# Case Study 1

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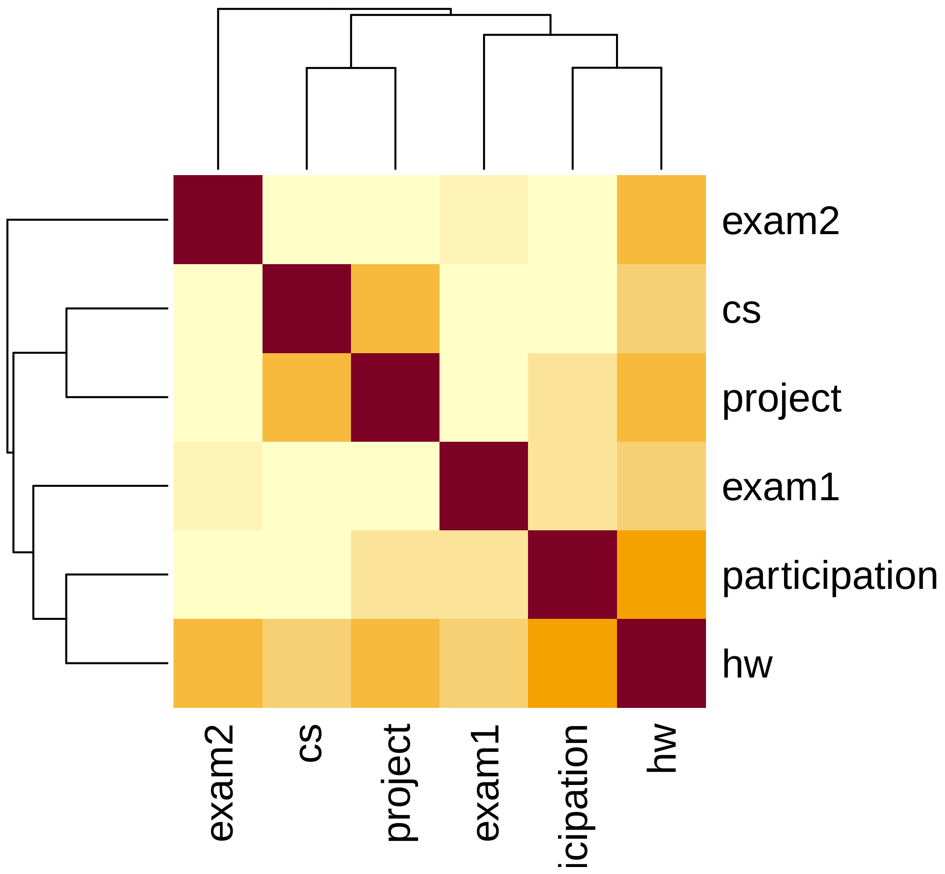
## Data Explorations and Summary Statistics

```r
grades <- read.csv("grades.csv", header=TRUE)
grades <- grades[1:6]
dim(grades)
```

```
## [1] 275   6
```

## Model Selection

```r
cor_matrix <- cor(grades)
heatmap(cor_matrix, symm = TRUE)
```



Looking at the correlation matrix, none of the variables are strongly correlated with another variable, so we do not need to drop any variables based on what we see from the correlation matrix.

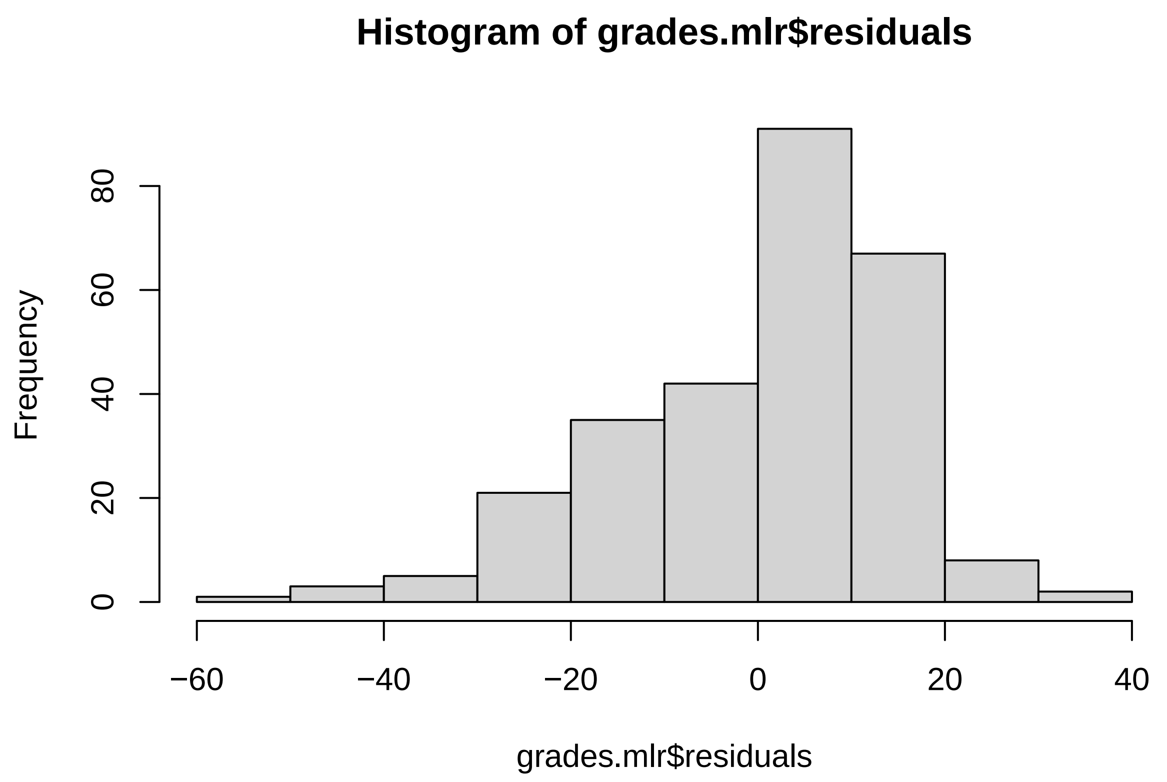
We want to make a model with 95% confidence (i.e. $\alpha = 0.05$)

```
grades.mlr <- lm(exam2 ~ hw + cs + participation + exam1 + project ,data=grades)
summary(grades.mlr)
```

