Project

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11/11/2021

Data processing

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

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

## -- Attaching packages --------------------------------------------------------------------------- tid

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

```r
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
```

```r
library(leaps)
```

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

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

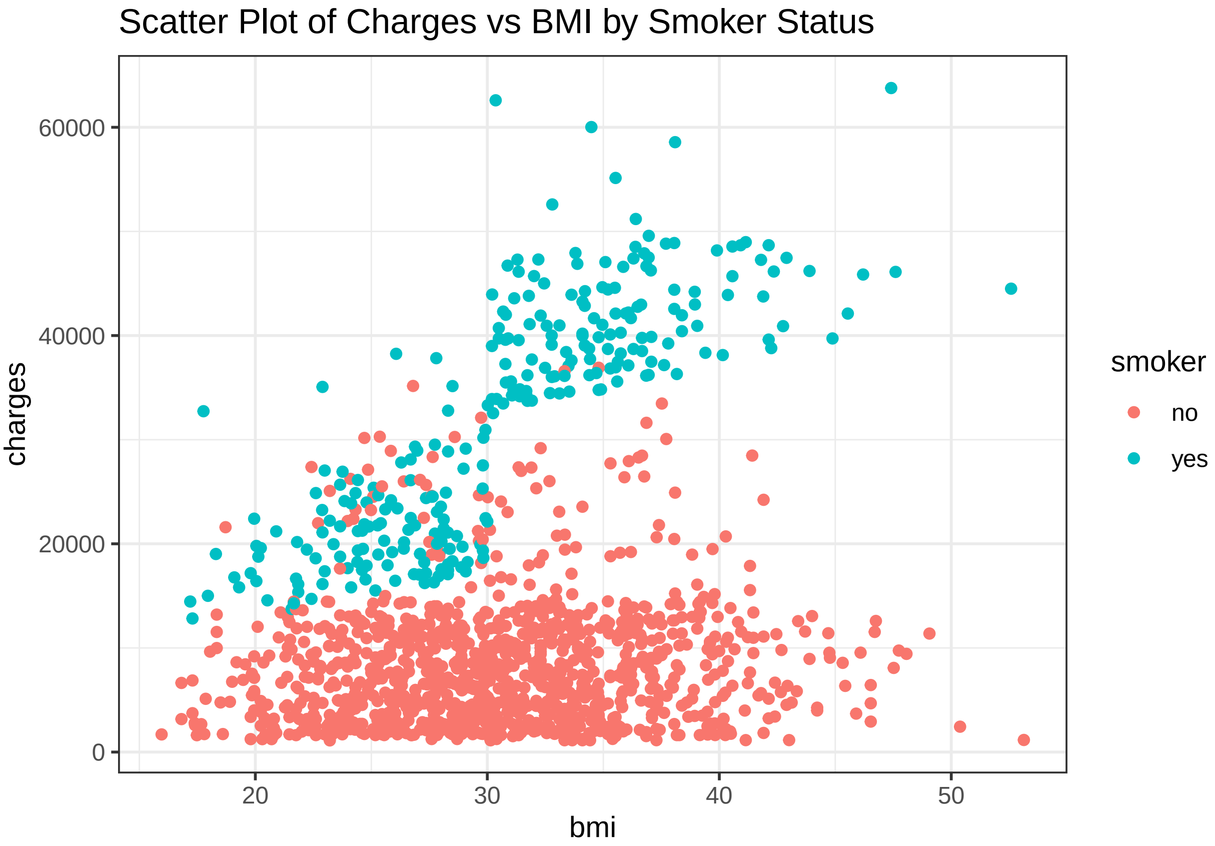
```
##   age    sex    bmi children smoker    region   charges
## 1  19 female 27.900        0    yes southwest 16884.924
## 2  18   male 33.770        1     no southeast  1725.552
## 3  28   male 33.000        3     no southeast  4449.462
## 4  33   male 22.705        0     no northwest 21984.471
## 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$charges))
data$smoker = as.factor(data$smoker)
data$region = as.factor(data$region)
head(data)
```

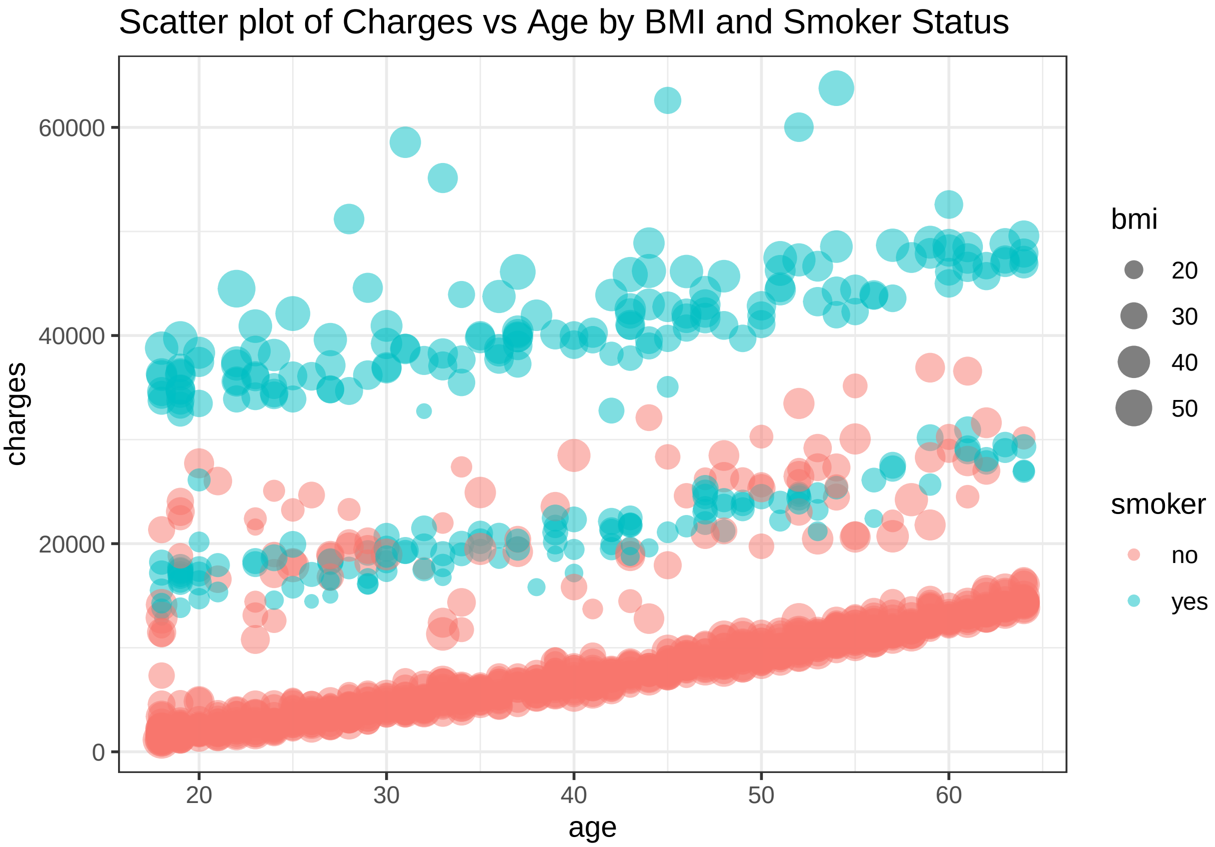
```
##   age    sex    bmi children smoker    region   charges significant.charge
## 1  19 female 27.900        0    yes southwest 16884.924               TRUE
## 2  18   male 33.770        1     no southeast  1725.552              FALSE
## 3  28   male 33.000        3     no southeast  4449.462              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
```

Initial EDA

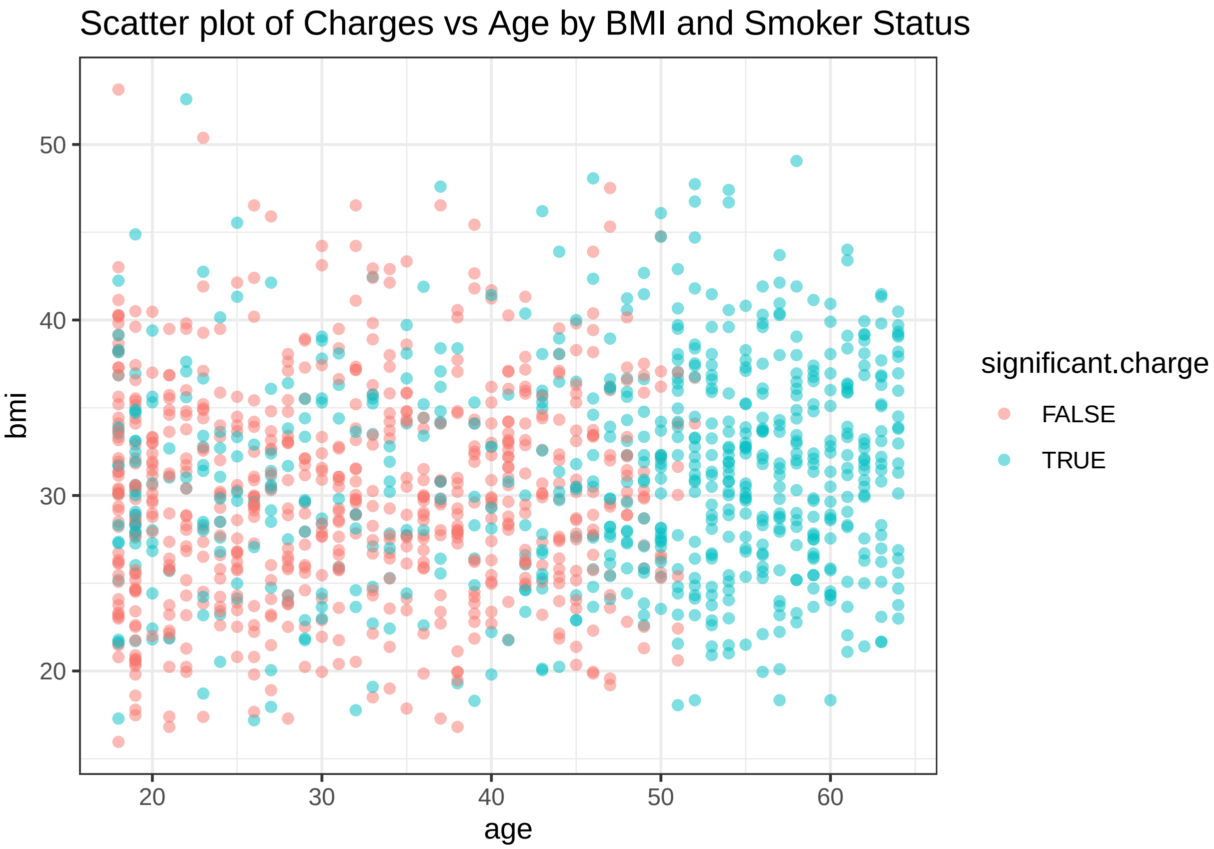
```
ggplot(aes(x=bmi, y=charges, color=smoker), data=data) +
  labs(title="Scatter Plot of Charges vs BMI by Smoker Status") +
  theme_bw() +
  geom_point()
```



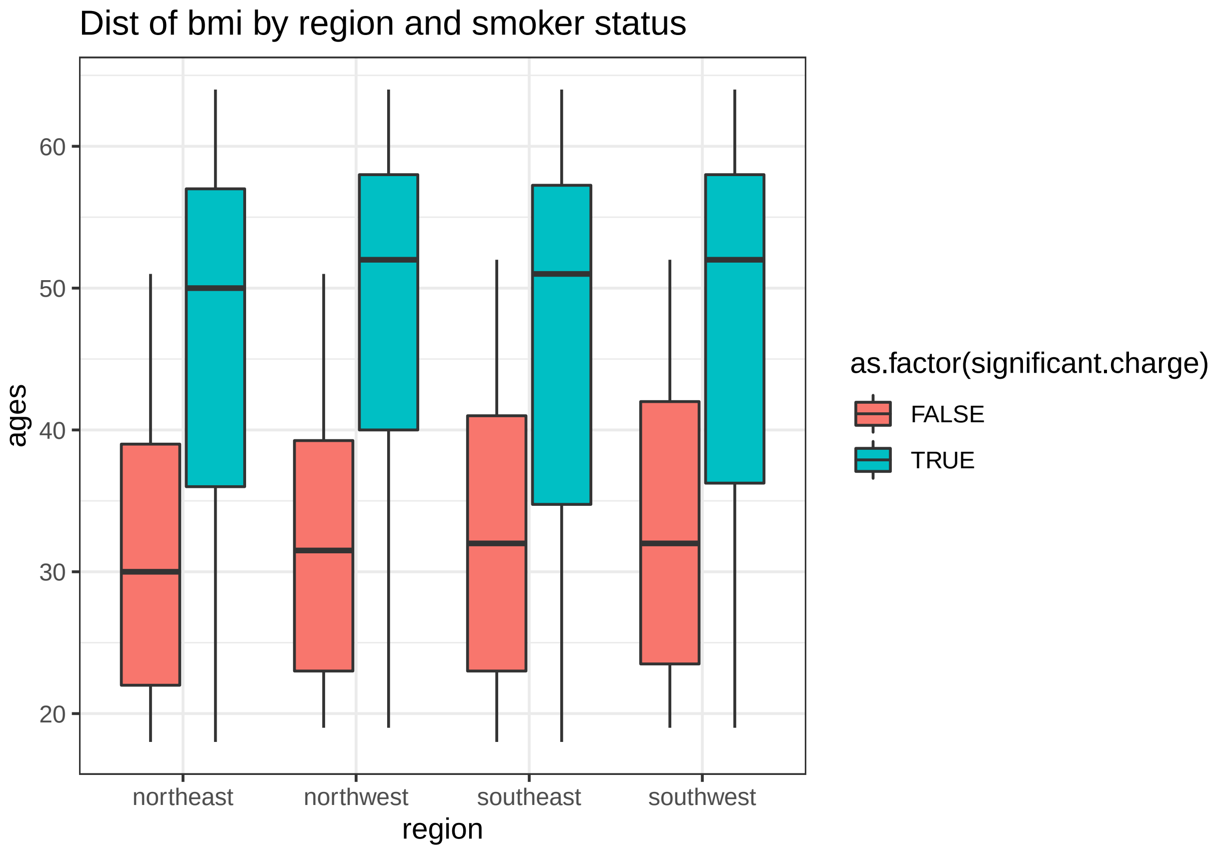
```r
ggplot(aes(x=age,y=charges, color=smoker, size=bmi), data=data) +
  labs(title="Scatter plot of Charges vs Age by BMI and Smoker Status") +
  theme_bw() +
  geom_point(alpha=0.5)
```



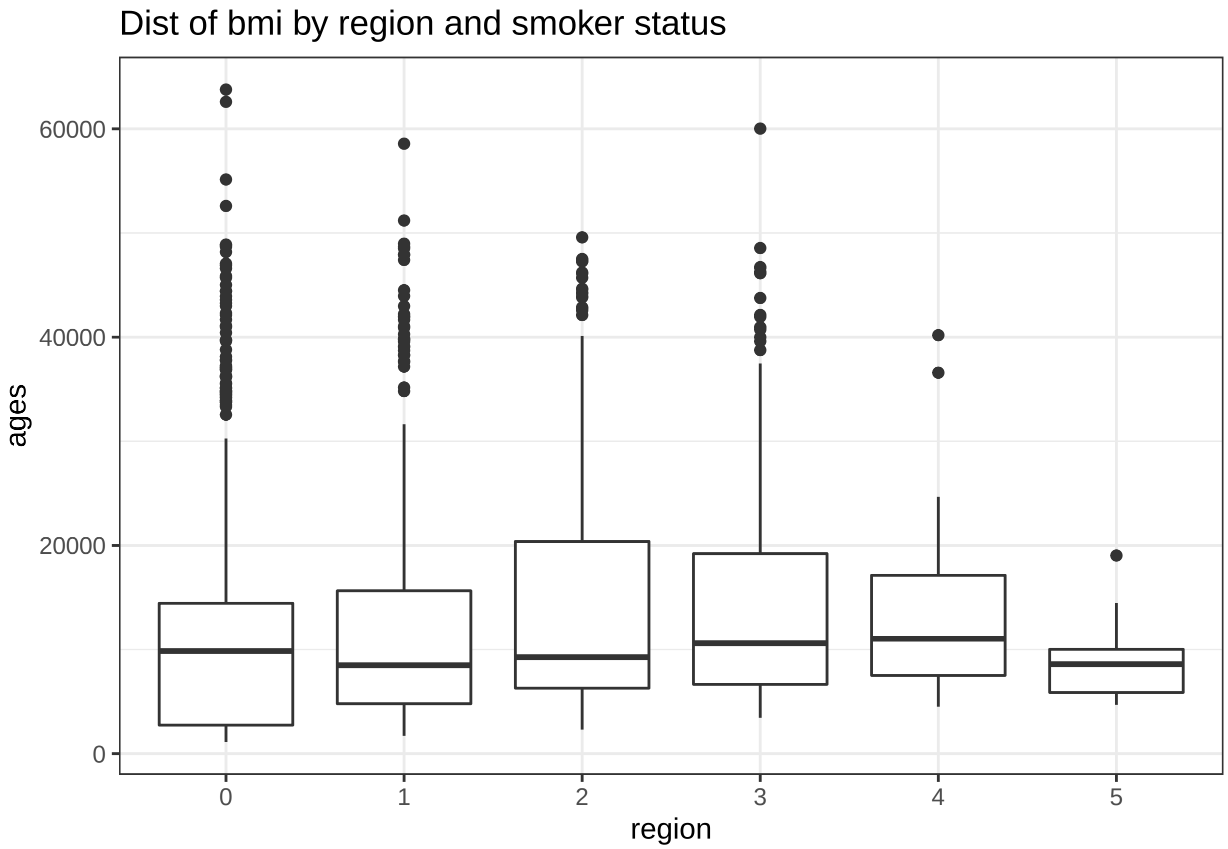
```r
ggplot(aes(x=age,y=bmi, color=significant.charge), data=data) +
  labs(title="Scatter plot of Charges vs Age by BMI and Smoker Status") +
  theme_bw() +
  geom_point(alpha=0.5)
```



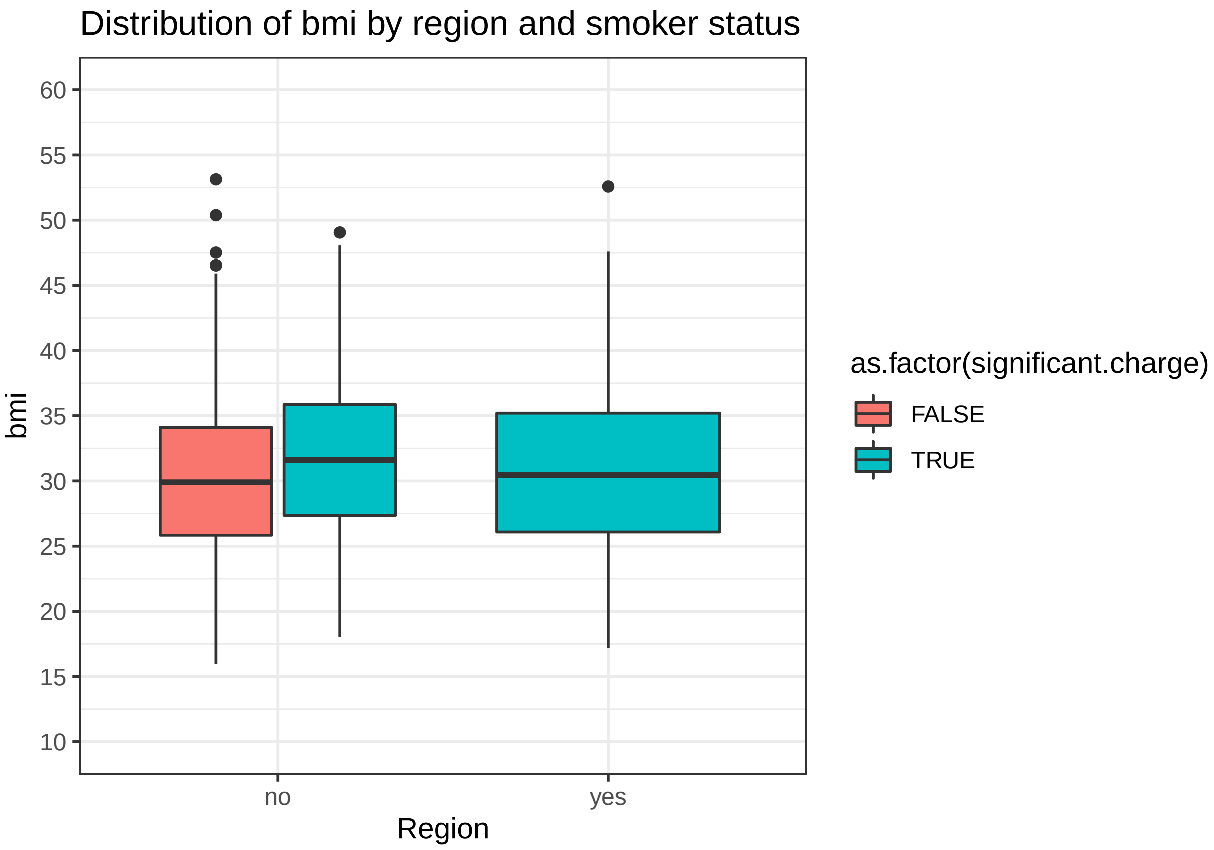
```
ggplot(data, aes(x=region, y=age, fill=as.factor(significant.charge)))+
  geom_boxplot() +
  theme_bw() +
  labs(x="region", y="ages", title="Dist of bmi by region and smoker status")
```



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

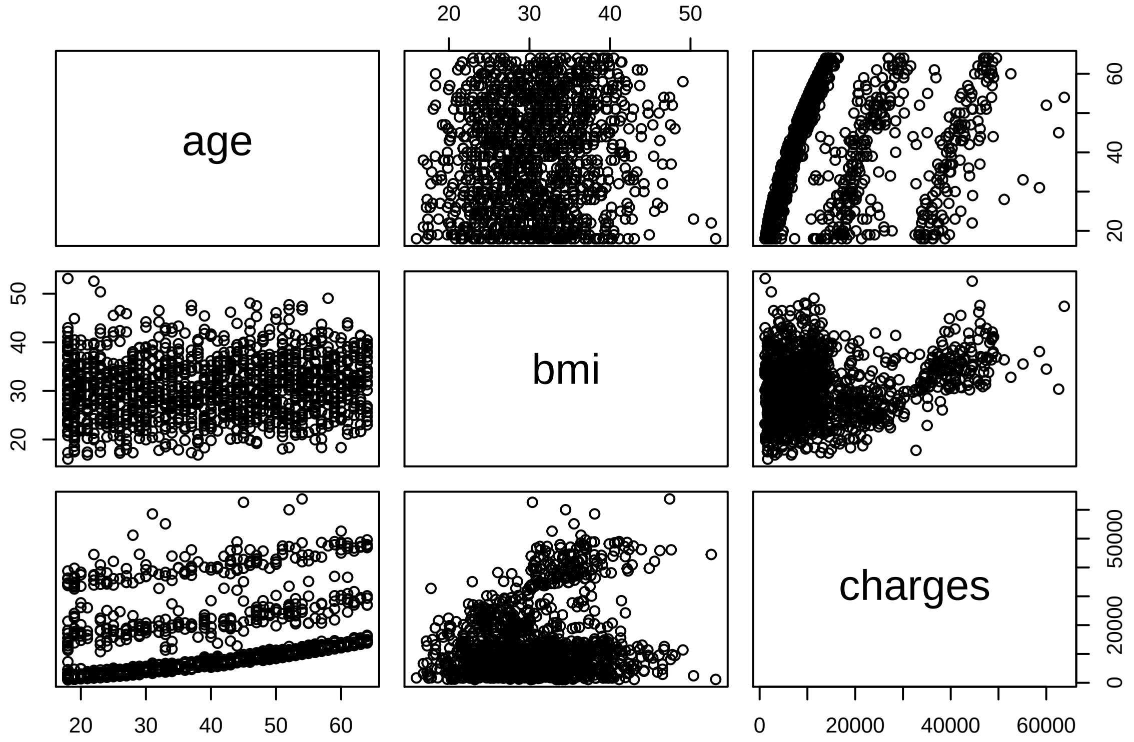


```
ggplot(data, aes(x=smoker, y=bmi, fill=as.factor(significant.charge)))+
  geom_boxplot() +
  theme_bw() +
  labs(x="Region", y="bmi", title="Distribution of bmi by region and smoker status") +  scale_y_continu
```



Correlation

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



```r
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
```

