YK_Final_P4

Yinan Kang

5/14/2019

```
rm(list=ls())
df.4 <- read.csv("/cloud/project/Question 4.csv")
```

Fit Model

```
require(lmtest)
```

```
## Loading required package: lmtest
```

```
## Loading required package: zoo
```

```
##
## Attaching package: 'zoo'
```

```
## The following objects are masked from 'package:base':
##
##     as.Date, as.Date.numeric
```

```
require(Hmisc)
```

```
## Loading required package: Hmisc
```

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

```
## Loading required package: survival
```

```
## Loading required package: Formula
```

```
## Loading required package: ggplot2
```

```
## Registered S3 methods overwritten by 'ggplot2':
##   method         from
##   [.quosures     rlang
##   c.quosures     rlang
##   print.quosures rlang
```

```
##
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
model.4 <- lm(Y~., data=df.4)
dwtest(model.4)
```

```
##
##  Durbin-Watson test
##
## data:  model.4
## DW = 1.9618, p-value = 0.2903
## alternative hypothesis: true autocorrelation is greater than 0
```

**Using Durbin Watson test, we find that there is no autocorrelation present* *

Using Cochrane-Orcutt Procedure

```
# et <- model.4$residuals
# et1 <- Lag(et,shift=1)
#
# d1 <- sum(na.omit((et1)*et))
# d2 <- sum(na.omit(et1)^2)
# rho <- d1/d2
#
# Ytnew <- df.4$Y - rho*Lag(df.4$Y,shift=1)
# X1tnew <- df.4$X1 - rho*Lag(df.4$X1,shift=1)
# X2tnew <- df.4$X2 - rho*Lag(df.4$X2,shift=1)
# X3tnew <- df.4$X3 - rho*Lag(df.4$X3,shift=1)
# X4tnew <- df.4$X4 - rho*Lag(df.4$X4,shift=1)
# X5tnew <- df.4$X5 - rho*Lag(df.4$X5,shift=1)
# X6tnew <- df.4$X6 - rho*Lag(df.4$X6,shift=1)
#
# model.new <- lm(Ytnew ~ X1tnew + X2tnew + X3tnew + X4tnew + X5tnew + X6tnew)
#
# dwtest(model.new)
```

YK_Final_P2

Yinan Kang

5/13/2019

```
require(dplyr)
require(leaps)
require(neuralnet)
require(readxl)
require(caret)
require(car)
require(rpart)
```

Problem 2

Load Data

```
rm(list=ls())
df <- read.csv("/cloud/project/Question 2.csv")
```

Split Data

```
set.seed(12345)
trainIndex <- createDataPartition(df$Y, p=0.7, list=FALSE)

train.df <- df[trainIndex,]
test.df <- df[-trainIndex,]
```

Fit Model with Development sample (a.k.a. 'train.df')

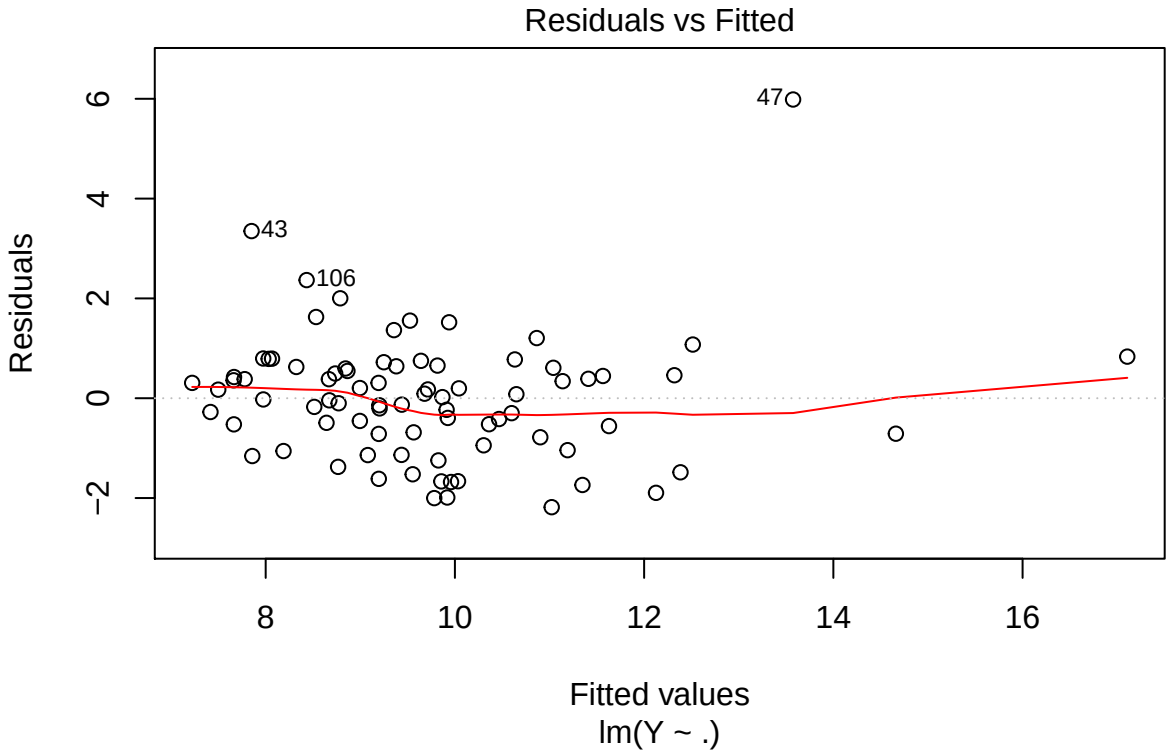
(a)

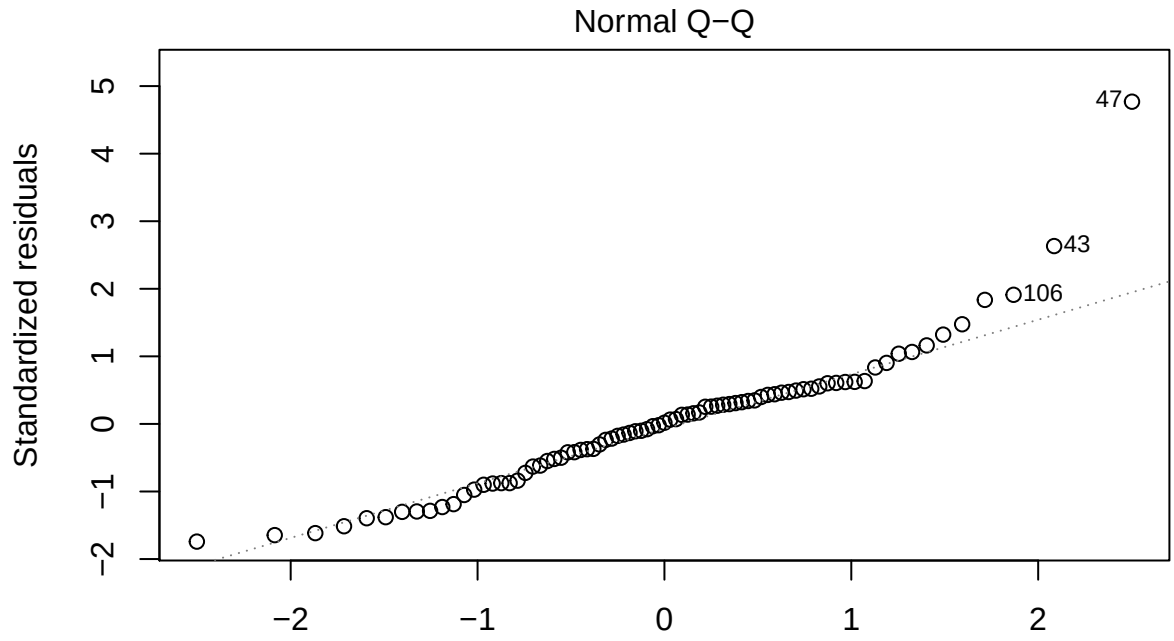
```
model <- lm(Y~. , data=train.df)

# Residual Analysis and Model Significance
summary(model)
```

