

# DATA 605 - Discussion 11

Joshua Sturm

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## 1. Data Exploration

```
library(tidyverse)
library(knitr)
library(corrplot)
library(gridExtra)
```

### 1.1 Import Dataset

```
ins <- read.csv("insurance.csv")
```

#### 1.1.1 Data Dictionary

```
defs <- c("An integer indicating the age of the primary beneficiary (excluding those above 64 years, since they are generally not covered by the plan)",
          "The policy holder's gender, either male or female",
          "The body mass index (BMI), which provides a sense of how over- or under-weight a person is relative to their height",
          "An integer indicating the number of children/dependents covered by the insurance plan",
          "A yes or no categorical variable that indicates whether the insured regularly smokes tobacco",
          "The beneficiary's place of residence in the US, divided into four geographic regions: northeast, southeast, southwest, and northwest",
          "Dependent variable - measures the medical costs each person charged to the insurance plan for the year")

ins.dict <- data.frame(names(ins), defs, stringsAsFactors = F)
names(ins.dict) <- c("Variable Name", "Definition")

kable(ins.dict)
```

Variable Name	Definition
age	An integer indicating the age of the primary beneficiary (excluding those above 64 years, since they are generally not covered by the plan)
sex	The policy holder's gender, either male or female
bmi	The body mass index (BMI), which provides a sense of how over- or under-weight a person is relative to their height
children	An integer indicating the number of children/dependents covered by the insurance plan
smoker	A yes or no categorical variable that indicates whether the insured regularly smokes tobacco
region	The beneficiary's place of residence in the US, divided into four geographic regions: northeast, southeast, southwest, and northwest
charges	Dependent variable - measures the medical costs each person charged to the insurance plan for the year

### 1.2 Data Structure

```
psych::describe(ins)
##          vars      n    mean      sd  median  trimmed   mad    min
## age          1 1338   39.21   14.05   39.00    39.01   17.79   18.00
```

```
## sex*      2 1338      1.51      0.50      2.00      1.51      0.00      1.00
## bmi       3 1338     30.66      6.10     30.40     30.50      6.20     15.96
## children  4 1338      1.09      1.21      1.00      0.94      1.48      0.00
## smoker*   5 1338      1.20      0.40      1.00      1.13      0.00      1.00
## region*   6 1338      2.52      1.10      3.00      2.52      1.48      1.00
## charges   7 1338 13270.42 12110.01 9382.03 11076.02 7440.81 1121.87
##          max      range skew kurtosis      se
## age        64.00     46.00  0.06    -1.25    0.38
## sex*        2.00      1.00 -0.02    -2.00    0.01
## bmi        53.13     37.17  0.28    -0.06    0.17
## children     5.00      5.00  0.94     0.19    0.03
## smoker*      2.00      1.00  1.46     0.14    0.01
## region*      4.00      3.00 -0.04    -1.33    0.03
## charges 63770.43 62648.55  1.51     1.59 331.07
```

The dataset has 7 variables, and 1338 cases.

## 1.3 Missing data

```
any(is.na(ins))
## [1] FALSE
```

Amazingly, this dataset has no missing cases, which will simplify our cleaning process!