Blind Full Model

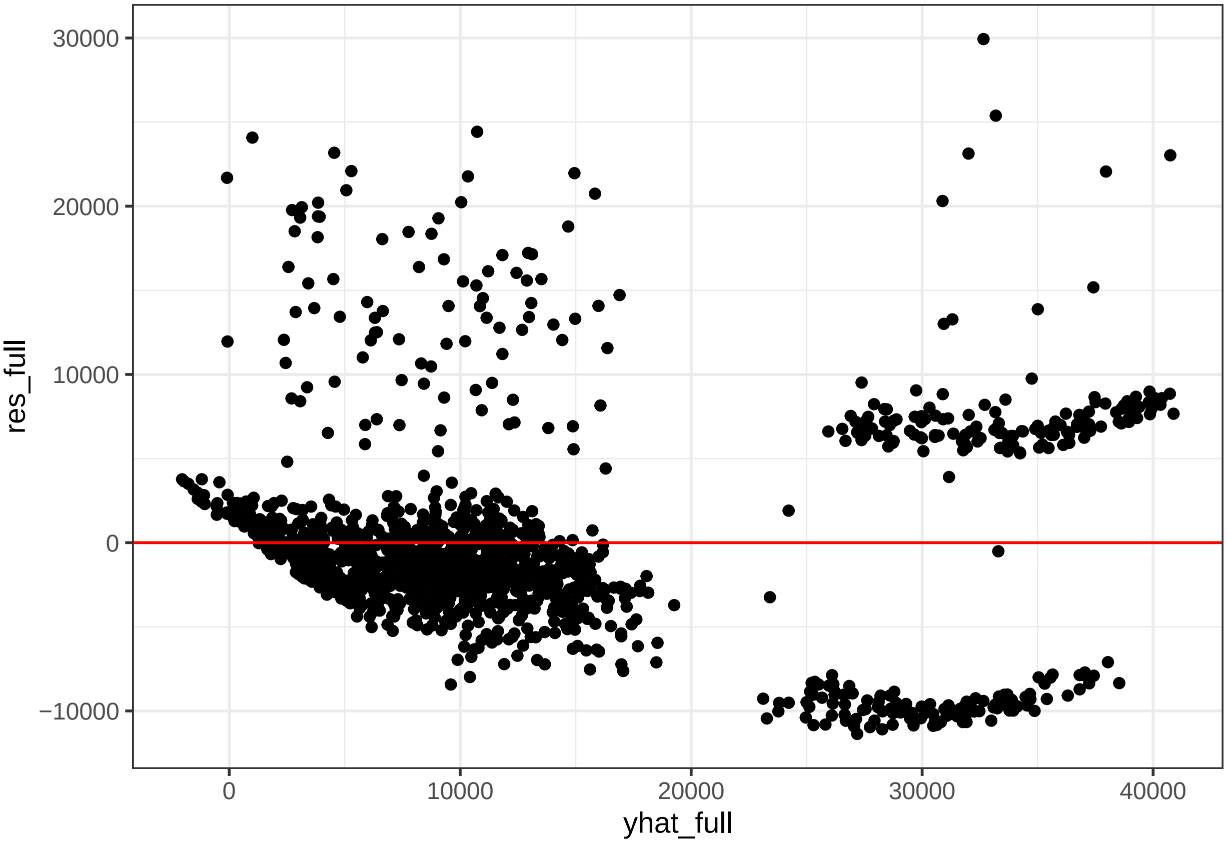
```r
mlr_full = lm(charges ~  age + bmi + children + smoker + region, data=data)
summary(mlr_full)
```

```
##
## 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.

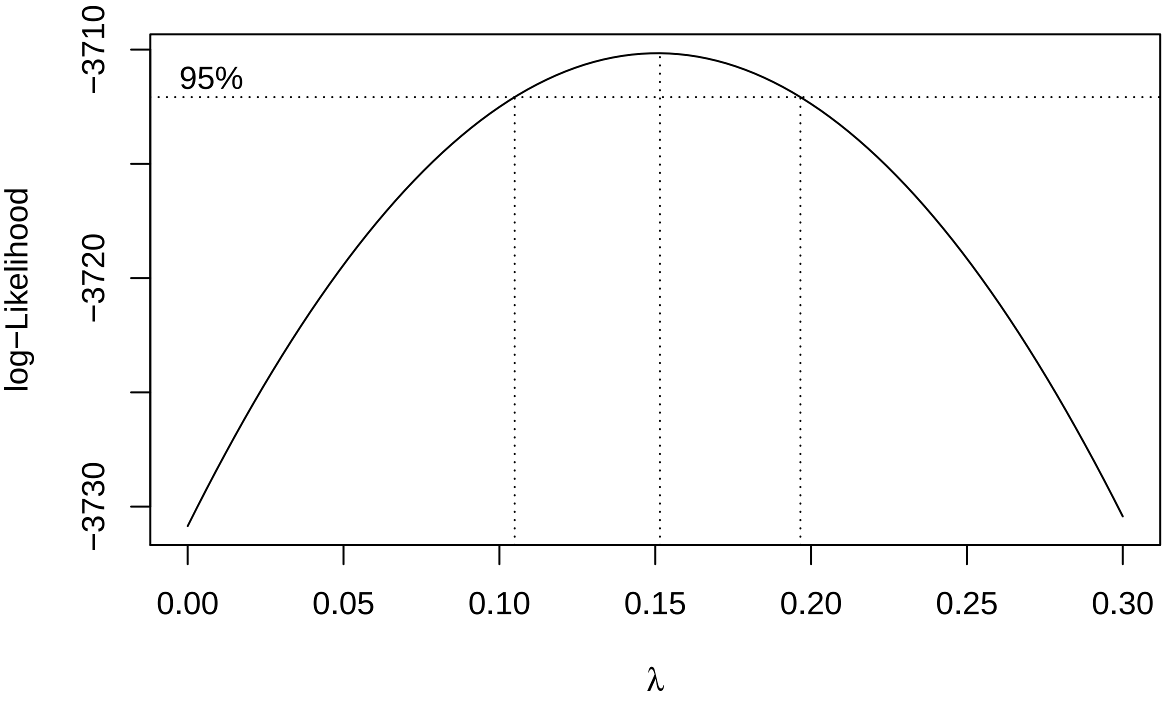
Assumption Check of Full Model

```
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.

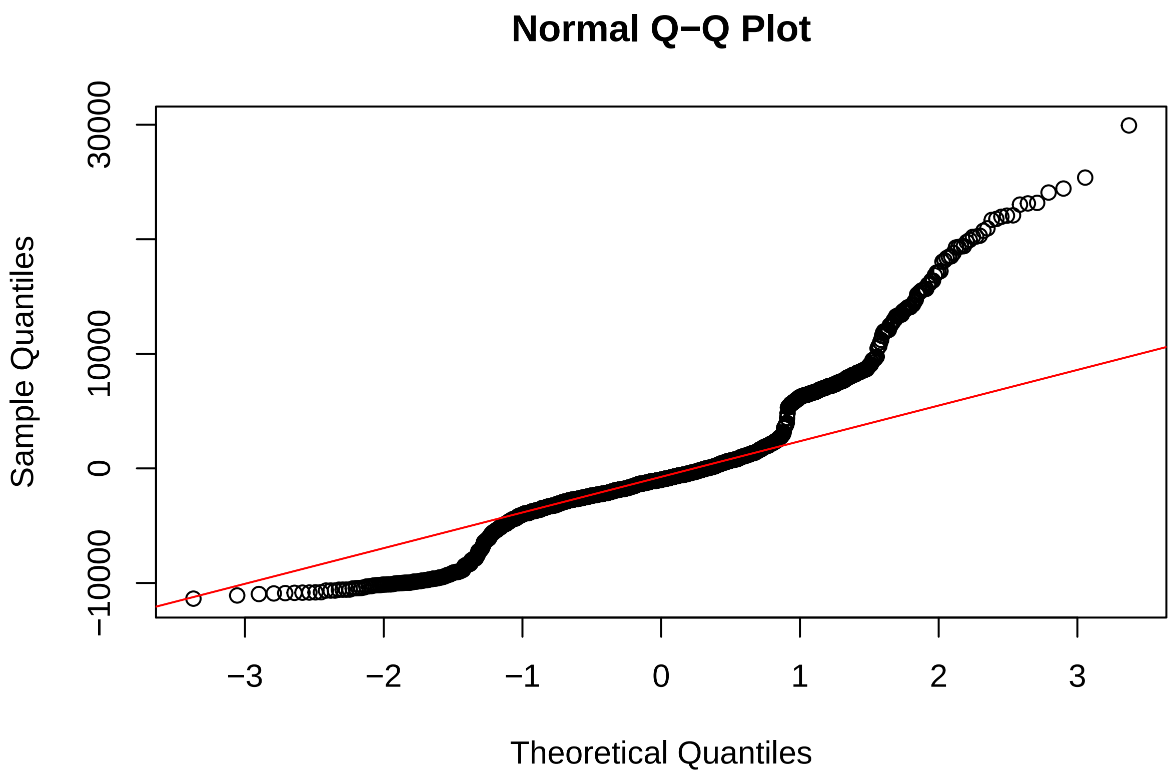
```r
boxcox(mlr_full, lambda=seq(0,0.3, 0.01))
```



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

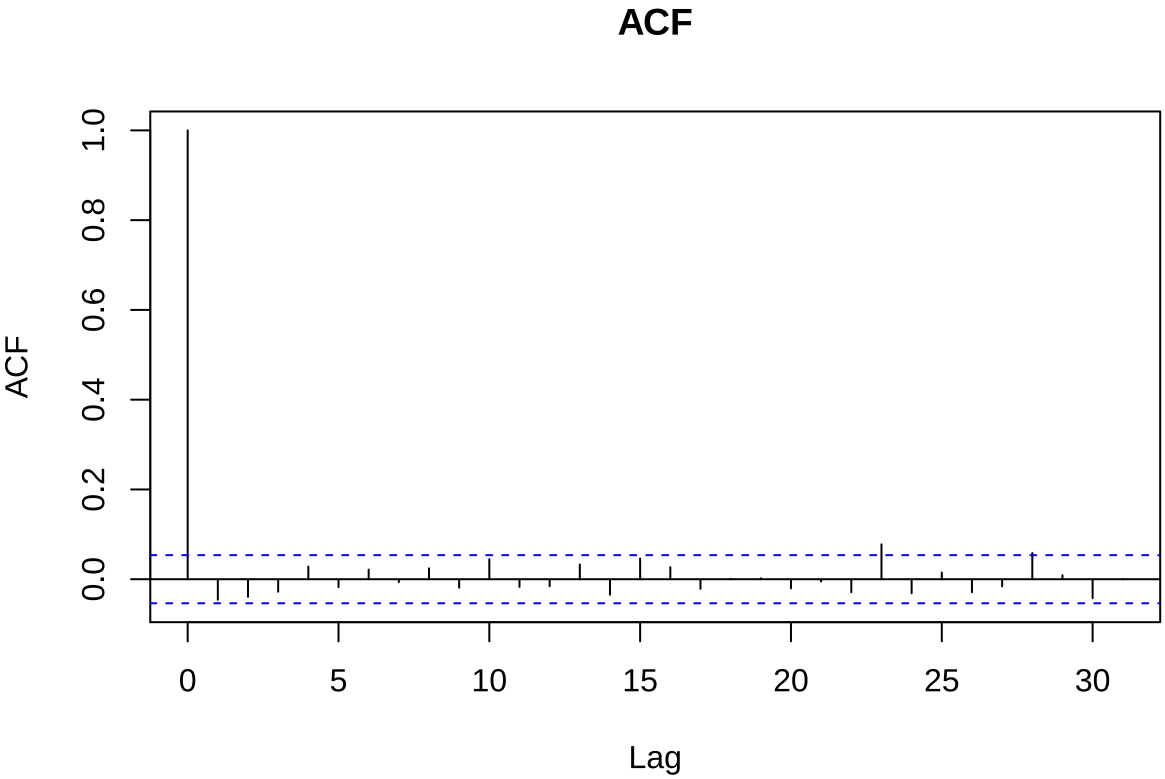
QQPlot Normality of Full Model

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



ACF of full model

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



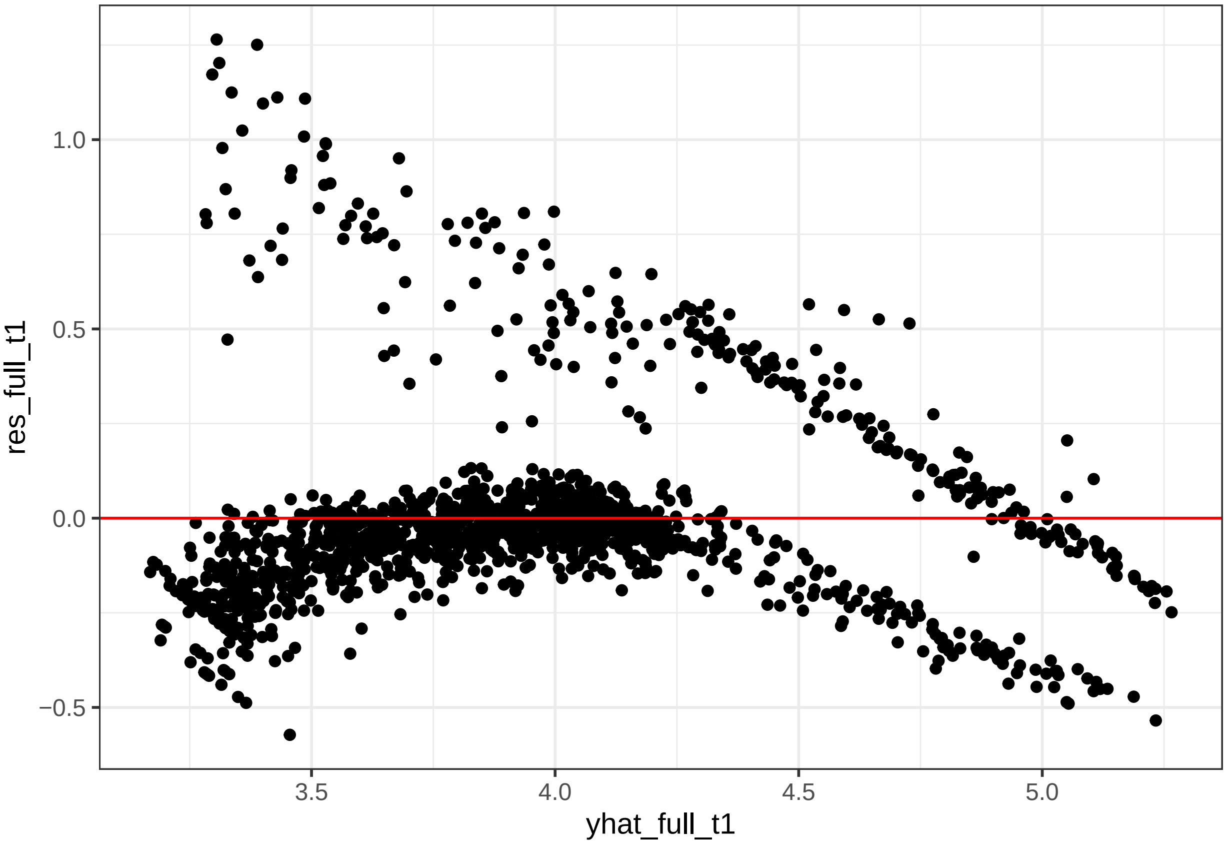
Transformation of full model

```
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
```

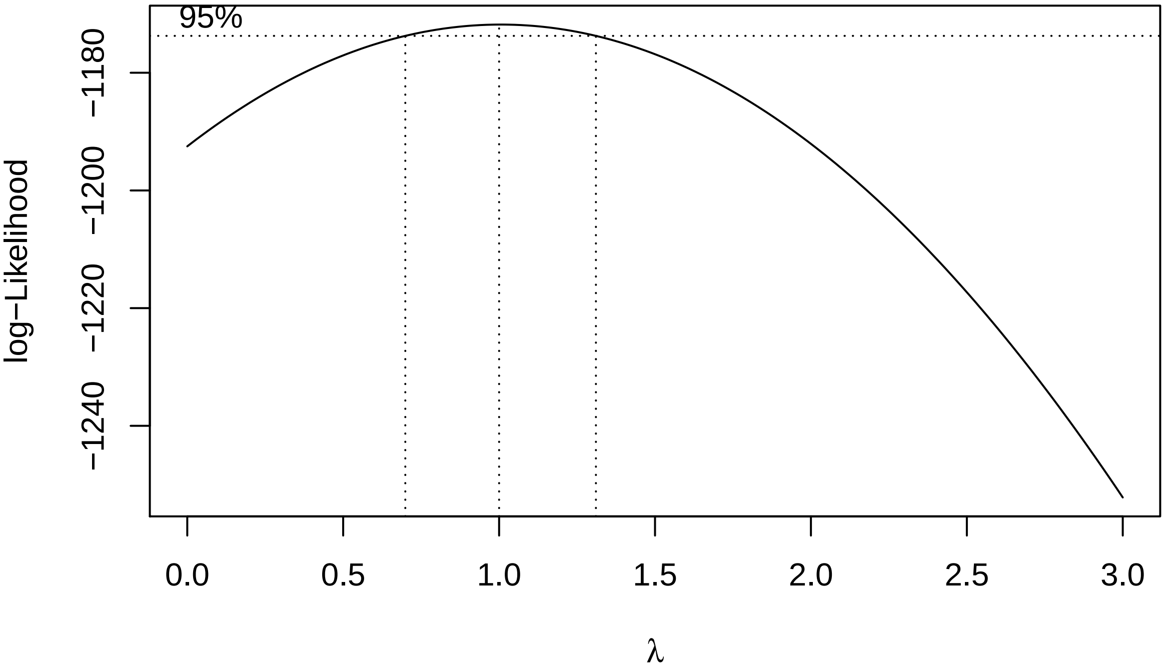
Residual Plot of the transformed model.

```
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")
```



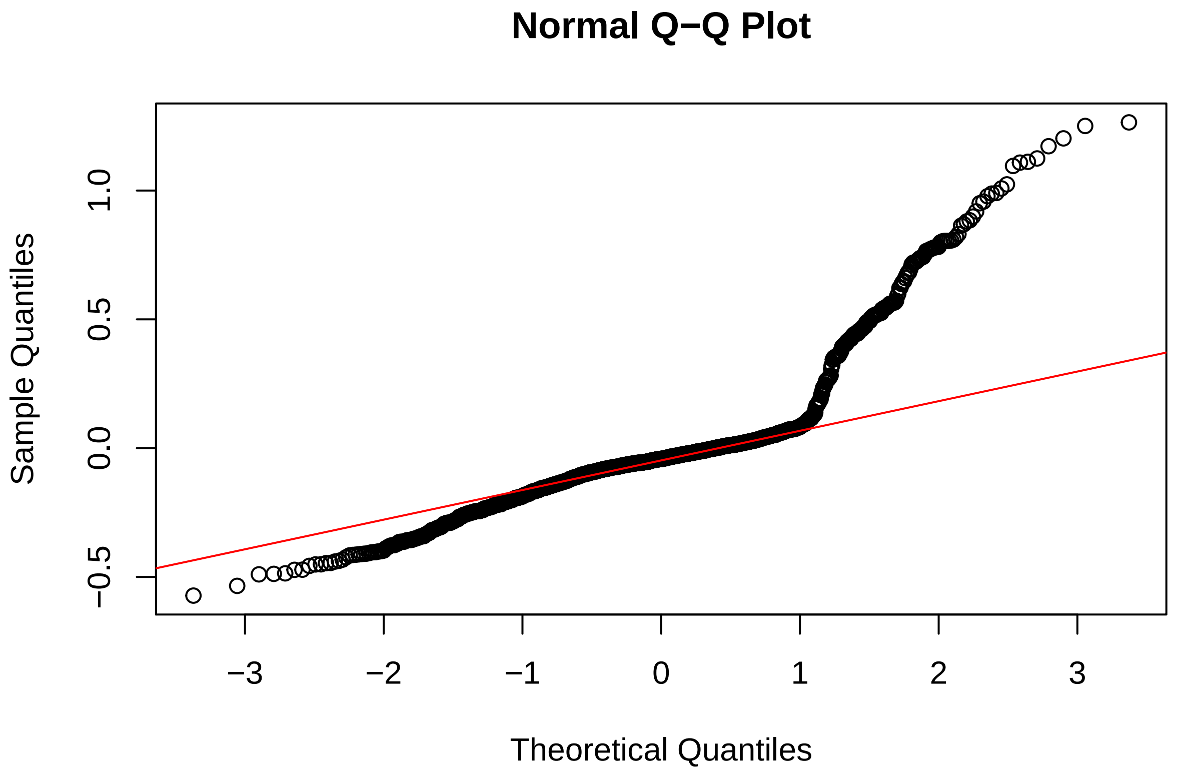
Violation in constant variance

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



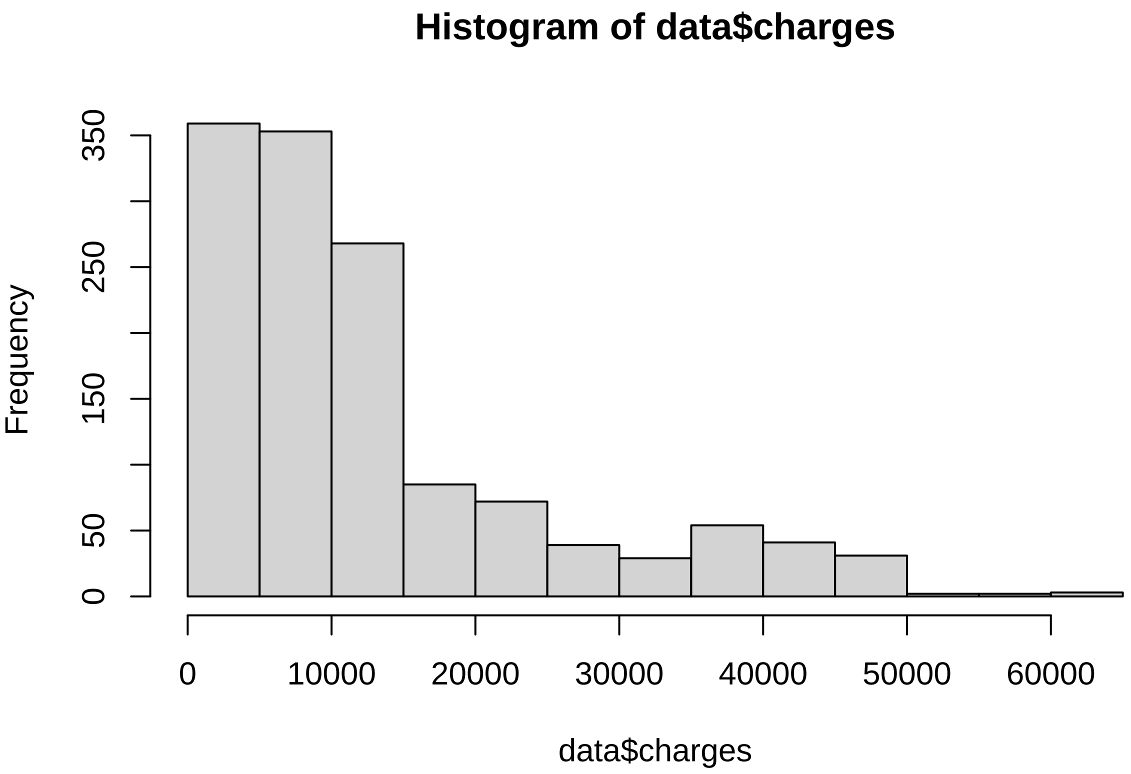
QQPLOT of transformed full model.

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

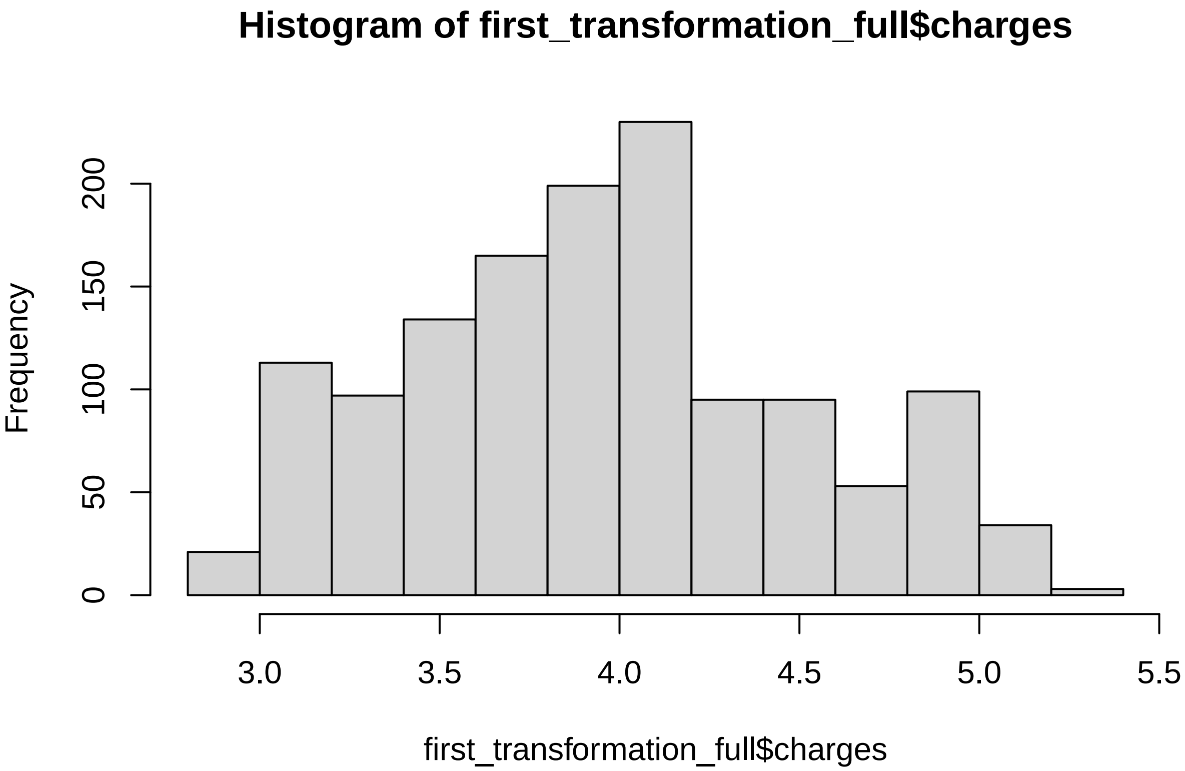


Why is this happening? Is there some weird behavior in the response variable?