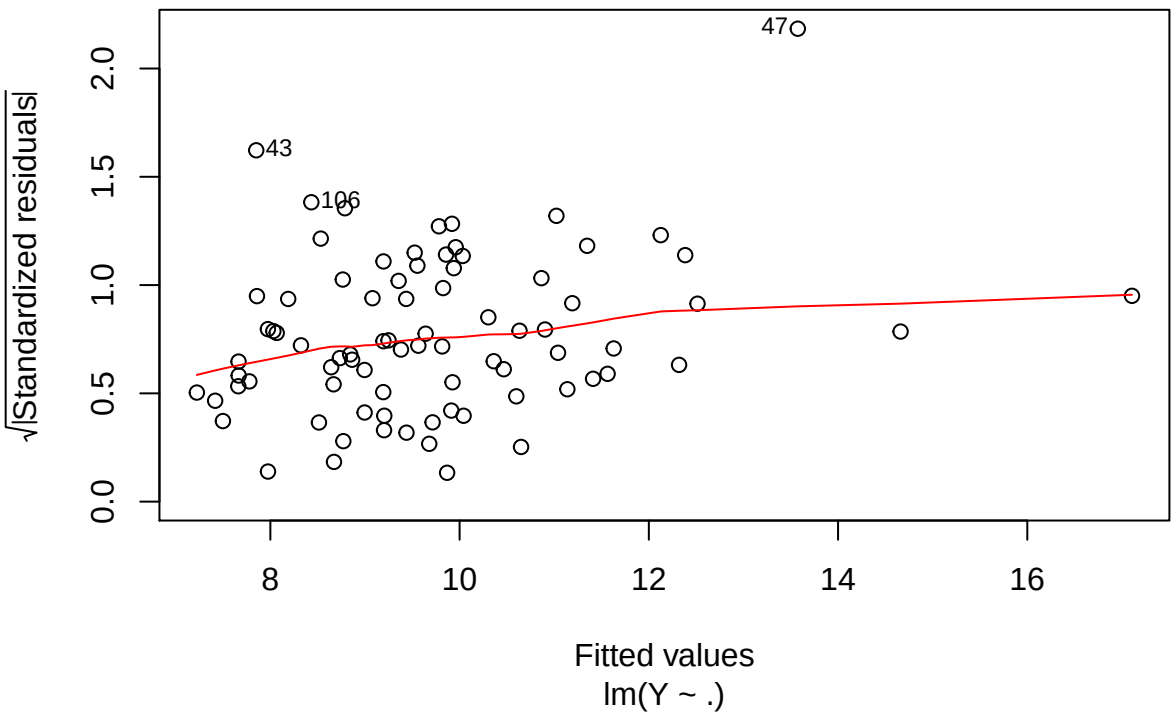
```
##
## Call:
## lm(formula = Y ~ ., data = train.df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.1832 -0.7152  0.0220  0.6097  5.9856
##
## Coefficients:
```

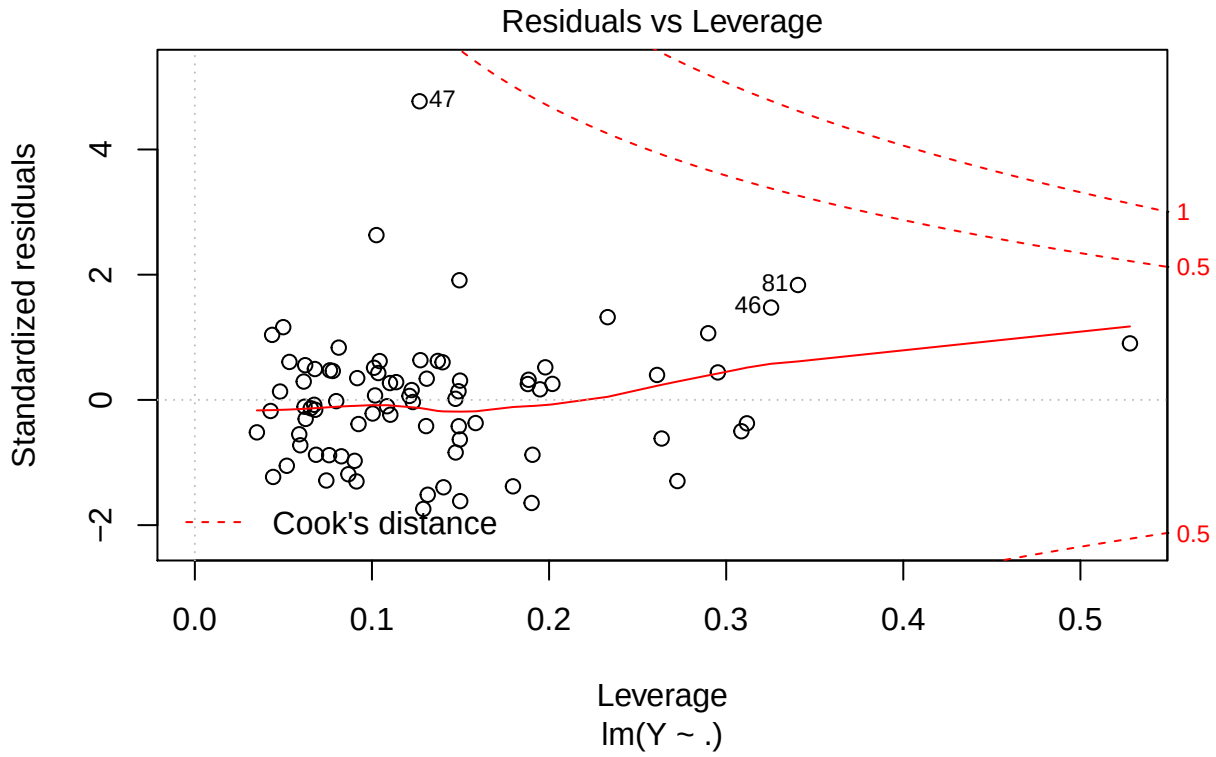
```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.5097992  2.5712076   0.976  0.33237
## X1           0.0851752  0.0355052   2.399  0.01911 *
## X2           0.4778835  0.1740312   2.746  0.00766 **
## X3           0.0006345  0.0221793   0.029  0.97726
## X4           0.0132255  0.0089821   1.472  0.14539
## X5          -0.0103232  0.0057853  -1.784  0.07869 .
## X6          -0.1159227  0.5899833  -0.196  0.84480
## X7          -0.4528421  0.1938593  -2.336  0.02236 *
## X8           0.0216602  0.0063384   3.417  0.00106 **
## X9          -0.0065853  0.0031066  -2.120  0.03757 *
## X10          0.0078747  0.0191298   0.412  0.68186
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.343 on 70 degrees of freedom
## Multiple R-squared:  0.6363, Adjusted R-squared:  0.5843
## F-statistic: 12.24 on 10 and 70 DF,  p-value: 6.101e-12
```

```
plot(model)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(Y ~ .)
47
43
106
−2
−1
0
1
2
3
4
5


Scale−Location
√|Standardized residuals|
Fitted values
lm(Y ~ .)
47
43
106
0.0
0.5
1.0
1.5
2.0
8
10
12
14
16




```
# Multicollinearity
vif(model)
```

```
##        X1        X2        X3        X4        X5        X6        X7
##  1.105343  2.405521  2.186076  1.570451 53.297022  2.234402  1.560107
##        X8        X9       X10
## 43.156298  8.085746  3.734094
```