## 1.4 Visualizations

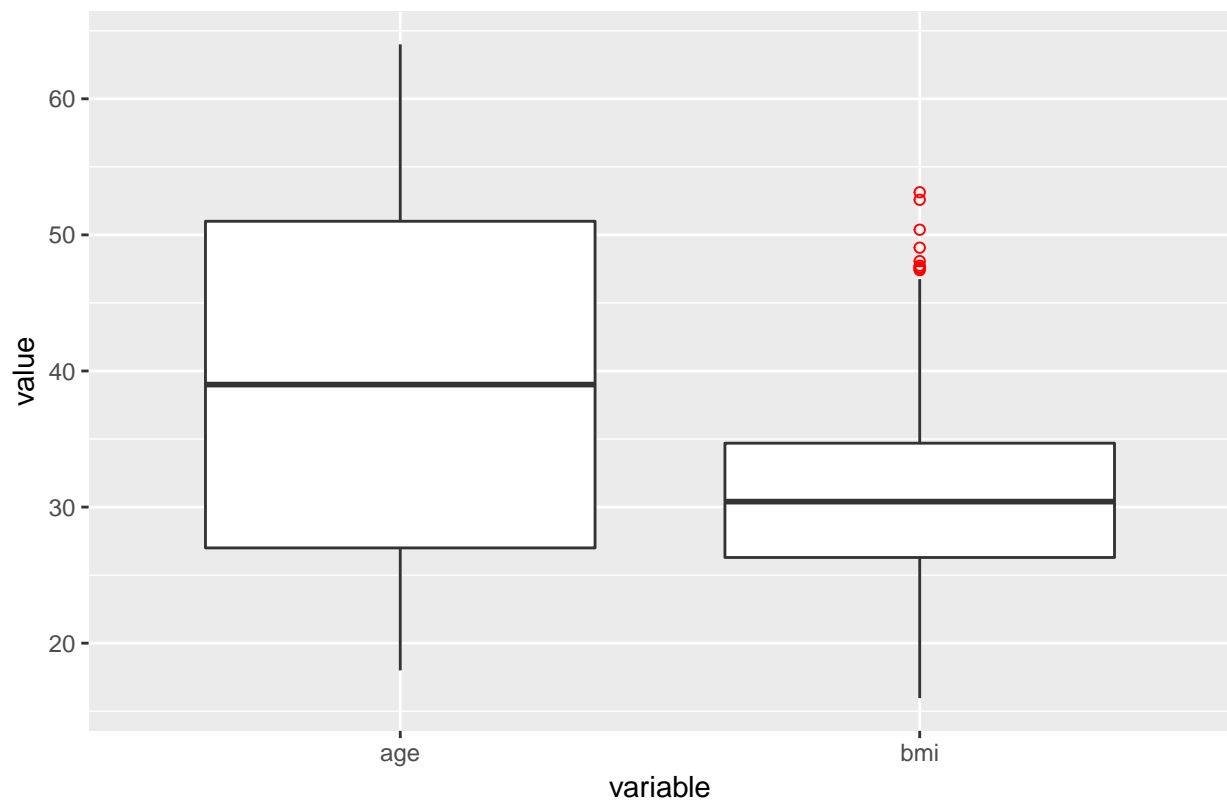
### 1.4.1 Boxplot

```
ins.bp <- ins %>%
  select(c(1, 3)) %>%
  gather()

summary.boxplot <- ggplot(ins.bp, aes(x = key, y = value)) +