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



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



Trial of other predictors to fullfill the linearity assumption.

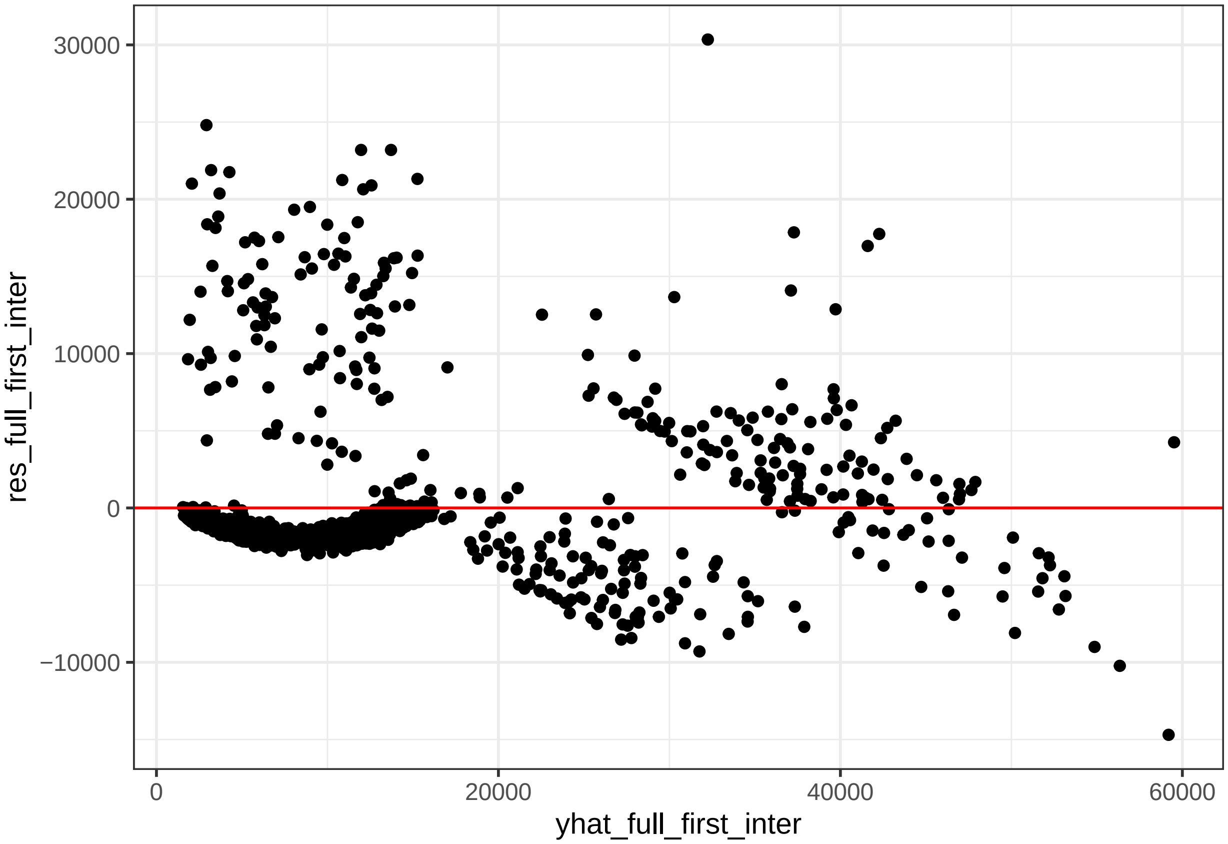
Maybe we can add some interaction terms to the model to see if we can fix the linearity assumption.

```
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
```

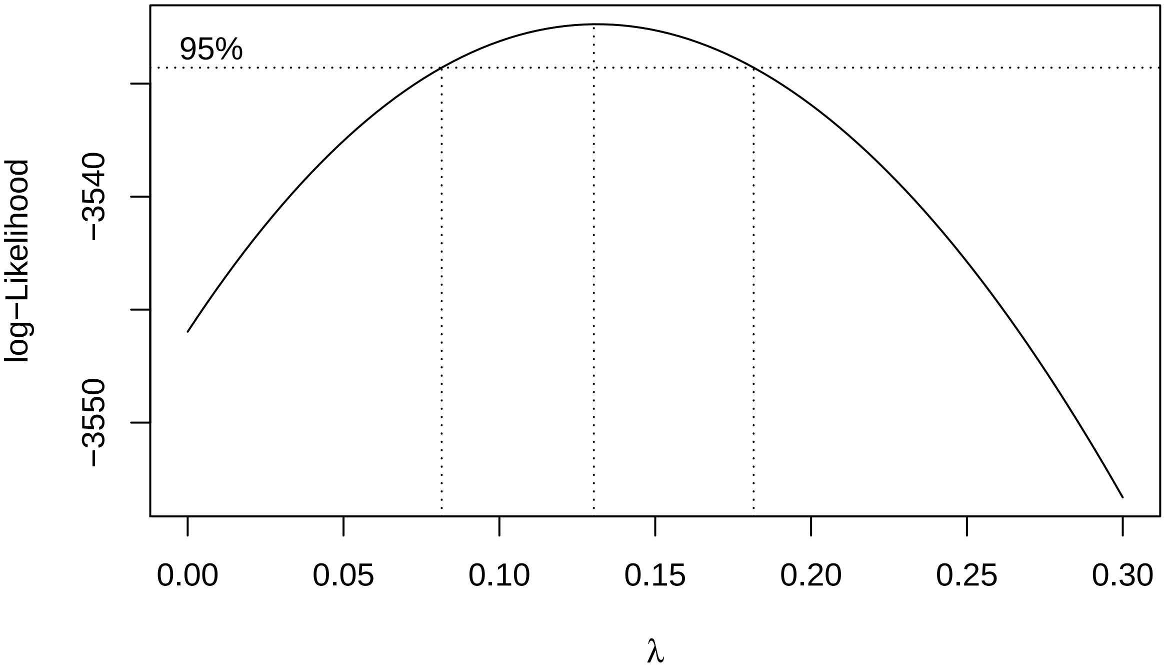
Residual Plot

```
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))
```



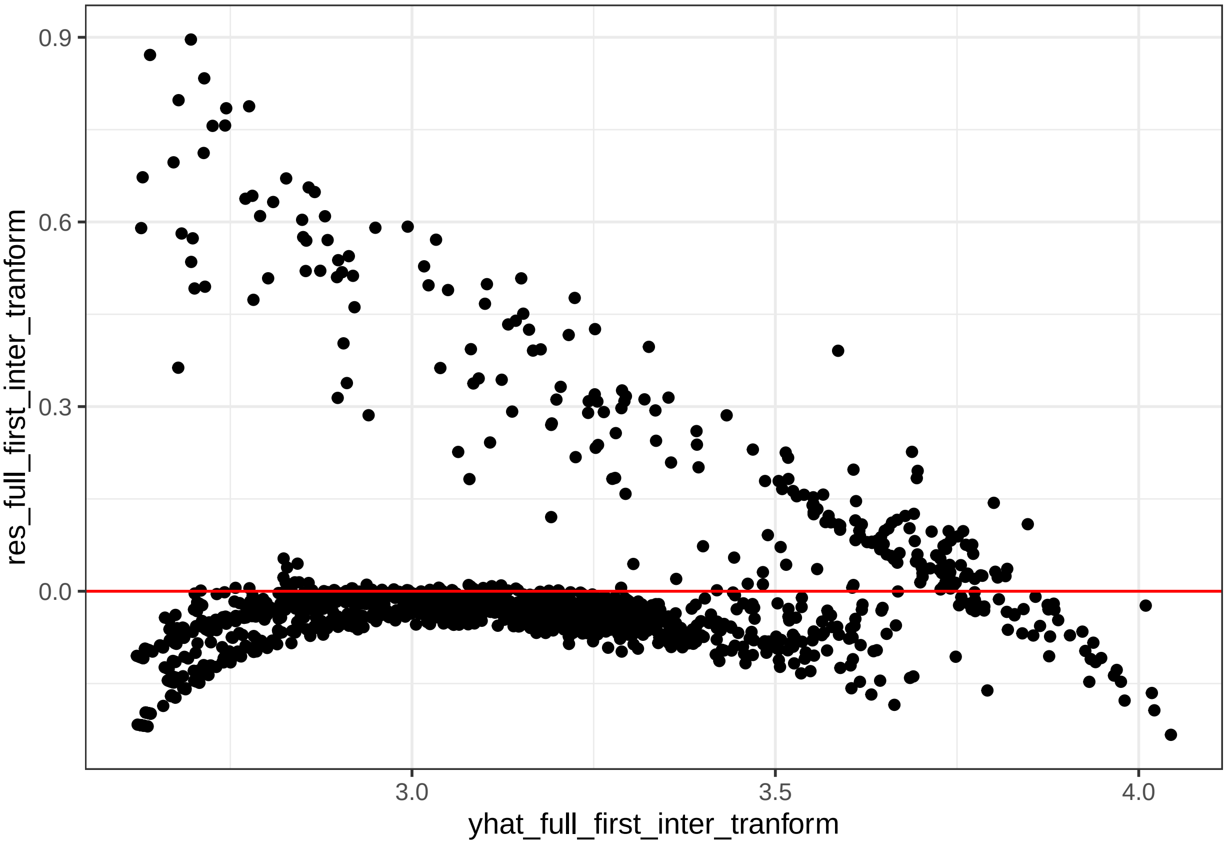
Maybe we can use a lambda value of 0.125

```
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
```

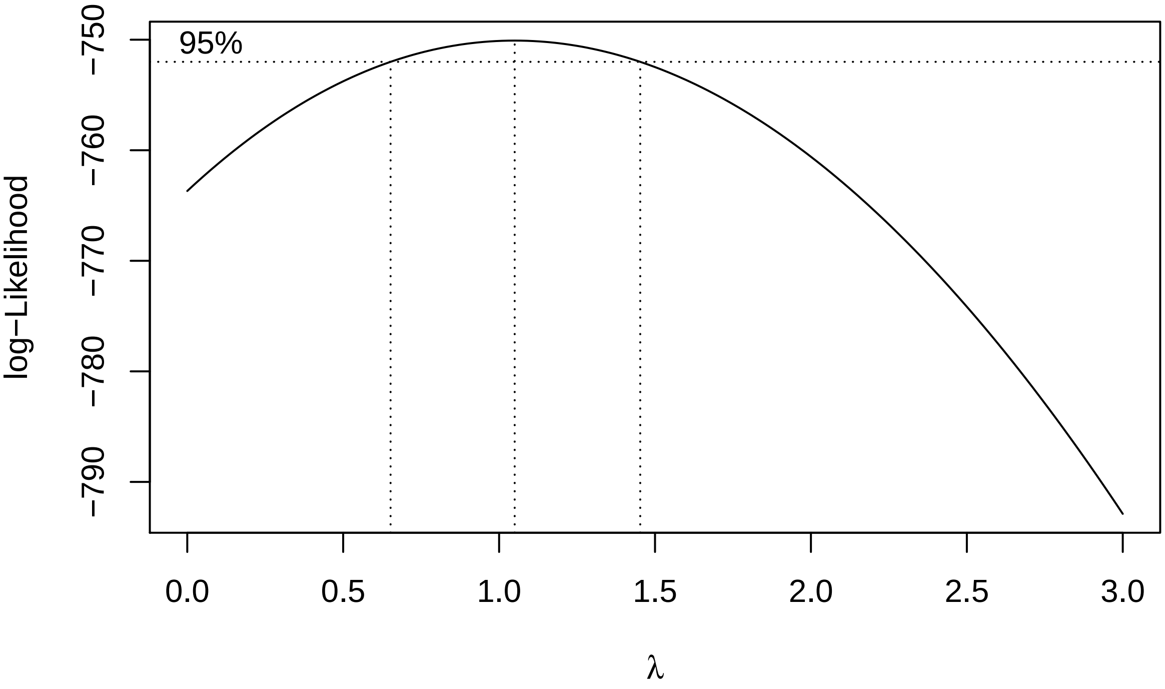
Recheck Residual Plot

```
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.

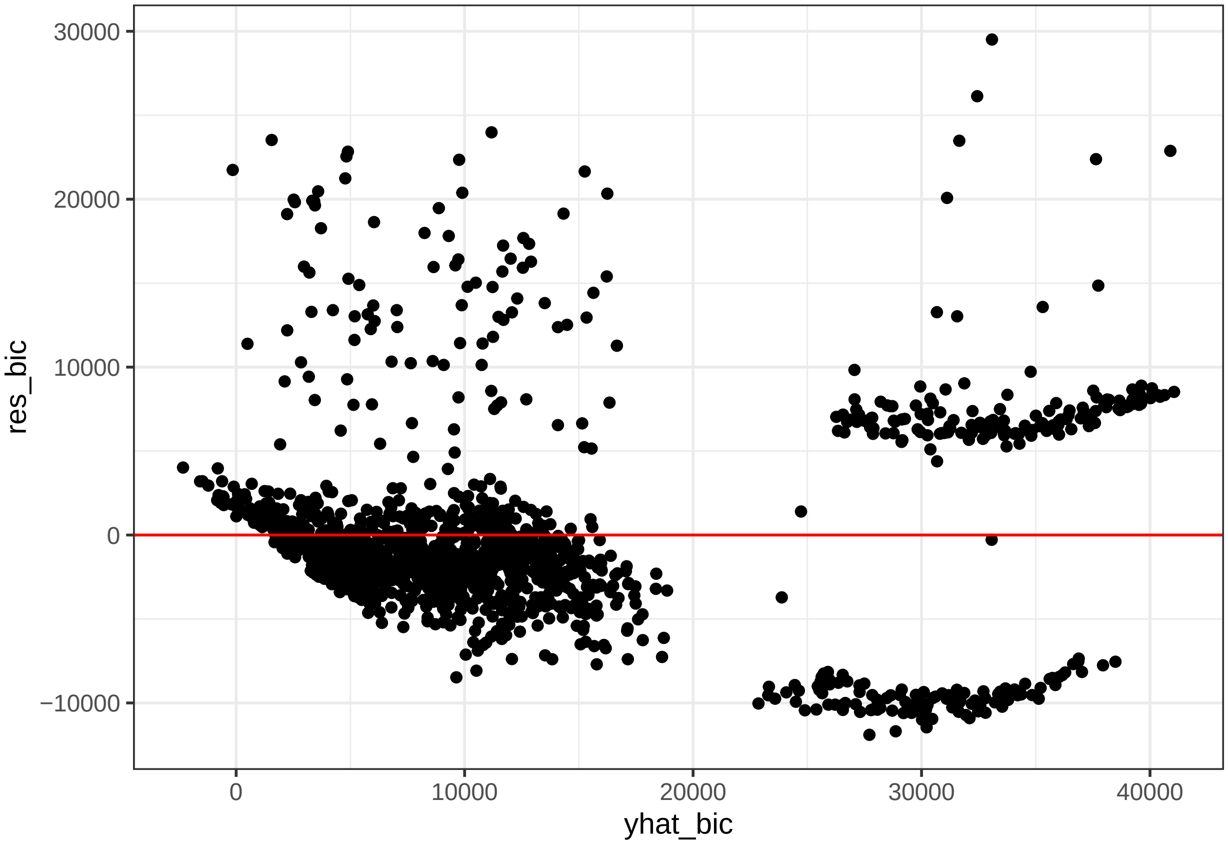
Try different models before splitting the data

```
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
```

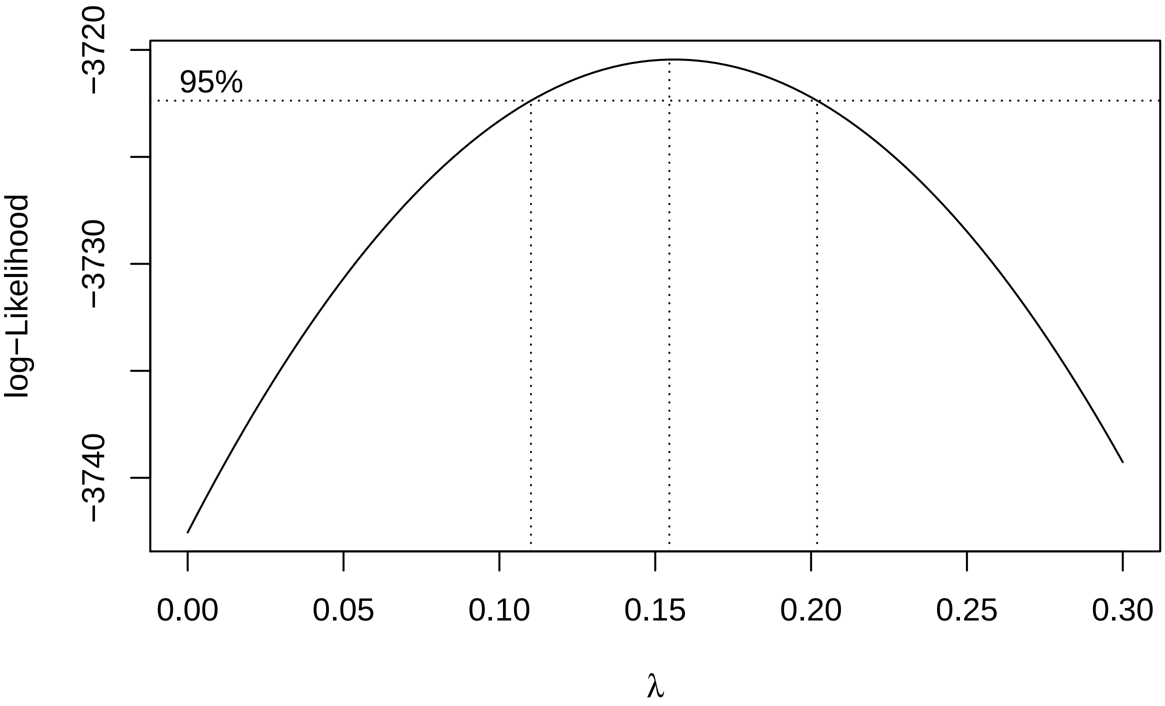
Residual Plot

```
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))
```



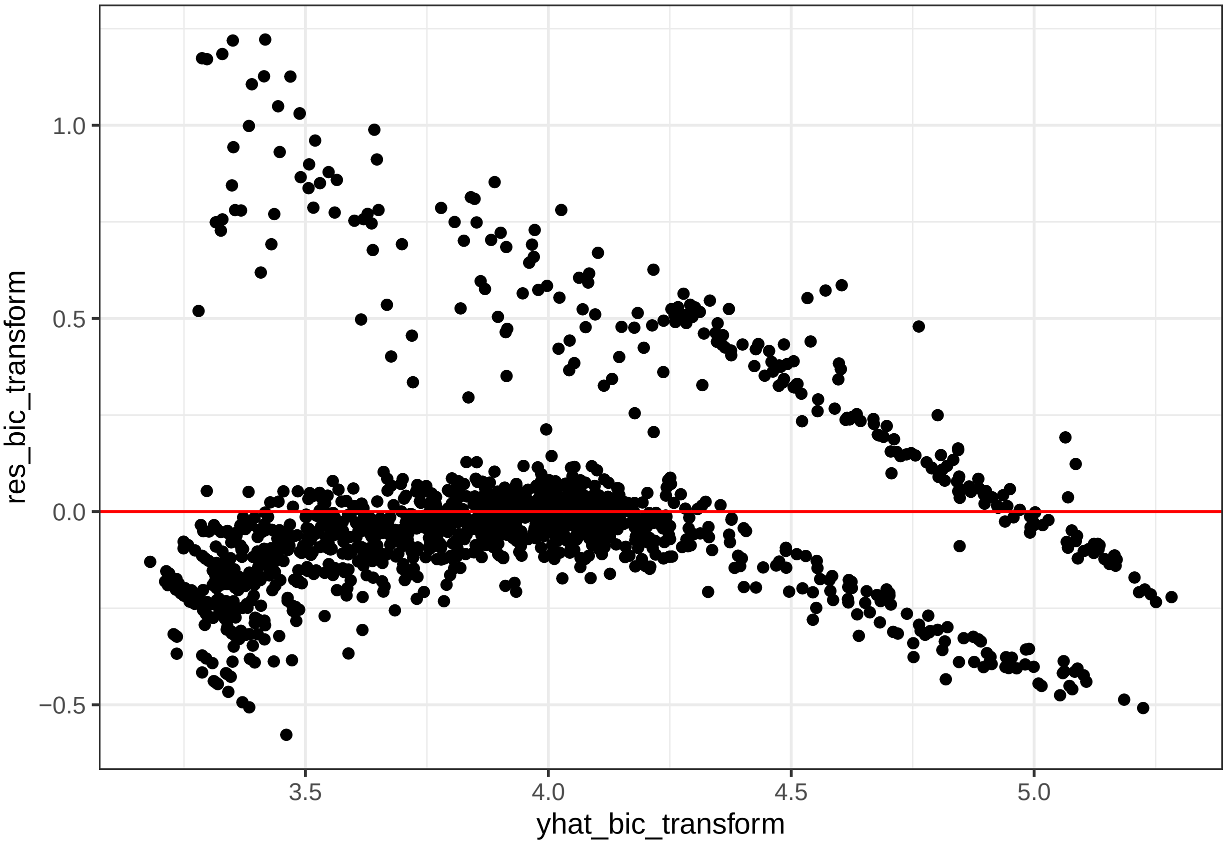
Again lambda of 0.15

```
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
```

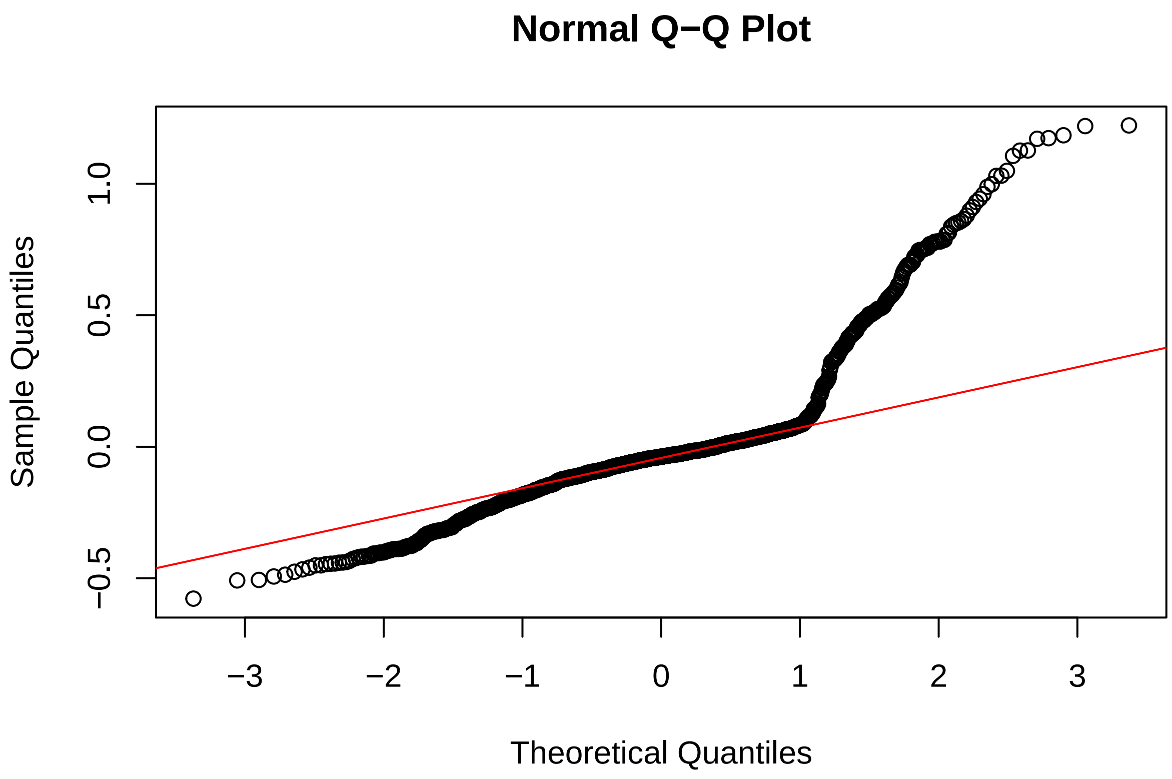
Residual Plot

