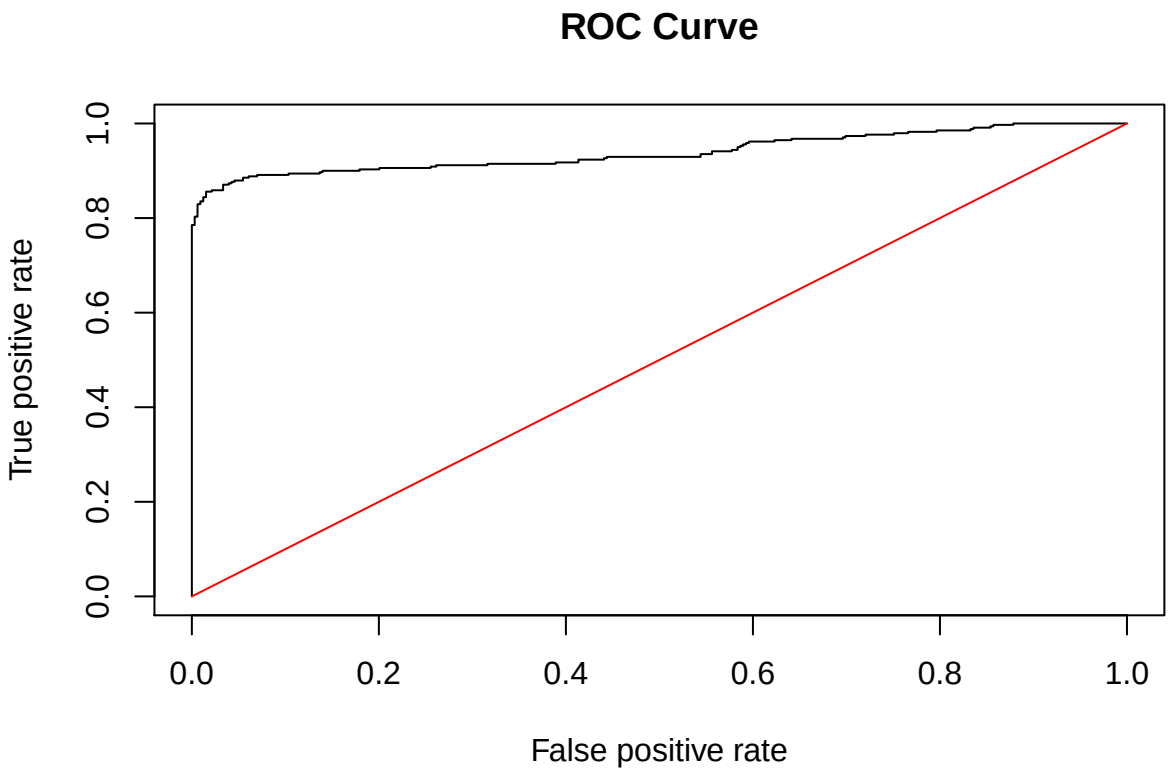
```
##
## Call:
## glm(formula = significant.charge ~ age + bmi + children + smoker +
##     region, family = "binomial", data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5477  -0.3328  -0.0757   0.3392   3.3986
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -9.80428    1.09743  -8.934   <2e-16 ***
## age               0.18932    0.01654  11.444   <2e-16 ***
## bmi               0.03258    0.02402   1.356    0.175
## children          0.19678    0.11015   1.786    0.074 .
```

```
## smokeryes         22.80340  693.10646   0.033    0.974
## regionnorthwest  -0.37231    0.38719  -0.962    0.336
## regionsoutheast  -0.47896    0.40576  -1.180    0.238
## regionsouthwest  -0.17324    0.38930  -0.445    0.656
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 927.25  on 668  degrees of freedom
## Residual deviance: 355.27  on 661  degrees of freedom
## AIC: 371.27
##
## Number of Fisher Scoring iterations: 18
```

```
library(ROCR)
```

```
## Warning: package 'ROCR' was built under R version 4.0.2
```

```
##predicted survival rate for test data based on training data
preds<-predict(result,newdata=test, type="response")
##transform the input data into a format that is suited for the
##performance() function
rates<-prediction(preds, test$significant.charge)
##store the true positive and false positive rates
roc_result<-performance(rates,measure="tpr", x.measure="fpr")
##plot ROC curve and overlay the diagonal line for random guessing
plot(roc_result, main="ROC Curve")
lines(x = c(0,1), y = c(0,1), col="red")
```



```
##compute the AUC
auc<-performance(rates, measure = "auc")
auc@y.values
```

```
## [[1]]
## [1] 0.9392187
```

Matrix

```
table(test$significant.charge, preds>0.5)
```

```
##
##         FALSE TRUE
##   FALSE   302   27
##   TRUE     37  303
```

Threshold value manipulation

```
table(test$significant.charge, preds>0.2)
```

```
##
##         FALSE TRUE
##   FALSE   235   94
##   TRUE     30  310
```

Doesn't play a huge role in decreasing the False Positive Rate. We want to make sure that when someone signs up for a plan that they don't get charged significantly given their condition.