```
mean(vif(model))
```

```
## [1] 11.93351
```

Analysis of (a): Upon seeing the overall summary model statistics, we find that overall, the model has a p-value = 6.101e-12, so overall the model IS statistically significant. The adj-R2 = 0.5843, which (without knowing context of dataset) we can generally say is between OK and mediocre variance accountability.

We see from the residual plot and the QQ-Normality plot that: * there is no severe normality issue (though a few noticeable observations - #43, #47)
* overall there is constant variance of the residuals

Multicollinearity: From the Variance Inflation Factor analysis, we find that there is relatively severe multicollinearity with the current model. Predictors X5 and X8 have VIF values >10, and overall the mean VIF = 11.93, which is >1 (benchmark).

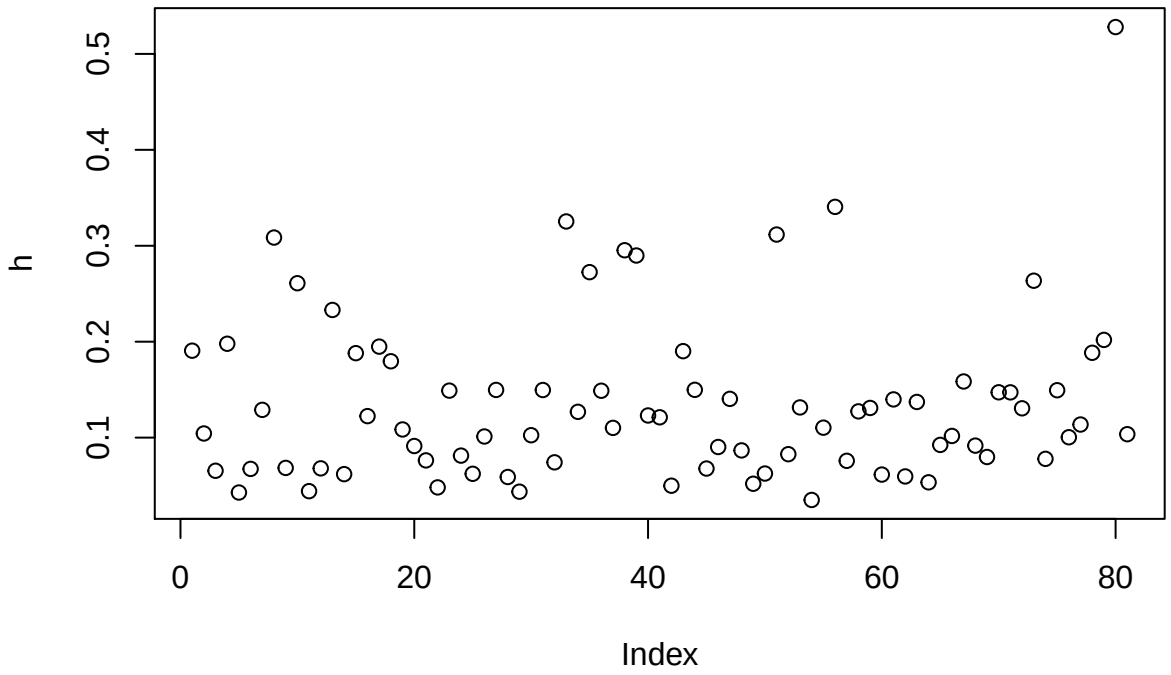
(b) Outliers and Influentials

```
summary(influence.measures(model))
```

```
## Potentially influential observations of
##   lm(formula = Y ~ ., data = train.df) :
##
```

```
##     dfb.1_ dfb.X1 dfb.X2 dfb.X3 dfb.X4 dfb.X5 dfb.X6 dfb.X7 dfb.X8 dfb.X9
## 11    0.06  -0.05   0.15  -0.09  -0.11  -0.03  -0.04   0.04   0.05  -0.17
## 13    0.00   0.08   0.06   0.05  -0.03   0.01  -0.11  -0.06  -0.05   0.06
## 43    0.49  -0.72  -0.14  -0.26   0.25  -0.14   0.02   0.18   0.17  -0.22
## 47   -0.83   0.66   0.89  -0.72   0.51  -0.43   0.31  -0.47   0.56  -0.33
## 52   -0.04   0.00  -0.01   0.05  -0.11   0.15   0.12  -0.05  -0.15   0.03
## 74   -0.05   0.00   0.04  -0.08   0.03   0.02   0.13   0.00   0.00   0.07
## 81    0.80  -0.59   0.08  -0.32  -0.13   0.49  -0.71  -0.20  -0.43  -0.76
## 104   0.23  -0.17  -0.06   0.07  -0.16   0.03  -0.06  -0.01  -0.06   0.10
## 112  -0.08   0.12  -0.15   0.22  -0.03  -0.33   0.00   0.05   0.60  -0.29
##     dfb.X10 dffit   cov.r   cook.d hat
## 11    0.04   -0.33    1.63_*  0.01   0.31
## 13   -0.04    0.24    1.55_*  0.01   0.26
## 43    0.22    0.93    0.41_*  0.07   0.10
## 47    0.21    2.20_*  0.02_*  0.30   0.13
## 52    0.01    0.28    1.61_*  0.01   0.30
## 74   -0.14   -0.25    1.67_*  0.01   0.31
## 81    0.37    1.34_*  1.03    0.16   0.34
## 104  -0.12   -0.37    1.50_*  0.01   0.26
## 112  -0.09    0.95    2.18_*  0.08   0.53_*
```

```r
# For hat values: 2p/n
p <- 10
n <- nrow(train.df)

h <- lm.influence(model)$hat
plot(h)
```



Influential Analysis: We displayed the key influential determination statistics (Cook's Distance, DFFITS, Hat, etc.). We also plotted the Hat values for a visual comparison.

The approximate threshold to be considered a highly influential case for Hat values was '2p/n' = 0.25. Some observations crossed this threshold slightly, but only Case 112 truly did (noticeable from plot as well, where it's Hat=0.53). For DFFITS, the threshold is '1', but those that crossed this threshold did not show high

leverage in the other metrics.

Thus, I would point to Case 112 as the only really influential case.

(c) Can X5, X6, X7 be dropped?

Note: I am assuming question is asking can X5, X6, X7 be dropped together from the model, as opposed to one-by-one

```
model.light <- lm(Y~X1+X2+X3+X4+X8+X9+X10, data=train.df)
anova(model.light, model)
```

```
## Analysis of Variance Table
##
## Model 1: Y ~ X1 + X2 + X3 + X4 + X8 + X9 + X10
## Model 2: Y ~ X1 + X2 + X3 + X4 + X5 + X6 + X7 + X8 + X9 + X10
##   Res.Df    RSS Df Sum of Sq      F  Pr(>F)
## 1     73 145.63
## 2     70 126.28  3    19.347 3.5748 0.01816 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Analysis: If we go by the alpha = 0.05 level... NO, we can't drop X5,X6,X7 as p-value < 0.05, indicating statistical significance.

(But, if we were to utilize the alpha = 0.01 level, then the opposite conclusion would be valid.)

