Regression Analysis Examples in R

Chapter 2 - Simple Linear Regression

Example. Airfreight Data

	1	2	3	4	5	6	7	8	9	10
Shipment Route (x)	1	0	2	0	3	1	0	1	2	0
Airfreight Breakage (y)	16	9	17	12	22	13	8	15	19	11

a) Compute the ANOVA table
b) Compute the confidence intervals for the parameters
c) Compute the confidence interval on the average (mean) response when $X = 1$.
d) What is the total variability in y explained by this model?

Solution.

Part a.

We can compute the anova table manually as follows,

$$S_{xx} = \sum_{i=1}^{n}(x_i - \bar{x})^2 = \sum_{i=1}^{n} x_i^2 - \frac{1}{n}\left(\sum_{i=1}^{n} x_i\right)^2 = 20 - \frac{1}{10}(100) = 10$$

$$S_{xy} = \sum_{i=1}^{n} y_i(x_i - \bar{x}) = \sum_{i=1}^{n} x_i y_i - \frac{1}{n}\sum_{i=1}^{n} x_i \sum_{i=1}^{n} y_i = 182 - \frac{1}{10}(10)(142) = 40$$

Therefore,

$$\hat{\beta}_1 = \frac{S_{xy}}{S_{xx}} = \frac{40}{10} = 4$$

Then, $\hat{\beta}_0 = \bar{y} - \hat{\beta}_1\bar{x}$, so

$$\hat{\beta}_0 = \frac{1}{10}(142) - 4 \cdot \frac{1}{10}(10) = 10.2$$

This gives us our linear model

$$\hat{y} = 10.2 + 4x$$

The sum of squares for regression is

$$SSR = \hat{\beta}_1^2 \sum_{i=1}^{n}(x_i - \bar{x})^2 = \hat{\beta}_1^2 S_{xx} = 16 \cdot 10 = 160$$

The total sum of squares is

$$SST = \sum_{i=1}^{n}(y_i - \bar{y})^2 = \sum_{i=1}^{n} y_i^2 - n\bar{y}^2 = 2194 - 10(14.2)^2 = 177.6$$

Then, the residual sum of squares is

$$SSE = SST - SSR = 177.6 - 160 = 17.6$$

Now we can construct the anova table

Source	Sum of Squares	DF	MS=SS/df	F = MSR/MSE
Regression	160	1	160	72.727
Error	17.6	8	2.2	
Total	177.6			

We conclude tbat the regression is highly significant since the F value is very large. We can also do this in R

```
x <- c(1,0,2,0,3,1,0,1,2,0)
y <- c(16,9,17,12,22,13,8,15,19,11)
model <- lm(formula = y ~ x)
print(model)
```

```
##
## Call:
## lm(formula = y ~ x)
##
## Coefficients:
## (Intercept)            x
##        10.2          4.0
```

```
anova(model)
```

```
## Analysis of Variance Table
##
## Response: y
##           Df Sum Sq Mean Sq F value    Pr(>F)
## x          1  160.0   160.0  72.727 2.749e-05 ***
## Residuals  8   17.6     2.2
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can see that we get the same results and reach the same conclusion, and we also get the p-value which is very small and we can conclude from there as well that the regression is highly significant.

Part b.

We can construct confidence intervals, first we need to compute $se(\hat{\beta}_1)$ and $se(\hat{\beta}_0)$.

$$se^2(\hat{\beta}_0) = MSE\left(\frac{1}{n} + \frac{\bar{x}}{S_{xx}}\right) = 2.2\left(\frac{1}{10} + \frac{1}{10}\right) = 0.44 \implies se(\hat{\beta}_0) = \sqrt{0.44} = 0.6633$$

$$se^2(\hat{\beta}_1) = \frac{MSE}{S_{xx}} = \frac{2.2}{10} = 0.22 \implies se(\hat{\beta}_1) = \sqrt{0.22} = 0.490$$

Then, we have to compute $t_{\alpha/2,n-2} = t_{0.025,8}$, we either use a t look up table or in R,

```r
qt(0.025, 8, lower.tail=FALSE)
```

```
## [1] 2.306004
```

Thus, our confidence intervals are

$$\hat{\beta}_0 - t_{\alpha/2,n-2}se(\hat{\beta}_0) \leq \hat{\beta}_0 \leq \hat{\beta}_0 + t_{\alpha/2,n-2}se(\hat{\beta}_0) \rightarrow 10.2 \pm 2.306(0.6633) = (8.6704, 11.7296)$$

$$\hat{\beta}_1 - t_{\alpha/2,n-2}se(\hat{\beta}_1) \leq \hat{\beta}_1 \leq \hat{\beta}_1 + t_{\alpha/2,n-2}se(\hat{\beta}_1) \rightarrow 4 \pm 2.306(0.490) = (2.9392, 5.0608)$$

We can compute these confidence intervals in R as well

```r
confint(model, level=0.95)
```

```
##                2.5 %    97.5 %
## (Intercept) 8.670370 11.729630
## x           2.918388  5.081612
```

Part c.

We want to compute first $E(y|x_0)$, where $x_0 = 1$. An unbiased estimator for $E(y|x_0)$ is

$$\widehat{E(y|x_0)} = \hat{\mu}_{y|x_0} = \hat{\beta}_0 + \hat{\beta}_1 x_0 = 10.2 + 4(1) = 14.2$$

Then, the confidence interval is

$$\left[\hat{\mu}_{y|x_0} \pm t_{\alpha/2,n-2}\sqrt{MSE\left(\frac{1}{n} + \frac{(x_0 - \bar{x})^2}{S_{xx}}\right)}\right] = \left[14.2 \pm 2.306\sqrt{2.2\left(\frac{1}{10} + \frac{(1-1)^2}{S_{xx}}\right)}\right] = (13.11839, 15.28161)$$

We can do this in R with

```r
predict(model, newdata = data.frame(x=1), interval = 'confidence', level=0.95)
```

```
##    fit      lwr      upr
## 1 14.2 13.11839 15.28161
```

Part d.

The total variability in y explained by the regressor x is measured by the coefficient of determination

$$R^2 = \frac{SSR}{SST} = \frac{160}{177.6} = 0.9009$$

We can also see this in the summary of the model in R

```r
summary(model)
```

```
##
## Call:
## lm(formula = y ~ x)
##
## Residuals:
##    Min     1Q Median     3Q    Max
```

```
##   -2.2   -1.2    0.3    0.8    1.8
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  10.2000     0.6633  15.377 3.18e-07 ***
## x             4.0000     0.4690   8.528 2.75e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.483 on 8 degrees of freedom
## Multiple R-squared:  0.9009, Adjusted R-squared:  0.8885
## F-statistic: 72.73 on 1 and 8 DF,  p-value: 2.749e-05
```

The R^2 value is 0.9009.

Chatper 3 - Multiple Linear Regression

Question 3.1

Consider the National Football League data in Table B.1

a. Fit a multiple linear regression model relating the number of games won to the team's passing yardage (x_2), the percentage of rushing plays (x_7), and the opponents' yards rushing (x_8).
b. Construct the analysis-of-variance table and test for significance of regression.
c. Calculate t statistics for the hypotheses $H_0 : \beta_2 = 0$, $H_0 : \beta_7 = 0$, and $H_0 : \beta_8 = 0$. What conclusions can you draw about the roles of variables in x_2, x_7, and x_8 play in the model?
d. Calculate R^2 and R^2_{Adj} for this model.
e. Using the partial F test, determine the contribution of x_7 to the model. How is the partial F statistic related to the t test for β_7 calculated in part c above?

Question 3.3

Refer to problem 3.1

a. Find a 95% CI for β_7.

b. Find a 95% CI on the mean number of games won by a team when $x_2 = 2300$, $x_7 = 56$, and $x_8 = 2100$.

Question 3.4

Reconsider the National Football League data from Problem 3.1. Fit a model to these data using only x_7 and x_8 as regressors.

a. Test for significance of regression.

b. Calculate R^2 and R^2_{Adj}. How do these quantities compare to the value computed for the model in Problem 3.1, which included an additional regressor (x_2)?

c. Calculate a 95% CI on β_7. Also find a 95% CI on the mean number of games won by a team when $x_7 = 56$, and $x_8 = 2100$. Compare the lengths of these CIs to the lengths of the corresponding CIs from Problem 3.3.

d. What conclusions can you draw from this problem about the consequences of omitting an important regressor from a model?

Solutions.

Question 3.1

Part a.

We can fit a linear model using the same R function,

```
# Table b1 was loaded ahead of time.
model <- lm(formula = y ~ x2 + x7 + x8, tableb1)
model
```

```
##
## Call:
## lm(formula = y ~ x2 + x7 + x8, data = tableb1)
##
## Coefficients:
## (Intercept)           x2           x7           x8
##   -1.808372     0.003598     0.193960    -0.004815
```

This gives us our linear model with the estimates $\hat{\beta}_0 = -1.808$, $\hat{\beta}_2 = 0.00360$, $\hat{\beta}_7 = 0.194$, and $\hat{\beta}_8 = -0.00482$.

$$y = -1.808 + 0.00360x_2 + 0.194x_7 - 0.00482x_8$$

Part b.

We test for significance of regession using the hypotheses

$$H_0 : \beta_2 = \beta_7 = \beta_8 = 0, \;\; H_1 : \beta_j \neq 0, j = 2, 7, 8$$

We use the F-statistic

$$F_0 = \frac{SSR/k}{SSE/(n-p)} = \frac{MSR}{MSE} \sim F_{k,n-p}$$

We reject the null hypothesis when $F > F_{\alpha,k,n-k-1}$, we compute these values in R. In this case, we have $k = 3$ regressors and coefficients, so $p = k + 1 = 4$, thus

```
n <- nrow(tableb1)
anova(model)
```

```
## Analysis of Variance Table
##
## Response: y
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## x2         1  76.193  76.193  26.172 3.100e-05 ***
## x7         1 139.501 139.501  47.918 3.698e-07 ***
## x8         1  41.400  41.400  14.221 0.0009378 ***
## Residuals 24  69.870   2.911
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
qf(0.05, 3, n-4, lower.tail=FALSE)
```

```
## [1] 3.008787
```

Source	Sum of Squares	DF	MS	F	P
x_2	76.193	1	76.193	26.172	$3.1 \cdot 10^{-5}$
x_7	139.501	1	139.501	47.918	$3.698 \cdot 10^{-7}$
x_8	41.400	1	41.400	14.221	0.0009378
Residuals	69.8790	24	2.911		

$$F_0 = \frac{SSR/k}{SSE/(n-p)} = \frac{(76.193 + 139.501 + 41.4)/3}{69.870/24} = 29.439$$

We can also obtain the F-statistic from the summary of the model,

```r
summary(model)
```

```
##
## Call:
## lm(formula = y ~ x2 + x7 + x8, data = tableb1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.0370 -0.7129 -0.2043  1.1101  3.7049
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.808372   7.900859  -0.229 0.820899
## x2           0.003598   0.000695   5.177 2.66e-05 ***
## x7           0.193960   0.088233   2.198 0.037815 *
## x8          -0.004816   0.001277  -3.771 0.000938 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.706 on 24 degrees of freedom
## Multiple R-squared:  0.7863, Adjusted R-squared:  0.7596
## F-statistic: 29.44 on 3 and 24 DF,  p-value: 3.273e-08
```

Therefore, we reject the null hypothesis $H_0 : \beta_2 = \beta_7 = \beta_8 = 0$, and conclude our regression is significant.

Part c.

We want to conduct tests on the indivudal coefficients, with the hypotheses $H_0 : \beta_2 = 0$, $H_0 : \beta_7 = 0$, and $H_0 : \beta_8 = 0$. We need the t-statistic

$$t_0 = \frac{\hat{\beta}_j}{se(\hat{\beta}_j)}$$

We reject the null hypothesis when $|t_0| > t_{\alpha/2, n-p}$,

```r
qt(0.025, n-4, lower.tail=FALSE)
```

```
## [1] 2.063899
```

We have all the information we need however in the summary of the model, we can see the estimate and the standard error for each coefficient, which tells us the t-value, but also the t-value is included. We can see that for all coefficents and their respective t-values, $|t_0| > t_{\alpha/2,n-p}$ so we reject all 3 of the null hypotheses.

Part d.

The R^2 value can be computed with

$$R^2 = \frac{SSR}{SST} = 1 - \frac{SSE}{SST} = \frac{76.193 + 139.501 + 41.4}{76.193 + 139.501 + 41.4 + 69.8790} = 0.7863$$

We get these values from the ANOVA table above and also in the summaryof our model, we have $R^2 = 0.7863$, and the adjusted R^2 value is

$$R^2_{Adj} = 1 - \frac{SSE/(n-k)}{SST/(n-1)} = 1 - \frac{68.8790/24}{326.973/27} = 0.7596$$

This value is also in the summary R output above.

Part e.

To conduct the partial F test to determine the contribution of x_7, we want to tes tthe hypotheses

$$H_0 : \beta_7 = 0, \ H_1 : \beta_7 \neq 0$$

We fit the model assuming the null hypothesis is true to get the reduced model and obtain the anova table,

```r
reduced_model <- lm(formula = y ~ x8 + x2, data=tableb1)
anova(reduced_model)
```

```
## Analysis of Variance Table
##
## Response: y
##           Df  Sum Sq Mean Sq F value    Pr(>F)
## x8         1 178.092 178.092  53.043 1.245e-07 ***
## x2         1  64.934  64.934  19.340 0.0001775 ***
## Residuals 25  83.938   3.358
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Then, we want to use the F statistic to test the hypotheses

$$F_0 = \frac{SSR(\beta_7|\beta_2, \beta_0)/r}{MSE}$$

So, we have

$$SRR(\beta_7|\beta_2, \beta_8) = SSR(\beta_7, \beta_2, \beta_8) - SSR(\beta_2, \beta_8) = 257.094 - (178.092 + 64.934) = 14.064$$

Therefore,

$$F_0 = \frac{SSR(\beta_7|\beta_2, \beta_8)}{MSE} = \frac{14.064}{2.911} \approx 4.831$$

we reject the null hypothesis if $F_0 > F_{\alpha,r,n-p}$,

```
qf(0.05, 1, 24, lower.tail=FALSE)
```

```
## [1] 4.259677
```

We conclude that x_7 contributed significantly to this model. We also notice that the F statistic is the square of the t test used in part c.