  labs(x = "variable", title = "Insurance Data Boxplot") +
  geom_boxplot(outlier.colour = "red", outlier.shape = 1)

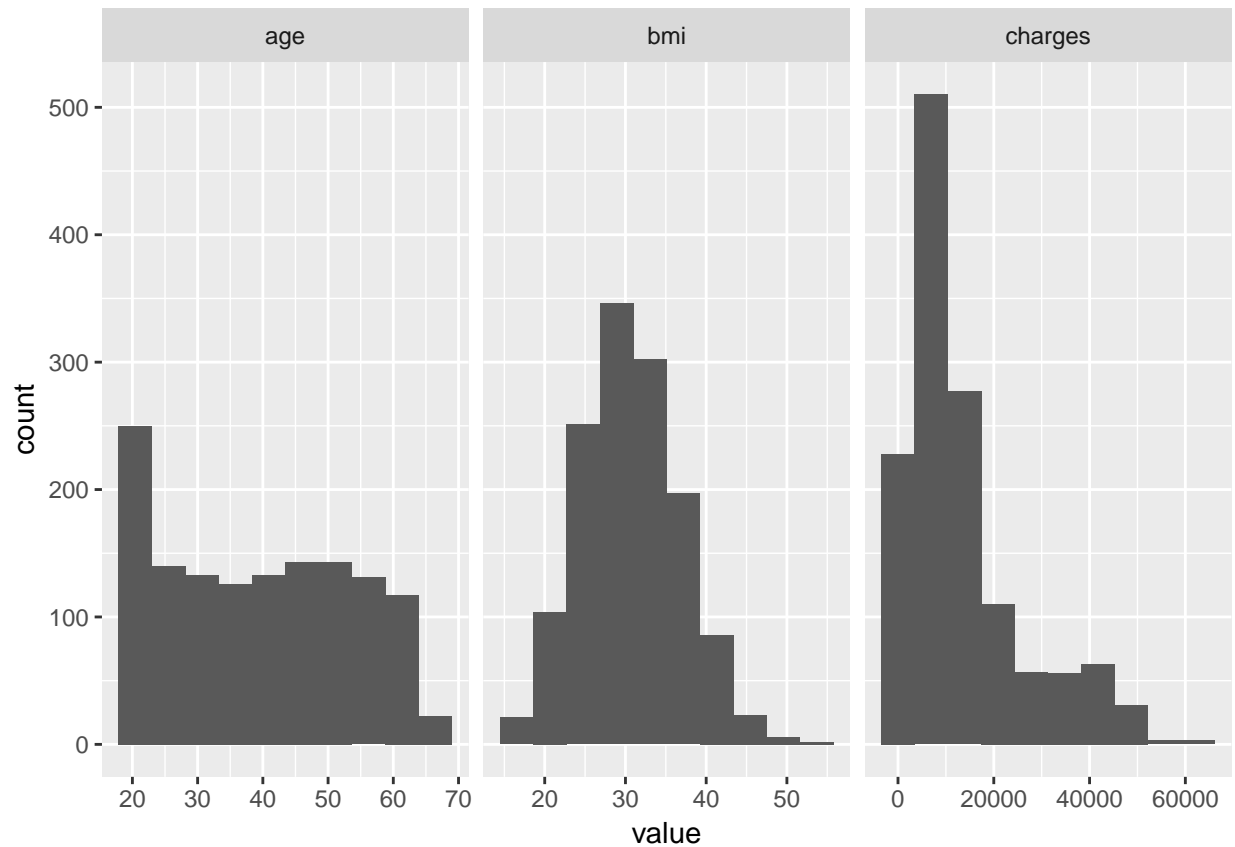
summary.boxplot
```