```
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")
```



QQPlot

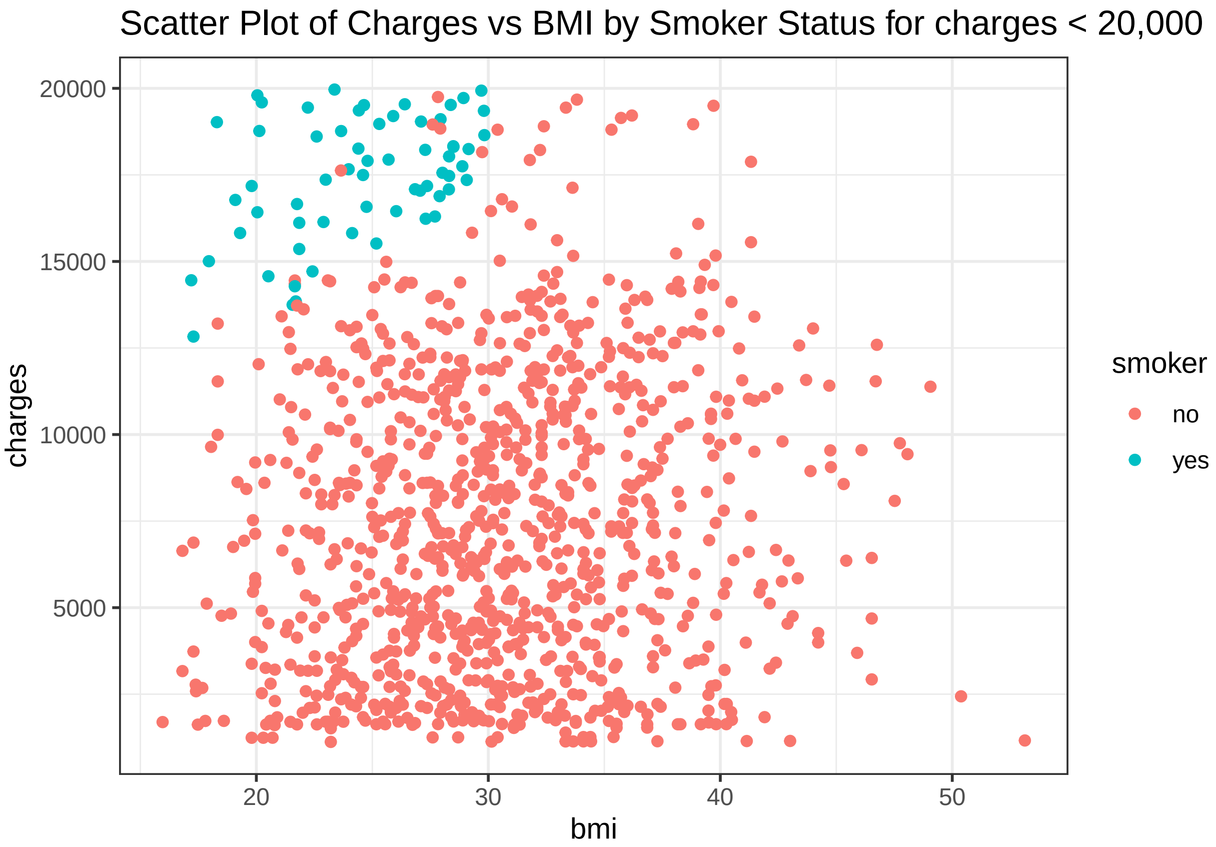
```
{
  qqnorm(bic_selection_model_transform$residuals)
  qqline(bic_selection_model_transform$residuals, col="red")
}
```



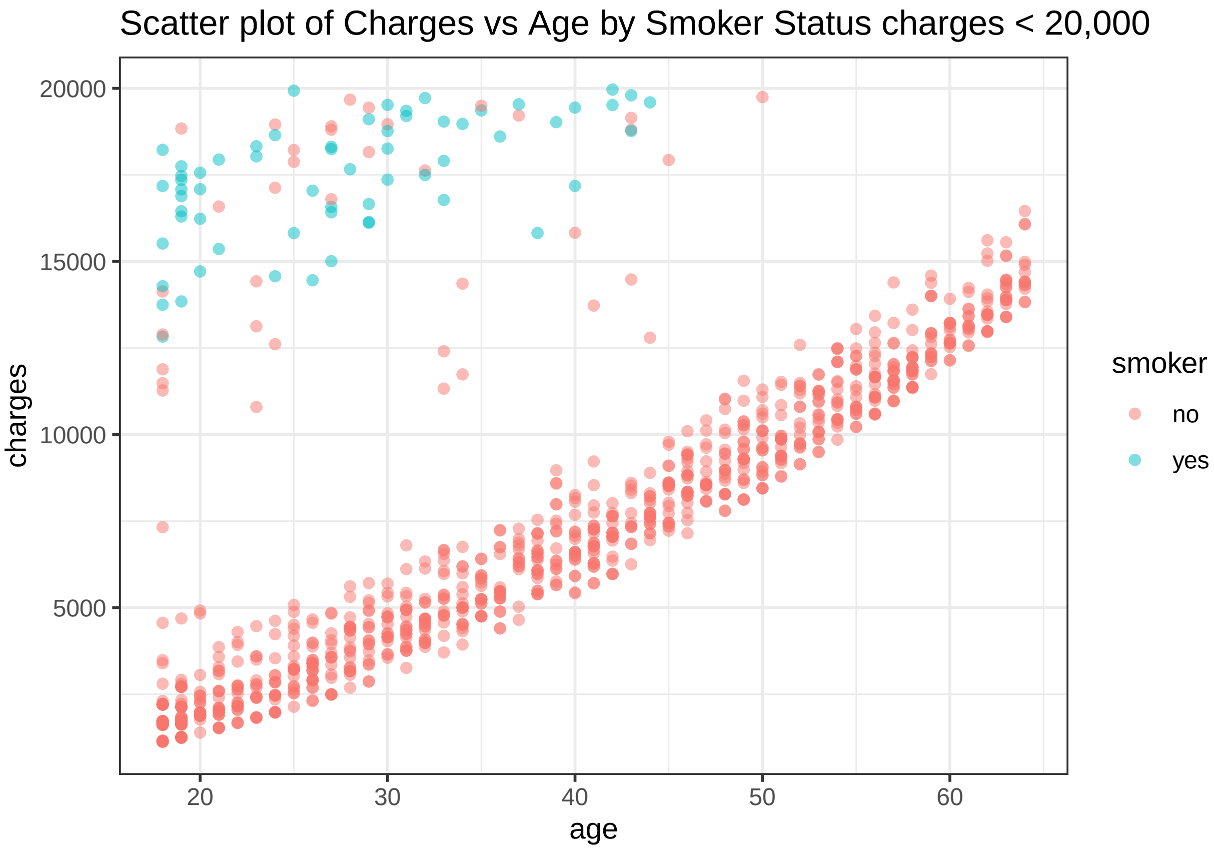
See the two groupings

Check the data points below and above 20,000

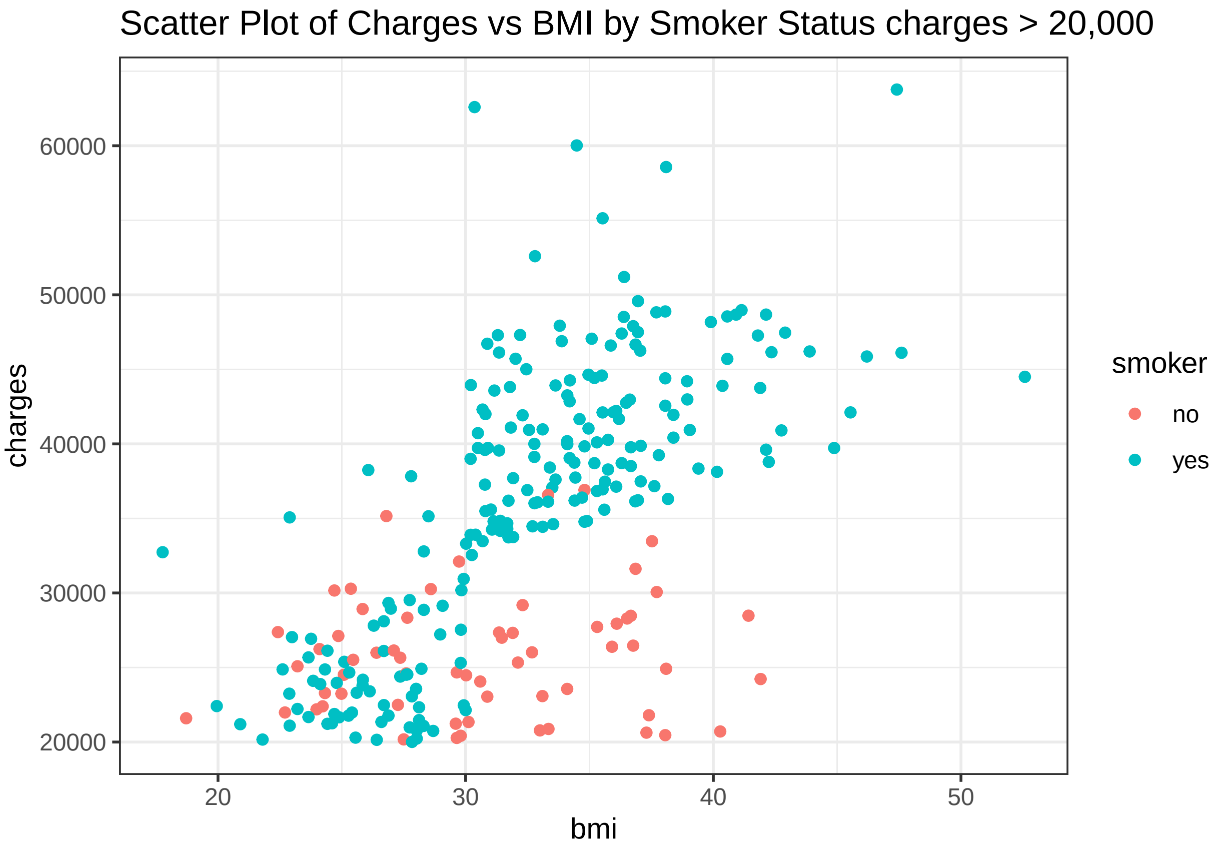
```
less_charge <- data[data$charges < 20000,]
more_change <- data[data$charges >= 20000, ]
library(tidyverse)
ggplot(aes(x=bmi, y=charges, color=smoker), data=less_charge) +
  labs(title="Scatter Plot of Charges vs BMI by Smoker Status for charges < 20,000") +
  theme_bw() +
  geom_point()
```



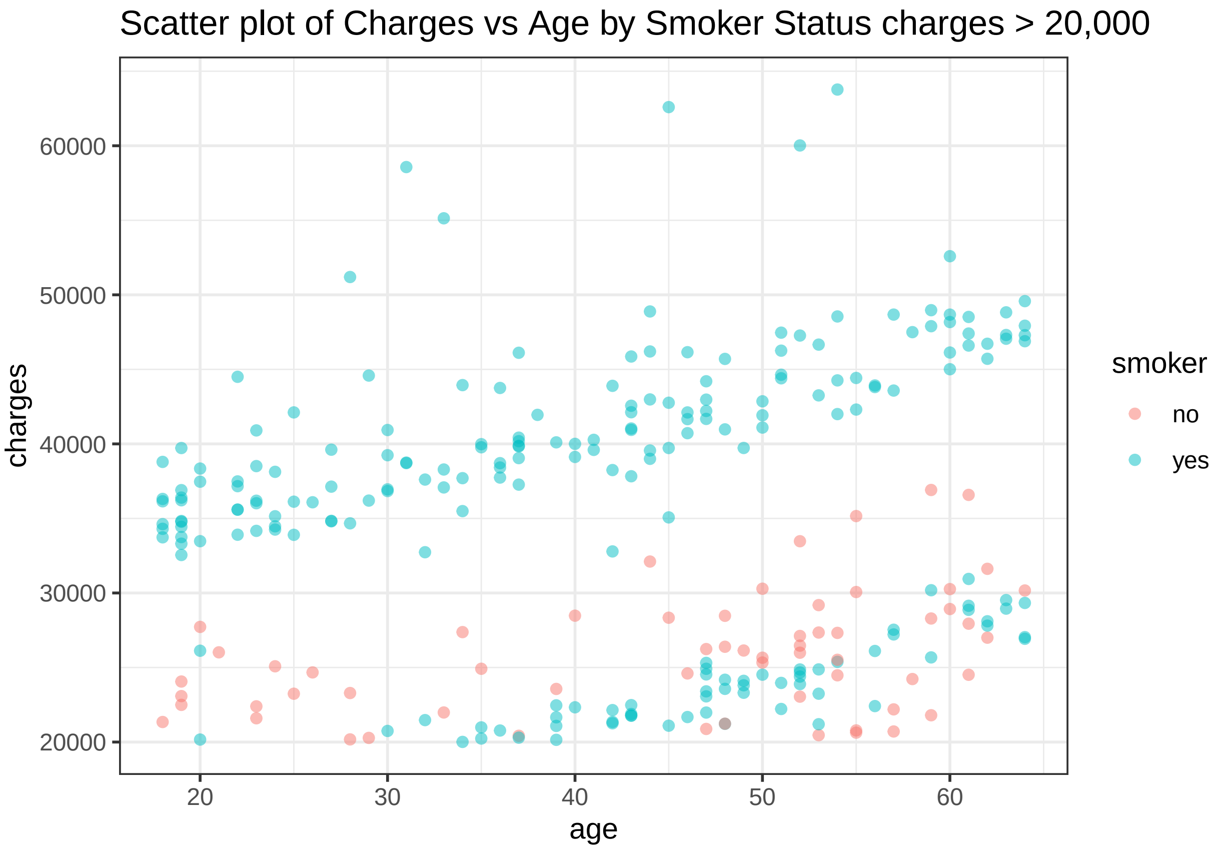
```
ggplot(aes(x=age,y=charges, color=smoker), data=less_charge) +
  labs(title="Scatter plot of Charges vs Age by Smoker Status charges < 20,000") +
  theme_bw() +
  geom_point(alpha=0.5)
```



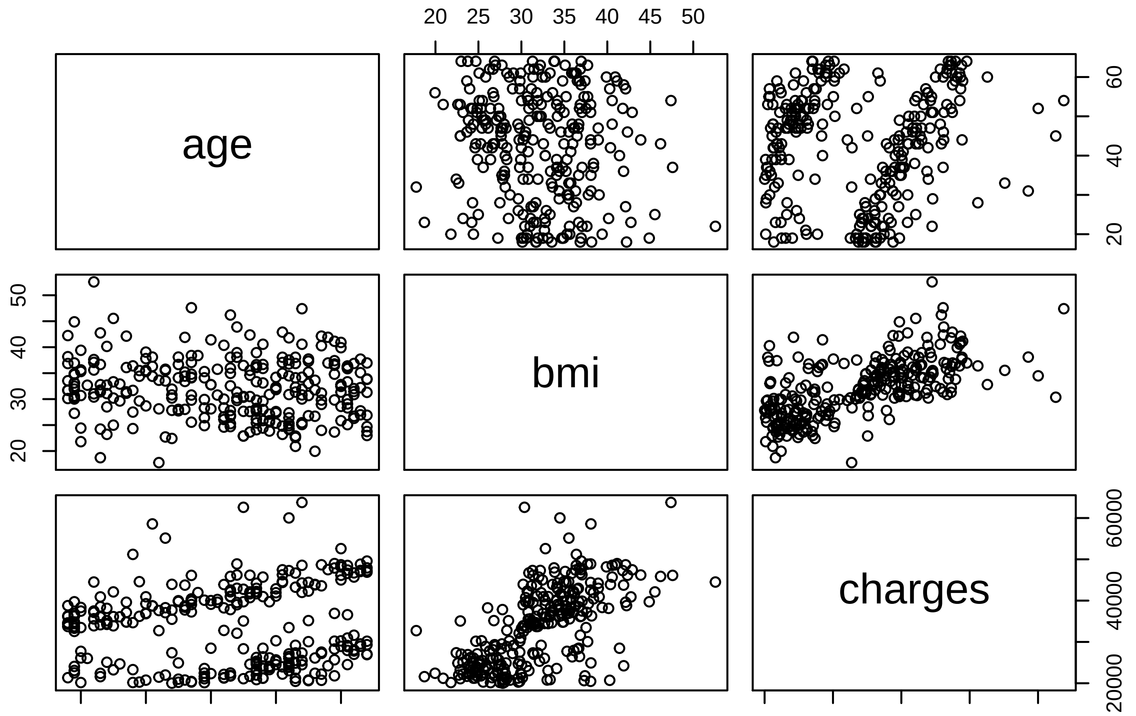
```
ggplot(aes(x=bmi, y=charges, color=smoker), data=more_change) +
  labs(title="Scatter Plot of Charges vs BMI by Smoker Status charges > 20,000") +
  theme_bw() +
  geom_point()
```



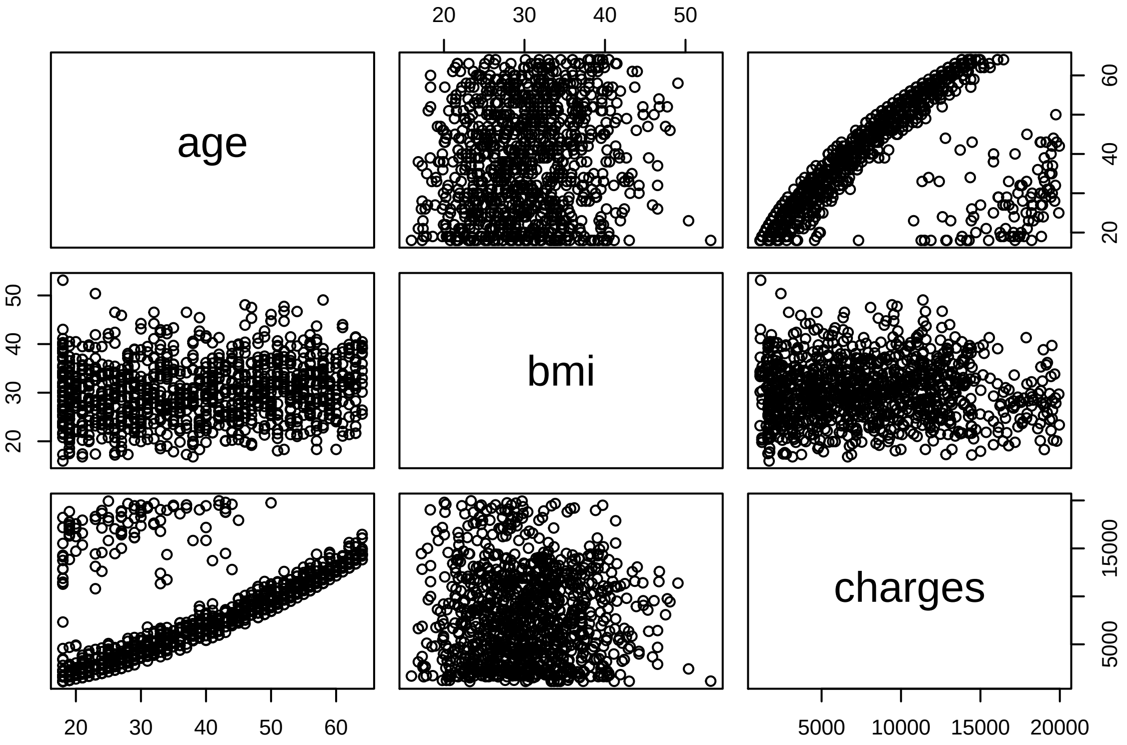
```
ggplot(aes(x=age,y=charges, color=smoker), data=more_change) +
  labs(title="Scatter plot of Charges vs Age by Smoker Status charges > 20,000") +
  theme_bw() +
  geom_point(alpha=0.5)
```



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

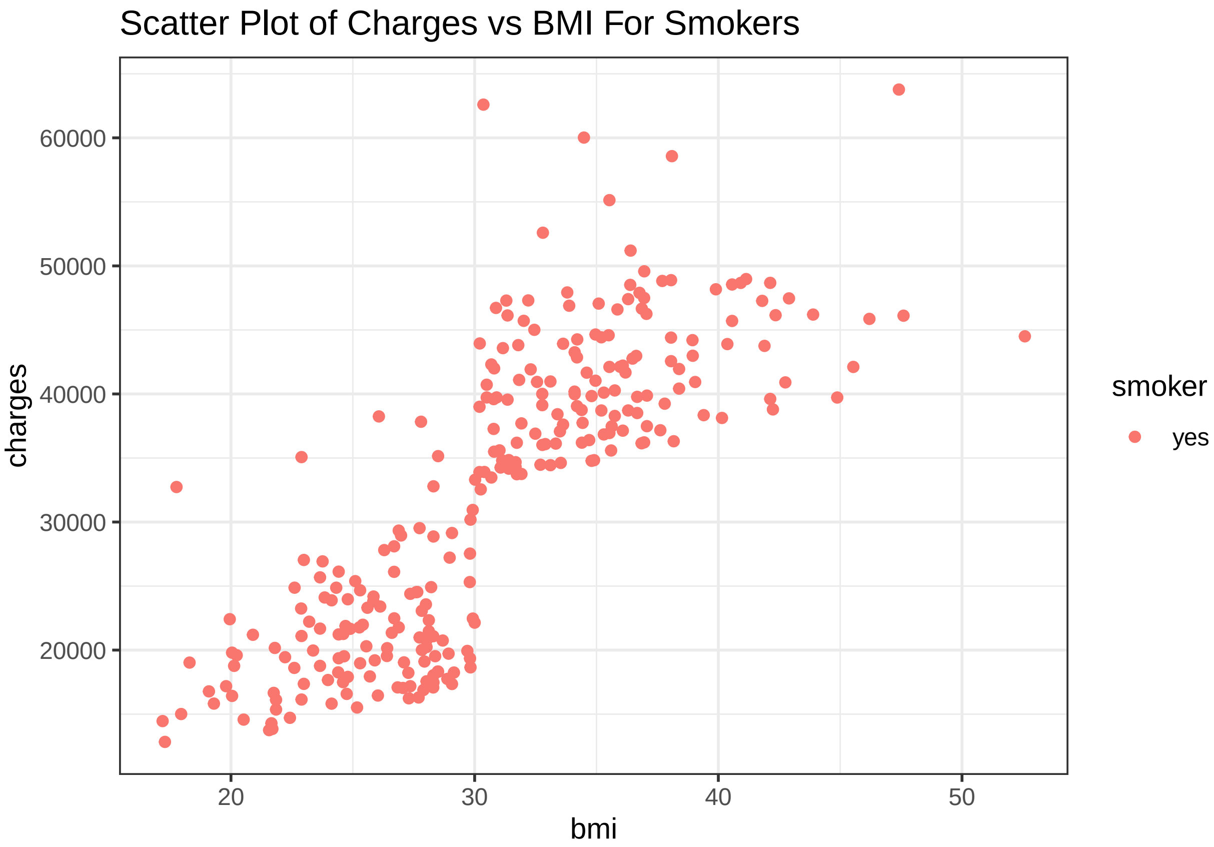


```
pairs(less_charge[c("age", "bmi", "charges")])
```

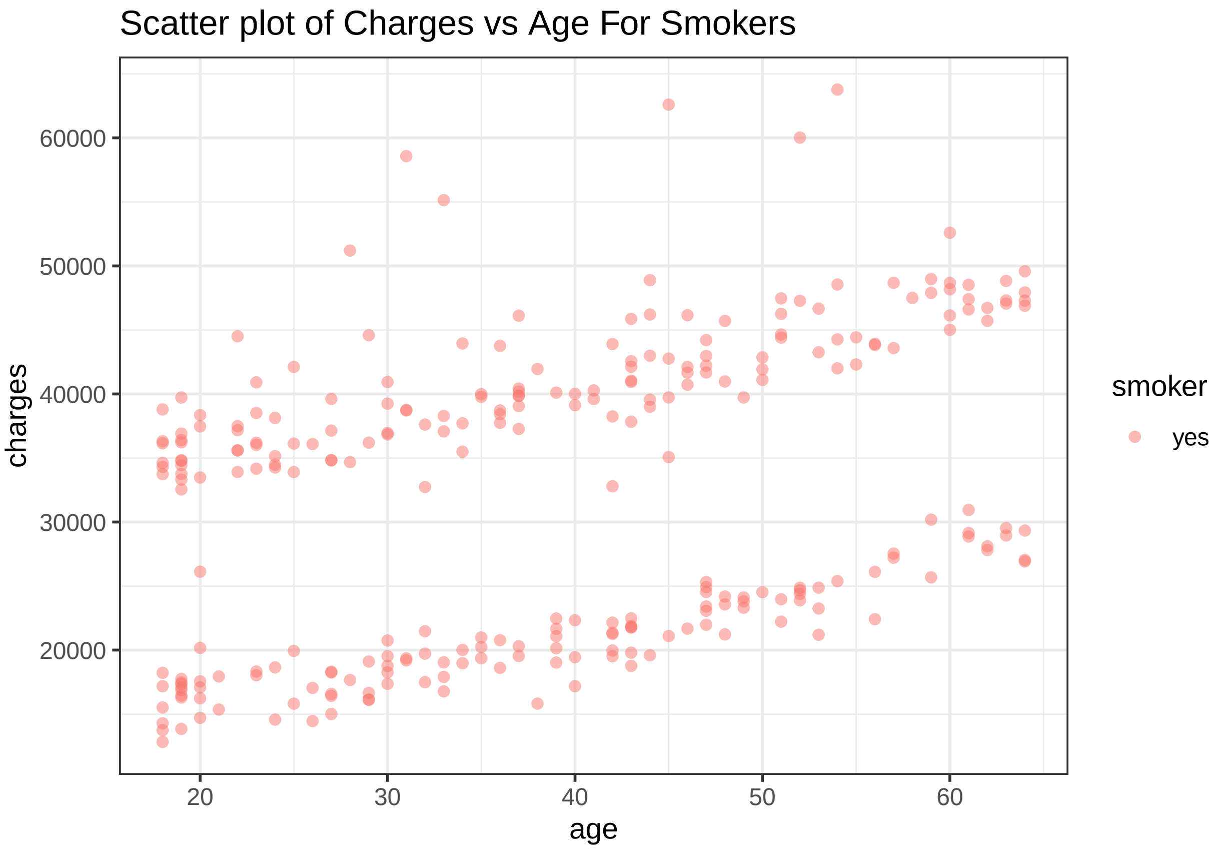


Split dataset by smoking status

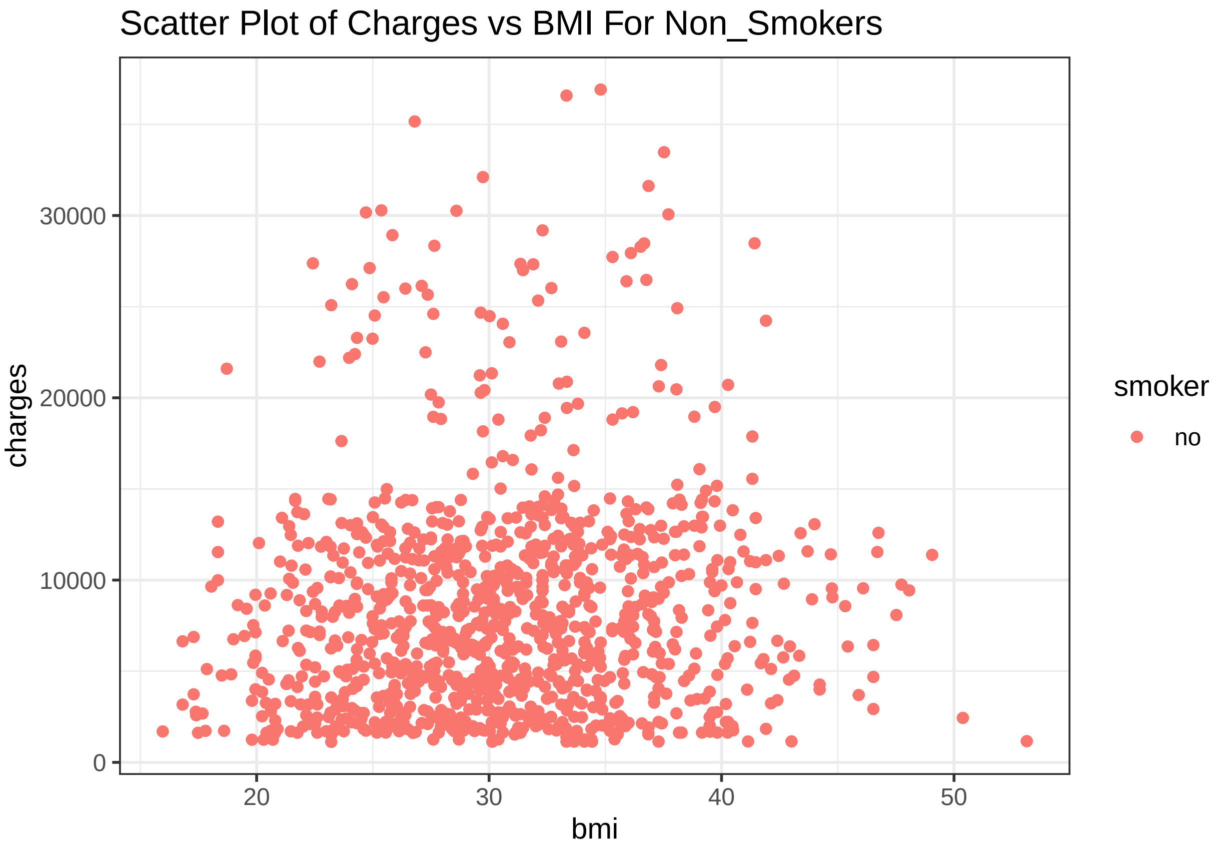
```
smokers <- data[data$smoker == 'yes',]
non_smokers <- data[data$smoker != 'yes',]