Question 3.3

Part a.

To consturct a confidence interval on β_7, we need to compute

$$\hat{\beta}_j - t_{\alpha/2,n-p}\sqrt{\hat{\sigma}^2 C_{jj}} \leq \beta_j \leq \hat{\beta}_j - t_{\alpha/2,n-p}\sqrt{\hat{\sigma}^2 C_{jj}}$$

We have the standard error for β_7 from the previous summary output from R, so $se(\hat{\beta}_j) = \sqrt{\hat{\sigma}^2 C_{jj}} = 0.088233$. Then, the t-value was also obtained earlier and we have $t_{\alpha/2,n-p} = 2.063899$, and the coefficient estimator $\hat{\beta}_7 = 0.193960$. Therefore, the confidence interval is

$$0.193960 \pm 2.063899 \cdot (0.088233) = (0.011856, 0.376064)$$

This can be also obtained in R

```
confint(model, "x7")
```

```
##         2.5 %    97.5 %
## x7 0.01185532 0.3760651
```

Part b.

The mean response at $x_2 = 2300$, $x_7 = 56$ and $x_8 = 2100$ is

$$y_0 = \beta_0 + \beta_2(2300) + \beta_7(56) + \beta_8(2100) = 7.215188$$

Then, the confidence interval on the mean response is

$$\left[\hat{y}_0 \pm t_{\alpha/2,n-p}\sqrt{\hat{\sigma}^2 x_0'(X'X)^{-1}x_0}\right]$$

This can be calculated in R with

```
predict(model, newdata=data.frame(x2 = 2300, x7 = 56, x8 = 2100),
        interval = 'confidence', level=0.95)
```

```
##        fit      lwr      upr
## 1 7.216424 6.436203 7.996645
```

Question 3.4

Part a

We want to test the hypotheses for significance,

$$H_0 : \beta_7 = \beta_8 = 0,\ H_1 : \beta_j \neq 0,\ j = 7, 8$$

We can fit the model and get the anova table,

```
model <- lm(formula = y ~ x7 + x8, tableb1)
anova(model)
```

```
## Analysis of Variance Table
##
## Response: y
##           Df  Sum Sq Mean Sq F value   Pr(>F)
## x7         1  97.238  97.238  16.437 0.000431 ***
## x8         1  81.828  81.828  13.832 0.001015 **
## Residuals 25 147.898   5.916
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We can see from the anova table that the regression is highly significant, but we can also use the F test statistic,

$$F_0 = \frac{SSR/k}{SSE/(n-k-1)} = \frac{(97.238 + 81.828)/2}{147.898/25} = \frac{89.533}{5.916} = 15.134$$

Then, we can compute $F_{\alpha,k,n-k-1}$,

```
qf(0.05, 3, 25, lower.tail=FALSE)
```

```
## [1] 2.991241
```

We can see that $F_0 > F_{\alpha,k,n-k-1}$ so we reject the null hypotheses that $H_0 : \beta_7 = \beta_8 = 0$, and conclude that the regression is significant.

Part b.

We can obtain a summary for the model and look at the R^2 and R^2_{Adj} values similar to the previous questions.

```
summary(model)
```

```
##
## Call:
## lm(formula = y ~ x7 + x8, data = tableb1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.7985 -1.5166 -0.5792  1.9927  4.5248
##
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 17.944319   9.862484   1.819  0.08084 .
## x7           0.048371   0.119219   0.406  0.68839
## x8          -0.006537   0.001758  -3.719  0.00102 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.432 on 25 degrees of freedom
## Multiple R-squared:  0.5477, Adjusted R-squared:  0.5115
## F-statistic: 15.13 on 2 and 25 DF,  p-value: 4.935e-05
```

We get an R-squared value $R^2 = 0.5477$ and the adjusted R-squared is $R^2_{Adj} = 0.5115$, we can see that these values are lower than when we had x_2 in the model. So, the model with x_2 was able to better explain the variablity in y and this suggests x_2 may have been contributing significantly to the model.

Part c.

```
confint(model, "x7")
```

```
##         2.5 %   97.5 %
## x7 -0.1971643 0.293906
```

A 95% confidence interval on β_7 is

$$(-0.1971643, 0.293906)$$

```
new_data <- data.frame(x7 = 56, x8=2100)
predict(model, newdata=new_data, interval='confidence', level=0.95)
```

```
##        fit      lwr      upr
## 1 6.926243 5.828643 8.023842
```

Our 95% confidence interval on the mean number of games one when $x_7 = 56$ and $x_8 = 2100$ is

$$(5.828643, 8.023842)$$

We can see that the length of both confidence intervals are greater than when x_2 was included in the model. This suggests we were more confident with our estimates when x_2 was included.

d.

We can conclude that omitting an important regressor (x_2) affected our estimates and standard error of coeffficients, resulting in larger lenghts in the confidence intervals and lower values for R^2.

Chapter 4 - Model Adequecy

Question 4.1

Consider the simple regression model fit to the National Football League team performance data in Problem 2.1. (Same data as previous questions, with the model y $x8$.

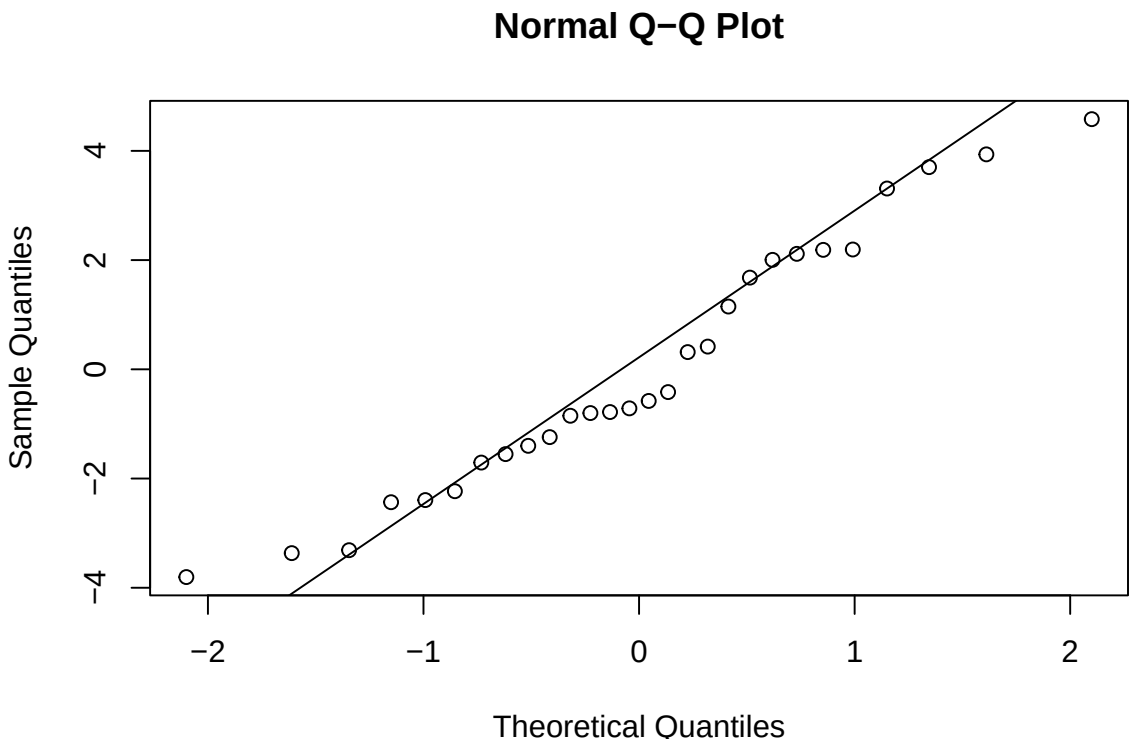
a. Construct a normal probability plot of the residuals. Does there seem to be any problem with the normality assumption?

b. Construct an interpret a plot of the residuals versus the predicted repsonse.

c. Plot the residuals versus the team passing yardage, x_2. DOes this plot indicate that the model will be improved by adding x_2 to the model?

Part a.

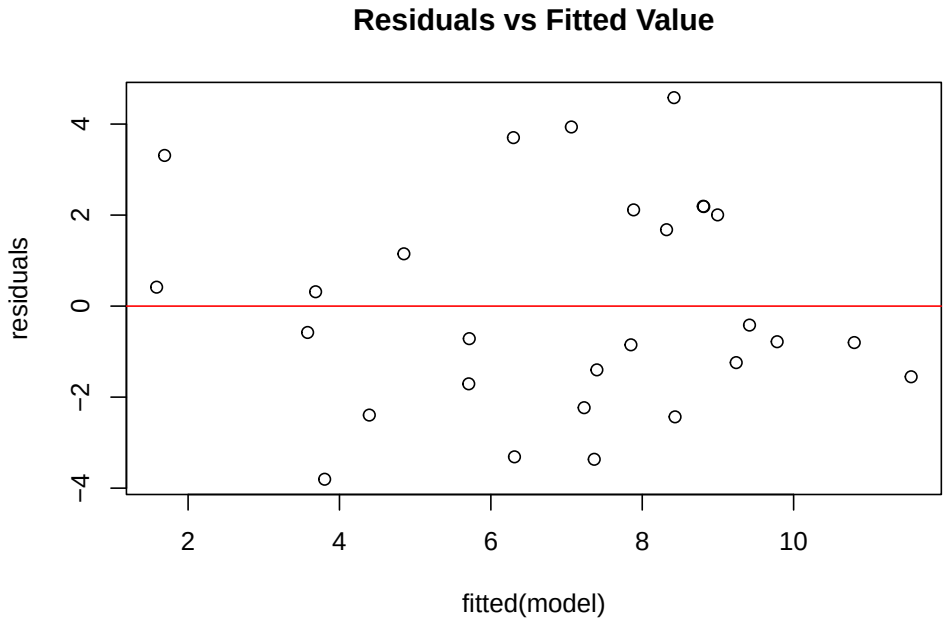
```
library(ggplot2)
model <- lm(formula = y ~ x8, tableb1)
residuals <- residuals(model)
qqnorm(residuals)
qqline(residuals)
```



It appears that the normality assumption is fine since the standardized residuals closely follow the theoretical quantiles for a normal distribution as observered in the quantile-quantile plot.

Part b.

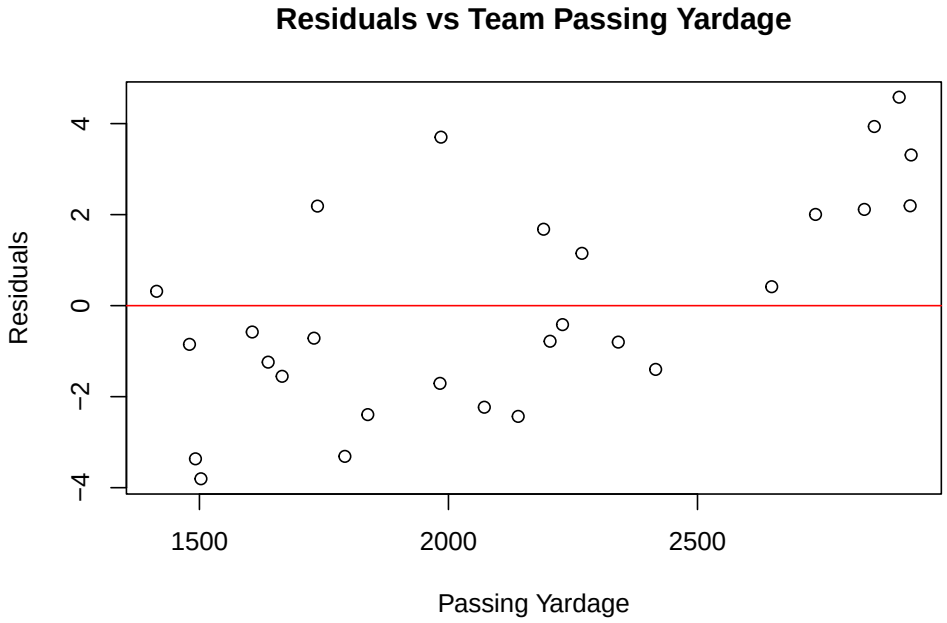
```
plot(fitted(model), residuals, main = "Residuals vs Fitted Value")
abline(h=0, col = 'red')
```



The model appears to be adequate since the residuals vs fitted values appear to be randomly distributed around 0, showing no patterns.

Part c.