(d) Regression Tree

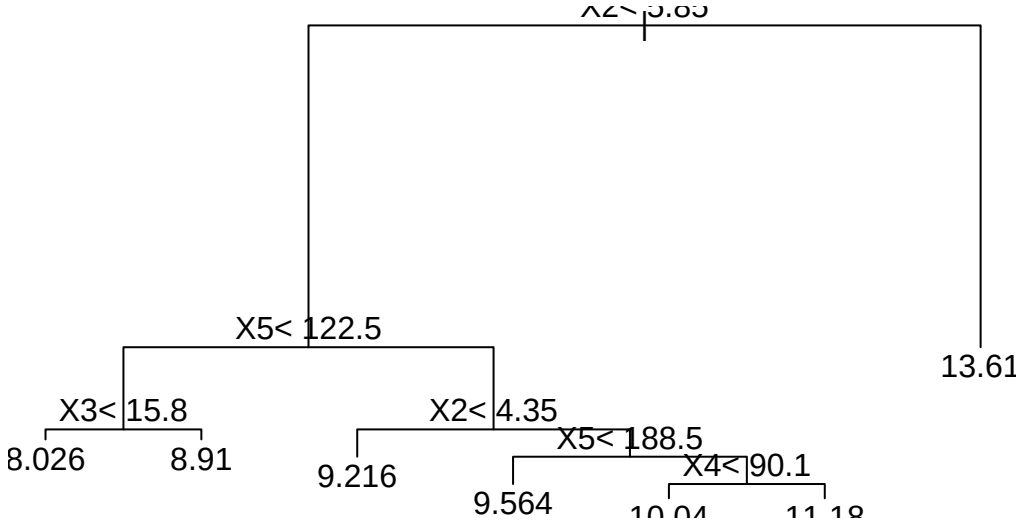
```
model.reg <- rpart(Y~., data=train.df)
summary(model.reg)
```

```
## Call:
## rpart(formula = Y ~ ., data = train.df)
##   n= 81
##
##           CP nsplit rel error    xerror      xstd
## 1 0.38600137      0 1.0000000 1.0264650 0.3458540
## 2 0.09857913      1 0.6139986 0.9862689 0.2675827
## 3 0.03068474      2 0.5154195 0.7569987 0.2040399
## 4 0.01534651      3 0.4847348 0.7790316 0.2047835
## 5 0.01201516      5 0.4540417 0.8028815 0.2049651
## 6 0.01000000      6 0.4420266 0.8013606 0.2049183
##
## Variable importance
##  X2  X3  X5  X9  X8 X10  X1  X4  X7
##  44  12  12  10   9   7   2   2   1
##
## Node number 1: 81 observations,    complexity param=0.3860014
##   mean=9.724568, MSE=4.286047
##   left son=2 (73 obs) right son=3 (8 obs)
##   Primary splits:
##       X2  < 5.85  to the left,  improve=0.3860014, (0 missing)
```

```
##       X5  < 305   to the left,  improve=0.2580972, (0 missing)
##       X8  < 250   to the left,  improve=0.2571419, (0 missing)
##       X10 < 50    to the left,  improve=0.2402275, (0 missing)
##       X9  < 130.5 to the left,  improve=0.2019305, (0 missing)
##   Surrogate splits:
##       X3 < 44    to the left,  agree=0.926, adj=0.25, (0 split)
##
## Node number 2: 73 observations,    complexity param=0.09857913
##   mean=9.298767, MSE=1.659033
##   left son=4 (24 obs) right son=5 (49 obs)
##   Primary splits:
##       X5  < 122.5 to the left,  improve=0.2825850, (0 missing)
##       X9  < 99.5  to the left,  improve=0.2800819, (0 missing)
##       X8  < 66.5  to the left,  improve=0.2545677, (0 missing)
##       X10 < 30    to the left,  improve=0.1981774, (0 missing)
##       X2  < 4.25  to the left,  improve=0.1954625, (0 missing)
##   Surrogate splits:
##       X8  < 94    to the left,  agree=0.945, adj=0.833, (0 split)
##       X9  < 83    to the left,  agree=0.918, adj=0.750, (0 split)
##       X10 < 35.7  to the left,  agree=0.863, adj=0.583, (0 split)
##       X2  < 2.85  to the left,  agree=0.795, adj=0.375, (0 split)
##       X1  < 55.95 to the right, agree=0.726, adj=0.167, (0 split)
##
## Node number 3: 8 observations
##   mean=13.61, MSE=11.50655
##
## Node number 4: 24 observations,    complexity param=0.01201516
##   mean=8.320417, MSE=0.8548457
##   left son=8 (16 obs) right son=9 (8 obs)
##   Primary splits:
##       X3  < 15.8  to the left,  improve=0.20331650, (0 missing)
##       X10 < 30    to the left,  improve=0.15790380, (0 missing)
##       X8  < 60    to the left,  improve=0.14193620, (0 missing)
##       X1  < 52.75 to the left,  improve=0.10585500, (0 missing)
##       X2  < 2.75  to the left,  improve=0.07611349, (0 missing)
##   Surrogate splits:
##       X1  < 50    to the right, agree=0.708, adj=0.125, (0 split)
##       X4  < 81.65 to the left,  agree=0.708, adj=0.125, (0 split)
##       X7  < 1.5   to the right, agree=0.708, adj=0.125, (0 split)
##       X9  < 73    to the left,  agree=0.708, adj=0.125, (0 split)
##       X10 < 32.85 to the left,  agree=0.708, adj=0.125, (0 split)
##
## Node number 5: 49 observations,    complexity param=0.03068474
##   mean=9.777959, MSE=1.354477
##   left son=10 (20 obs) right son=11 (29 obs)
##   Primary splits:
##       X2 < 4.35  to the left,  improve=0.16050800, (0 missing)
##       X4 < 96    to the left,  improve=0.10494870, (0 missing)
##       X8 < 212   to the left,  improve=0.09400911, (0 missing)
##       X5 < 183   to the left,  improve=0.08514898, (0 missing)
##       X7 < 2.5   to the right, improve=0.07494387, (0 missing)
##   Surrogate splits:
##       X3 < 7.85  to the left,  agree=0.735, adj=0.35, (0 split)
##       X9 < 127   to the left,  agree=0.735, adj=0.35, (0 split)
```

```
##       X1 < 45.35 to the left,  agree=0.653, adj=0.15, (0 split)
##       X4 < 57.95 to the left,  agree=0.653, adj=0.15, (0 split)
##       X5 < 138.5 to the left,  agree=0.653, adj=0.15, (0 split)
##
## Node number 8: 16 observations
##   mean=8.025625, MSE=0.4226621
##
## Node number 9: 8 observations
##   mean=8.91, MSE=1.1978
##
## Node number 10: 20 observations
##   mean=9.2165, MSE=1.313343
##
## Node number 11: 29 observations,    complexity param=0.01534651
##   mean=10.16517, MSE=1.015508
##   left son=22 (9 obs) right son=23 (20 obs)
##   Primary splits:
##       X5  < 188.5 to the left,  improve=0.1599134, (0 missing)
##       X8  < 152   to the left,  improve=0.1599134, (0 missing)
##       X2  < 5.4   to the left,  improve=0.1343526, (0 missing)
##       X10 < 50    to the left,  improve=0.1336582, (0 missing)
##       X4  < 94.55 to the left,  improve=0.1310009, (0 missing)
##   Surrogate splits:
##       X8  < 152   to the left,  agree=1.000, adj=1.000, (0 split)
##       X9  < 164   to the left,  agree=0.897, adj=0.667, (0 split)
##       X10 < 41.45 to the left,  agree=0.793, adj=0.333, (0 split)
##       X1  < 57.7  to the right, agree=0.759, adj=0.222, (0 split)
##       X3  < 25.8  to the right, agree=0.724, adj=0.111, (0 split)
##
## Node number 22: 9 observations
##   mean=9.564444, MSE=0.2281802
##
## Node number 23: 20 observations,    complexity param=0.01534651
##   mean=10.4355, MSE=1.134335
##   left son=46 (13 obs) right son=47 (7 obs)
##   Primary splits:
##       X4  < 90.1  to the left,  improve=0.26210460, (0 missing)
##       X1  < 52.65 to the left,  improve=0.19582880, (0 missing)
##       X7  < 2.5   to the right, improve=0.09871465, (0 missing)
##       X10 < 50    to the left,  improve=0.06785769, (0 missing)
##       X2  < 5.1   to the left,  improve=0.06575969, (0 missing)
##   Surrogate splits:
##       X9  < 176   to the right, agree=0.80, adj=0.429, (0 split)
##       X10 < 40    to the right, agree=0.80, adj=0.429, (0 split)
##       X3  < 26.15 to the left,  agree=0.75, adj=0.286, (0 split)
##       X5  < 202.5 to the right, agree=0.75, adj=0.286, (0 split)
##       X7  < 1.5   to the right, agree=0.75, adj=0.286, (0 split)
##
## Node number 46: 13 observations
##   mean=10.03538, MSE=1.009733
##
## Node number 47: 7 observations
##   mean=11.17857, MSE=0.5162694
```

```
plot(model.reg)
text(model.reg)
```



(d) and (e) Using holdout sample to score the model, and also to compare with regression tree model

```
model.pred <- predict(model,newdata=test.df)
model.ei <- model.pred - test.df$Y

tree.pred <- predict(model.reg, newdata=test.df)
tree.ei <- tree.pred - test.df$Y

# Using MAE as criteria
mean(abs(model.ei))
```

```
## [1] 0.8360067
```

```
mean(abs(tree.ei))
```

```
## [1] 1.208188
```

(d) second part: We see that, using mean absolute error as the criteria, the linear model in (a) performed better than the regression tree model.

Re-calibrate model and compare with model in (c)

Confused by the wording... I am going to re-calibrate model from (a) with holdout data to detect stability, then fit holdout data with model in (c) and compare.

[Main confusion... what is meant by 'final model' in (c)? We never decided (c) was 'final' model.]

```
model.end <- lm(Y~., data=test.df)
summary(model.end) # Holdout
```

```
##
## Call:
## lm(formula = Y ~ ., data = test.df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.1463 -0.4101  0.0541  0.2869  2.0243
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  6.484464   2.645779   2.451 0.023096 *
## X1           0.065061   0.037822   1.720 0.100108
## X2           0.378929   0.150200   2.523 0.019777 *
## X3           0.017632   0.021746   0.811 0.426563
## X4           0.003781   0.011132   0.340 0.737524
## X5           0.001210   0.003670   0.330 0.744929
## X6          -0.121216   0.714414  -0.170 0.866892
## X7          -0.676796   0.146053  -4.634 0.000143 ***
## X8           0.004417   0.006257   0.706 0.487951
## X9          -0.002534   0.003387  -0.748 0.462671
## X10         -0.035624   0.017592  -2.025 0.055772 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8064 on 21 degrees of freedom
## Multiple R-squared:  0.7738, Adjusted R-squared:  0.6661
## F-statistic: 7.185 on 10 and 21 DF,  p-value: 7.767e-05
```

```
summary(model) # Original
```

```
##
## Call:
## lm(formula = Y ~ ., data = train.df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.1832 -0.7152  0.0220  0.6097  5.9856
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.5097992  2.5712076   0.976  0.33237
## X1           0.0851752  0.0355052   2.399  0.01911 *
## X2           0.4778835  0.1740312   2.746  0.00766 **
## X3           0.0006345  0.0221793   0.029  0.97726
## X4           0.0132255  0.0089821   1.472  0.14539
## X5          -0.0103232  0.0057853  -1.784  0.07869 .
## X6          -0.1159227  0.5899833  -0.196  0.84480
## X7          -0.4528421  0.1938593  -2.336  0.02236 *
## X8           0.0216602  0.0063384   3.417  0.00106 **
## X9          -0.0065853  0.0031066  -2.120  0.03757 *
## X10          0.0078747  0.0191298   0.412  0.68186
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.343 on 70 degrees of freedom
```

```
## Multiple R-squared:  0.6363, Adjusted R-squared:  0.5843
## F-statistic: 12.24 on 10 and 70 DF,  p-value: 6.101e-12
```

Analysis: We see that using the holdout sample, certain X predictors gained/lost significance, indicating potential instability with our modeling.