Insurance Data Boxplot



#### 1.4.2 Histogram

```
ins.h <- ins %>%  
  select(c(1, 3, 7)) %>%  
  gather()  
  
ins.hist <- ggplot(data = ins.h, mapping = aes(x = value)) +  
  geom_histogram(bins = 10) +  
  facet_wrap(~key, scales = 'free_x')  
  
ins.hist
```

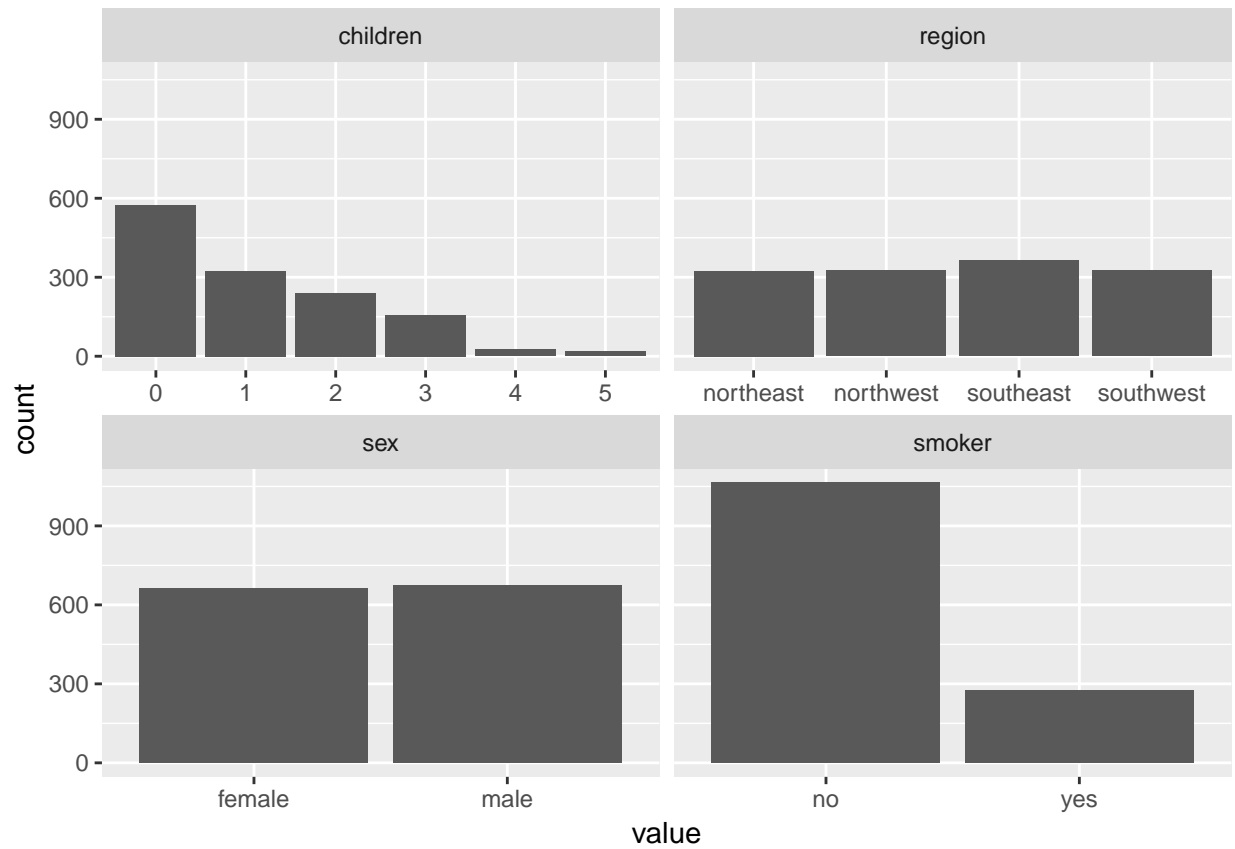


### 1.4.3 Bar Chart

```
ins.b <- ins %>%
  select(c(2, 4:6)) %>%
  gather()

ins.bar <- ggplot(data = ins.b, mapping = aes(x = value)) +
  geom_bar() +
  facet_wrap(~key, scales = 'free_x')

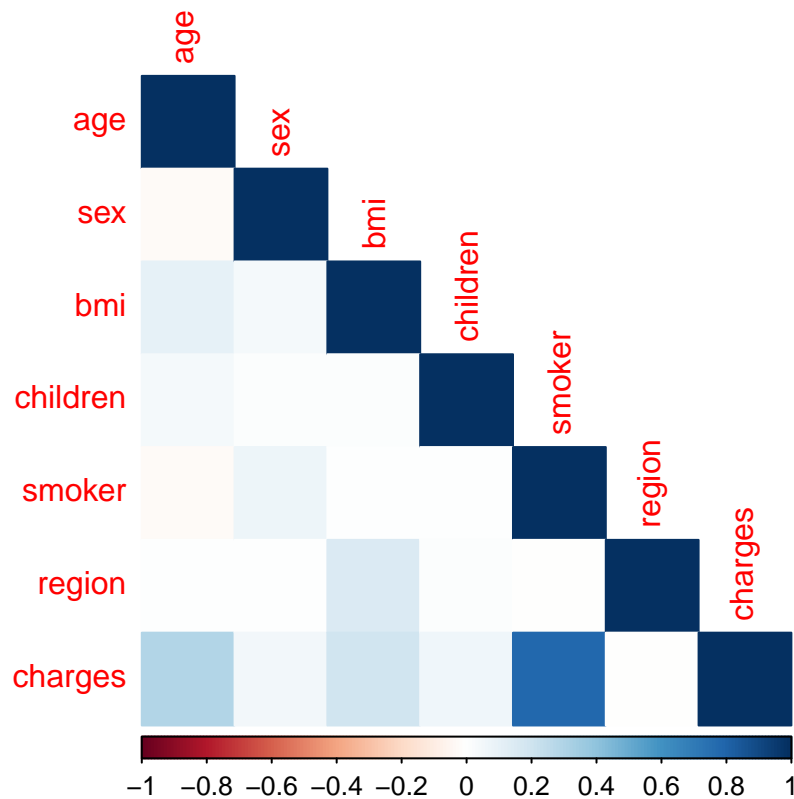
ins.bar
```