```
residuals <- residuals(model)
plot(tableb1$x2, residuals, xlab="Passing Yardage",
     ylab="Residuals", main="Residuals vs Team Passing Yardage")
abline(h=0, col="red")
```



The model appears to be improved when adding x_2 since the residuals appear to be more close to 0.

Lack of Fit Example

We are going to use this data to conduct a lack of fit test.

x	1	1	2	3.3	3.3	4	4	4	4.7	5
y	10.84	9.30	16.35	22.88	24.35	24.56	25.86	29.16	24.59	22.25
x	5.6	5.6	5.6	6.0	6.0	6.5	6			
y	25.90	27.20	25.61	25.45	26.56	21.03	21.46			

We can count that there are $m = 10$ levels, and $n = 17$ observations, so

$$\sum_{i=1}^{n} n_i = 2 + 1 + 3 + \cdots = 17$$

We can compute then fit a model with this data in R,

```
x <- c(1,1,2,3.3,3.3,4,4,4,4.7,5,5.6,5.6,5.6,6,6,6.5,6)
y <- c(10.84 , 9.30 , 16.35 ,22.88  ,24.35 , 24.56, 25.86 ,29.16
      ,24.59, 22.25,25.90 , 27.20 , 25.61 , 25.45 , 26.56 , 21.03 ,21.46)
model <- lm(formula = y ~ x)
print(model)
```

```
##
## Call:
## lm(formula = y ~ x)
##
## Coefficients:
## (Intercept)            x
##      12.523        2.316
```

```
anova(model)
```

```
## Analysis of Variance Table
##
## Response: y
##           Df Sum Sq Mean Sq F value    Pr(>F)
## x          1 260.44 260.439  17.196 0.0008606 ***
## Residuals 15 227.17  15.145
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We get the linear model

$$\hat{y}_i = 12.5323 + 2.316x_i$$

Then, we can compute lack of fit and pure error with

$$SS_{PE} = \sum_{i=1}^{m}\sum_{j=1}^{n_i}(y_{ij} - \bar{y}_i)^2, SS_{LOF} = SSE - SS_{PE}$$

In R, we get

```r
library(EnvStats)
anovaPE(model)
```

```
##               Df  Sum Sq Mean Sq F value    Pr(>F)
## x              1 260.439 260.439 71.0262 2.996e-05 ***
## Lack of Fit    7 197.840  28.263  7.7078  0.004971 **
## Pure Error     8  29.334   3.667
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Our F-statistic is 7.70, and the critical value is $F_{\alpha,m-2,n-m}$, which we can compute in R or look at a table.

```r
qf(0.05, 8, 7, lower.tail=FALSE)
```

```
## [1] 3.725725
```

Therefore, we reject the null hypothesis $H_0 : E(y_i) = \beta_0 + \beta_1 x_i$.

Interprolating Values From Look-up Table

Say we want to find the t-value for t_{α_0} where α_0 is not located on the look up table, we then choose the 2 closest α values, call them α_1, α_2, so that $\alpha_1 < \alpha_0 < \alpha_2$. Then, we use the following formula to interprolate the t-value as

$$t_{\alpha_0} \approx t_{\alpha_1} + \frac{(\alpha_0 - \alpha_1)(t_{\alpha_2} - t_{\alpha_1})}{\alpha_2 - \alpha_1}$$

Example.

Suppose you have the critical value $\alpha_0 = 0.015$, the 2 closest values would be $\alpha_1 = 0.01$, and $\alpha_2 = 0.025$. So, we get

$$t_{0.015} \approx \frac{(0.015 - 0.01)(t_{0.025} - t_{0.01})}{0.025 - 0.01}$$

```r
noint <- lm(formula = y~ 0)
print(noint)
```

```
##
## Call:
## lm(formula = y ~ 0)
##
## No coefficients
```

```r
anova(noint)
```

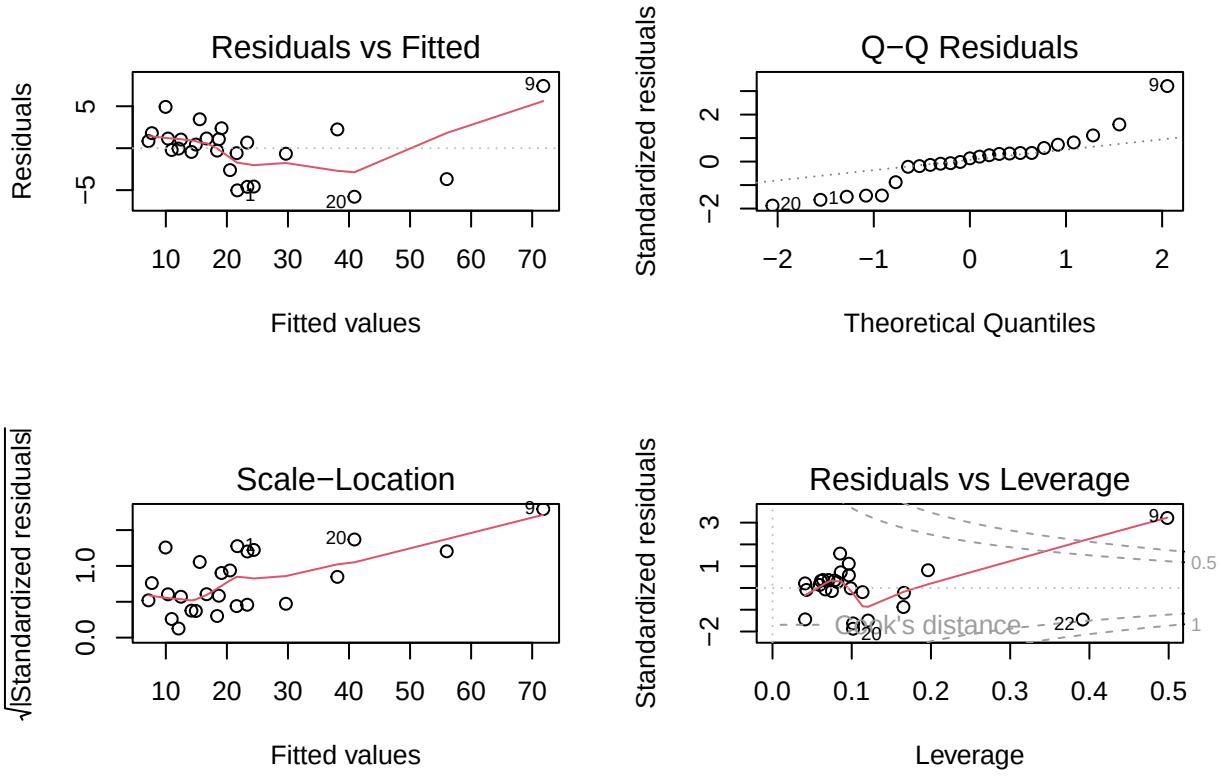
```
## Analysis of Variance Table
##
## Response: y
##           Df Sum Sq Mean Sq F value Pr(>F)
## Residuals 17 9132.2  537.19
```

Chapter 5 - Weighted Least Squared and Transformations

Example of checking for model adequecy with BP test

Using the delivery time data, we can examine the model adequecy of

```
delivery <- read.table("./Data/delivery.txt",header=TRUE, sep='\t')
X1 = delivery$Number.of.Cases
X2 = delivery$Distance
Y = delivery$Delivery.Time
fit = lm(Y~X1+X2, data=delivery)
par(mfrow=c(2,2))
plot(fit)
```



We can see in the qq-plot that the residuals do not follow the theoretical quantiles of a normal distribution, so there is likely an issue with the normality assumption of the model. The residuals vs fitted appear to have some pattern resembling a parabola.

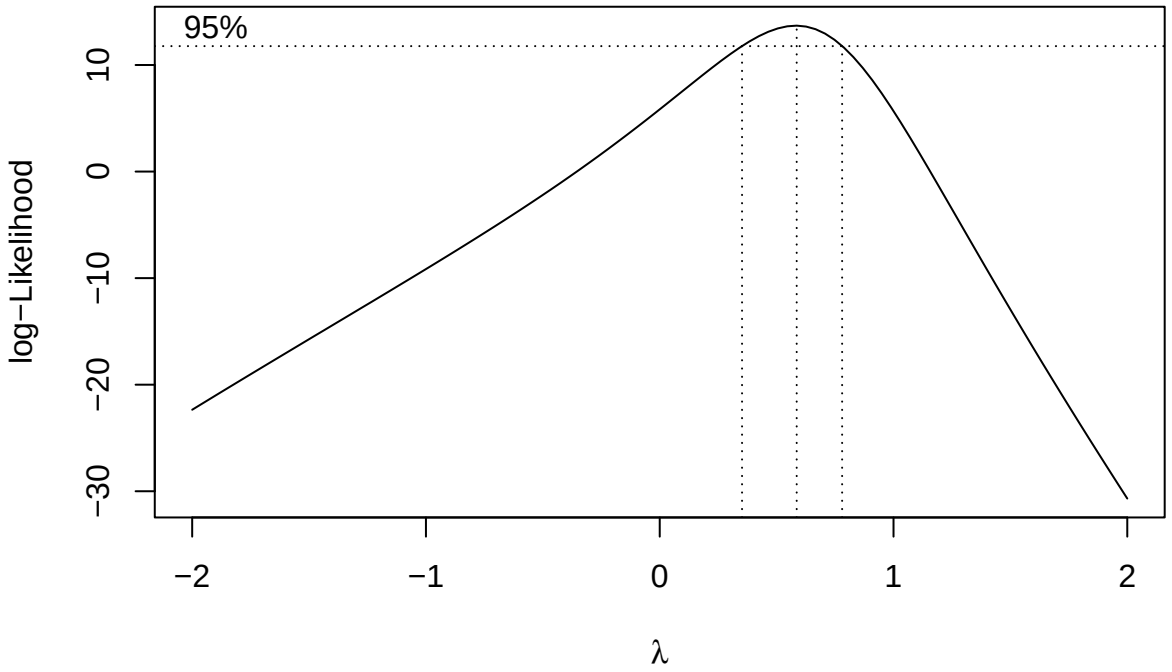
```
library(lmtest)
bptest(fit)
```

```
##
##  studentized Breusch-Pagan test
##
## data:  fit
## BP = 11.988, df = 2, p-value = 0.002493
```

We can see that the p-value that it is low, so we reject the null hypothesis that the variance is constant.

We can attempt to remede the issue with the residuals by applying a boxcox transformation.

```
library(MASS)
boxcox(fit)
b <- boxcox(fit)
```

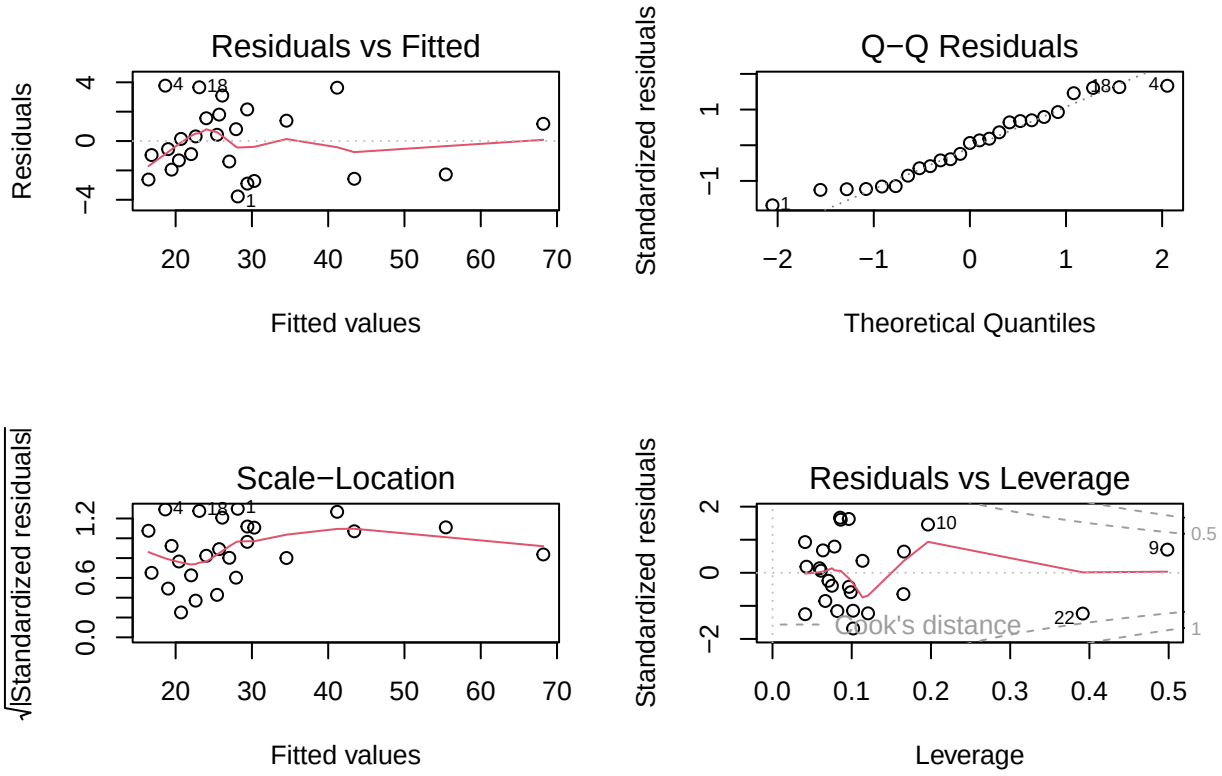