Comparing with Model in (c)

```
model.light.end <- lm(Y~X1+X2+X3+X4+X8+X9+X10, data=test.df)
summary(model.light.end) # Model in (c)
```

```
##
## Call:
## lm(formula = Y ~ X1 + X2 + X3 + X4 + X8 + X9 + X10, data = test.df)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.86074 -0.66180 -0.02693  0.49506  2.21545
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  3.894681   2.920243   1.334   0.1948
## X1           0.069574   0.049457   1.407   0.1723
## X2           0.429827   0.197128   2.180   0.0393 *
## X3           0.037291   0.024062   1.550   0.1343
## X4           0.009690   0.014584   0.664   0.5127
## X8           0.007155   0.004329   1.653   0.1114
## X9          -0.002571   0.004039  -0.637   0.5304
## X10         -0.050809   0.023010  -2.208   0.0370 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.093 on 24 degrees of freedom
## Multiple R-squared:  0.5251, Adjusted R-squared:  0.3866
## F-statistic: 3.791 on 7 and 24 DF,  p-value: 0.006588
```

```
summary(model.end) # Model in (e) with holdout sample
```

```
##
## Call:
## lm(formula = Y ~ ., data = test.df)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -1.1463 -0.4101  0.0541  0.2869  2.0243
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  6.484464   2.645779   2.451 0.023096 *
## X1           0.065061   0.037822   1.720 0.100108
## X2           0.378929   0.150200   2.523 0.019777 *
## X3           0.017632   0.021746   0.811 0.426563
## X4           0.003781   0.011132   0.340 0.737524
```

```
## X5           0.001210   0.003670   0.330 0.744929
## X6          -0.121216   0.714414  -0.170 0.866892
## X7          -0.676796   0.146053  -4.634 0.000143 ***
## X8           0.004417   0.006257   0.706 0.487951
## X9          -0.002534   0.003387  -0.748 0.462671
## X10         -0.035624   0.017592  -2.025 0.055772 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.8064 on 21 degrees of freedom
## Multiple R-squared:  0.7738, Adjusted R-squared:  0.6661
## F-statistic: 7.185 on 10 and 21 DF,  p-value: 7.767e-05
```

When both used the holdout sample, the Full model (all X's included) performed much better than the model in (c).

Full model adj-R2: 0.67, (c) model adj-R2: 0.39.

YK_Final_P3

Yinan Kang

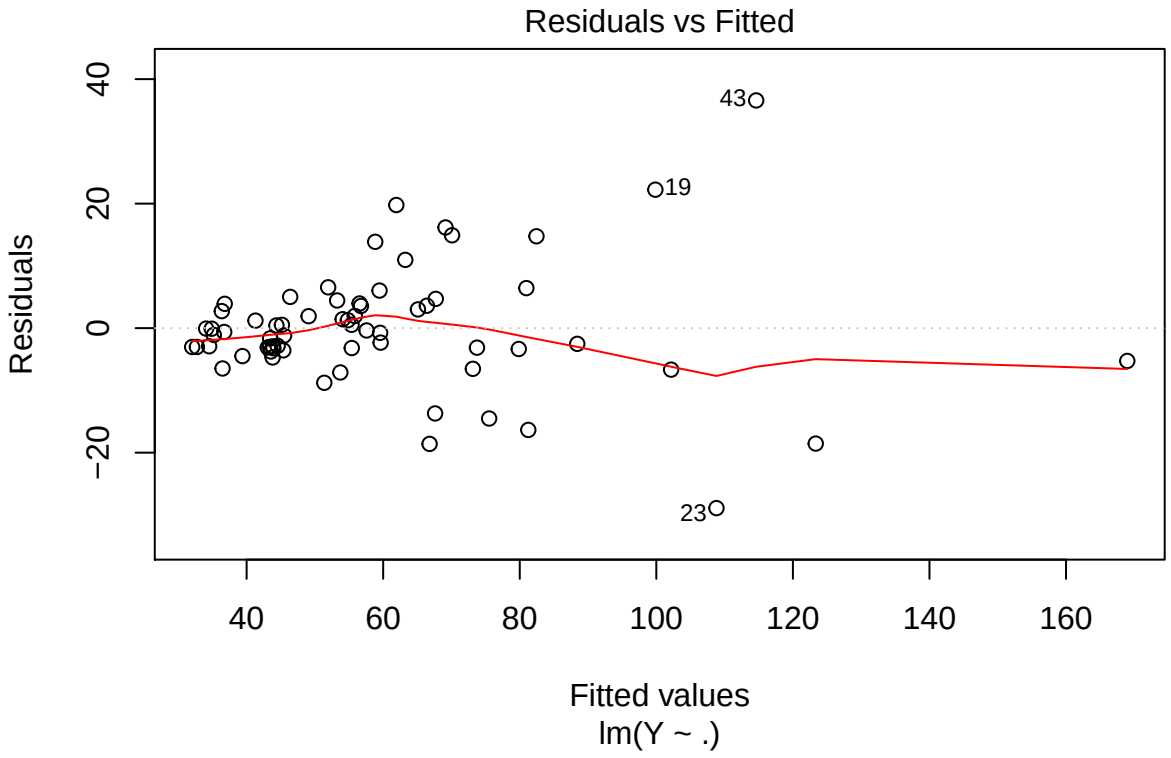
5/13/2019

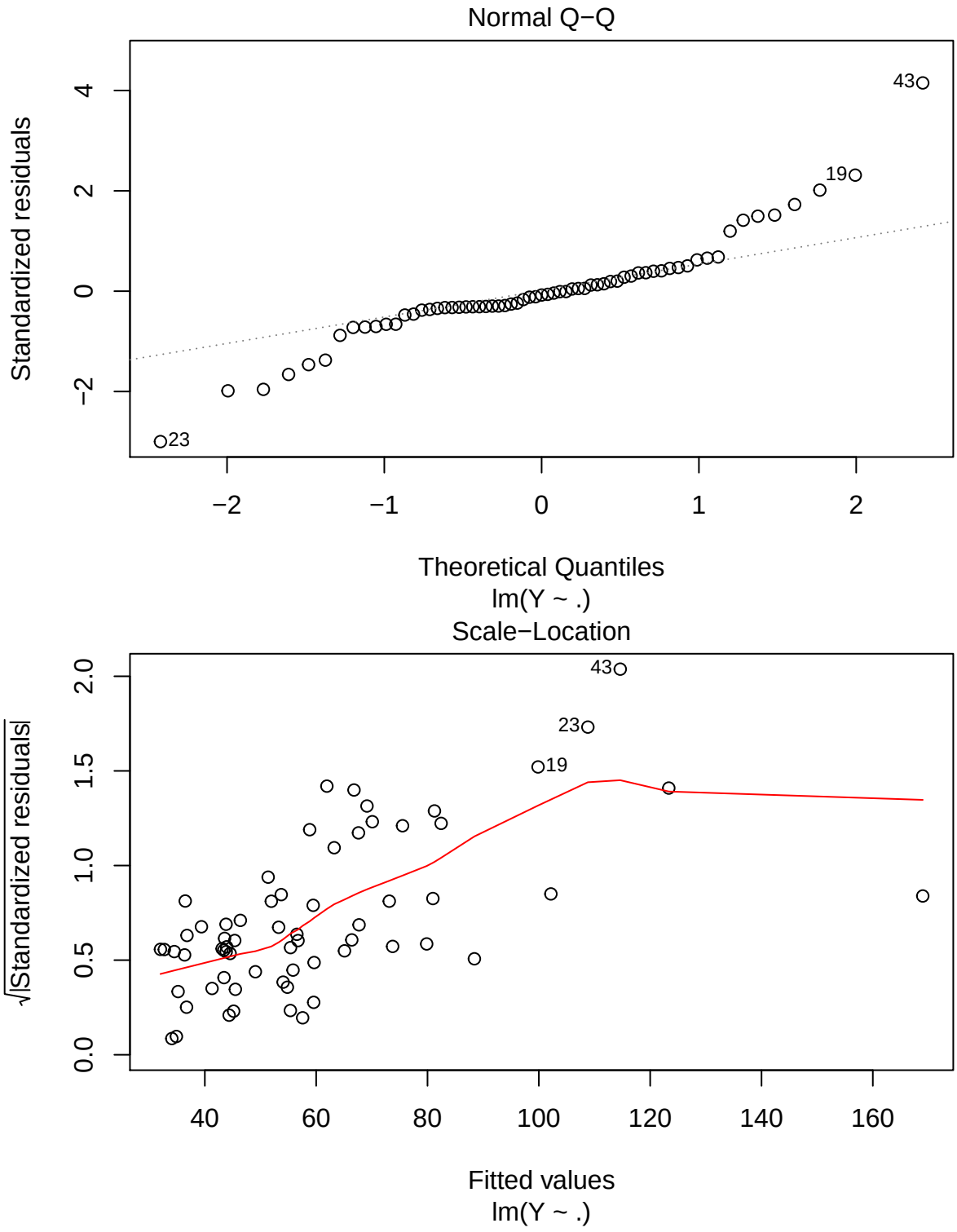
```
require(dplyr)
require(leaps)
require(neuralnet)
require(readxl)
require(caret)
require(lmtest)
```