## 1.4.4 Correlation

### 1.4.4.1 Correlation Heatmap

```
ins.c <- mutate_all(ins, funs(as.numeric))  
corrplot(cor(ins.c), method = "color", type = "lower")
```



#### 1.4.4.2 Correlation (with dependent) table

```
corp <- apply(ins.c[, -7], 2, function(x) cor.test(x, y=ins.c$charges)$p.value)
cortable <- cor(ins.c[, -7], ins.c$charges)
kable(cbind(as.character(corp), cortable), col.names = c("P-value", "Correlation with dependent"))
```

	P-value	Correlation with dependent
age	4.88669333171859e-29	0.299008193330648
sex	0.0361327210059298	0.0572920622020254
bmi	2.45908553511669e-13	0.198340968833629
children	0.0128521285201365	0.0679982268479048
smoker	8.2714358421744e-283	0.787251430498477
region	0.82051783646525	-0.00620823490944446

Based on the above correlation analyses, one can see that most variables, especially **smoker** and **age**, are positively correlated with the dependent variable **charges**, while **region** has a negative correlation.

## 2. Data Preparation

### 2.1 Missing Data

As noted earlier, the dataset is remarkably whole, so we may proceed without worrying about having to impute any data.

### 2.2 Normality of Predictor Variables

As can be seen in the distribution plots in section 1.4.2, `bmi` appears to be nearly normal, while `age` has a slight right skew. Linear regression does not make any assumptions on the normality of any variables, so I will keep the variables as is.

### 2.4 Variable Transformation

For one of my models, I will transform `bmi` to a binary variable, with any case having a value inside the accepted range as described in the data dictionary being marked 0, and all others marked 1.

### 2.5 Outliers

From section 1.4.1, only `bmi` has outliers. I believe that transforming it to a continuous variable, as outlined in the preceding section.

## 3. Build Models

### 3.1 Model 1

For the first model, I will include all variables as is, to serve as a baseline with which to compare future models that may have transformed variables.

```
m1 <- lm(formula = charges ~ .,
          data = ins)
summary(m1)
##
## Call:
## lm(formula = charges ~ ., data = ins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -11304.9  -2848.1   -982.1   1393.9  29992.8
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -11938.5     987.8  -12.086 < 2e-16 ***
## age             256.9       11.9   21.587 < 2e-16 ***
## sexmale       -131.3      332.9   -0.394 0.693348
## bmi            339.2       28.6   11.860 < 2e-16 ***
## children       475.5      137.8    3.451 0.000577 ***
## smokeryes     23848.5     413.1   57.723 < 2e-16 ***
```

```
## regionnorthwest    -353.0      476.3   -0.741 0.458769
## regionsoutheast    -1035.0     478.7   -2.162 0.030782 *
## regionsouthwest    -960.0     477.9   -2.009 0.044765 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6062 on 1329 degrees of freedom
## Multiple R-squared:  0.7509, Adjusted R-squared:  0.7494
## F-statistic: 500.8 on 8 and 1329 DF,  p-value: < 2.2e-16
```

### 3.1.1 Model 1 Interpretation

The model summary reveals several variables that are insignificant toward predicting the target variable - sexmale, and regionnorthwest. I'll build a second model, and see if I can improve on this.

## 3.2 Model 2

```
m2 <- lm(formula = charges ~ . -sex -region,
          data = ins)
summary(m2)
##
## Call:
## lm(formula = charges ~ . - sex - region, data = ins)
##
## 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
```

### 3.2.1 Compare models

```
anova(m2, m1)
## Analysis of Variance Table
##
## Model 1: charges ~ (age + sex + bmi + children + smoker + region) - sex -
##      region
```



```
## Model 2: charges ~ age + sex + bmi + children + smoker + region
##   Res.Df      RSS Df Sum of Sq    F Pr(>F)
## 1   1333 4.9078e+10
## 2   1329 4.8840e+10  4 238917273 1.6253 0.1654
```

It seems that the original model is preferred over the second.