```
lambda <- b$x[which.max(boxcox(fit)$y)]
lambda
```

```
## [1] 0.5858586
```

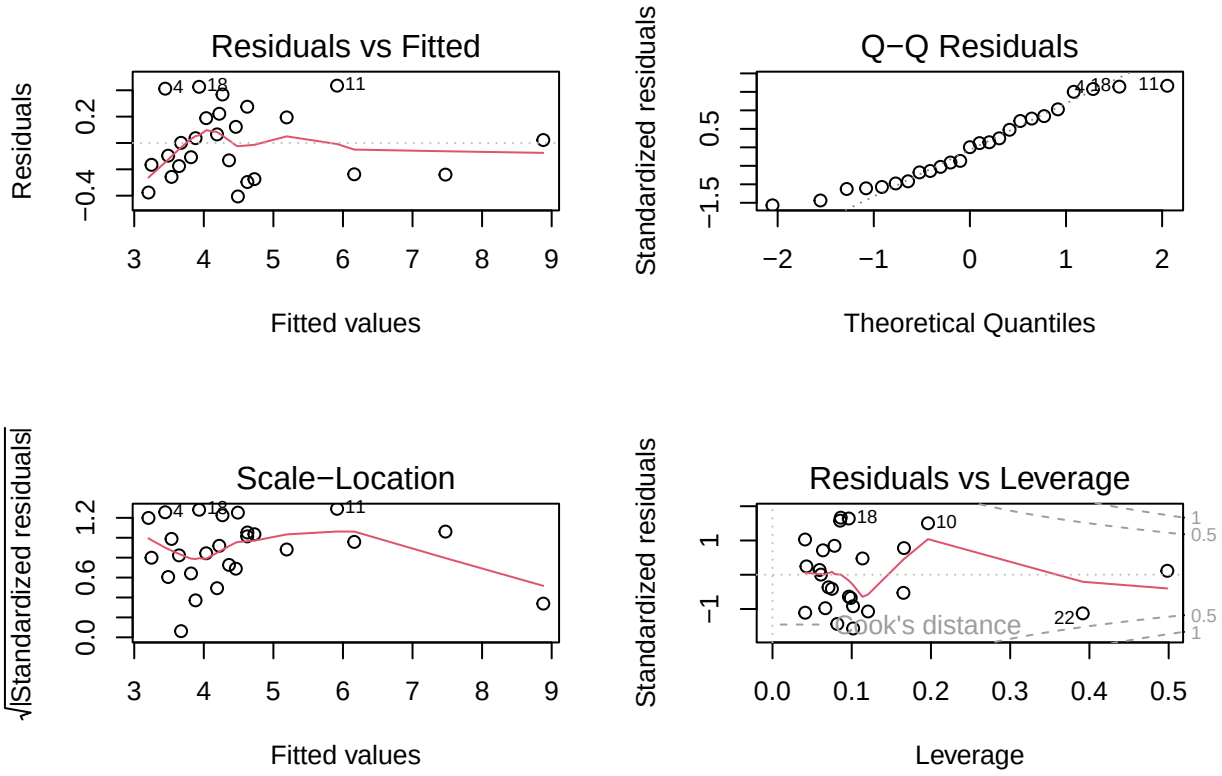
Now using our lambda value, we can transform y and refit the model,

```
n = length(Y)

y_dot <- exp(1/n * sum(log(Y)))

Y_transformed <- (Y^lambda - 1) / (lambda * y_dot^(lambda - 1))

new_model <- lm(Y_transformed ~ X1 + X2, data=delivery)

par(mfrow=c(2,2))

plot(new_model)
```



We can see that the qq-plot looks better now and the residuals appear fairly normally distributed, as well as the residuals vs fitted look more random, so we also can conclude that there is no longer an issue with the constant variance assumption. Another approach to this problem is to use another transformation on y. Since the reponse variable y is the time, which is count, the simplest probabilistic model for count data is the Poisson distribution, thus we transform $y' = \sqrt{y}$, and we plot this model.

```
y_prime <- sqrt(Y)

sqrt_y_model <- lm(y_prime ~ X1 + X2, data=delivery)

par(mfrow=c(2,2))

plot(sqrt_y_model)
```



We see that we get fairly similar results to the boxcox transformation, and can conlude the assumption of constant variance is no longer violated.

Example of Weighted Least Squares

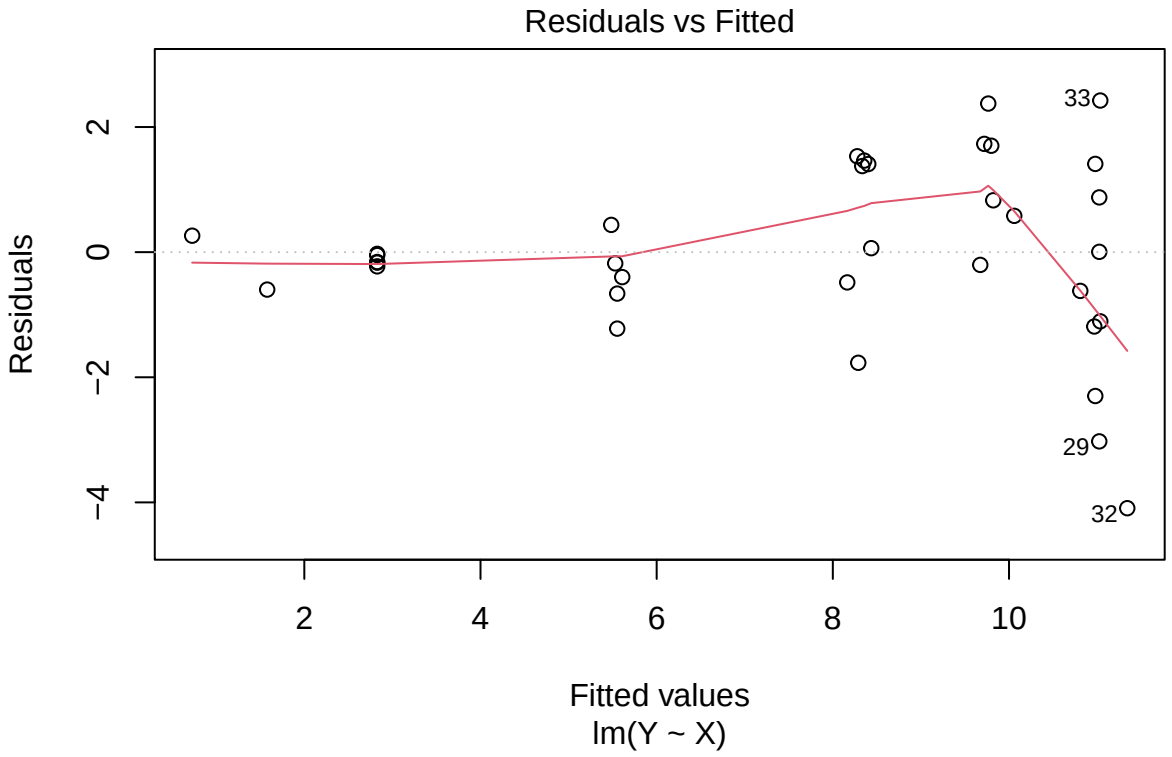
Using the weighted Turkey data, we can fit a model an examine the residuals.

```
turkey <- read.table("./Data/weighted.txt",header=TRUE, sep='\t')



fit <- lm(Y ~ X, data=turkey)

summary(fit)
```

```
##
## Call:
## lm(formula = Y ~ X, data = turkey)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.0928 -0.6087 -0.0473  1.1256  2.4238
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.57895    0.67919  -0.852      0.4
## X            1.13540    0.08622  13.169 1.09e-14 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.457 on 33 degrees of freedom
## Multiple R-squared:  0.8401, Adjusted R-squared:  0.8353
## F-statistic: 173.4 on 1 and 33 DF,  p-value: 1.089e-14
```

```
plot(fit,1)
```



As we can see, there appears to be a telescoping effect. One way to proceed is to perform the usual regression. Then, group the data using the X variable. Estimate the variances s_i^2 of the Y_i for each group. Then fit the variances against the averages of the X_i of the groups. Next we computed averages and variances for subsets of the data and then fitted the variances against the averages.

```
turkey
```

```
##         X     Y
## 1    1.15  0.99
## 2    1.90  0.98
## 3    3.00  2.60
## 4    3.00  2.67
## 5    3.00  2.66
## 6    3.00  2.78
## 7    3.00  2.80
## 8    5.34  5.92
## 9    5.38  5.35
## 10   5.40  4.33
## 11   5.40  4.89
```

```
## 12  5.45  5.21
## 13  7.70  7.68
## 14  7.80  9.81
## 15  7.81  6.52
## 16  7.85  9.71
## 17  7.87  9.82
## 18  7.91  9.81
## 19  7.94  8.50
## 20  9.03  9.47
## 21  9.07 11.45
## 22  9.11 12.14
## 23  9.14 11.50
## 24  9.16 10.65
## 25  9.37 10.64
## 26 10.17  9.78
## 27 10.18 12.39
## 28 10.22 11.03
## 29 10.22  8.00
## 30 10.22 11.90
## 31 10.18  8.68
## 32 10.50  7.25
## 33 10.23 13.46
## 34 10.03 10.19
## 35 10.23  9.93
```

We can see that we have many data points at 3, 5.4, 7.8, 9.1, and 10.2. These aren't perfect groupings but there are many points at this X value or very close to it, so we will use these as our groups. Now we can compute the variances at each of these points.

```
s1 <- round(var(turkey[turkey$X == 3, ]$Y),4)
s2 <- round(var(subset(turkey, X >= 5.34 & X <= 5.45)$Y),4)
s3 <- round(var(subset(turkey, X >= 7.7 & X <= 7.94)$Y),4)
s4 <- round(var(subset(turkey, X >= 9.03 & X <= 9.37)$Y),4)
s5 <- round(var(subset(turkey, X >= 10.03 & X <= 10.5)$Y),4)

s <- c(s1, s2, s3, s4, s5)

df <- data.frame(X = c(3, 5.4, 7.8, 9.1, 10.2), s = s)
df
```

```
##      X      s
## 1  3.0 0.0072
## 2  5.4 0.3440
## 3  7.8 1.7404
## 4  9.1 0.8683
## 5 10.2 3.8964
```

So now that we have our dataframe, we can fit a model with s as the response and the averages that we picked,

```r
fit2 <- lm(s ~ X + I(X^2), data=df)
summary(fit2)
```

```
##
## Call:
## lm(formula = s ~ X + I(X^2), data = df)
##
## Residuals:
##       1       2       3       4       5
## -0.1198  0.1980  0.5586 -1.2990  0.6621
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.53291    3.78395   0.405    0.725
## X           -0.73343    1.28494  -0.571    0.626
## I(X^2)       0.08826    0.09666   0.913    0.458
##
## Residual standard error: 1.116 on 2 degrees of freedom
## Multiple R-squared:  0.7427, Adjusted R-squared:  0.4853
## F-statistic: 2.886 on 2 and 2 DF,  p-value: 0.2573
```

Now, we have the regression model

$$\hat{s}^2 = 1.5329 - 0.7334\bar{X} + 0.0883\bar{X}^2$$

The weights are then computes as inverses of the predicted variances,

```r
weights <- 1/predict(fit2, newdata = data.frame(X = turkey$X))

weighted_model <- lm(Y ~ X, data=turkey, weights=weights)
summary(weighted_model)
```

```
##
## Call:
## lm(formula = Y ~ X, data = turkey, weights = weights)
##
## Weighted Residuals:
##     Min      1Q  Median      3Q     Max
## -2.8010 -0.5572  0.1544  0.9843  1.6397
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.88908    0.30058  -2.958  0.00569 **
## X            1.16469    0.05945  19.590  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.139 on 33 degrees of freedom
```

```
## Multiple R-squared:  0.9208, Adjusted R-squared:  0.9184
## F-statistic: 383.8 on 1 and 33 DF,  p-value: < 2.2e-16
```

The original model was

$$\hat{Y} = -0.579 + 1.14X$$

The new weighted model becomes

$$\hat{Y} = -0.89 + 1.16X$$

Chapter 6 - Regression Diagnostics and Measures of Influence

We will examine the bank dataset and fit a model to the data. Then examine the residuals and look for any outliers or influential points.

```
library(olsrr)
```

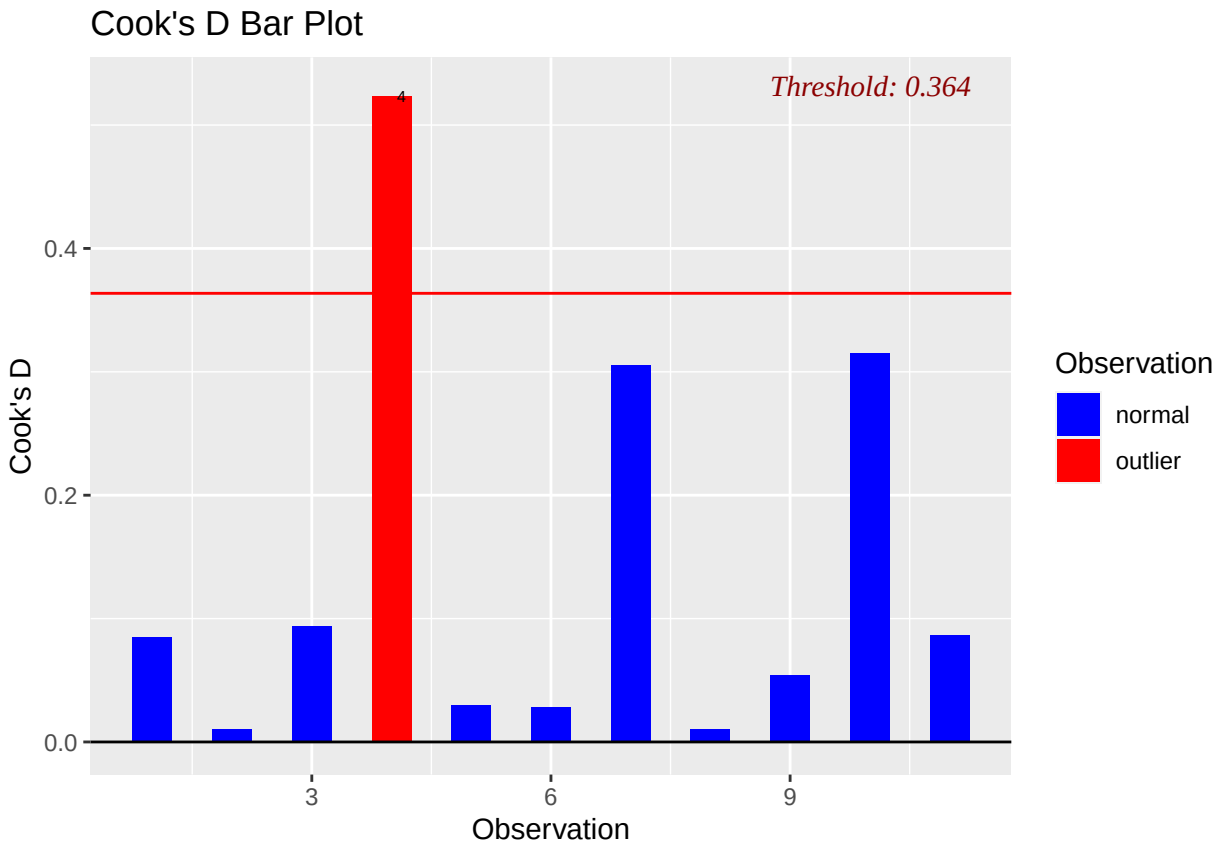
```
##
## Attaching package: 'olsrr'
```