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



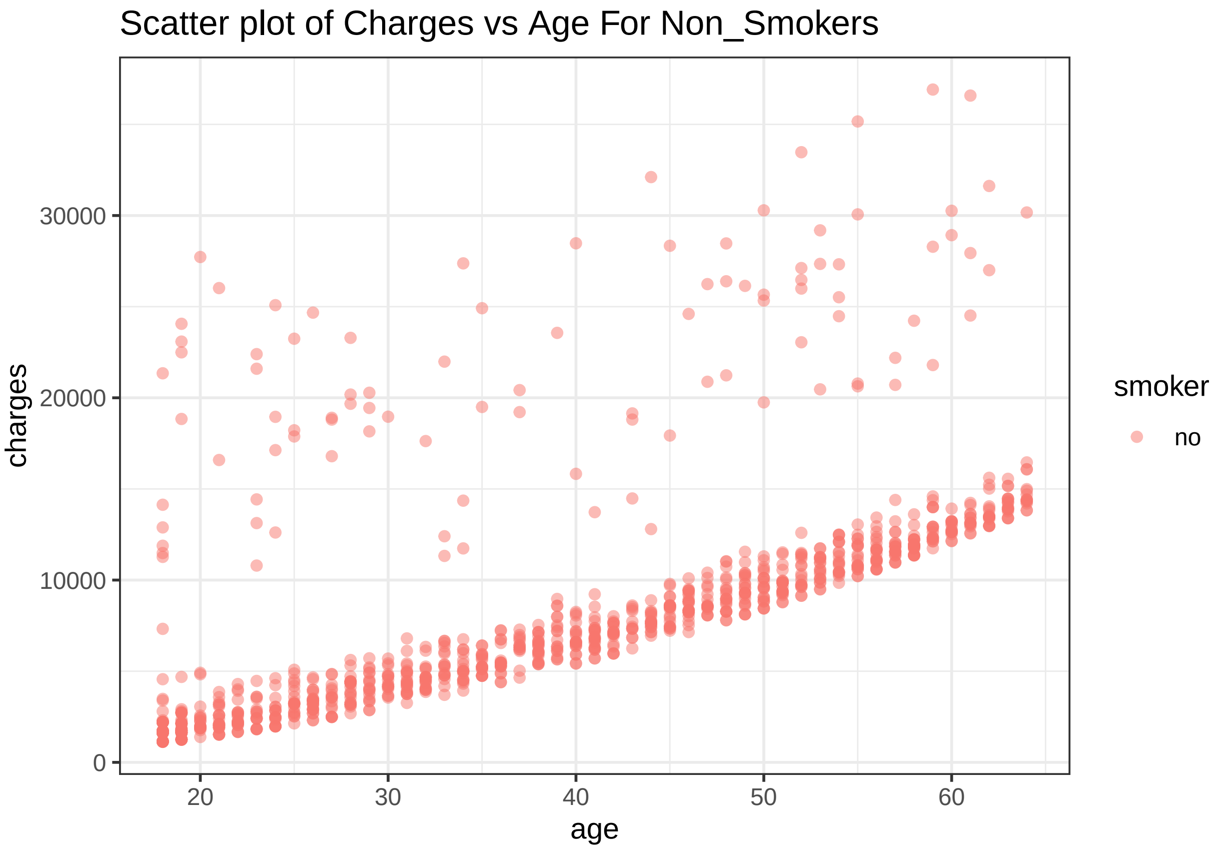
```
ggplot(aes(x=age,y=charges, color=smoker), data=smokers) +
  labs(title="Scatter plot of Charges vs Age For Smokers") +
  theme_bw() +
  geom_point(alpha=0.5)
```



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



```
ggplot(aes(x=age,y=charges, color=smoker), data=non_smokers) +
  labs(title="Scatter plot of Charges vs Age For Non_Smokers") +
  theme_bw() +
  geom_point(alpha=0.5)
```


Scatter plot of Charges vs Age For Non_Smokers

Smokers forward selection

```
## Smokers
##intercept only model
regnull_smoker <- lm(charges~1, data=smokers)
##model with all predictors
regfull_smoker <- lm(charges ~ age + sex + bmi + children + region , data=smokers)
```

Forward Selection

```
step(regnull_smoker, scope=list(lower=regnull_smoker, upper=regfull_smoker), direction="forward")
```

```
## Start:  AIC=5126.83
## charges ~ 1
##
##              Df  Sum of Sq        RSS    AIC
## + bmi         1 2.3653e+10 1.2713e+10 4840.9
## + age         1 4.9308e+09 3.1435e+10 5088.9
## + region      3 1.2923e+09 3.5073e+10 5122.9
## + sex         1 3.7263e+08 3.5993e+10 5126.0
## <none>                     3.6366e+10 5126.8
## + children    1 4.6986e+07 3.6319e+10 5128.5
##
## Step:  AIC=4840.86
## charges ~ bmi
##
##              Df  Sum of Sq        RSS    AIC
## + age       1 3739448620 8.9736e+09 4747.4
## <none>                   1.2713e+10 4840.9
## + children  1   77371010 1.2636e+10 4841.2
## + sex       1   12609906 1.2700e+10 4842.6
## + region    3  112969895 1.2600e+10 4844.4
##
## Step:  AIC=4747.41
## charges ~ bmi + age
##
##            Df Sum of Sq        RSS    AIC
## <none>                  8973564816 4747.4
## + region    3 149563719 8824001097 4748.8
## + children  1  14356763 8959208053 4749.0
## + sex       1   7002694 8966562122 4749.2
```

```
##
## Call:
## lm(formula = charges ~ bmi + age, data = smokers)
##
## Coefficients:
## (Intercept)          bmi          age
##    -22367.4       1438.1        266.3
```

Non Smokers forward selection

```
#Non smokers
regnull_non_smokers <- lm(charges~1, data=non_smokers)
##model with all predictors
regfull_non_smokers <- lm(charges ~ age + sex + bmi + children + region , data=non_smokers)
```

Forward Selection

```
step(regnull_non_smokers, scope=list(lower=regnull_non_smokers, upper=regfull_non_smokers), direction="
```

```
## Start:  AIC=18511.36
## charges ~ 1
##
##            Df  Sum of Sq        RSS   AIC
## + age       1 1.5058e+10 2.3130e+10 17980
## + children  1 7.3709e+08 3.7452e+10 18493
## + bmi       1 2.6969e+08 3.7919e+10 18506
## + sex       1 1.2113e+08 3.8068e+10 18510
## + region    3 2.3153e+08 3.7957e+10 18511
## <none>                   3.8189e+10 18511
##
## Step:  AIC=17979.87
## charges ~ age
##
##            Df Sum of Sq        RSS   AIC
## + children  1 531956489 2.2598e+10 17957
## + region    3 248975743 2.2881e+10 17974
## + sex       1  68342342 2.3062e+10 17979
## <none>                  2.3130e+10 17980
## + bmi       1   1914187 2.3128e+10 17982
##
```

```
## Step:  AIC=17957.12
## charges ~ age + children
##
##          Df Sum of Sq        RSS   AIC
## + region  3 262141210 2.2336e+10 17951
## + sex     1  69429619 2.2529e+10 17956
## <none>                2.2598e+10 17957
## + bmi     1   1065536 2.2597e+10 17959
##
## Step:  AIC=17950.7
## charges ~ age + children + region
##
##        Df Sum of Sq        RSS   AIC
## + sex   1  72093470 2.2264e+10 17949
## <none>              2.2336e+10 17951
## + bmi   1  11274021 2.2325e+10 17952
##
## Step:  AIC=17949.26
## charges ~ age + children + region + sex
##
##        Df Sum of Sq        RSS   AIC
## <none>              2.2264e+10 17949
## + bmi   1  12614493 2.2251e+10 17951
```

```
##
## Call:
## lm(formula = charges ~ age + children + region + sex, data = non_smokers)
##
## Coefficients:
##     (Intercept)              age         children  regionnorthwest
##         -1695.9            265.5            589.1           -550.2
## regionsoutheast  regionsouthwest          sexmale
##          -913.2          -1373.0           -521.0
```

We get different models (first smokers)

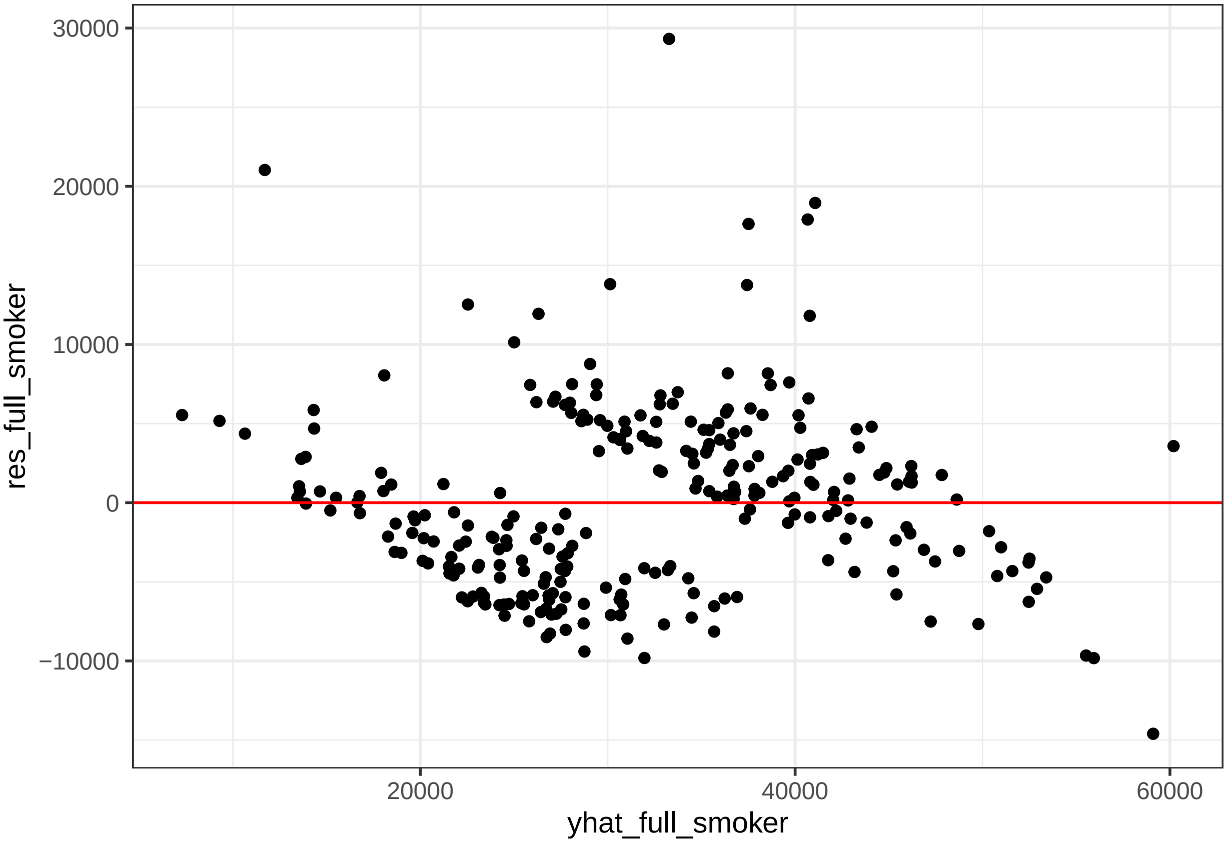
```
mlr_full_smoker = lm(charges ~  bmi+age , data=smokers)
summary(mlr_full_smoker)
```

```
##
## Call:
## lm(formula = charges ~ bmi + age, data = smokers)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14604.4  -4315.1   -240.5   3638.0  29316.7
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -22367.45    1931.86  -11.58   <2e-16 ***
## bmi           1438.09      55.22   26.05   <2e-16 ***
## age            266.29      25.06   10.63   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

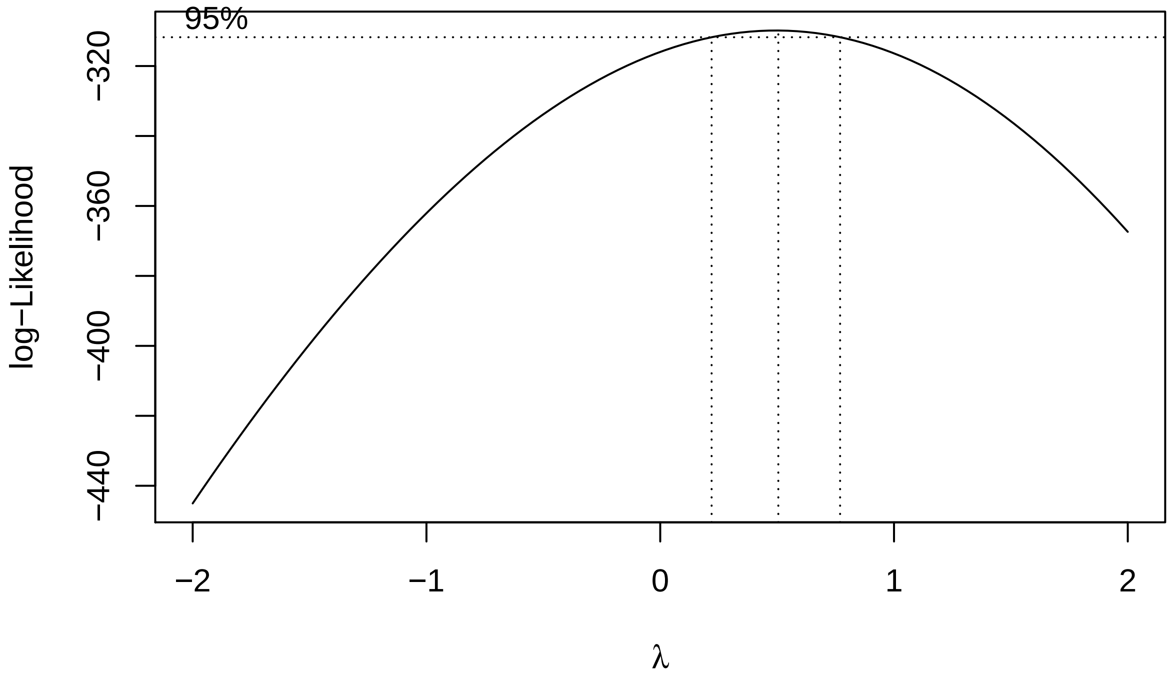
```
##
## Residual standard error: 5754 on 271 degrees of freedom
## Multiple R-squared:  0.7532, Adjusted R-squared:  0.7514
## F-statistic: 413.6 on 2 and 271 DF,  p-value: < 2.2e-16
```

Residual Plot of smokers looks the best so far.

```
yhat_full_smoker <- mlr_full_smoker$fitted.values
res_full_smoker <- mlr_full_smoker$residuals
smokers %>%
  ggplot(aes(yhat_full_smoker, res_full_smoker)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



```
boxcox(mlr_full_smoker)
```



Rseponse needs to be transformed

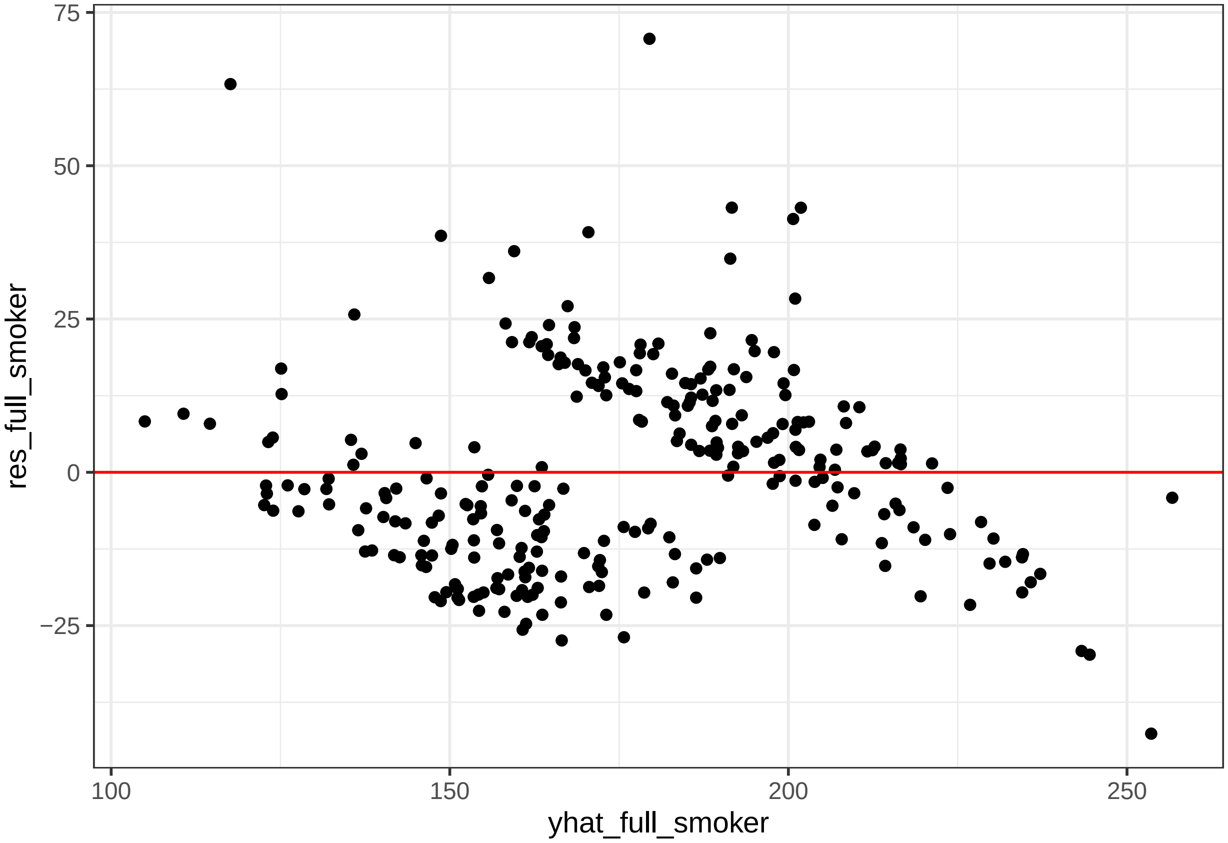
```
smokers_transform <- smokers
smokers_transform$charges <- smokers_transform$charges^0.5
mlr_full_smoker_transform = lm(charges ~  bmi+age , data=smokers_transform)
mlr_full_smoker_transform_full = lm(charges ~  bmi+age + sex + region , data=smokers_transform)
summary(mlr_full_smoker_transform)
```

```
##
## Call:
## lm(formula = charges ~ bmi + age, data = smokers_transform)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -42.622 -12.877  -1.715  10.868  70.699
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  19.9145     5.4586   3.648 0.000317 ***
## bmi           4.1245     0.1560  26.436  < 2e-16 ***
## age           0.7634     0.0708  10.781  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.26 on 271 degrees of freedom
## Multiple R-squared:  0.7587, Adjusted R-squared:  0.7569
## F-statistic: 426.1 on 2 and 271 DF,  p-value: < 2.2e-16
```

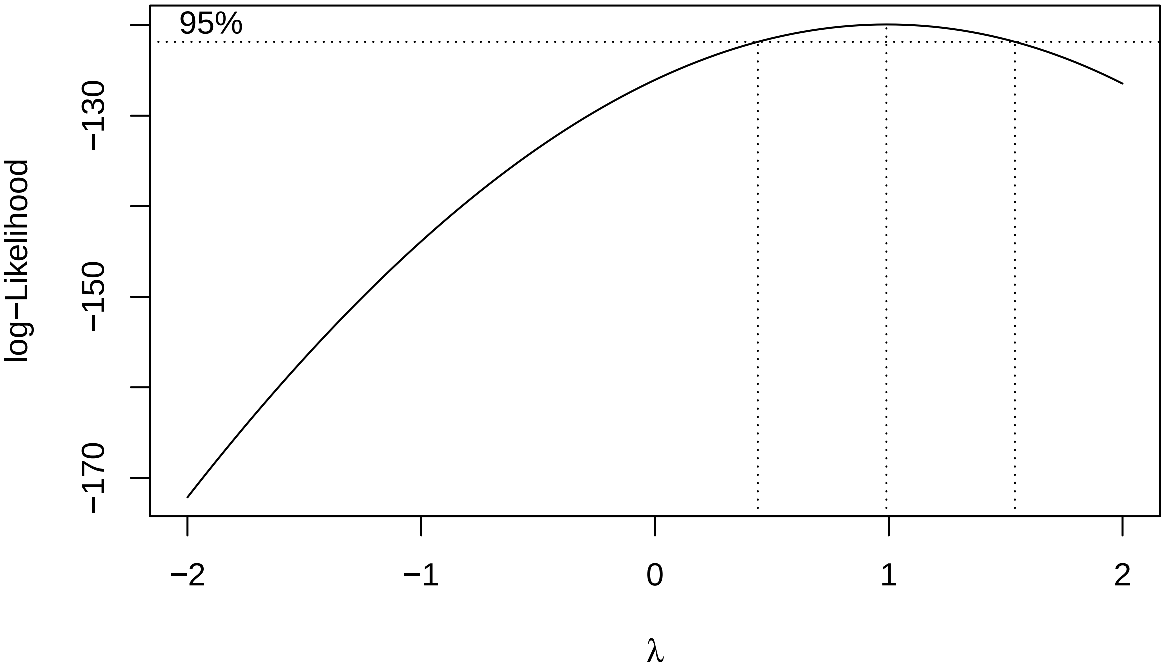
residual plot for transformed response variable for smoerks

```
yhat_full_smoker <- mlr_full_smoker_transform$fitted.values
res_full_smoker <- mlr_full_smoker_transform$residuals
smokers %>%
  ggplot(aes(yhat_full_smoker, res_full_smoker)) +
```

```r
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```

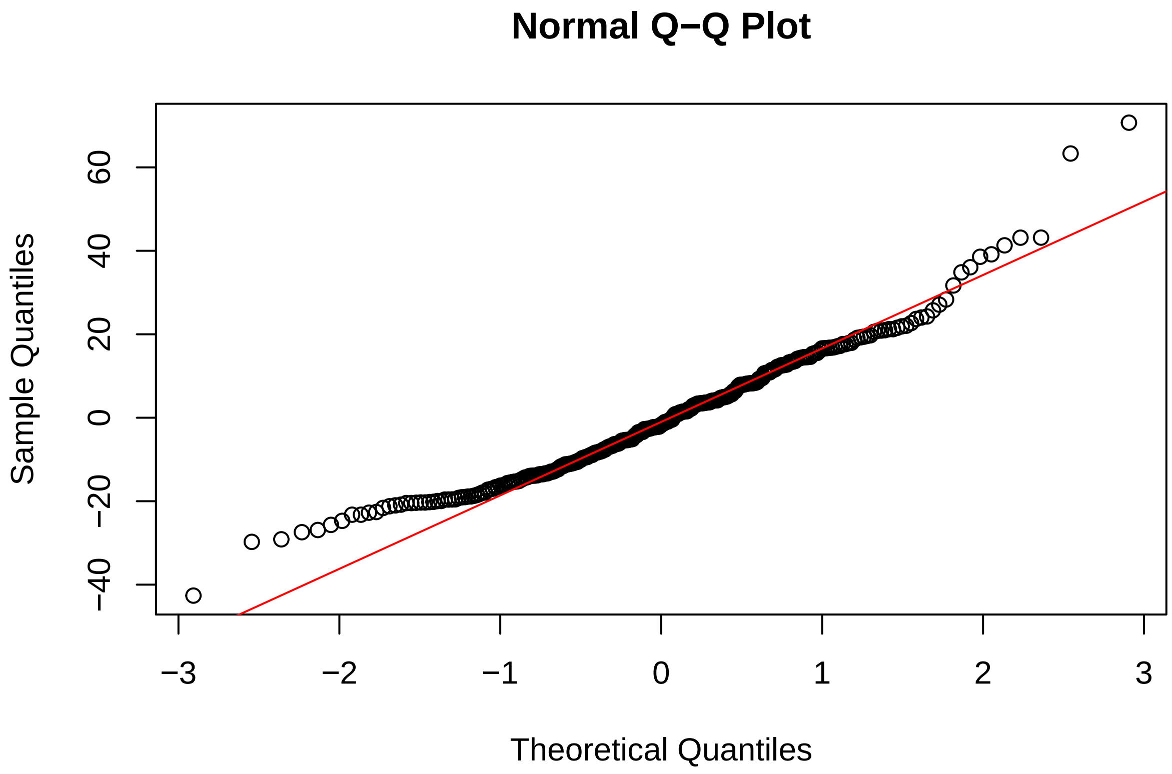