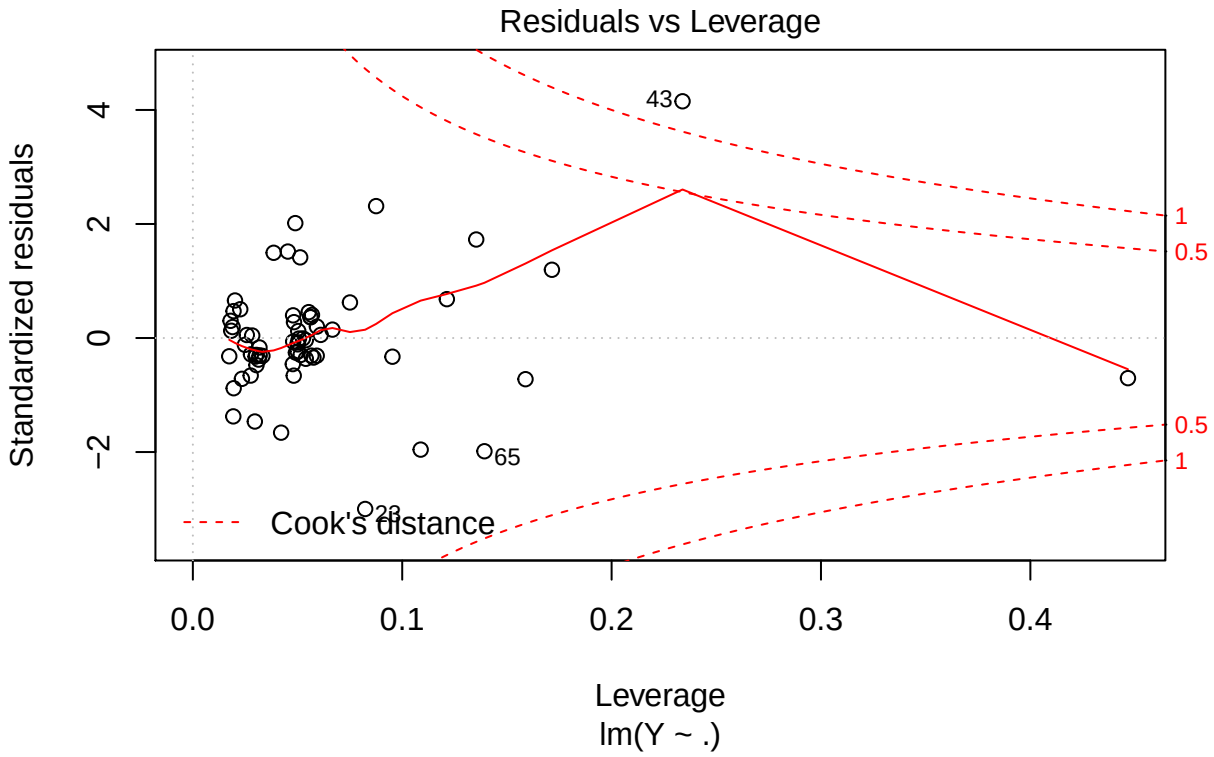
```
rm(list=ls())
df.3 <- read.csv("/cloud/project/Question 3.csv")
```

Fit Model

```
model.3 <- lm(Y~., data=df.3)
plot(model.3)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(Y ~ .)
43
19
23
−2
−1
0
1
2
4
Scale−Location
√|Standardized residuals|
Fitted values
lm(Y ~ .)
0.0
0.5
1.0
1.5
2.0
40
60
80
100
120
140
160



Analysis: We see unequal variance (Megaphone shape) in the Residuals Plot

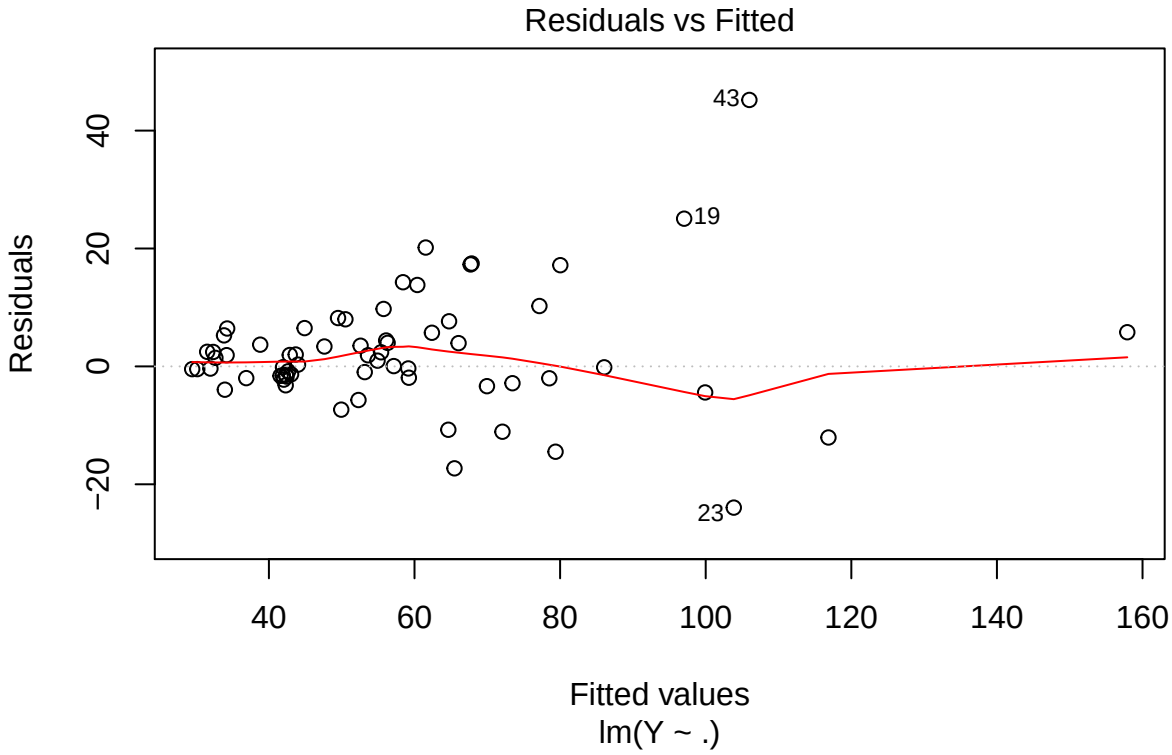
Using Weighted Least Squares

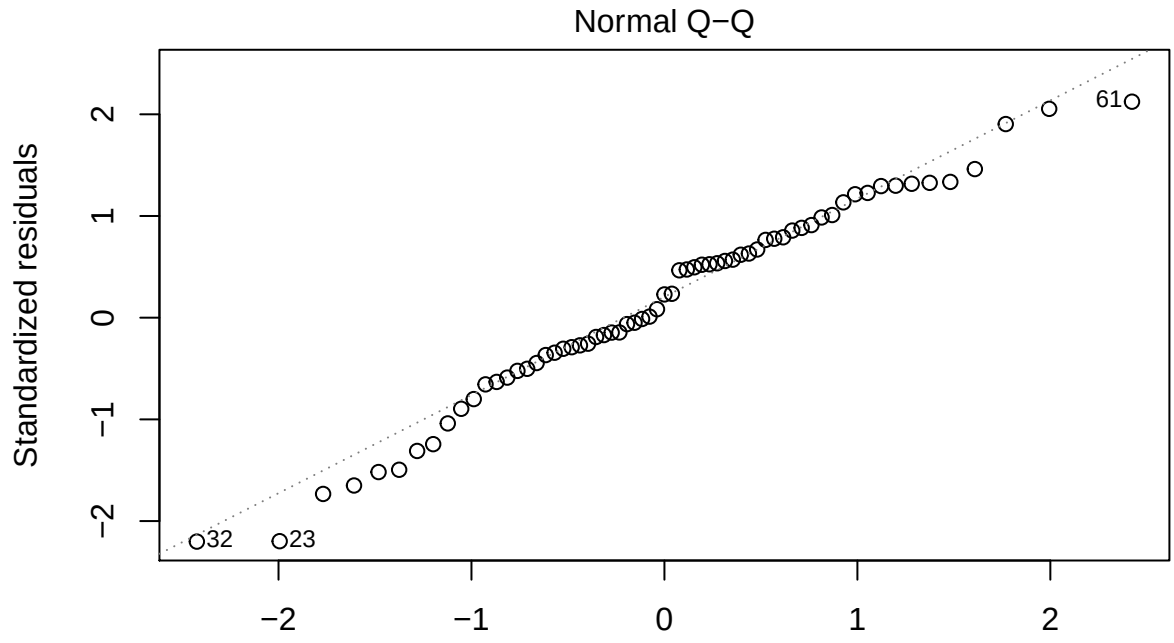
```
ei <- model.3$residuals
abs.ei <- abs(ei)
model.3.1 <- lm(abs.ei ~ ., data=df.3)