```
## The following object is masked from 'package:MASS':
##
##     cement
```

```
## The following object is masked from 'package:MPV':
##
##     cement
```

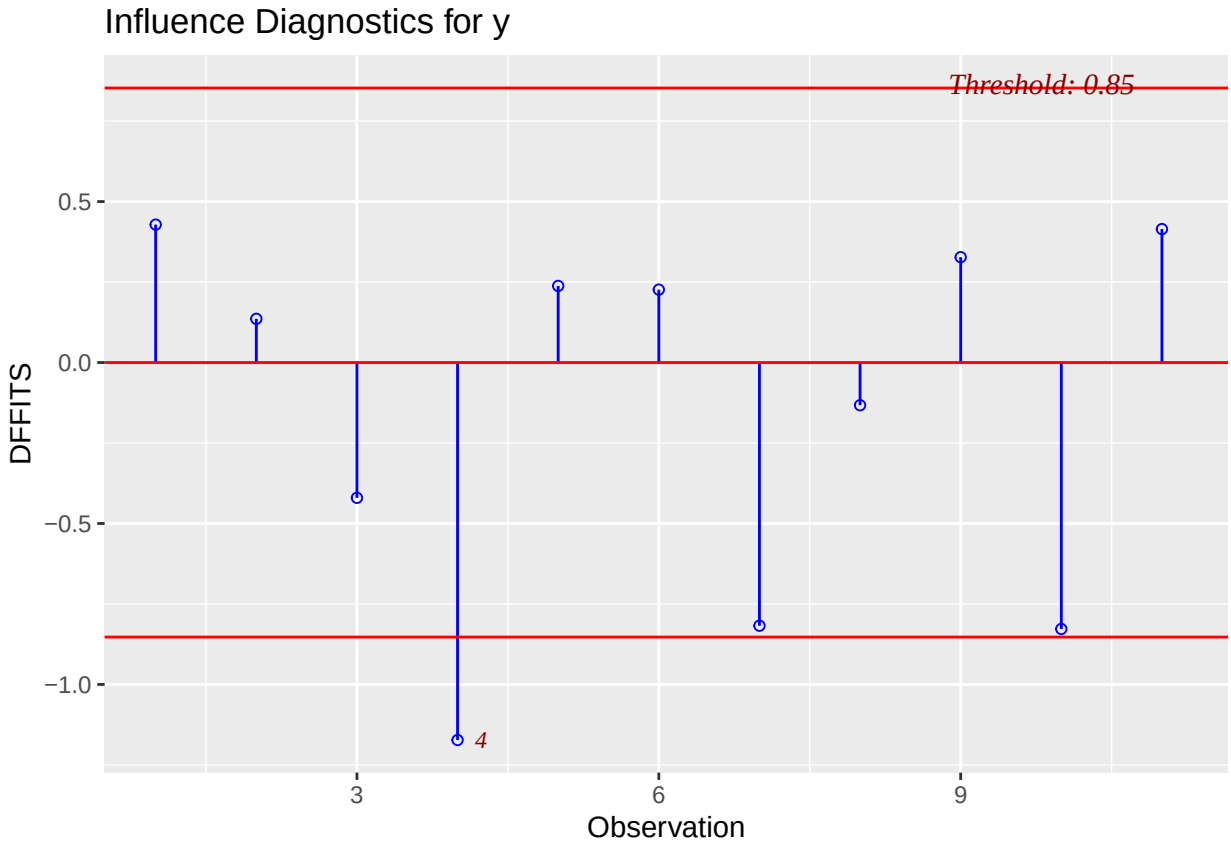
```
## The following object is masked from 'package:datasets':
##
##     rivers
```

```
bank <- read.table("./Data/bank.txt",header=TRUE, sep='\t')

y <- bank$Number.New.accounts
x <- bank$Minimum.Deposit
fit <- lm(y~x)
# Cook's Distance vs. Observations
ols_plot_cooksd_bar(fit)
```



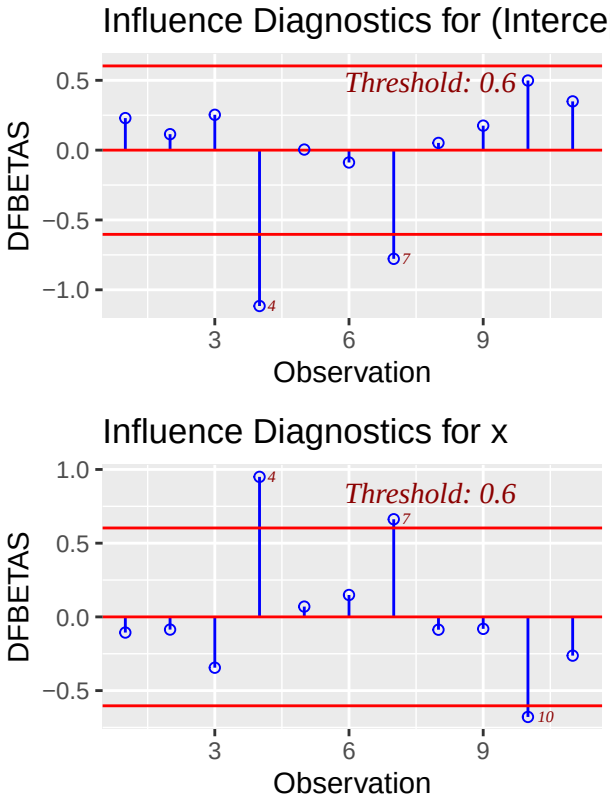
From the Cook's distant plot, we see that the 4th observation is influential on the fitted values at all X values. We can look at the plot for DFFITS,

```
ols_plot_dffits(fit)
```



We see again that the 4th observation is influential on the 4th fitted value of the model. We can also look at the DFBETAS plot,

```
ols_plot_dfbetas(fit)
```



From the DFBETAS vs Observation plots, we see that the 4th, 7th, and 10th observations are influential on the slope, and the 4th and 7th oberservations are influential on the intercept. To summarize, we can examine the measures of influence with

```
influence.measures(fit)
```

```
## Influence measures of
##   lm(formula = y ~ x) :
##
##      dfb.1_   dfb.x  dffit cov.r  cook.d    hat inf
## 1   0.22952 -0.1062  0.428 0.951 0.08506 0.0969
## 2   0.11433 -0.0860  0.136 1.454 0.01024 0.1518
## 3   0.25317 -0.3446 -0.420 1.566 0.09395 0.2775
## 4  -1.11603  0.9498 -1.173 0.787 0.52318 0.2644   *
## 5   0.00406  0.0698  0.238 1.241 0.02993 0.0995
## 6  -0.08838  0.1486  0.226 1.409 0.02790 0.1597
## 7  -0.77818  0.6623 -0.818 1.133 0.30507 0.2644
## 8   0.05173 -0.0870 -0.133 1.472 0.00977 0.1597
## 9   0.17533 -0.0811  0.327 1.108 0.05356 0.0969
## 10  0.49853 -0.6786 -0.828 1.171 0.31504 0.2775
## 11  0.34910 -0.2626  0.415 1.189 0.08634 0.1518
```

Chapter 7 - Polynomial and Indicator Regression

Example using Indicator Variables

We will use the turkey dataset

```
turkey <- read.table("./Data/turkey.txt",header=TRUE, sep='\t')
turkey
```

```
##    Age Weight Origin Z1 Z2
## 1   28   13.3      G  1  0
## 2   20    8.9      G  1  0
## 3   32   15.1      G  1  0
## 4   22   10.4      G  1  0
## 5   29   13.1      V  0  1
## 6   27   12.4      V  0  1
## 7   28   13.2      V  0  1
## 8   26   11.8      V  0  1
## 9   21   11.5      W  0  0
## 10  27   14.2      W  0  0
## 11  29   15.4      W  0  0
## 12  23   13.1      W  0  0
## 13  25   13.8      W  0  0
```

We can see that we have a catagorical variable "origin", which has 3 levels, G, V, and W. So, we create 2 dummy variables Z_1 and Z_2 to represent the levels. In this case, it was done for us with $(Z_1, Z_2) = (0,0) \implies W$, $(Z_1, Z_2) = (0,1) \implies V$, and $(Z_1, Z_2) = (1,0) \implies G$. 1 dummy variables allows for $2^1 = 2$ levels, 2 dummy variables gives us $2^2 = 4$ levels, and so on.

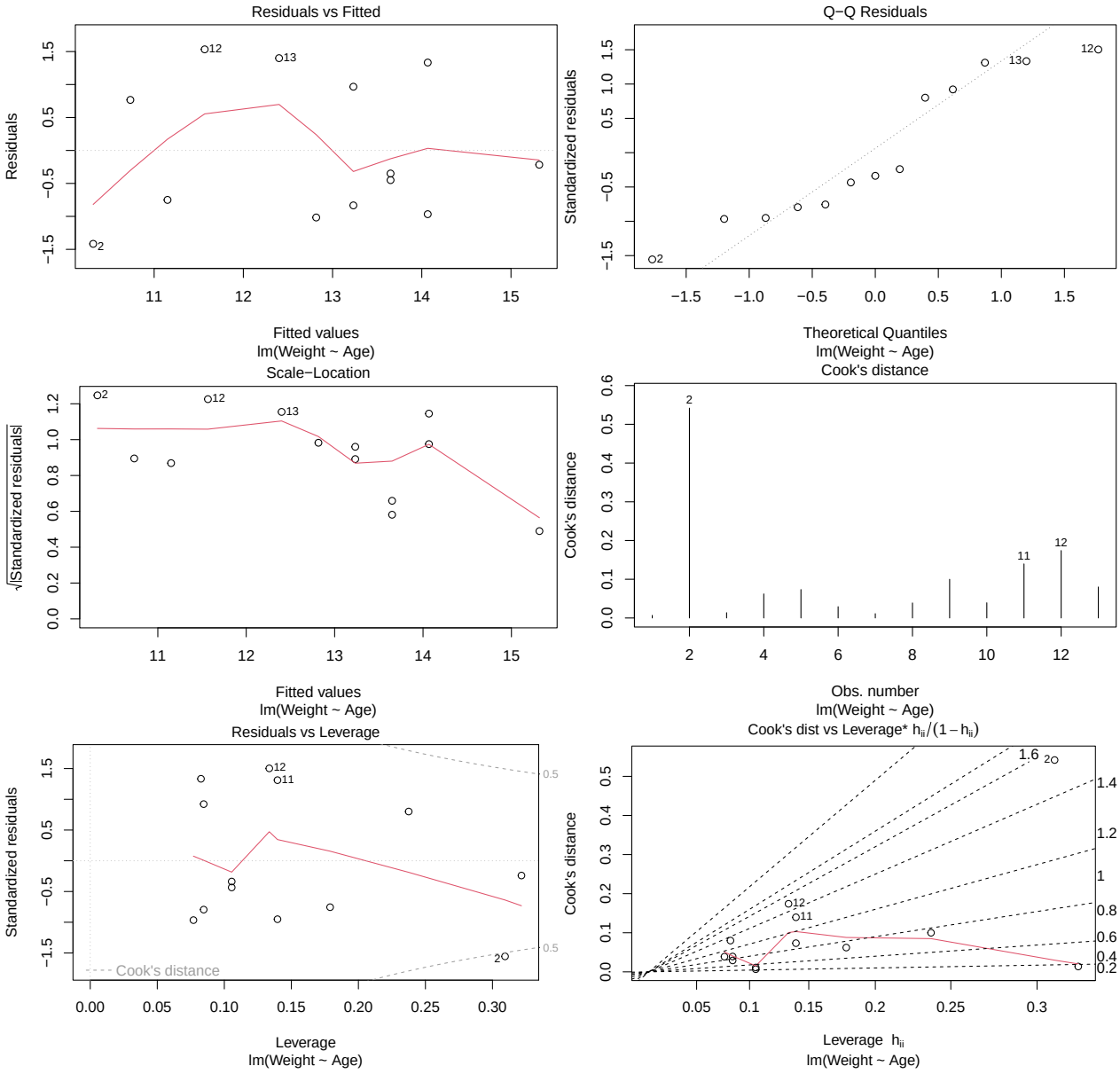
We can plot a model using just age and weight,