```r
boxcox(mlr_full_smoker_transform)
```



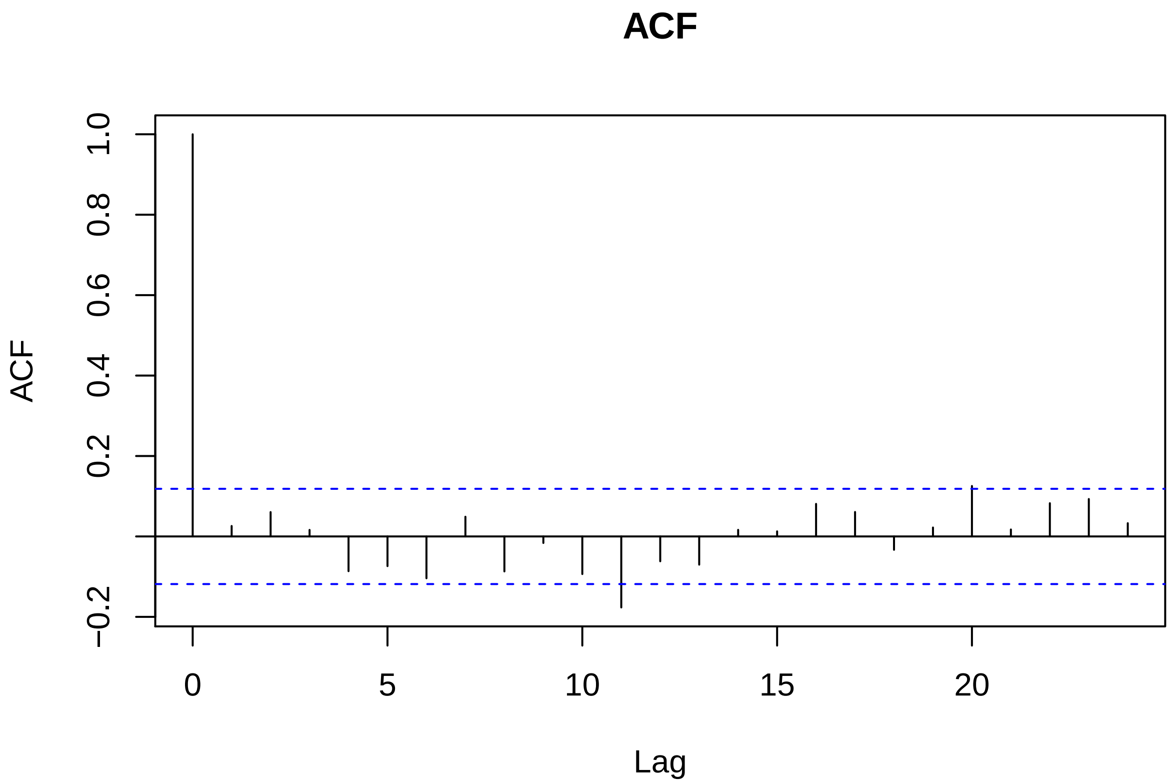
QQPlot Smokers

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



ACF for somkers

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



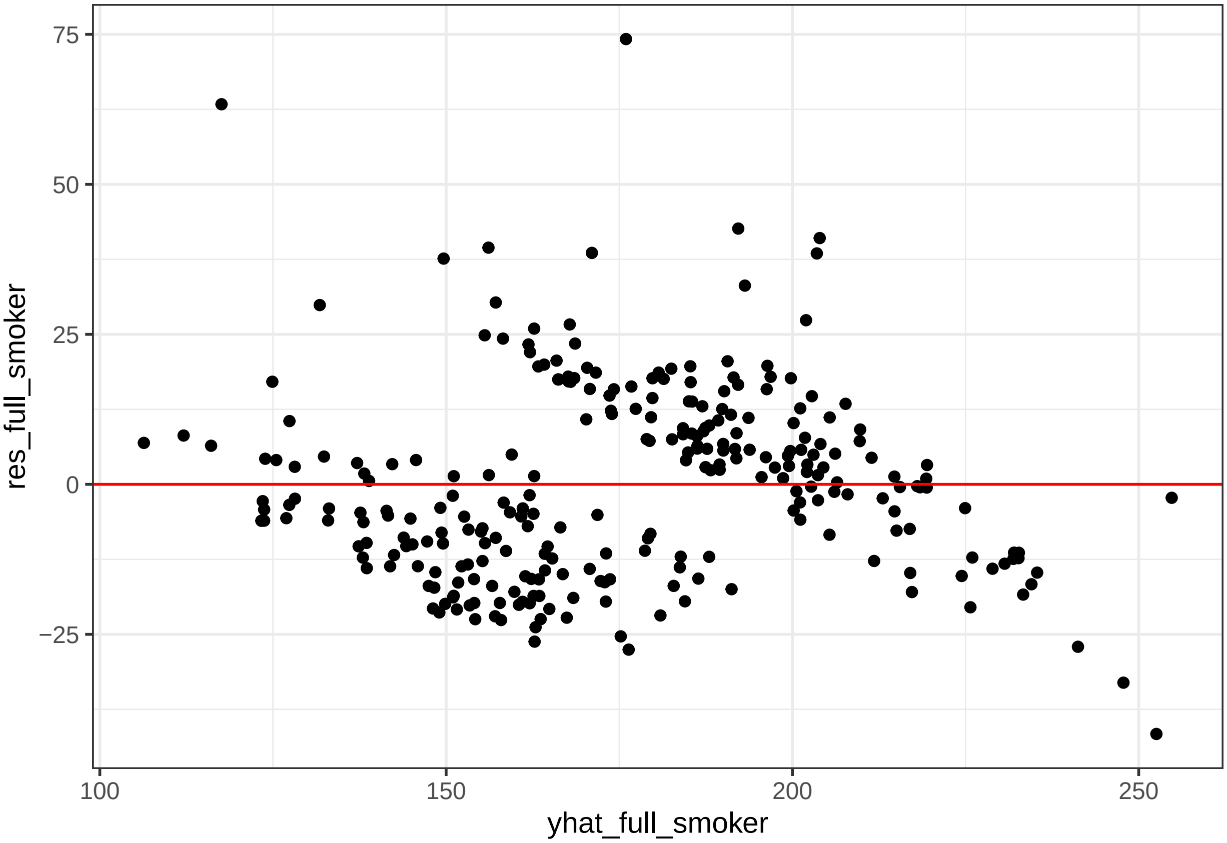
Can we drop the other predictors?

```
mlr_full_smoker_full = lm(charges ~  bmi+age+children+region , data=smokers_transform)
summary(mlr_full_smoker_full)
```

```
##
## Call:
## lm(formula = charges ~ bmi + age + children + region, data = smokers_transform)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -41.603 -12.339  -0.845   9.705  74.211
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)     18.58918    5.66726   3.280  0.00118 **
## bmi              4.21653    0.16320  25.837  < 2e-16 ***
## age              0.76698    0.07129  10.759  < 2e-16 ***
## children         0.53142    0.85647   0.620  0.53547
## regionnorthwest -1.53030    2.92036  -0.524  0.60071
## regionsoutheast -5.14260    2.71691  -1.893  0.05946 .
## regionsouthwest -0.93879    2.94778  -0.318  0.75038
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.23 on 267 degrees of freedom
## Multiple R-squared:  0.763,  Adjusted R-squared:  0.7577
## F-statistic: 143.3 on 6 and 267 DF,  p-value: < 2.2e-16
```

Residual of full model for smokers

```
yhat_full_smoker <- mlr_full_smoker_full$fitted.values
res_full_smoker <- mlr_full_smoker_full$residuals
smokers %>%
  ggplot(aes(yhat_full_smoker, res_full_smoker)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



Residual Seems Fine, can we drop these predictors using partial F - test.

```
summary(mlr_full_smoker_transform)
```

```
##
## Call:
## lm(formula = charges ~ bmi + age, data = smokers_transform)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -42.622 -12.877  -1.715  10.868  70.699
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  19.9145     5.4586   3.648 0.000317 ***
## bmi           4.1245     0.1560  26.436  < 2e-16 ***
## age           0.7634     0.0708  10.781  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.26 on 271 degrees of freedom
## Multiple R-squared:  0.7587, Adjusted R-squared:  0.7569
## F-statistic: 426.1 on 2 and 271 DF,  p-value: < 2.2e-16
```

```
anova(mlr_full_smoker_transform,mlr_full_smoker_transform_full )
```

```
## Analysis of Variance Table
##
## Model 1: charges ~ bmi + age
## Model 2: charges ~ bmi + age + sex + region
##   Res.Df   RSS Df Sum of Sq      F Pr(>F)
## 1    271 71645
## 2    267 70442  4    1202.7 1.1396 0.3382
```

We can drop these other predictors since p-value is above 0.05

Outliers detection

```
##critical value using Bonferroni procedure
n<-dim(smokers_transform)[1]
p<-3
crit<-qt(1-0.05/(2*n), n-1-p)
##externally studentized residuals
ext.student.res<-rstudent(mlr_full_smoker_transform)
##identify
ext.student.res[abs(ext.student.res)>crit]
```

```
##      129     1301
## 4.041989 4.510779
```

```
##leverages
lev<-lm.influence(mlr_full_smoker_transform)$hat
##identify
round(lev[lev>2*p/n],4)
```

```
##    251    293    413    544    550    665    804    861   1048   1125   1157
## 0.0268 0.0284 0.0226 0.0326 0.0258 0.0224 0.0251 0.0301 0.0547 0.0225 0.0307
```

```
DFFITS<-dffits(mlr_full_smoker_transform)
round(DFFITS[abs(DFFITS)>2*sqrt(p/n)],3)
```

```
##    129    293    550    578    820    861    918   1048   1157   1231   1301
##  0.569 -0.231 -0.297  0.260  0.218 -0.329  0.246 -0.656 -0.225  0.244  0.302
```

```
DFBETAS<-dfbetas(mlr_full_smoker_transform)
tempdfbetas = abs(DFBETAS)>2/sqrt(n)
tempdfbetas[(tempdfbetas[,1] == TRUE | tempdfbetas[,2] == TRUE | tempdfbetas[,3] == TRUE ) ,]
```

```
##      (Intercept)   bmi   age
## 35         FALSE  TRUE FALSE
## 95         FALSE FALSE  TRUE
## 129         TRUE  TRUE FALSE
## 293        FALSE  TRUE FALSE
## 477        FALSE FALSE  TRUE
## 531         TRUE FALSE FALSE
## 550         TRUE  TRUE FALSE
## 578        FALSE  TRUE FALSE
## 675         TRUE  TRUE FALSE
## 820        FALSE  TRUE FALSE
## 861         TRUE  TRUE FALSE
## 918         TRUE  TRUE FALSE
## 952         TRUE  TRUE FALSE
## 1048        TRUE  TRUE  TRUE
## 1140       FALSE FALSE  TRUE
## 1147       FALSE FALSE  TRUE
## 1157       FALSE  TRUE FALSE
## 1197       FALSE FALSE  TRUE
## 1224        TRUE FALSE  TRUE
## 1231        TRUE FALSE  TRUE
## 1232        TRUE FALSE FALSE
## 1301       FALSE FALSE  TRUE
## 1302       FALSE FALSE  TRUE
```

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

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

Non Smokers Analysis

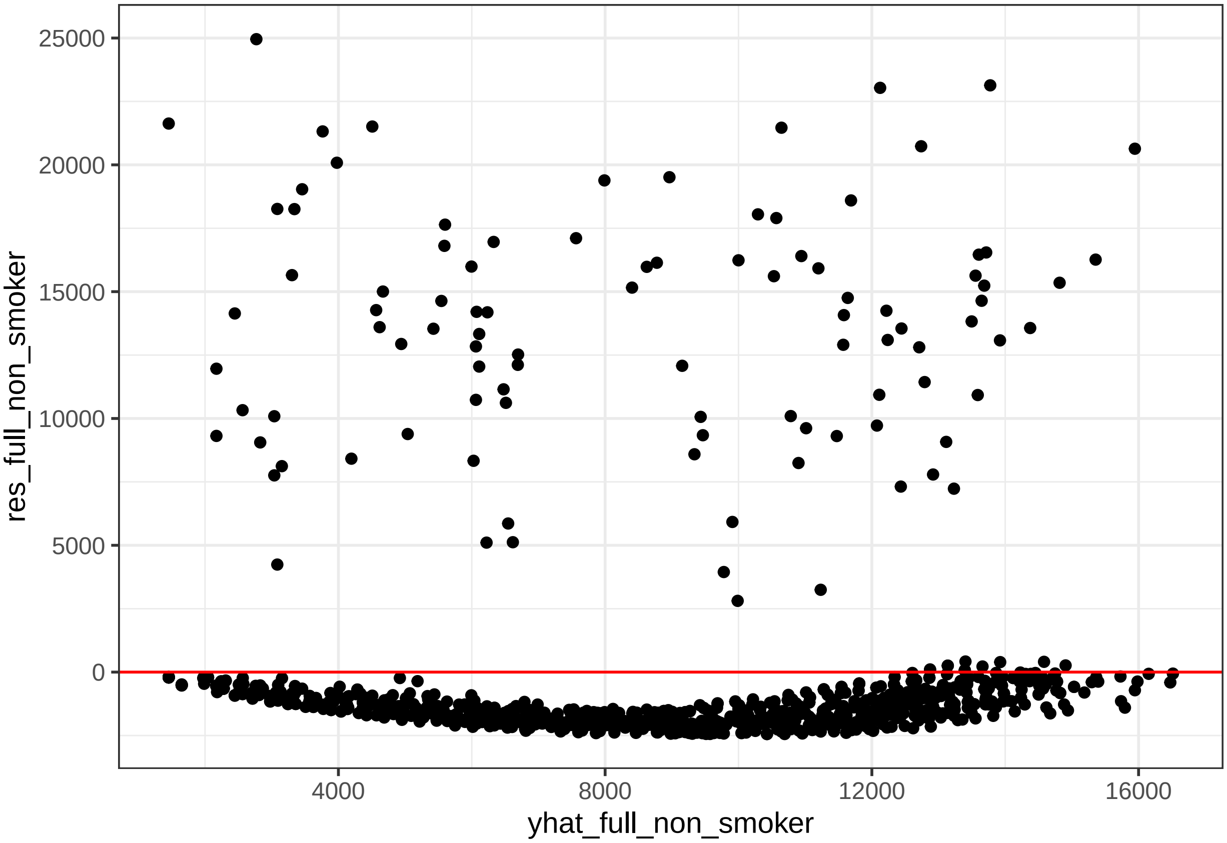
Predictors from forward selection process.

```
mlr_full_non_smoker = lm(formula = charges ~ age + children + region + sex, data = non_smokers)
summary(mlr_full_non_smoker)
```

```
##
## Call:
## lm(formula = charges ~ age + children + region + sex, data = non_smokers)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2441.2 -1870.1 -1380.6  -673.9 24954.7
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -1695.87     520.71  -3.257 0.001162 **
## age               265.53      10.01  26.524  < 2e-16 ***
## children          589.06     115.67   5.093 4.18e-07 ***
## regionnorthwest  -550.17     401.17  -1.371 0.170544
## regionsoutheast  -913.18     398.99  -2.289 0.022293 *
## regionsouthwest -1372.97     401.23  -3.422 0.000646 ***
## sexmale          -521.01     281.62  -1.850 0.064585 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4589 on 1057 degrees of freedom
## Multiple R-squared:  0.417,  Adjusted R-squared:  0.4137
## F-statistic:   126 on 6 and 1057 DF,  p-value: < 2.2e-16
```

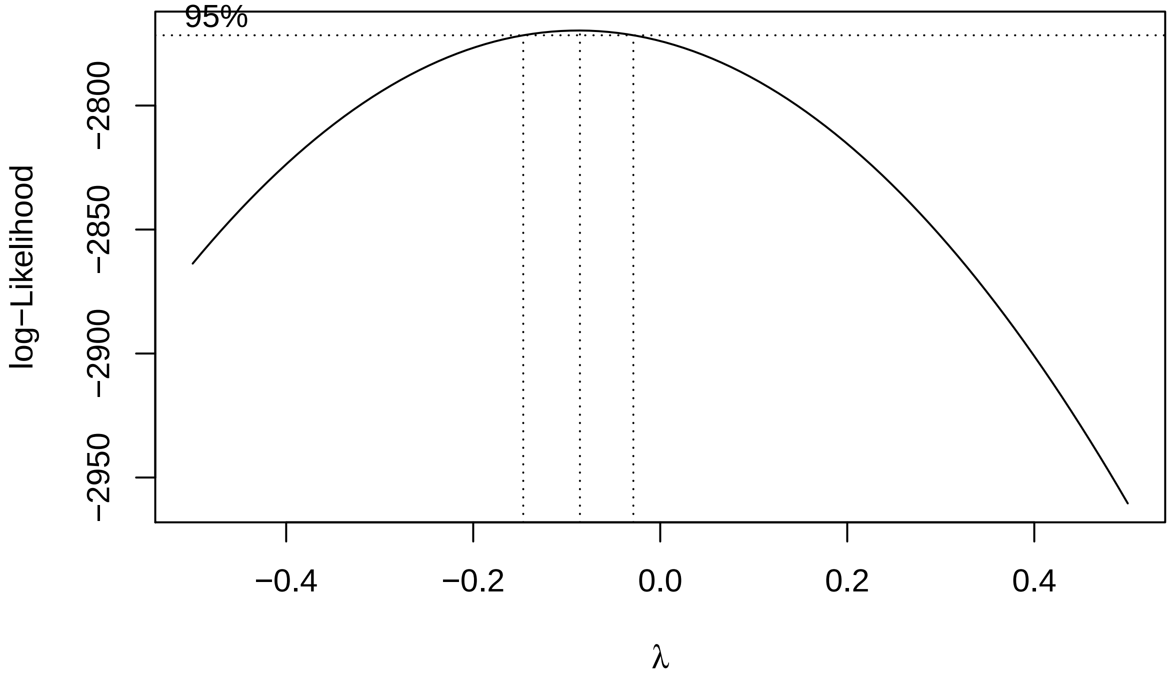
```
yhat_full_non_smoker <- mlr_full_non_smoker$fitted.values
res_full_non_smoker <- mlr_full_non_smoker$residuals
non_smokers %>%
```

```r
ggplot(aes(yhat_full_non_smoker, res_full_non_smoker)) +
geom_point() +
theme_bw() +
geom_hline(yintercept = 0, color="red")
```



Can we transform the response variable?

```r
boxcox(mlr_full_non_smoker, c(-0.5, 0.5, 0.1))
```

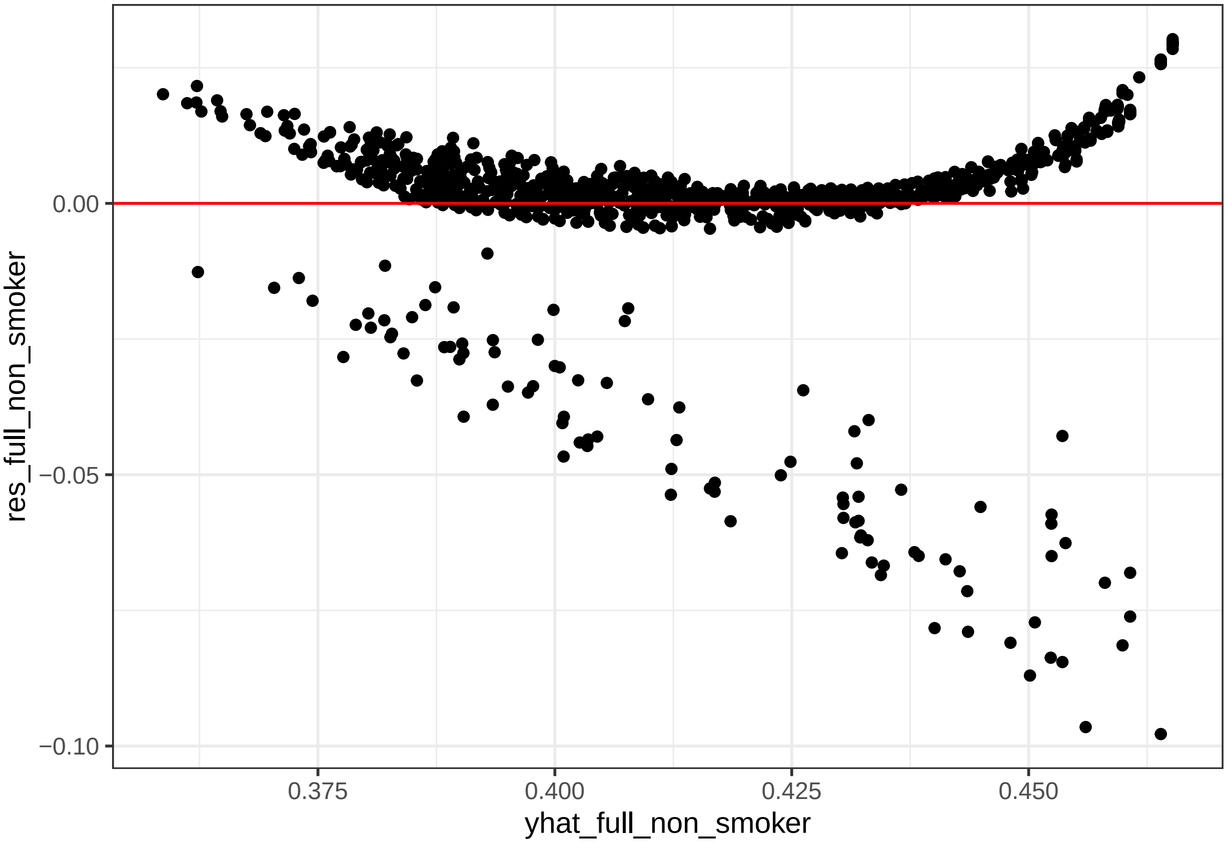


```
non_smoker_transform <- non_smokers
non_smoker_transform$charges <- non_smoker_transform$charges^(-0.1)
mlr_full_non_smoker_transform = lm(formula = charges ~ age + children + region + sex, data = non_smoker_
summary(mlr_full_non_smoker_transform)
```