s <- model.3.1$fitted.values
wi <- 1/(s^2)

model.3.new <- lm(Y~., weights=wi, data=df.3)
summary(model.3.new)
```

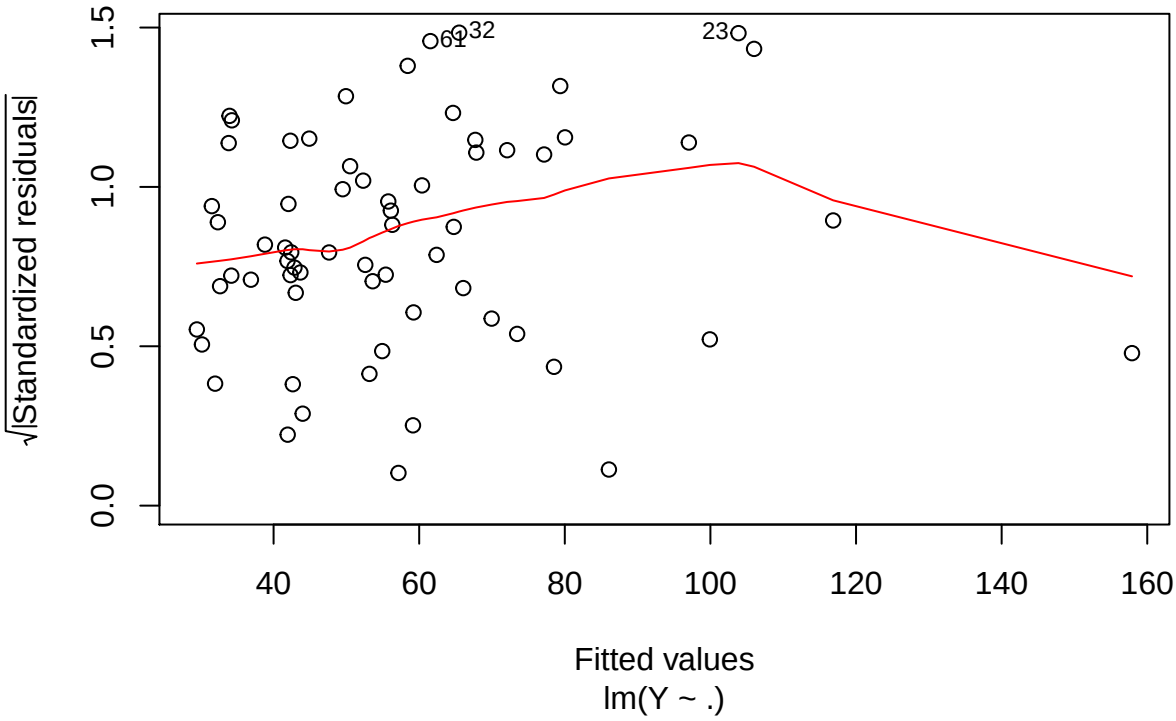
```
##
## Call:
## lm(formula = Y ~ ., data = df.3, weights = wi)
##
## Weighted Residuals:
##     Min      1Q  Median      3Q     Max
## -2.3041 -0.4933  0.2369  0.9425  2.3723
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  16.2356     1.5265  10.636 1.60e-15 ***
## X1           12.4000     0.7930  15.636  < 2e-16 ***
## X2            1.2718     0.1861   6.833 4.49e-09 ***
## X3            1.5929     0.3179   5.011 4.93e-06 ***
```

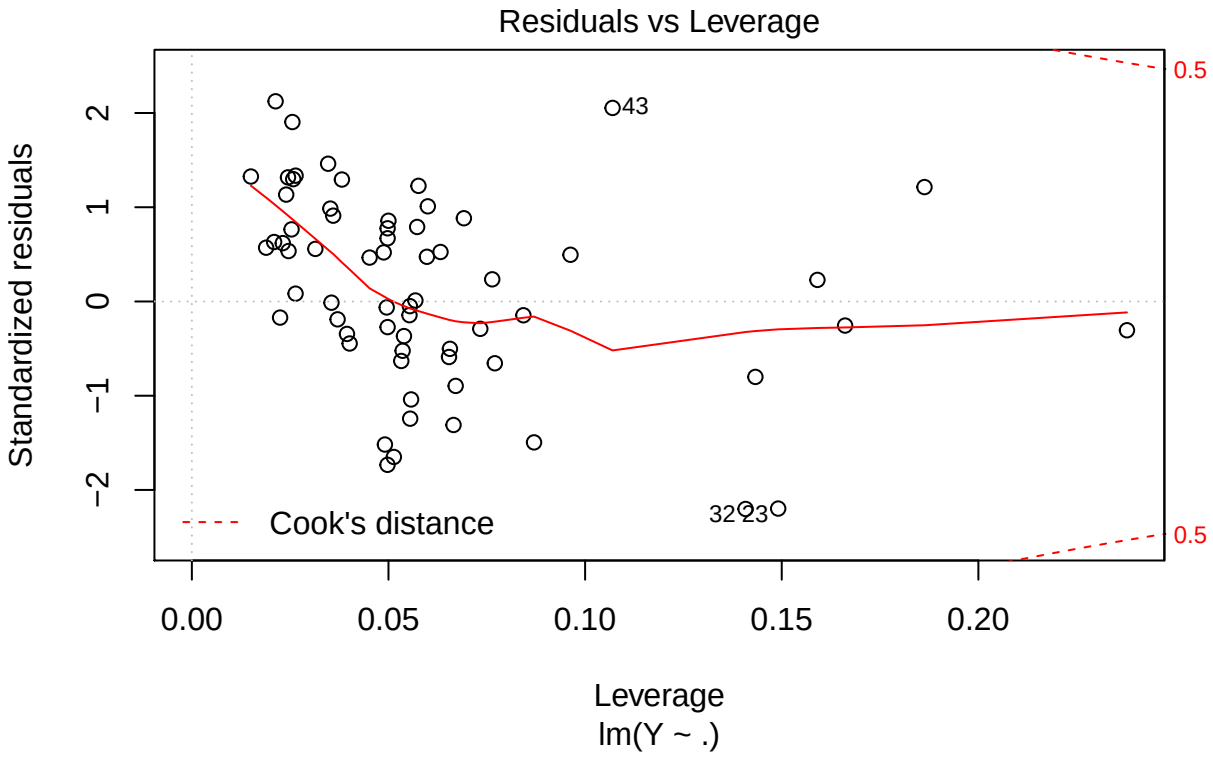
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.129 on 61 degrees of freedom
## Multiple R-squared:  0.8878, Adjusted R-squared:  0.8823
## F-statistic: 160.9 on 3 and 61 DF,  p-value: < 2.2e-16
```

```
plot(model.3.new)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(Y ~ .)
61
32
23
−2
−1
0
1
2


Scale−Location
√|Standardized residuals|
Fitted values
lm(Y ~ .)
61
32
23
0.0
0.5
1.0
1.5
40
60
80
100
120
140
160


Residuals vs Leverage
Standardized residuals
Leverage
lm(Y ~ .)
Cook's distance
0.5
0.5
43
32
23
0.00
0.05
0.10
0.15
0.20
−2
−1
0
1
2

YK_Final_P5

Yinan Kang

5/14/2019