```
model1 <- lm(Weight ~ Age, data=turkey)
summary(model1)
```

```
##
## Call:
## lm(formula = Weight ~ Age, data = turkey)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.4167 -0.8333 -0.3500  0.9667  1.5333
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.98333    2.33273    0.85 0.413327
## Age          0.41667    0.08922    4.67 0.000682 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.096 on 11 degrees of freedom
## Multiple R-squared:  0.6647, Adjusted R-squared:  0.6343
```

```
## F-statistic: 21.81 on 1 and 11 DF,  p-value: 0.0006824
```

We see that there is a significant relationship between age and weight, the R^2 value is a bit low at 0.66, we can examine the model adequency.



We can see from the qq-plot, that the normally assumption of the residuals may not be reasonable. We can also see from the residuals vs fitted plot that there is a curve in the data, which tells us that our linear model may not be a good fit. Using the criteria that an observation is influential when Cook's distance $D_i > 1$, we see there are no influential points.

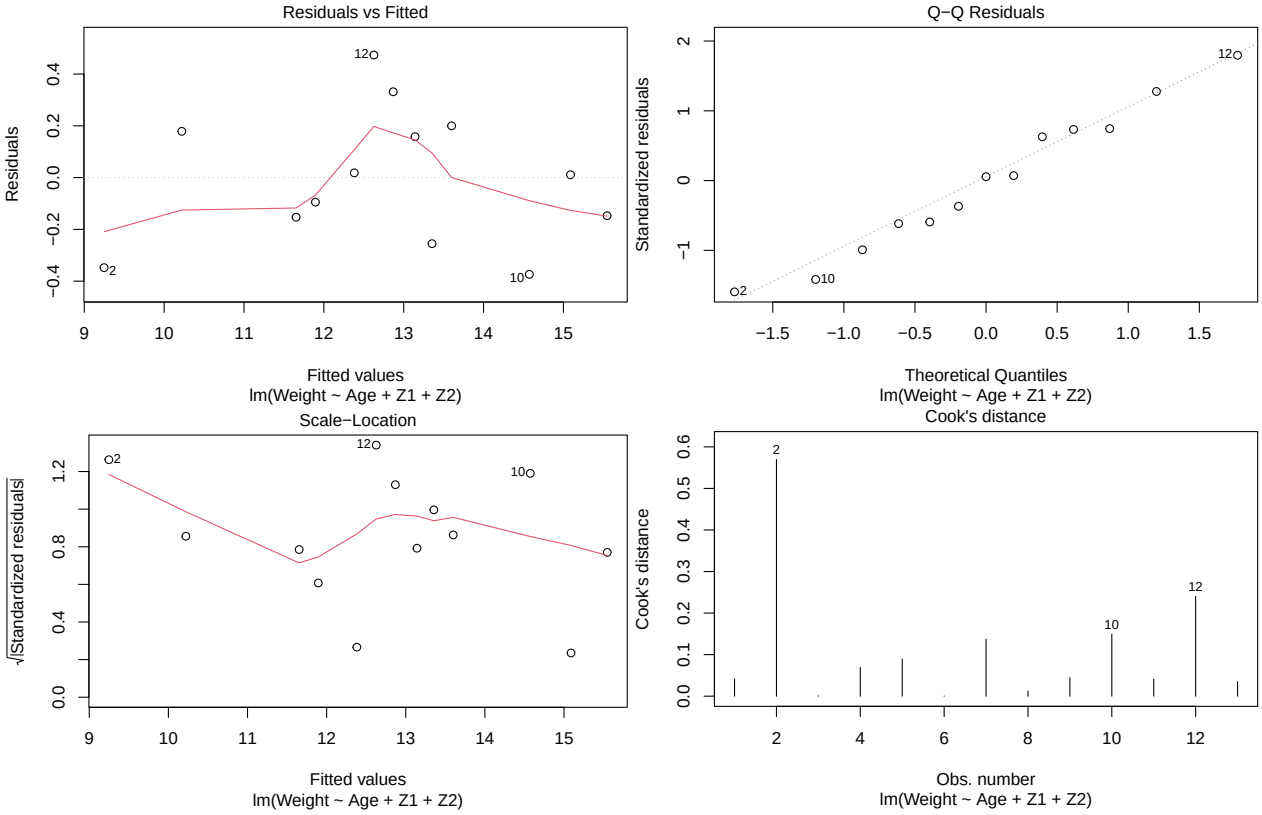
Now we can try fitting the model with our 2 dummy variables to see if it improves,

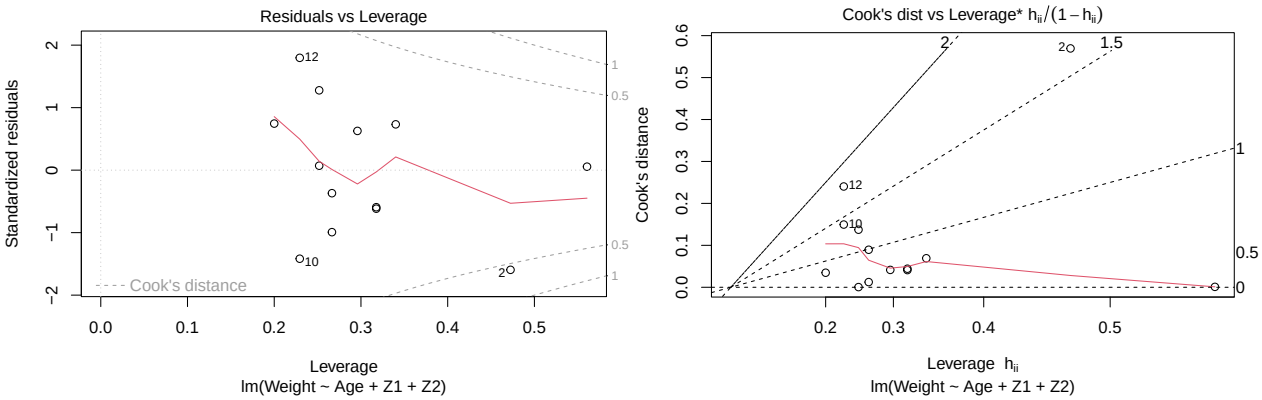
```
model2 <- lm(Weight ~ Age + Z1 + Z2, data=turkey)
summary(model2)
```

```
##
```

```
## Call:
## lm(formula = Weight ~ Age + Z1 + Z2, data = turkey)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.37353 -0.15294  0.01103  0.17868  0.47353
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.43088    0.65744   2.176   0.0575 .
## Age          0.48676    0.02574  18.908 1.49e-08 ***
## Z1          -1.91838    0.20180  -9.506 5.45e-06 ***
## Z2          -2.19191    0.21143 -10.367 2.65e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3002 on 9 degrees of freedom
## Multiple R-squared:  0.9794, Adjusted R-squared:  0.9726
## F-statistic: 142.8 on 3 and 9 DF,  p-value: 6.6e-08
```

We see that all the predictors are significant, and our R^2 value has increased significantly. We can examine the model adequency again,



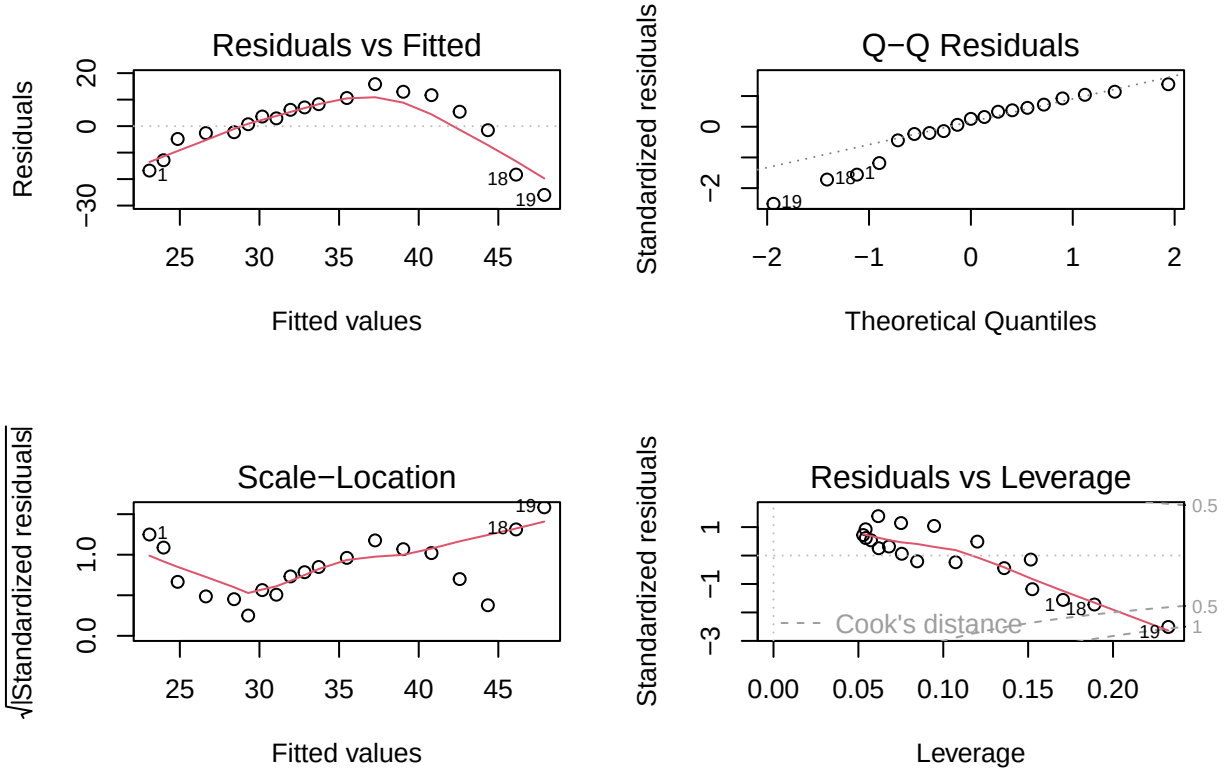


The qq-plot shows the assumption of normally distributed residuals is more reasonable now, and the residuals vs fitted is looking more random, however there still is a slight curve which could require more adjustments.

Example with Polynomial Regression

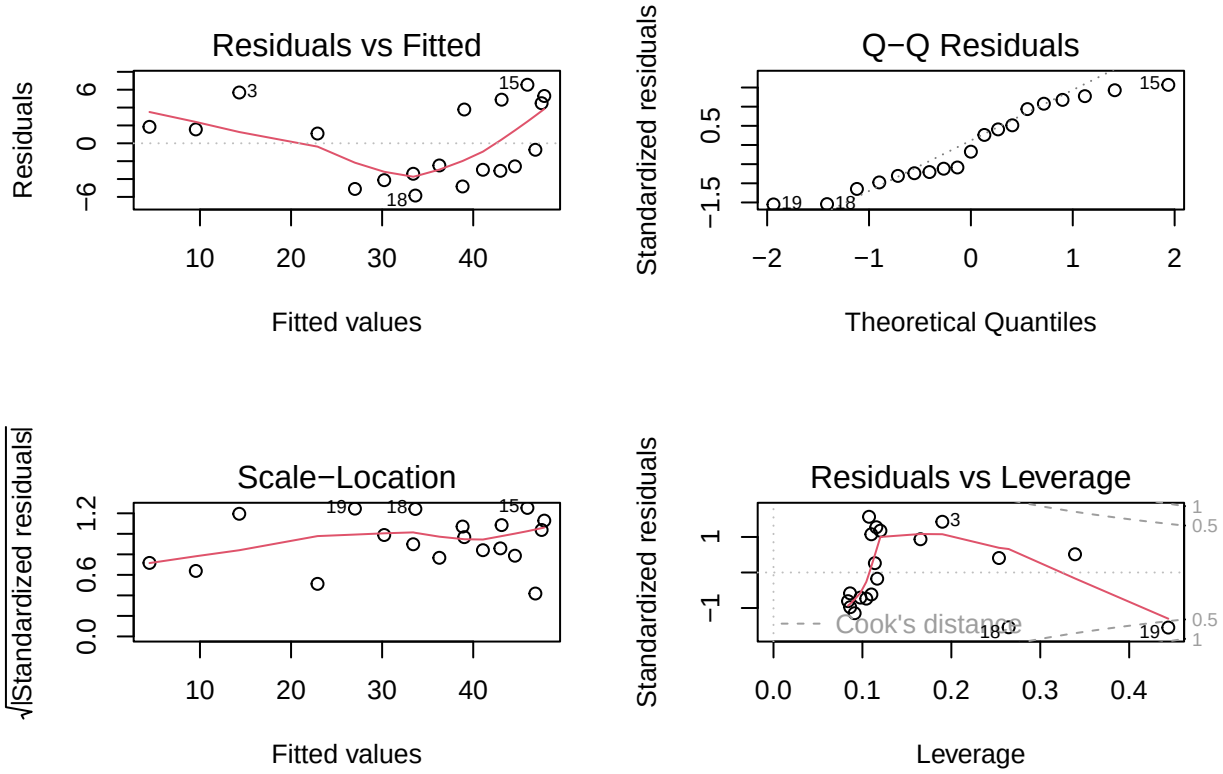
For this example we will use the hardwood dataset, we'll start by fitting a simple model and examining its adequecy,

```
hardwood <- read.table("./Data/hardwood.txt",header=TRUE, sep='\t')
x <- hardwood$Concentration
y <- hardwood$Tensile.Strength.Y
model1 <- lm(y ~ x)
par(mfrow=c(2,2))
plot(model1)
```



We can see from the residuals vs fitted, a very clear parabola shape is present, which indicates that there may be a non linear relationship our model is failing to account for. So, we will try to fit a quadratic model,

```
model2 <- lm(y ~ x + I(x^2))
par(mfrow=c(2,2))
plot(model2)
```



We can see now that the residuals vs fitted is slightly more random, however there is still a curve which indicates that there is evidence of a non linear relationship, and that the assumption of constant variance may not be reasonable. A higher order polynomial may be needed to fit the data better. We can also examine the differences in the R^2 values that we get from the 2 models,

```
summary(model1)$r.squared
```

```
## [1] 0.3053739
```

```
summary(model2)$r.squared
```

```
## [1] 0.908502
```

As we can see, the R^2 value for the quadratic model is much higher, so we can conclude that the quadratic model is a better fit.

Chapter 8 - Multicolinearity

We will use the acetylene dataset for this example.