I will build one last model, where I'll transform the `bmi` variable from continuous to binary.

```
m3 <- ins %>%
  mutate(overweight = if_else(bmi > 24.9, 1, 0)) %>%
  select(-c(bmi, region, sex))

m3 <- lm(formula = charges ~ .,
         data = m3)
summary(m3)
##
## Call:
## lm(formula = charges ~ ., data = m3)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -13017  -2500  -1713   1536  28693
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -5349.50     622.63  -8.592  < 2e-16 ***
## age          264.20      12.21   21.641  < 2e-16 ***
## children     497.99      141.62    3.516 0.000452 ***
## smokeryes    23920.52     422.76  56.582  < 2e-16 ***
## overweight   3439.77     445.08    7.728 2.13e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6236 on 1333 degrees of freedom
## Multiple R-squared:  0.7356, Adjusted R-squared:  0.7348
## F-statistic: 927.1 on 4 and 1333 DF,  p-value: < 2.2e-16
anova(m3, m1)
## Analysis of Variance Table
##
## Model 1: charges ~ age + children + smoker + overweight
## Model 2: charges ~ age + sex + bmi + children + smoker + region
##   Res.Df      RSS Df Sum of Sq    F    Pr(>F)
## 1   1333 5.1844e+10
## 2   1329 4.8840e+10  4 3004332616 20.438 2.338e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Once again, the first model outperforms the newer one, so we will use model 1 for our predictions.

## 4. Model Selection

### 4.1 Split Data

```
set.seed(858)

# Split data into training and testing partitions
train <- ins %>%
  sample_frac(., size = 0.7, replace = F)
test <- anti_join(ins, train)
```

### 4.3 Prediction

```
model1 <- lm(formula = charges ~ .,
             data = train)

predicted.charges <- predict(object = model1, newdata = test, type = "response")

model1 <- lm(formula = charges ~ .,
             data = train)

rp1 <- ggplot(model1, aes(.fitted, .resid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(se = FALSE) +
  labs(title = "Residuals vs Fitted")

rp2 <- ggplot(model1, aes(.fitted, .stdresid)) +
  geom_point() +
  geom_hline(yintercept = 0) +
  geom_smooth(se = FALSE)

rp3 <- ggplot(model1) +
  stat_qq(aes(sample = .stdresid)) +
  geom_abline()

rp4 <- ggplot(model1, aes(.fitted, sqrt(abs(.stdresid)))) +
  geom_point() +
  geom_smooth(se = FALSE) +
  labs(title = "Scale-Location")

rp5 <- ggplot(model1, aes(seq_along(.cooks), .cooks)) +
  geom_col() +
  ylim(0, 0.0075) +
  labs(title = "Cook's Distance")

rp6 <- ggplot(model1, aes(.hat, .stdresid)) +
  geom_point(aes(size = .cooks)) +
  geom_smooth(se = FALSE, size = 0.5) +
  labs(title = "Residuals vs Leverage")