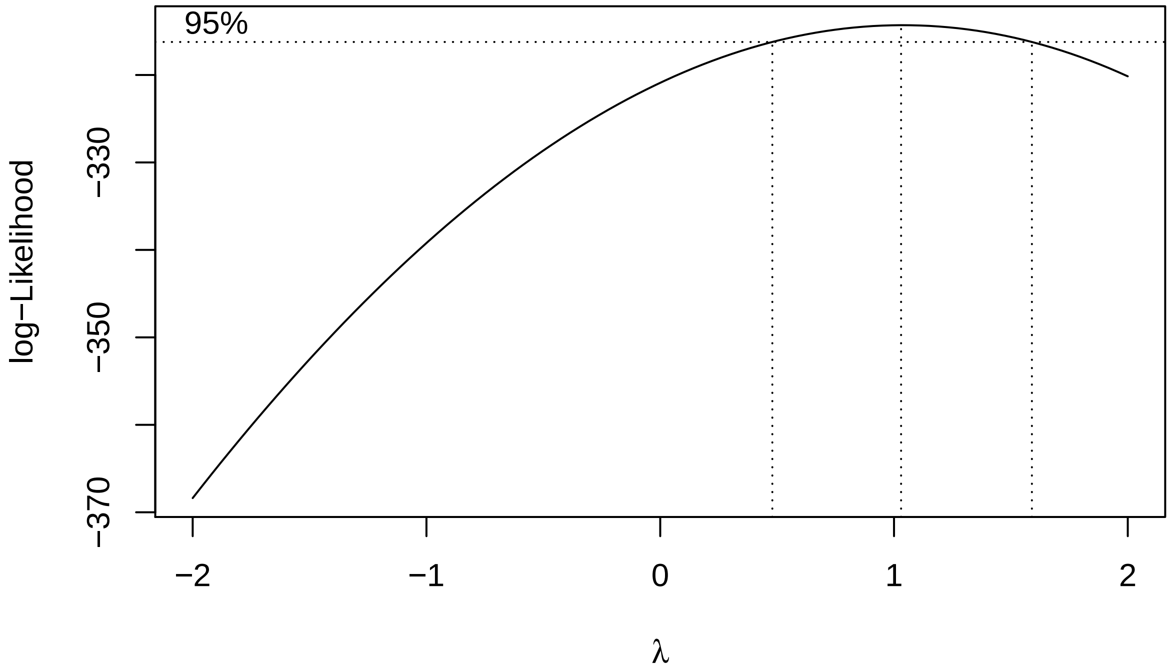
```
##
## Call:
## lm(formula = charges ~ age + children + region + sex, data = non_smoker_transform)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.097790 -0.000251  0.002357  0.006879  0.030263
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)       4.853e-01  1.947e-03 249.214  < 2e-16 ***
## age              -1.762e-03  3.744e-05 -47.072  < 2e-16 ***
## children         -5.651e-03  4.326e-04 -13.065  < 2e-16 ***
## regionnorthwest   3.100e-03  1.500e-03   2.066   0.0391 *
## regionsoutheast   7.149e-03  1.492e-03   4.792 1.89e-06 ***
## regionsouthwest   7.667e-03  1.500e-03   5.110 3.82e-07 ***
## sexmale           4.482e-03  1.053e-03   4.256 2.27e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01716 on 1057 degrees of freedom
## Multiple R-squared:  0.7023, Adjusted R-squared:  0.7006
## F-statistic: 415.6 on 6 and 1057 DF,  p-value: < 2.2e-16
```

Residual plot of transformed response variable with forward selection for non smokers

```
yhat_full_non_smoker <- mlr_full_non_smoker_transform$fitted.values
res_full_non_smoker <- mlr_full_non_smoker_transform$residuals
non_smokers %>%
  ggplot(aes(yhat_full_non_smoker, res_full_non_smoker)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```

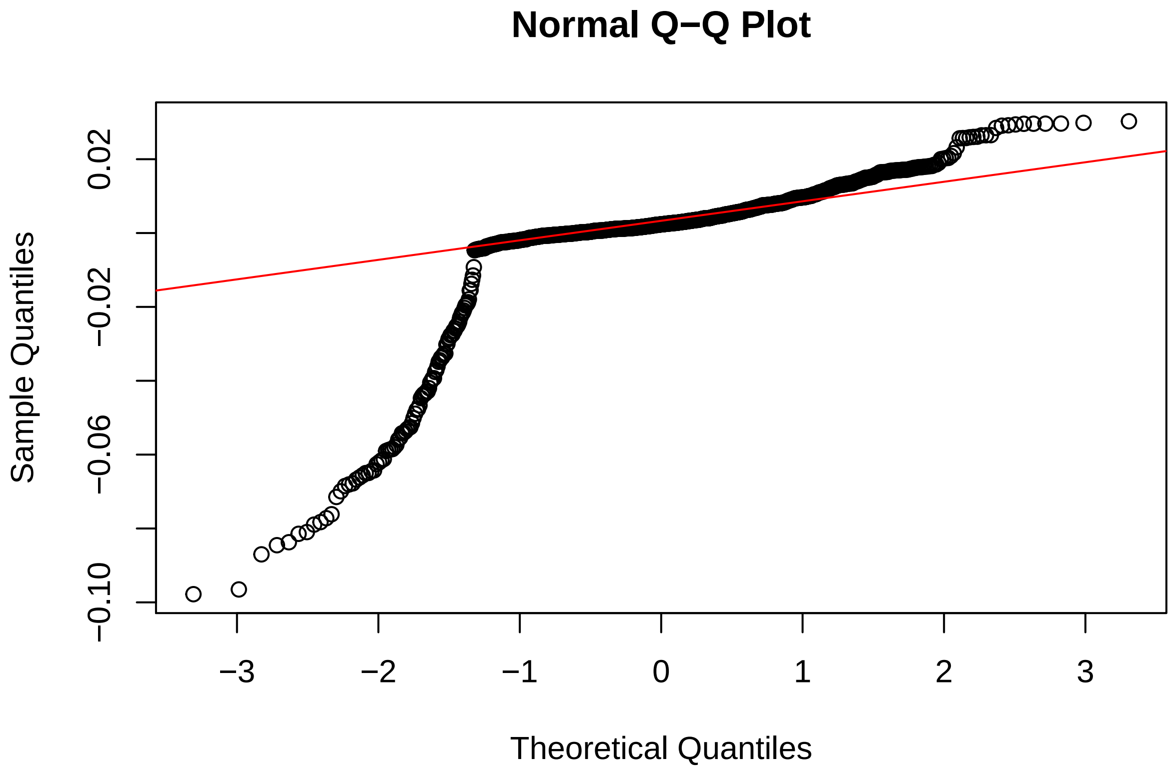


```
boxcox(mlr_full_non_smoker_transform)
```



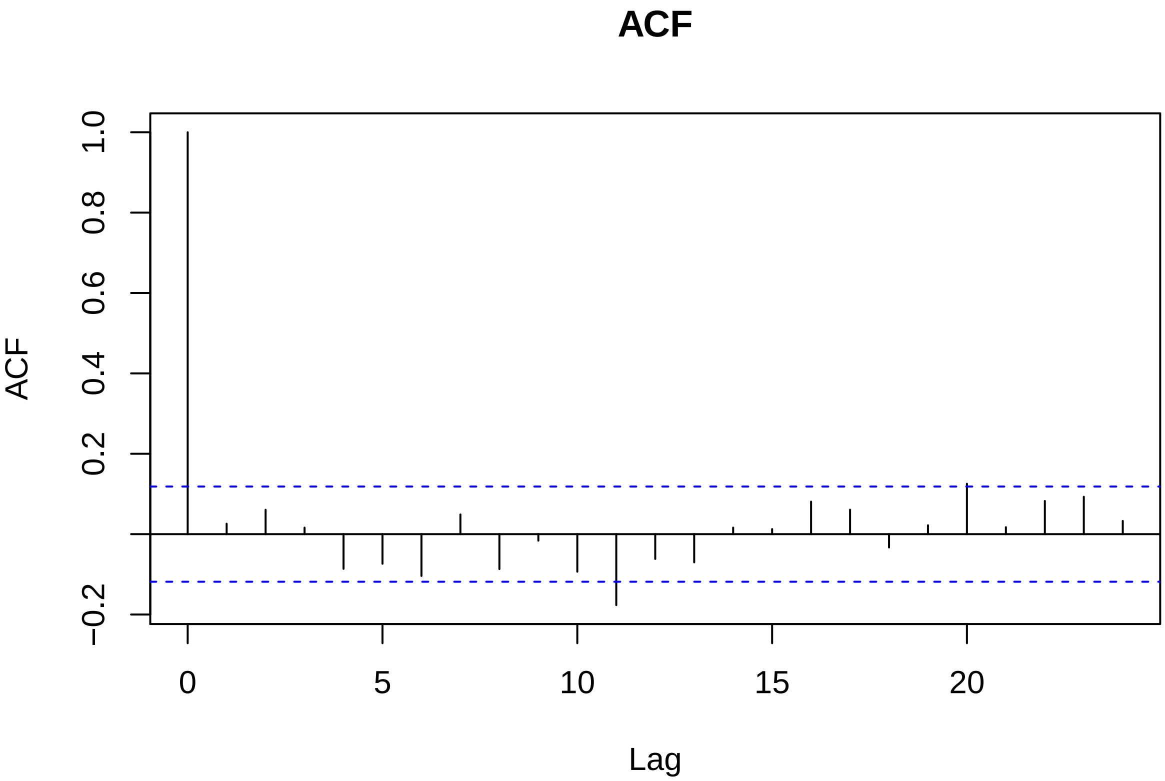
QQPlot

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



ACF

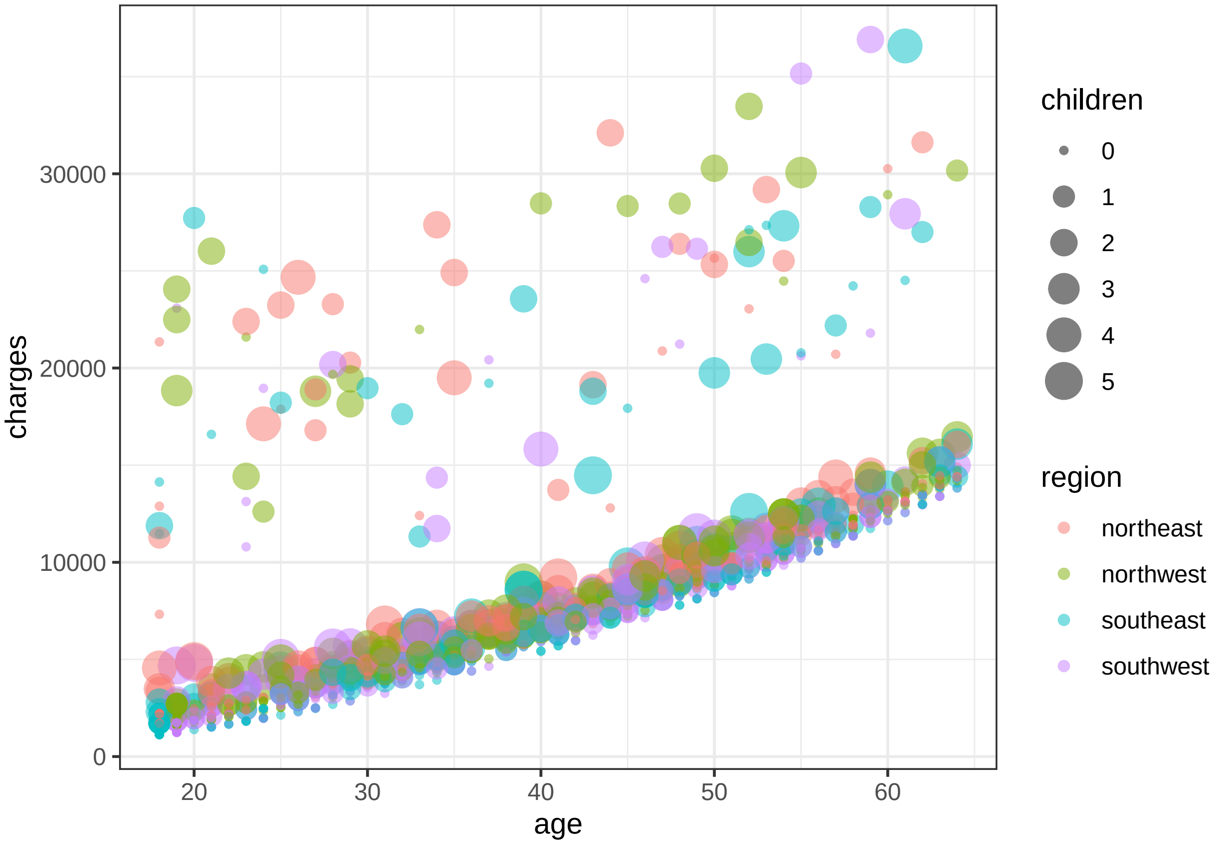
```
acf(mlr_full_smoker_transform$residuals, main="ACF")
```



Dropping of outliers

We transformed and tried many steps, but we can see that the outliers are actually small sub populations. It could be that they are some clients with preeixsting conditions, if that is the case they will follow a different trend and will be classified as outliers for our multiple linear regression model.

```
non_smokers %>%
  ggplot(aes(x=age, y=charges, color=region, size=children)) +
  theme_bw() +
  geom_point(alpha=0.5)
```



Lets drop these outliers using dffits

```
drop_outleirs <- non_smokers
DFFITS_drop1<-dffits(mlr_full_non_smoker)
want_drop1 = names(DFFITS_drop1[abs(DFFITS_drop1)>2*sqrt(5/dim(non_smokers)[1])])
drop_outleirs = non_smokers[setdiff(rownames(non_smokers), want_drop1),]
percent_dropped = (dim(non_smokers)[1] - dim(drop_outleirs)[1]) / dim(non_smokers)[1]
percent_dropped*100
```

```
## [1] 8.364662
```

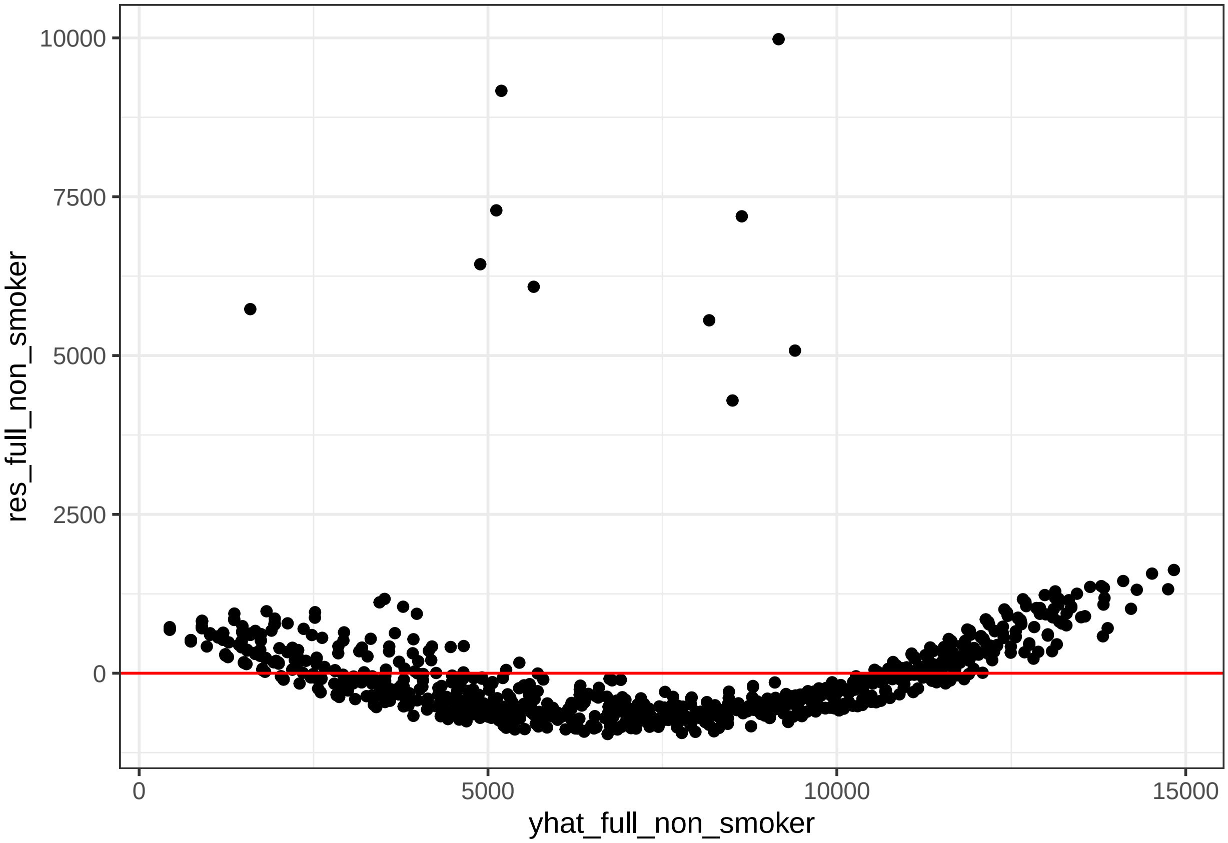
Make a multiple linear regression model after dropping the outliers

```
mlr_full_non_smoker_transform_drop = lm(formula = charges ~  region + age + children + sex, data = drop_
summary(mlr_full_non_smoker_transform_drop)
```

```
##
## Call:
## lm(formula = charges ~ region + age + children + sex, data = drop_outleirs)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -957.1 -528.9 -157.0  377.4 9979.3
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -3191.858    106.474 -29.978  < 2e-16 ***
## regionnorthwest   -380.203     81.624  -4.658 3.64e-06 ***
## regionsoutheast   -693.456     81.505  -8.508  < 2e-16 ***
## regionsouthwest  -656.634     81.119  -8.095 1.71e-15 ***
## age               265.832      2.041 130.242  < 2e-16 ***
## children          463.159     23.342  19.842  < 2e-16 ***
## sexmale          -461.038     57.043  -8.082 1.88e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 889.8 on 968 degrees of freedom
## Multiple R-squared:  0.9486, Adjusted R-squared:  0.9483
## F-statistic:  2979 on 6 and 968 DF,  p-value: < 2.2e-16
```

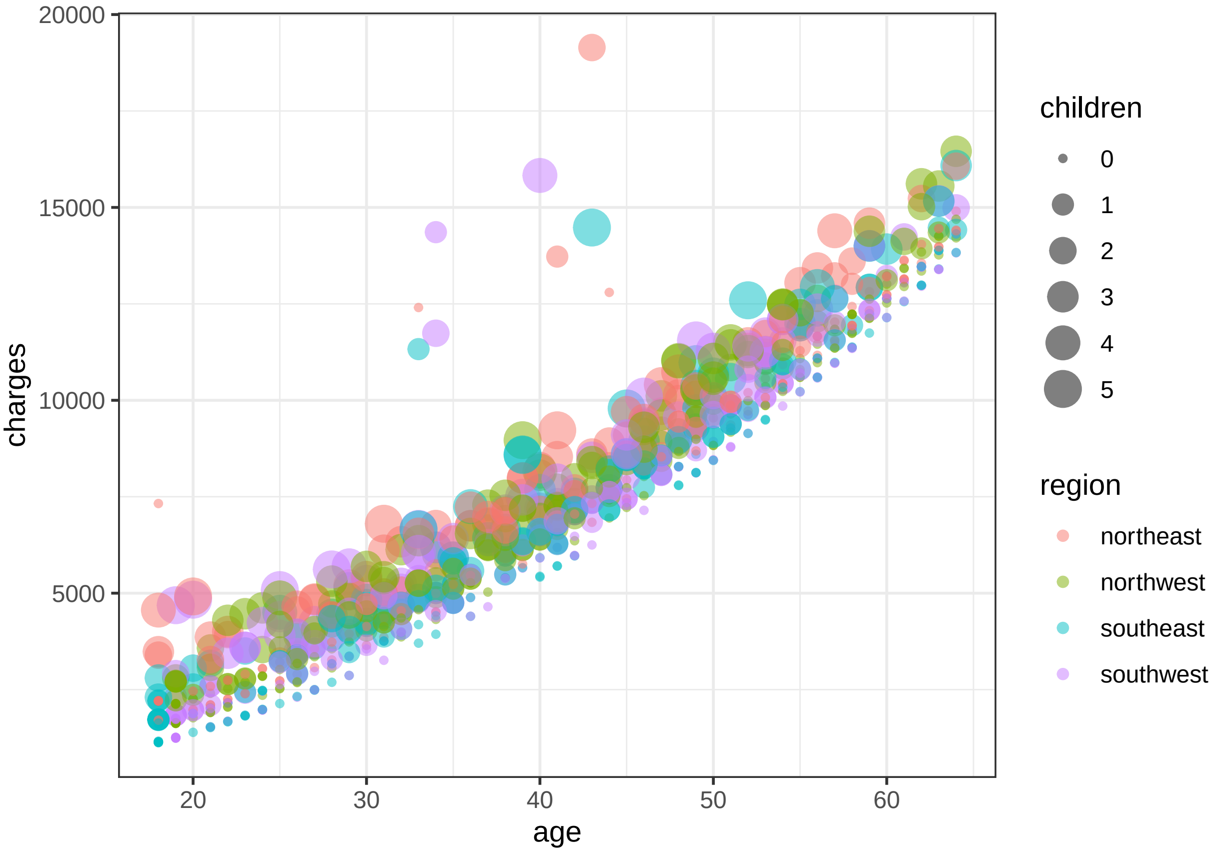
Residual plot of the model constructed after dropping the first set of outliers

```
yhat_full_non_smoker <- mlr_full_non_smoker_transform_drop$fitted.values
res_full_non_smoker <- mlr_full_non_smoker_transform_drop$residuals
drop_outleirs %>%
  ggplot(aes(yhat_full_non_smoker, res_full_non_smoker)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



Double checking EDA to see if the top section was fully dropped.

```
drop_outleirs %>%
  ggplot(aes(x=age, y=charges, color=region, size=children)) +
  theme_bw() +
  geom_point(alpha=0.5)
```



Since not all points were dropped, lets try dropping again based on outliers for DFFITS.

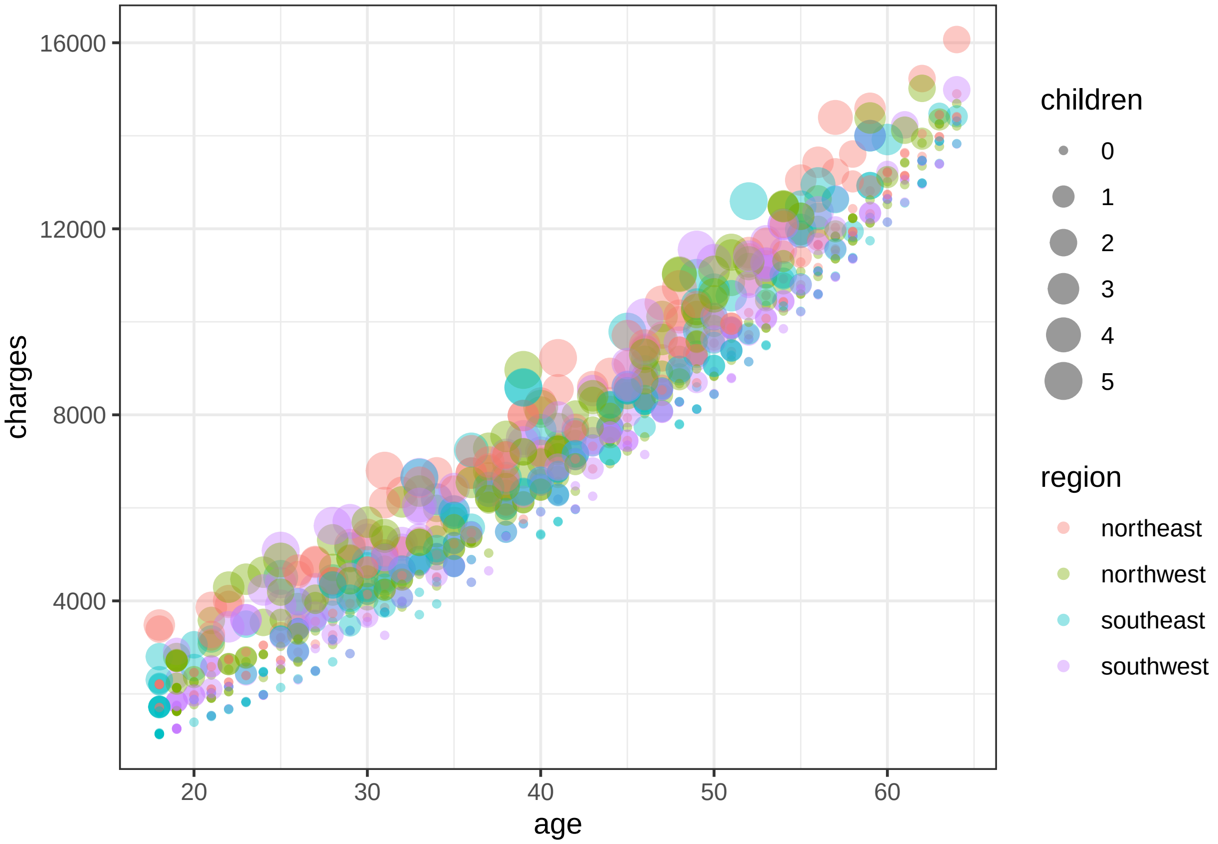
```
drop_outleirs2 <- drop_outleirs
DFFITS_drop2<-dffits(mlr_full_non_smoker_transform_drop)
want_drop2 = names(DFFITS_drop2[abs(DFFITS_drop2)>2*sqrt(5/dim(drop_outleirs)[1])])
drop_outleirs2 = drop_outleirs[setdiff(rownames(drop_outleirs), want_drop2),]
(dim(drop_outleirs)[1] - dim(drop_outleirs2)[1]) / dim(drop_outleirs)[1]
```

```
## [1] 0.02051282
```

```
(dim(non_smokers)[1] - dim(drop_outleirs2)[1]) / dim(non_smokers)[1]
```

```
## [1] 0.1024436
```