```
rm(list=ls())
df <- read.csv("/cloud/project/Question 5.csv")

require(ResourceSelection)
```

```
## Loading required package: ResourceSelection
```

```
## ResourceSelection 0.3-4   2019-01-08
```

(a) Fit model with first orders plus all interactions

```
model <- glm(Y~X1+X2+X3+X4+X1*X2+X1*X3+X1*X4+X2*X3+X2*X4+X3*X4, family="binomial",data=df)
summary(model)
```

```
##
## Call:
## glm(formula = Y ~ X1 + X2 + X3 + X4 + X1 * X2 + X1 * X3 + X1 *
##     X4 + X2 * X3 + X2 * X4 + X3 * X4, family = "binomial", data = df)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -2.3440  -0.9089   0.4209   0.7961   2.0514
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  0.551402   1.590243   0.347    0.729
## X1           0.056505   0.045956   1.230    0.219
## X2          -1.250346   0.674971  -1.852    0.064 .
## X3           0.613566   1.008733   0.608    0.543
## X4          -1.780009   1.830666  -0.972    0.331
## X1:X2        0.001105   0.011955   0.092    0.926
## X1:X3       -0.019941   0.022211  -0.898    0.369
## X1:X4        0.020090   0.025639   0.784    0.433
## X2:X3        0.177436   0.430328   0.412    0.680
## X2:X4       -0.055230   0.476060  -0.116    0.908
## X3:X4        0.908936   0.818335   1.111    0.267
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 270.06  on 195  degrees of freedom
## Residual deviance: 213.50  on 185  degrees of freedom
## AIC: 235.5
##
## Number of Fisher Scoring iterations: 5
```

(b) Likelihood Ratio Test for dropping Interaction Terms

Full Model: Pi = [1+exp(-X'BetaFull)] ^-1
where X*BetaFull* = *Beta0* + *Beta1*X1 + ... Beta10*(X3*X4)

Reduced Model: Pi = [1+exp(-X'BetaReduced)] ^-1
where X*BetaFull* = *Beta0* + *Beta1*X1 + ... Beta4*X4

Hypotheses:
H0: Beta 5 = Beta 6 .... = Beta 10 = 0 (All Beta's with Interaction terms = 0)
Ha: Not All Betas in H0 = 0

Decision Rule:
If G2 <= Chi-Sq(1-alpha, p-q), conclude H0
If G2 > Chi-Sq(1-alpha, p-1), conclude Ha

Assume alpha = 0.05

```
model.r <- glm(Y~X1+X2+X3+X4, family = "binomial", data=df)
anova(model, model.r, test="Chisq")
```

```
## Analysis of Deviance Table
##
## Model 1: Y ~ X1 + X2 + X3 + X4 + X1 * X2 + X1 * X3 + X1 * X4 + X2 * X3 +
##     X2 * X4 + X3 * X4
## Model 2: Y ~ X1 + X2 + X3 + X4
##   Resid. Df Resid. Dev Df Deviance Pr(>Chi)
## 1       185     213.50
## 2       191     215.65 -6  -2.1492   0.9055
```

Decision:

We use the 'anova' function to compare our full and reduced models. We see that the p-value associated with the Chi-Sq distribution is > 0.05.
This interpretation is different than the formal one stated in the Decision Rule above. This p-value lets us know that there is no statistical significance in adding the interactions, so they can be DROPPED.

(c) Backward elimination

```
step(model, scope = formula(model), direction="backward")
```

```
## Start:  AIC=235.5
## Y ~ X1 + X2 + X3 + X4 + X1 * X2 + X1 * X3 + X1 * X4 + X2 * X3 +
##     X2 * X4 + X3 * X4
##
##         Df Deviance    AIC
## - X1:X2  1   213.51 233.51
## - X2:X4  1   213.52 233.52
## - X2:X3  1   213.67 233.67
## - X1:X4  1   214.14 234.14
## - X1:X3  1   214.30 234.30
## - X3:X4  1   214.75 234.75
## <none>       213.50 235.50
##
## Step:  AIC=233.51
## Y ~ X1 + X2 + X3 + X4 + X1:X3 + X1:X4 + X2:X3 + X2:X4 + X3:X4
```

```
##
##         Df Deviance    AIC
## - X2:X4  1   213.52 231.52
## - X2:X3  1   213.68 231.68
## - X1:X4  1   214.15 232.15
## - X1:X3  1   214.40 232.40
## - X3:X4  1   214.78 232.78
## <none>       213.51 233.51
##
## Step:  AIC=231.52
## Y ~ X1 + X2 + X3 + X4 + X1:X3 + X1:X4 + X2:X3 + X3:X4
##
##         Df Deviance    AIC
## - X2:X3  1   213.68 229.68
## - X1:X4  1   214.15 230.15
## - X1:X3  1   214.41 230.41
## - X3:X4  1   214.84 230.84
## <none>       213.52 231.52
##
## Step:  AIC=229.68
## Y ~ X1 + X2 + X3 + X4 + X1:X3 + X1:X4 + X3:X4
##
##         Df Deviance    AIC
## - X1:X4  1   214.32 228.32
## - X1:X3  1   214.53 228.53
## - X3:X4  1   215.04 229.04
## <none>       213.68 229.68
## - X2     1   240.51 254.51
##
## Step:  AIC=228.32
## Y ~ X1 + X2 + X3 + X4 + X1:X3 + X3:X4
##
##         Df Deviance    AIC
## - X1:X3  1   214.81 226.81
## - X3:X4  1   215.44 227.44
## <none>       214.32 228.32
## - X2     1   240.74 252.74
##
## Step:  AIC=226.81
## Y ~ X1 + X2 + X3 + X4 + X3:X4
##
##         Df Deviance    AIC
## - X3:X4  1   215.65 225.65
## <none>       214.81 226.81
## - X1     1   229.00 239.00
## - X2     1   240.83 250.83
##
## Step:  AIC=225.65
## Y ~ X1 + X2 + X3 + X4
##
##        Df Deviance    AIC
## - X4    1   215.66 223.66
## <none>      215.65 225.65
## - X3    1   220.39 228.39
```

```
## - X1    1   230.16 238.16
## - X2    1   241.92 249.92
##
## Step:  AIC=223.66
## Y ~ X1 + X2 + X3
##
##        Df Deviance    AIC
## <none>      215.66 223.66
## - X3    1   220.67 226.67
## - X1    1   230.85 236.85
## - X2    1   242.00 248.00
```

```
##
## Call:  glm(formula = Y ~ X1 + X2 + X3, family = "binomial", data = df)
##
## Coefficients:
## (Intercept)           X1           X2           X3
##     0.20085      0.03584     -0.97722      0.77005
##
## Degrees of Freedom: 195 Total (i.e. Null);  192 Residual
## Null Deviance:       270.1
## Residual Deviance: 215.7     AIC: 223.7
```

Analysis: Using Backward step, we see that X1, X2, X3 are retained.

Re-fitting model for rest of problem !!

```
model <- glm(Y~X1+X2+X3, family="binomial", data=df)
```

(d) Hoslem-Lameshow Goodness-of-Fit

Hypotheses:

H0: Logistic response is appropriate
Ha: Logistic Response is not appropriate

Alternatives:

If X.test <= Chi-Sq(0.95,c-2), conclude H0
If X.test > Chi-Sq(0.95,c-2), conclude Ha

```
hoslem.test(model$y,fitted(model),g=5)
```

```
##
##  Hosmer and Lemeshow goodness of fit (GOF) test
##
## data:  model$y, fitted(model)
## X-squared = 1.223, df = 3, p-value = 0.7475
```

Decision: As X.test < Chi-Sq, we conclude H0, that a Logistic response is appropriate.

(e) Prediction

```
pred.data <- data.frame(X1=c(33,6), X2 =c(1,1), X3 = c(1,1), X4 = c(0,0))

pred <- predict(model, newdata=pred.data)
print(pred)
```

```
##         1         2
## 1.1764354 0.2087265
```

```
# Ran out of time to do joint confidence interval
```