rp7 <- ggplot(model1, aes(.hat, .cooks)) +
```

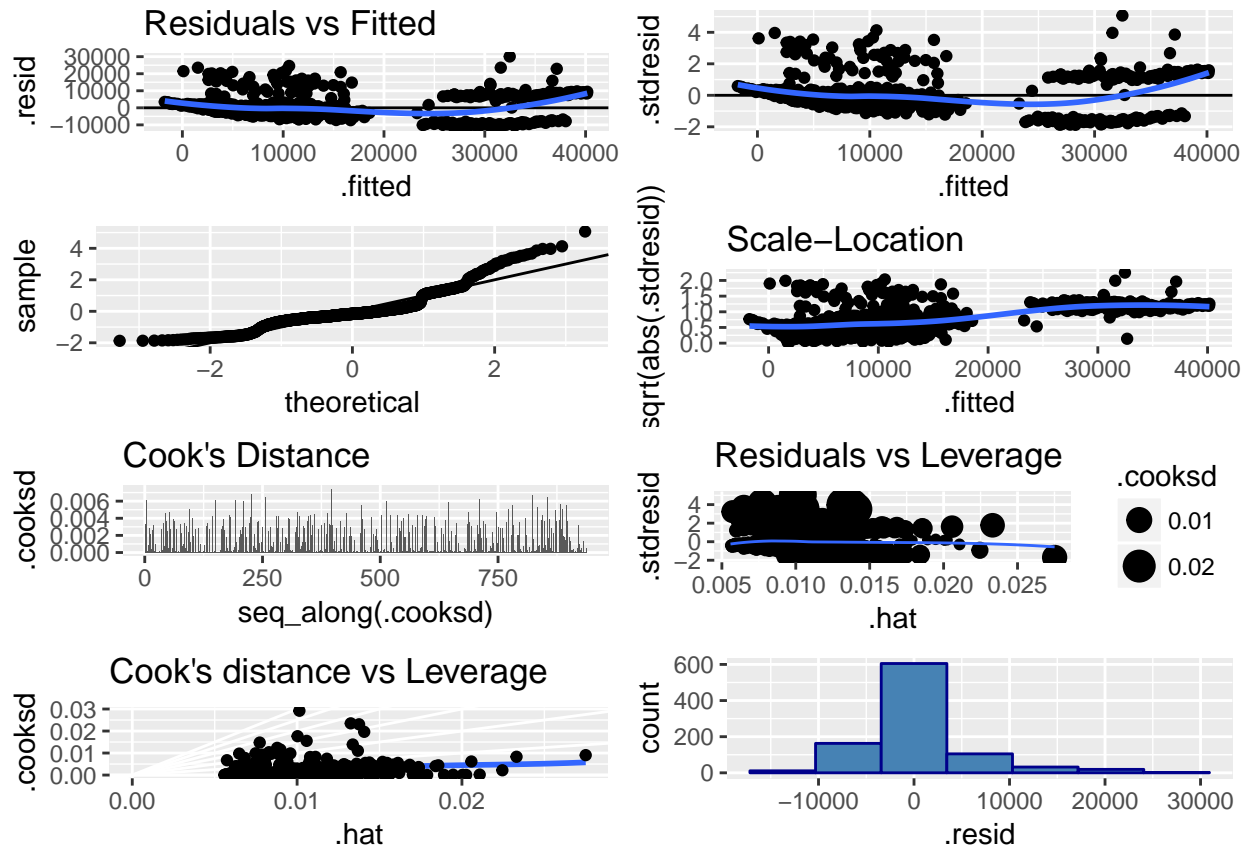
```

geom_vline(xintercept = 0, colour = NA) +
geom_abline(slope = seq(0, 3, by = 0.5), colour = "white") +
geom_smooth(se = FALSE) +
geom_point() +
labs(title = "Cook's distance vs Leverage")

rp8 <- ggplot(model1, aes(.resid)) +
  geom_histogram(bins = 7, color="darkblue", fill="steelblue")

grid.arrange(rp1, rp2, rp3, rp4, rp5, rp6, rp7, rp8, ncol = 2)

```



From the above visualizations, the residuals appear to be close enough to normal, so I'll proceed with using the model to make predictions.

## 4.4 Prediction Results

```

results.df <- data.frame(cbind(actuals = test$charges, predicted = predicted.charges))

results.df <- results.df %>%
  mutate(error = results.df$actuals - results.df$predicted) %>%
  round(., 2)
results.df <- results.df %>%
  mutate(perccolor = paste0(round(results.df$error/results.df$actuals*100,2),"%"))

kable(head(results.df))

```

actuals	predicted	error	percerror
4449.46	6702.10	-2252.64	-50.63%
3756.62	4105.21	-348.59	-9.28%
6406.41	8537.00	-2130.59	-33.26%
1826.84	4332.64	-2505.80	-137.17%
11090.72	14850.72	-3760.01	-33.9%
36837.47	29908.33	6929.14	18.81%

```
sprintf("The mean percent error is: %s%%", round(mean(results.df$error/results.df$actuals*100), 2))
## [1] "The mean percent error is: -19.31%"
```

## 5. Remarks

Our model was able to predict the insurance premium for policy holders with a mean difference of ~19%.

While **sex** and **region** were not major contributors to the model, the model with those variables removed actually performed slightly worse. Perhaps if **region** was further broken down by state, it might provide more explanatory power.

As one would expect, **smoker** is *highly* correlated with **charges** - that is, a smoker is very likely to have a higher premium.