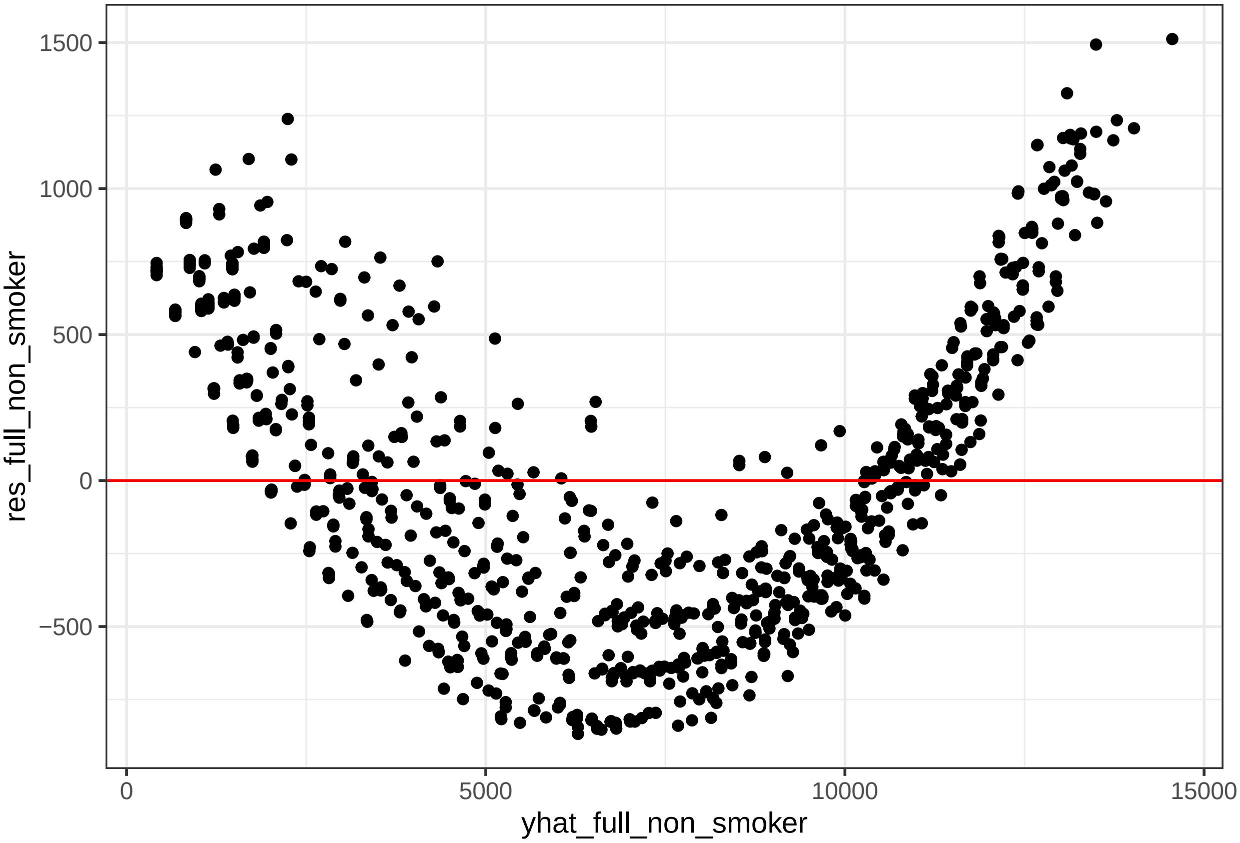
```
drop_outleirs2 %>%
  ggplot(aes(x=age, y=charges, color=region, size=children)) +
  geom_point(alpha = 0.4) + theme_bw()
```



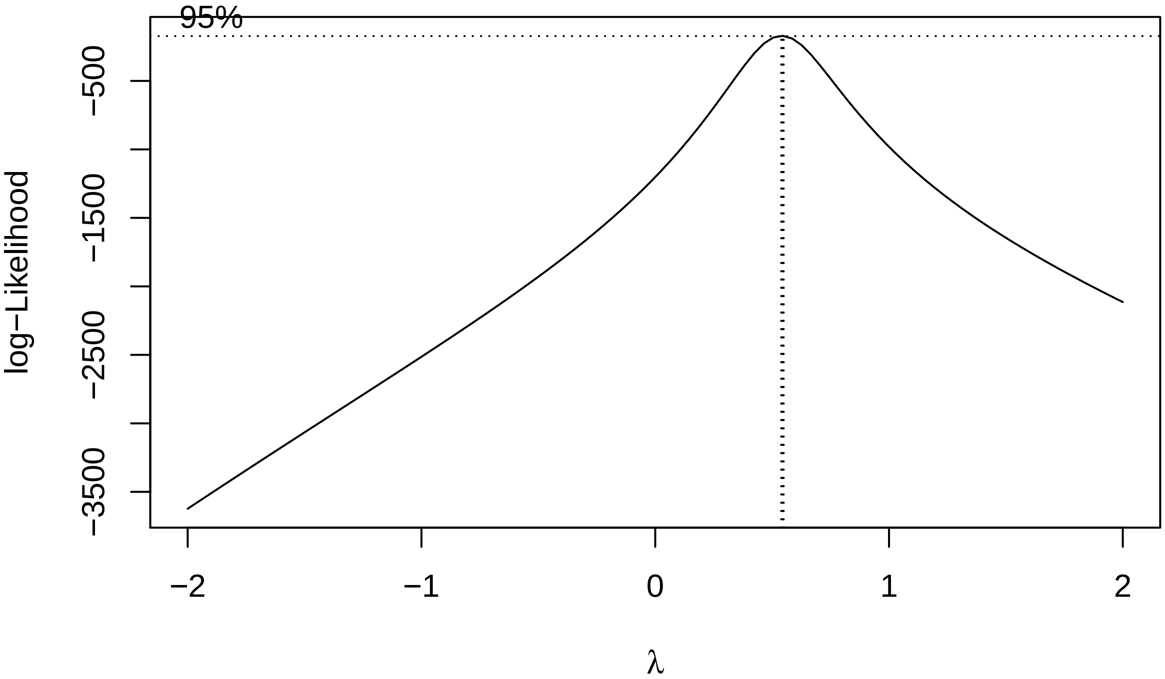
```
mlr_full_non_smoker_transform_drop2 = lm(formula = charges ~  region + age + children + sex, data = drop
summary(mlr_full_non_smoker_transform_drop2)
```

```
##
## Call:
## lm(formula = charges ~ region + age + children + sex, data = drop_outleirs2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -867.65 -444.78  -69.59  421.12 1512.12
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -3325.599     64.154 -51.838  < 2e-16 ***
## regionnorthwest  -238.085     48.721  -4.887  1.2e-06 ***
## regionsoutheast  -593.915     48.708 -12.193  < 2e-16 ***
## regionsouthwest  -601.035     48.534 -12.384  < 2e-16 ***
## age               266.590      1.224 217.796  < 2e-16 ***
## children          410.395     14.308  28.682  < 2e-16 ***
## sexmale          -460.787     34.023 -13.544  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 525.2 on 948 degrees of freedom
## Multiple R-squared:  0.9813, Adjusted R-squared:  0.9812
## F-statistic:  8284 on 6 and 948 DF,  p-value: < 2.2e-16
```

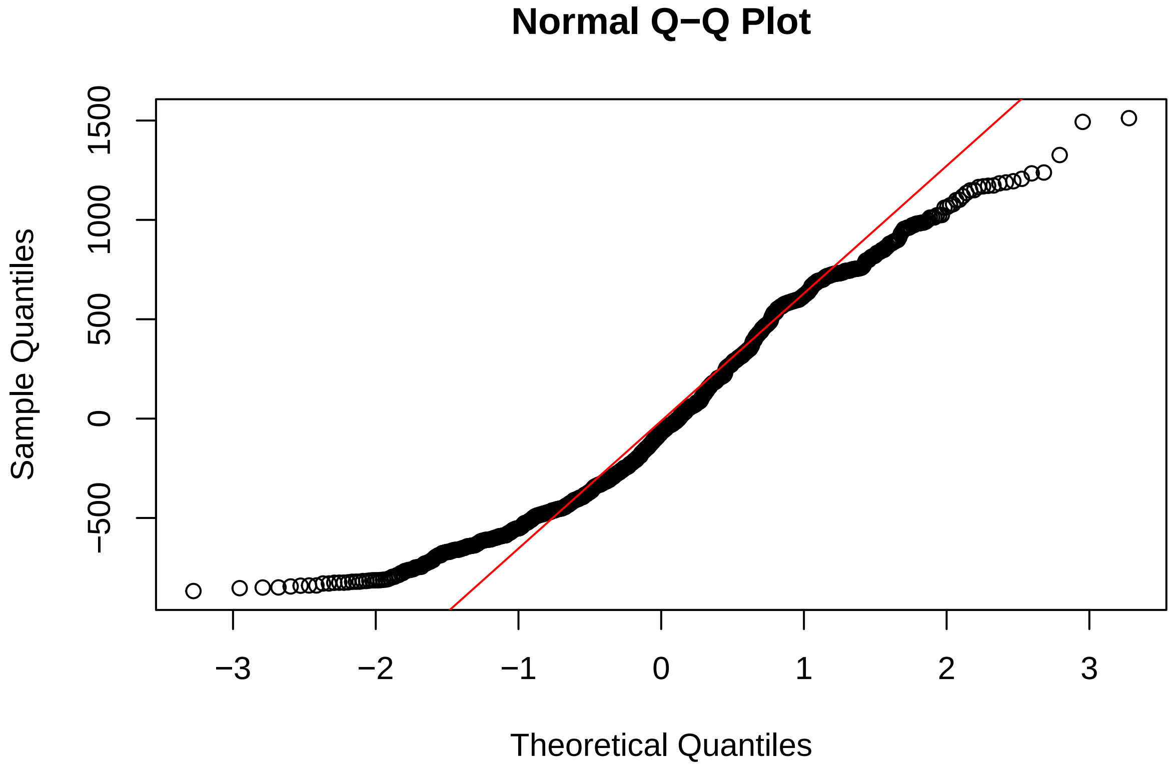
```
yhat_full_non_smoker <- mlr_full_non_smoker_transform_drop2$fitted.values
res_full_non_smoker <- mlr_full_non_smoker_transform_drop2$residuals
drop_outleirs2 %>%
  ggplot(aes(yhat_full_non_smoker, res_full_non_smoker)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



```
boxcox(mlr_full_non_smoker_transform_drop2)
```



```
{
  qqnorm(mlr_full_non_smoker_transform_drop2$residuals)
  qqline(mlr_full_non_smoker_transform_drop2$residuals, col="red")
}
```



Final transformation

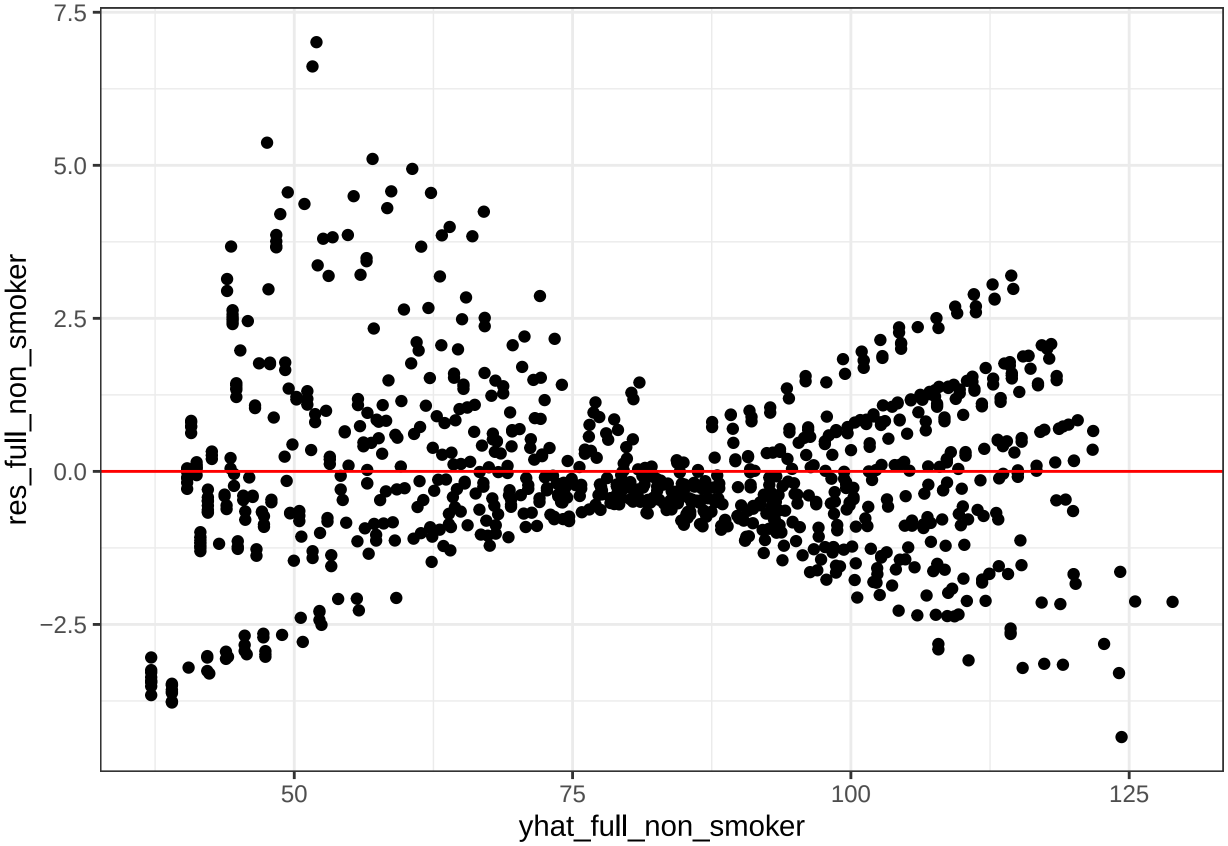
```
mlr_full_non_smoker_transform_drop3 = lm(formula = (charges)^0.5 ~  region + age + children + sex, data
```

```r
summary(mlr_full_non_smoker_transform_drop3)
```

```
##
## Call:
## lm(formula = (charges)^0.5 ~ region + age + children + sex, data = drop_outleirs2)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.3396 -0.7682 -0.1984  0.8051  7.0115
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)     14.228190   0.183533  77.524   <2e-16 ***
## regionnorthwest -1.339762   0.139383  -9.612   <2e-16 ***
## regionsoutheast -4.080085   0.139346 -29.280   <2e-16 ***
## regionsouthwest -3.897769   0.138846 -28.073   <2e-16 ***
## age              1.679522   0.003502 479.625   <2e-16 ***
## children         3.588815   0.040934  87.674   <2e-16 ***
## sexmale         -3.230161   0.097332 -33.187   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.502 on 948 degrees of freedom
## Multiple R-squared:  0.9962, Adjusted R-squared:  0.9961
## F-statistic: 4.103e+04 on 6 and 948 DF,  p-value: < 2.2e-16
```

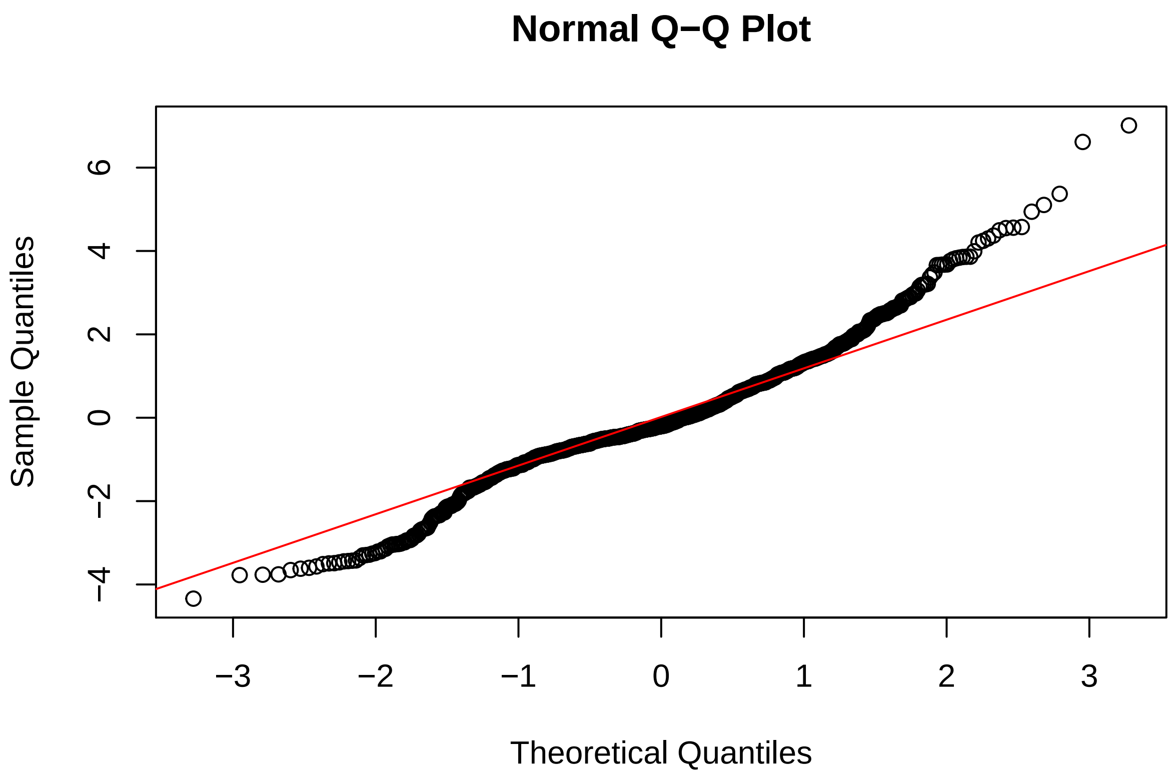
Residual Plot

```r
yhat_full_non_smoker <- mlr_full_non_smoker_transform_drop3$fitted.values
res_full_non_smoker <- mlr_full_non_smoker_transform_drop3$residuals
drop_outleirs2 %>%
  ggplot(aes(yhat_full_non_smoker, res_full_non_smoker)) +
  geom_point() +
  theme_bw() +
  geom_hline(yintercept = 0, color="red")
```



QQ PLOT

```
{
  qqnorm(mlr_full_non_smoker_transform_drop3$residuals)
  qqline(mlr_full_non_smoker_transform_drop3$residuals, col="red")
}
```



Logistic

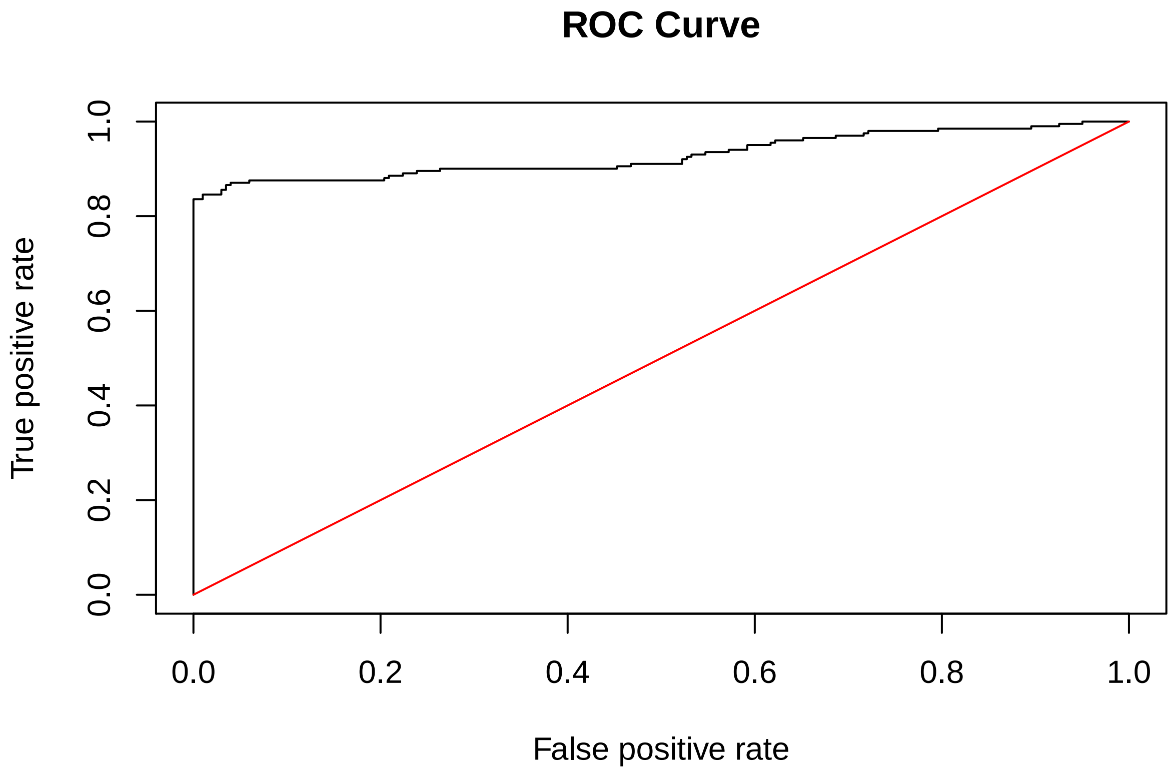
```
set.seed(6021) ##for reproducibility
sample<-sample.int(nrow(data), floor(.70*nrow(data)), replace = F)
train<- data[sample, ] ##training data frame
test<-data[-sample, ] ##test data frame
result<-glm(significant.charge ~ age + bmi + children + smoker + region + sex, family="binomial", data=
summary(result)
```

```
##
## Call:
## glm(formula = significant.charge ~ age + bmi + children + smoker +
##     region + sex, family = "binomial", data = train)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -1.5205  -0.3475  -0.0284   0.3683   3.4962
##
## Coefficients:
##                  Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -9.26037    0.89751 -10.318   <2e-16 ***
## age               0.18490    0.01342  13.781   <2e-16 ***
## bmi               0.03984    0.01999   1.993   0.0463 *
## children          0.18946    0.09252   2.048   0.0406 *
## smokeryes        22.76270  597.59493   0.038   0.9696
## regionnorthwest  -0.47986    0.32161  -1.492   0.1357
## regionsoutheast  -0.85665    0.33588  -2.551   0.0108 *
## regionsouthwest  -0.50317    0.32335  -1.556   0.1197
## sexmale          -0.56716    0.22860  -2.481   0.0131 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 1297.57  on 935  degrees of freedom
## Residual deviance:  500.78  on 927  degrees of freedom
## AIC: 518.78
##
## Number of Fisher Scoring iterations: 18
```

```r
library(ROCR)
```

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

```r
##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")
```



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

```
## [[1]]
## [1] 0.9288631
```

Matrix

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

```
##
##          FALSE TRUE
##   FALSE    182   19
##   TRUE      25  176
```

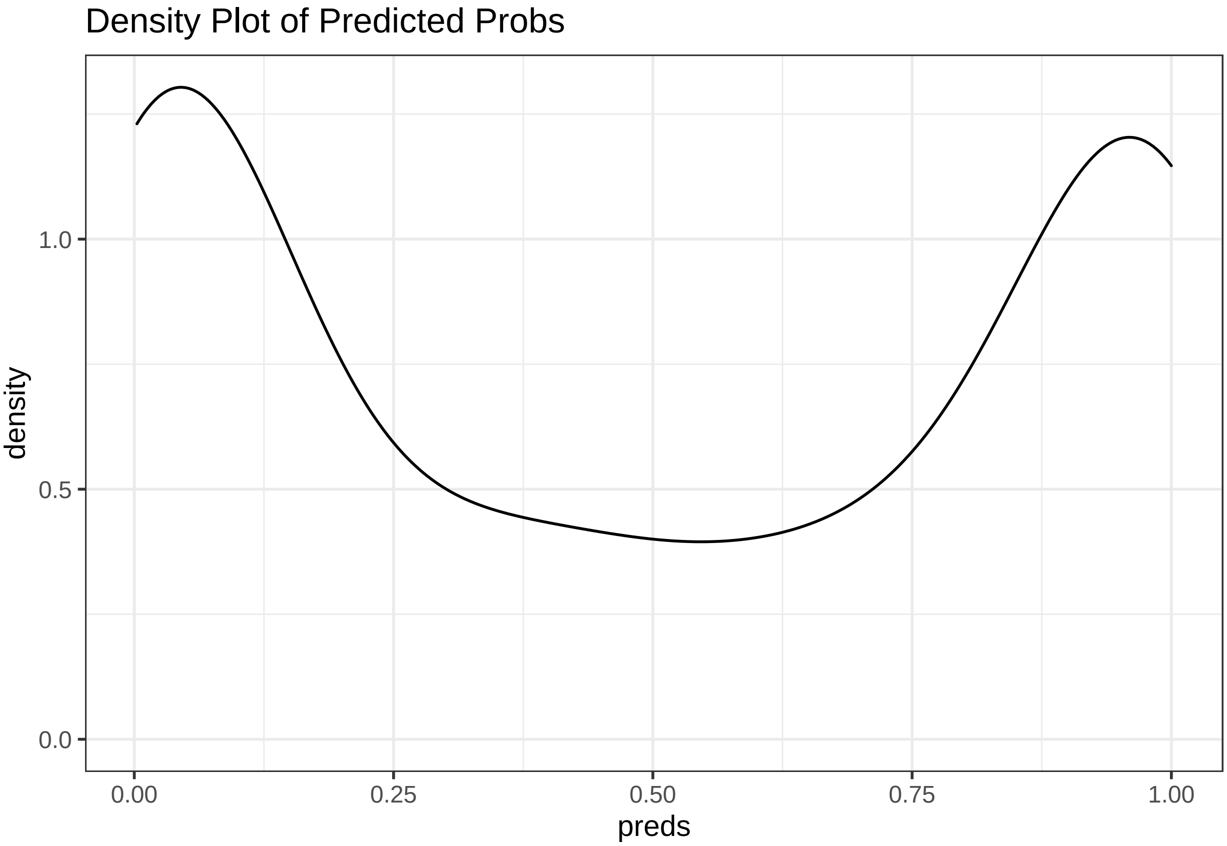
Threshold value manipulation

```
table(test$significant.charge, preds>0.25)
```

```
##
##          FALSE TRUE
##   FALSE    143   58
##   TRUE      20  181
```

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.

```
test<-data.frame(test,preds)
ggplot(test,aes(x=preds))+
geom_density()+
labs(title="Density Plot of Predicted Probs") + theme_bw()
```


Density Plot of Predicted Probs
density
preds