```
acetylene <- read.table("./Data/acetylene.txt",header=TRUE, sep='\t')
acetylene
```

```
##    Acetylene Temperature Ratio Contact.Time
## 1       49.0        1300   7.5       0.0120
## 2       50.2        1300   9.0       0.0120
## 3       50.5        1300  11.0       0.0115
## 4       48.5        1300  13.5       0.0130
## 5       47.5        1300  17.0       0.0135
## 6       44.5        1300  23.0       0.0120
## 7       28.0        1200   5.3       0.0400
## 8       31.5        1200   7.5       0.0380
## 9       34.5        1200  11.0       0.0320
## 10      35.0        1200  13.5       0.0260
## 11      38.0        1200  17.0       0.0340
## 12      38.5        1200  23.0       0.0410
## 13      15.0        1100   5.3       0.0840
## 14      17.0        1100   7.5       0.0980
## 15      20.5        1100  11.0       0.0920
## 16      29.5        1100  17.0       0.0860
```

We want to consider the full quadratic model which takes into account the interactions as well, and we want each of the regression to be scaled using the unit normal scaling (subtract mean and divide by standard deviation).

```
P <- acetylene$Acetylene
T <- scale(acetylene$Temperature)
H <- scale(acetylene$Ratio)
C <- scale(acetylene$Contact.Time)

model <- lm(P ~ T + H + C + I(T^2) + I(H^2) + I(C^2) + T*H + T*C + H*C)
summary(model)
```

```
##
## Call:
## lm(formula = P ~ T + H + C + I(T^2) + I(H^2) + I(C^2) + T * H +
##     T * C + H * C)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.3499 -0.3411  0.1297  0.5011  0.6720
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  35.8958     1.0916  32.884 5.26e-08 ***
## T             4.0038     4.5087   0.888 0.408719
## H             2.7783     0.3071   9.048 0.000102 ***
## C            -8.0423     6.0707  -1.325 0.233461
## I(T^2)      -12.5236    12.3238  -1.016 0.348741
```

```
## I(H^2)       -0.9727     0.3746  -2.597 0.040844 *
## I(C^2)      -11.5932     7.7063  -1.504 0.183182
## T:H          -6.4568     1.4660  -4.404 0.004547 **
## T:C         -26.9804    21.0213  -1.283 0.246663
## H:C          -3.7681     1.6553  -2.276 0.063116 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.9014 on 6 degrees of freedom
## Multiple R-squared:  0.9977, Adjusted R-squared:  0.9943
## F-statistic: 289.7 on 9 and 6 DF,  p-value: 3.225e-07
```

This gives us our model

$$\hat{P} = 35.8958 + 4.0038T + 2.7783H - 8.0423C - 6.4568TH - 26.9804TC$$
$$-3.7681HC - 12.5236T^2 - 0.9727H^2 - 11.5932C^2$$

We can examine the correlation between our predictors

```
predictors <- c(T,H,C, T*H, T*C, H*C, T^2, H^2, C^2)

df <- data.frame(T, H, C, T*H, H*C, T*C, T^2, H^2, C^2)
round(cor(df), 3)
```

```
##            T      H      C  T...H  H...C  T...C    T.2    H.2    C.2
## T      1.000  0.224 -0.958 -0.132  0.206  0.443 -0.271  0.031 -0.577
## H      0.224  1.000 -0.240  0.039 -0.023  0.192 -0.148  0.498 -0.224
## C     -0.958 -0.240  1.000  0.195 -0.274 -0.661  0.501 -0.018  0.765
## T...H -0.132  0.039  0.195  1.000 -0.974 -0.265  0.246  0.398  0.275
## H...C  0.206 -0.023 -0.274 -0.974  1.000  0.324 -0.279 -0.375 -0.359
## T...C  0.443  0.192 -0.661 -0.265  0.324  1.000 -0.972  0.126 -0.972
## T.2   -0.271 -0.148  0.501  0.246 -0.279 -0.972  1.000 -0.124  0.894
## H.2    0.031  0.498 -0.018  0.398 -0.375  0.126 -0.124  1.000 -0.158
## C.2   -0.577 -0.224  0.765  0.275 -0.359 -0.972  0.894 -0.158  1.000
```

As we can see, there's high correlation between temperataure and contact time, and there are other large correlations between x_1x_2 and x_2x_3, x_1x_3 and x_1^2, and x_1^2 and x_3^3. This is not surprising since these variables are generated from the linear terms and involve highly correlated regressors x_1 and x_3.

We can compute the variance inflation factors for each of the predictors,

```
library(car)
vif(model)
```

```
##           T           H           C      I(T^2)      I(H^2)      I(C^2)
##  375.247759    1.740631  680.280039 1762.575365    3.164318 1156.766284
##         T:H         T:C         H:C
##   31.037059 6563.345193   35.611286
```

As we can see many of these have very high VIF, which certainly indicates multicollinearity. We can also compute the condition number κ and condition indices $\kappa_j = \frac{\lambda_{\max}}{\lambda_j}$. Note that λ_j are the eigenvalues for the matrix $X'X$.

```
eigen_values <- eigen(cor(df))$values
eigen_values
```

```
## [1] 4.205230e+00 2.161999e+00 1.138677e+00 1.040475e+00 3.852305e-01
## [6] 4.953807e-02 1.362526e-02 5.127803e-03 9.693644e-05
```

```
kappa <- max(eigen_values) / min(eigen_values)
kappa
```

```
## [1] 43381.31
```

```
kappa_j <- max(eigen_values) / eigen_values
kappa_j
```

```
## [1]     1.000000     1.945066     3.693085     4.041644    10.916141
## [6]    84.888858   308.634770   820.084287 43381.314197
```

As we can see, the condition number $\kappa = 43381.31$ is very large which indicates severe multicollinearity. The condition indices greater than 1000 indicate severe multicollinearity, those between 100 and 1000 indicate moderate to strong multicollinearity, and those bellow 100 have no indication of multicollinearity.

We can compute the tolerance values as well

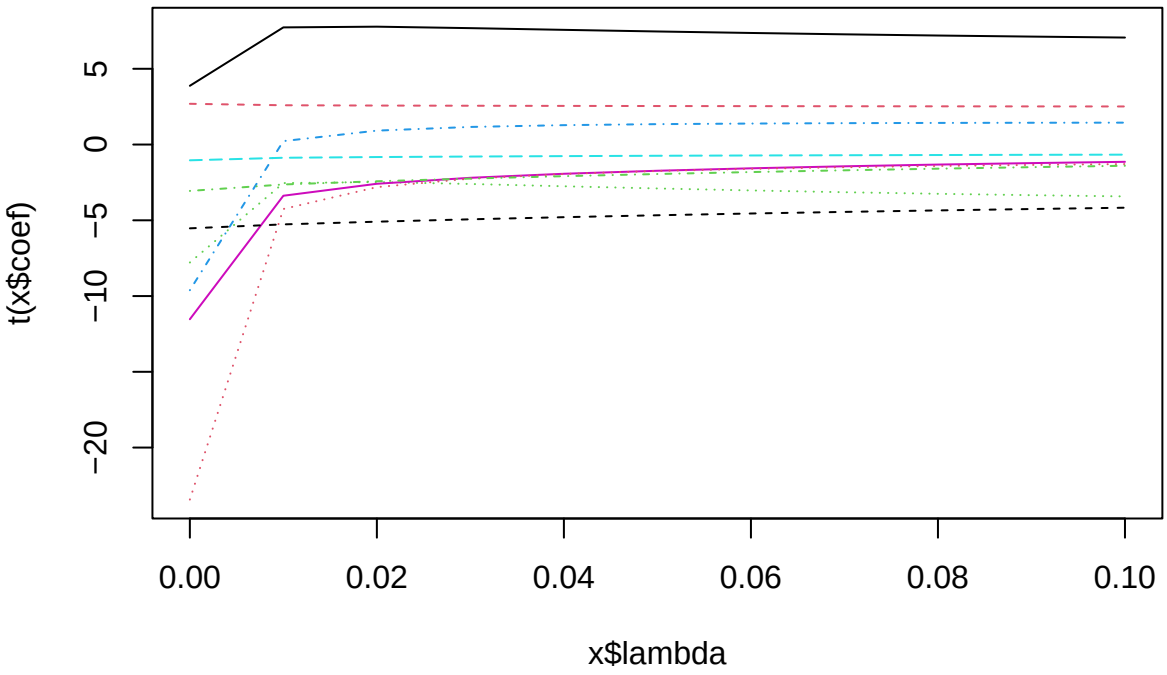
```
ols_coll_diag(model)$vif_t
```

```
##   Variables    Tolerance         VIF
## 1         T 0.0026649060  375.247759
## 2         H 0.5745042909    1.740631
## 3         C 0.0014699829  680.280039
## 4    I(T^2) 0.0005673516 1762.575365
## 5    I(H^2) 0.3160238460    3.164318
## 6    I(C^2) 0.0008644789 1156.766284
## 7       T:H 0.0322195480   31.037059
## 8       T:C 0.0001523613 6563.345193
## 9       H:C 0.0280809849   35.611286
```

Tolerance is the amount of variability in one independent variable that is not explained by the other independent variables. To compute it, regress the kth predictor on the other predictors in the model and compute the R^2 value, then Tolerance $= 1 - R^2$. Tolerance values less than 0.10 indicate collinearity.

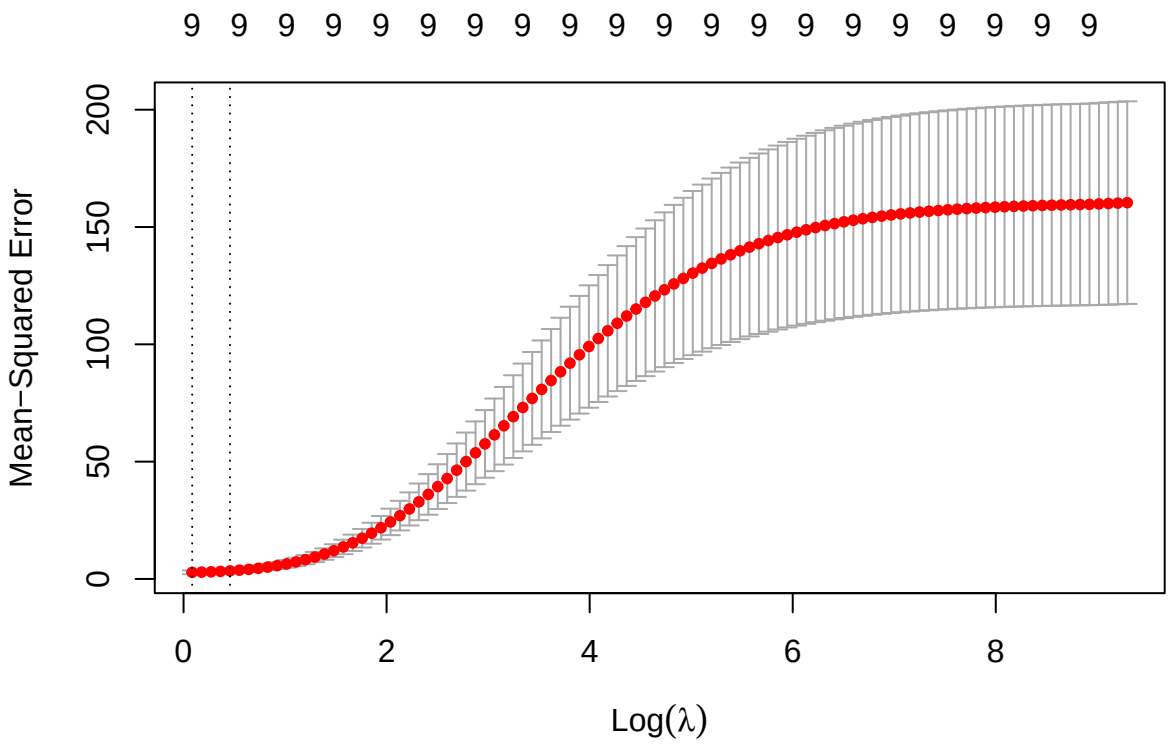
We can preform ridge regression now as well

```
ridge_model <- lm.ridge(P ~ T + H + C + I(T^2) + I(H^2) + I(C^2)
                        + T*H + T*C + H*C, lambda=seq(0,0.1,0.01))
plot(ridge_model)
```



The y axis represents the coefficient $\hat{\beta}_R$ which is the solution to the equation $(X'X + cI)\hat{\beta}_R = X'Y$, the x-axis is those values of c that we are looking for. We want to choose c large enough to provide stable coefficients but not too large. Now we want to preform cross validation and obtain the best value for c.

```
library(glmnet)

x = data.matrix(df)
y = P
model <- glmnet(x,y, alpha=0)
cv_model <- cv.glmnet(x,y, alpha=0)
plot(cv_model)
```



Now we can extract the optimal value of lambda and create the best model,

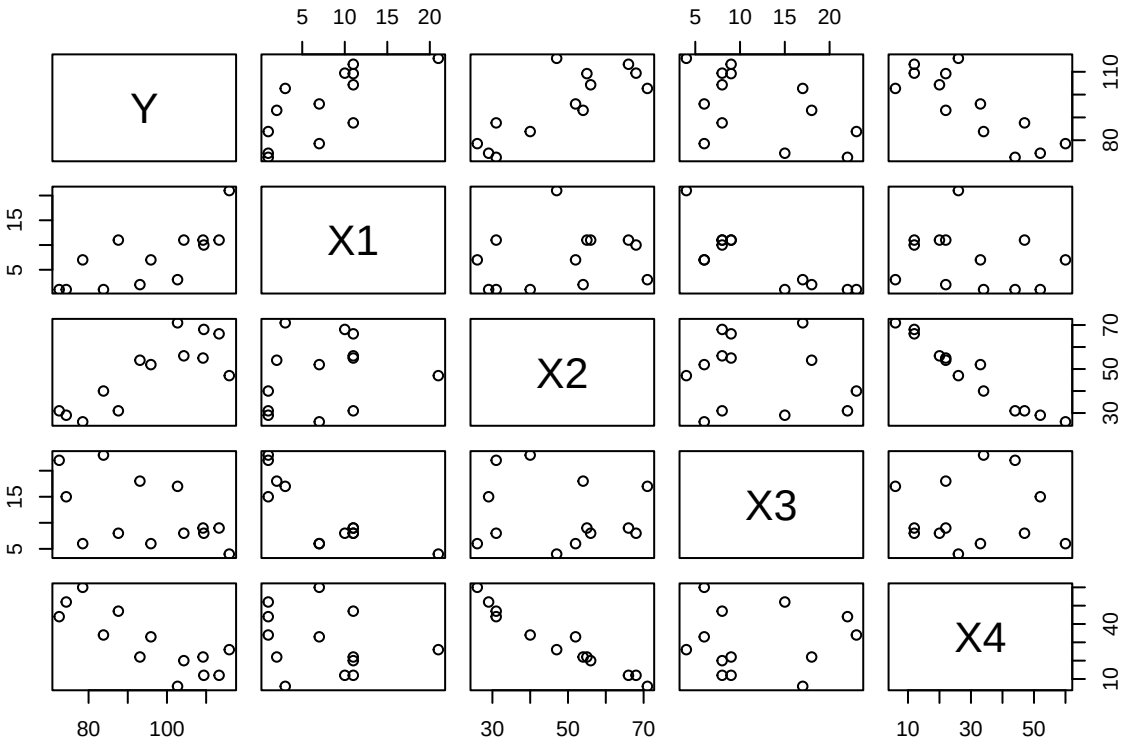
```
lambda <- cv_model$lambda.min
ridge_model <- glmnet(x,y, alpha=0, lambda=lambda)
coef(ridge_model)
```

```
## 10 x 1 sparse Matrix of class "dgCMatrix"
##                      s0
## (Intercept) 35.2178148
## T            5.8931581
## H            2.4034813
## C           -4.4901599
## T...H       -2.2227495
## H...C        1.0499186
## T...C       -0.6879354
## T.2          1.8762583
## H.2         -0.4899215
## C.2         -0.3485636
```

Chapter 9 - Model Selection

We will use the Hald Cement dataset for this example.

```
cement <- read.table("./Data/cement.txt",header=TRUE, sep='\t')
plot(cement)
```



Looking at the scatterplots, we can see there may be some multicollinearity between X_2 and X_4. Examining this further we find

```
cor(cement)
```

```
##              Y         X1         X2         X3         X4
## Y   1.0000000  0.7307175  0.8162526 -0.5346707 -0.8213050
## X1  0.7307175  1.0000000  0.2285795 -0.8241338 -0.2454451
## X2  0.8162526  0.2285795  1.0000000 -0.1392424 -0.9729550
## X3 -0.5346707 -0.8241338 -0.1392424  1.0000000  0.0295370
## X4 -0.8213050 -0.2454451 -0.9729550  0.0295370  1.0000000
```

```
model <- lm(Y ~ X1 + X2 + X3 + X4, data=cement)
ols_coll_diag(model)$vif_t
```

```
##   Variables   Tolerance       VIF
## 1        X1 0.025976582  38.49621
## 2        X2 0.003930460 254.42317
## 3        X3 0.021336344  46.86839
## 4        X4 0.003539662 282.51286
```

We can see that there is severe multicollinearity between X_2 and X_4 and shown by the tolerance being less than 0.1 for both, as well as a very large VIF. We can also see that X_1 and X_3 have a large correlation and also high VIF and low tolerance.

This suggests we want to try models that do not include all the predictotrs. We first try all possible regressions,

```
ols_step_all_possible(model)
```

```
##    Index N  Predictors  R-Square Adj. R-Square Mallow's Cp
## 4      1 1          X4 0.6745420     0.6449549  138.730833
## 2      2 1          X2 0.6662683     0.6359290  142.486407
## 1      3 1          X1 0.5339480     0.4915797  202.548769
## 3      4 1          X3 0.2858727     0.2209521  315.154284
## 5      5 2       X1 X2 0.9786784     0.9744140    2.678242
## 7      6 2       X1 X4 0.9724710     0.9669653    5.495851
## 10     7 2       X3 X4 0.9352896     0.9223476   22.373112
## 8      8 2       X2 X3 0.8470254     0.8164305   62.437716
## 9      9 2       X2 X4 0.6800604     0.6160725  138.225920
## 6     10 2       X1 X3 0.5481667     0.4578001  198.094653
## 12    11 3    X1 X2 X4 0.9823355     0.9764473    3.018233
## 11    12 3    X1 X2 X3 0.9822847     0.9763796    3.041280
## 13    13 3    X1 X3 X4 0.9812811     0.9750415    3.496824
## 14    14 3    X2 X3 X4 0.9728200     0.9637599    7.337474
## 15    15 4 X1 X2 X3 X4 0.9823756     0.9735634    5.000000
```

We can see that the model with 3 predictors X_1,X_2, and X_4 has the C_p value closest to the number of predictors, as well as one of the highest R^2 values. However, we know there is strong multicollinearity between X_2 and X_4, and the model with X_1, X_2 and X_3 had a slightly higher C_p value and a similar R^2. But, we run into the same issue since we know X_1 and X_3 have multicollinearity, so the next best option would be the model with only X_1 and X_2. It has a lower R^2 value but it is still very high at 0.979, and the C_p value is 2.67 which is also close to the number of predictors. So, we will select the model with X_1 and X_2.

Now using best subset selection,

```
ols_step_best_subset(model)
```

```
##  Best Subsets Regression
## --------------------------
## Model Index    Predictors
## --------------------------
##      1         X4
##      2         X1 X2
##      3         X1 X2 X4
##      4         X1 X2 X3 X4
## --------------------------
##
##                                                    Subsets Regression Summary
## ------------------------------------------------------------------------------------------------
##                         Adj.        Pred
## Model    R-Square    R-Square    R-Square      C(p)        AIC       SBIC        SBC
## ------------------------------------------------------------------------------------------------
##   1        0.6745      0.6450      0.5603    138.7308    97.7440    55.5401    99.4389    10
##   2        0.9787      0.9744      0.9654      2.6782    64.3124    29.2437    66.5722
##   3        0.9823      0.9764      0.9686      3.0182    63.8663    31.1723    66.6910
##   4        0.9824      0.9736      0.9594      5.0000    65.8367    34.4130    69.2264
## ------------------------------------------------------------------------------------------------
```

```
## AIC: Akaike Information Criteria
##  SBIC: Sawa's Bayesian Information Criteria
##  SBC: Schwarz Bayesian Criteria
##  MSEP: Estimated error of prediction, assuming multivariate normality
##  FPE: Final Prediction Error
##  HSP: Hocking's Sp
##  APC: Amemiya Prediction Criteria
```

We can see that the best model in terms of the C_p statistic and the R^2 value is again the model with X_1, X_2 and X_4. But, as we previously mentioned this model suffers from multicollinearity due to X_2 and X_4 being present. So, we pick the second best model which is X_1 and X_2 again.

Now using forward selection,

```
ols_step_forward_p(model)
```

```
##
##                             Selection Summary
## ------------------------------------------------------------------------
##         Variable                    Adj.
## Step    Entered     R-Square    R-Square      C(p)        AIC        RMSE
## ------------------------------------------------------------------------
##    1    X4            0.6745      0.6450    138.7308    97.7440    8.9639
##    2    X1            0.9725      0.9670      5.4959    67.6341    2.7343
##    3    X2            0.9823      0.9764      3.0182    63.8663    2.3087
## ------------------------------------------------------------------------
```

We can see that first X_4 was entered, then X_1, then X_2 resulting in the same model that we saw was the best in the previous 2 methods. However, selecting this model would lead to multicollinearity as we've discussed.

With backwards elimination,

```
ols_step_backward_p(model)
```

```
##
##
##                           Elimination Summary
## ------------------------------------------------------------------------
##         Variable                    Adj.
## Step    Removed     R-Square    R-Square     C(p)       AIC       RMSE
## ------------------------------------------------------------------------
##    1    X3            0.9823      0.9764    3.0182    63.8663    2.3087
## ------------------------------------------------------------------------
```

We can see that we only removed X_3, giving us the same model again X_1, X_2 and X_3.

Now using stepwise selection,

```
ols_step_both_p(model)
```

```
##
##                              Stepwise Selection Summary
```

```
## ----------------------------------------------------------------------------------
##                       Added/                   Adj.
## Step    Variable     Removed     R-Square    R-Square      C(p)        AIC       RMSE
## ----------------------------------------------------------------------------------
##    1       X4       addition       0.675       0.645    138.7310    97.7440    8.9639
##    2       X1       addition       0.972       0.967      5.4960    67.6341    2.7343
##    3       X2       addition       0.982       0.976      3.0180    63.8663    2.3087
## ----------------------------------------------------------------------------------
```

Once again, we end up with X_1, X_2 and X_4.

Chapter 10 - Logistic Regression and GLM's

Example of Logistic Regression

We'll fit a logistic regression model to the prgoramming experience dataset.

```
experience <- read.table("./Data/experience.txt",header=TRUE, sep='\t')

mlogit <- glm(Success ~ Experience, data=experience, family="binomial")
summary(mlogit)
```

```
##
## Call:
## glm(formula = Success ~ Experience, family = "binomial", data = experience)
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.05970    1.25935  -2.430   0.0151 *
## Experience   0.16149    0.06498   2.485   0.0129 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 34.296  on 24  degrees of freedom
## Residual deviance: 25.425  on 23  degrees of freedom
## AIC: 29.425
##
## Number of Fisher Scoring iterations: 4
```

We can see from the summary that our equation for our logistic regression model

$$\hat{\pi} = \frac{\exp(-3.05970 + 0.16149X_i)}{1 + \exp(-3.05970 + 0.16149X_i)}$$

And we conclude that the regression is significant so we reject the null hypothesis $H_0 : \beta_1 = 0$. We can compute the confidence intervals using

$$\hat{\beta}_j \pm z_{\alpha/2} se(\hat{\beta}_j)$$

We can find the z value with

```
qnorm(0.025, lower.tail=FALSE)
```

```
## [1] 1.959964
```

So the confidence intervals are

$$-3.05970 \pm 1.960 \cdot 1.25935 = (-5.528026, -0.591374)$$

$$0.16149 \pm 1.960 \cdot 0.06498 = (0.0341292, 0.2888508)$$

```
confint.default(mlogit)
```

```
##                    2.5 %     97.5 %
## (Intercept) -5.52797622 -0.5914155
## Experience   0.03412744  0.2888444
```

As we can see we get the same outputs in R (slightly off due to inaccuracy from lookup table).

We can also construct a confidence interval on the odds ratio, with (e^{0.0341292}, e^{0.2888508}),

```
exp(0.0341292)
```

```
## [1] 1.034718
```

```
exp(0.2888508)
```

```
## [1] 1.334893
```

```
exp(cbind(OR = coef(mlogit), confint.default(mlogit)))
```

```
##                      OR       2.5 %    97.5 %
## (Intercept) 0.04690196 0.003974024 0.5535432
## Experience  1.17525591 1.034716464 1.3348840
```

As we can see we obtain the same answer of (1.035, 1.335) for the confidence interval on the odds ratio.

Example of Poisson Regression

We will use the aircraft damage dataset for this example and fit a Poisson regression model.

```
aircraft <- read.table("./Data/aircraft.txt",header=TRUE, sep='\t')
model <- glm(Y ~ X1 + X2 + X3, data=aircraft, family="poisson")
summary(model)
```

```
##
## Call:
## glm(formula = Y ~ X1 + X2 + X3, family = "poisson", data = aircraft)
```

```
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept) -0.406023   0.877489  -0.463   0.6436
## X1           0.568772   0.504372   1.128   0.2595
## X2           0.165425   0.067541   2.449   0.0143 *
## X3          -0.013522   0.008281  -1.633   0.1025
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 53.883  on 29  degrees of freedom
## Residual deviance: 25.953  on 26  degrees of freedom
## AIC: 87.649
##
## Number of Fisher Scoring iterations: 5
```

This gives us our poisson regression model

$$Y_i = \exp(-0.406023 + 0.568772X_{i1} + 0.165425X_{i2} - 0.013522X_{i3})$$

We can examine now if the model has over dispersion or under dispersion. If the residual deviance is greater than the degrees of freedom, then we have over dispersion. This means that the estimates are correct, but the standard errors (standard deviation) are wrong and unaccounted for by the model.

The Null deviance shows how well the response variable is predicted by a model that includes only the intercept (grand mean) whereas residual with the inclusion of independent variables.