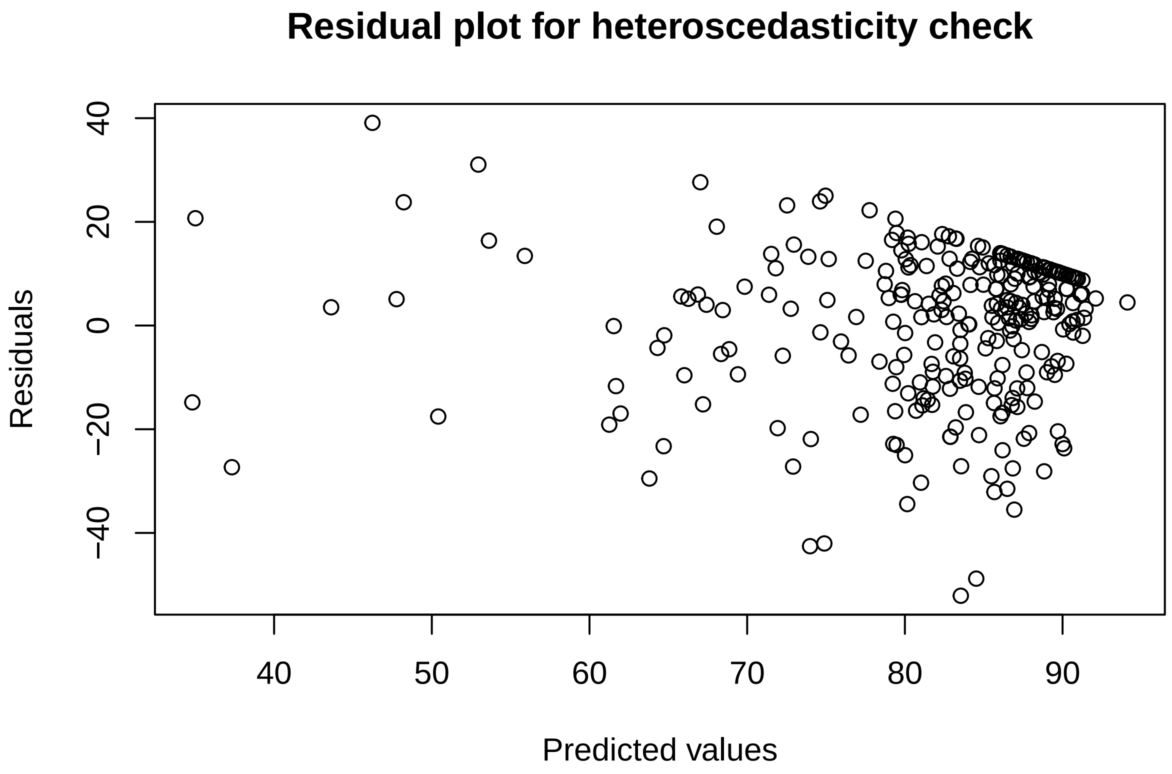
```
##
## Call:
## lm(formula = exam2 ~ hw + cs + participation + exam1 + project,
##     data = grades)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -52.116  -9.270   3.431  10.486  39.096
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   25.51074    6.52460   3.910 0.000117 ***
## hw             0.50233    0.07506   6.692 1.27e-10 ***
## cs             0.02096    0.07030   0.298 0.765805
## participation -0.09622    0.06259  -1.537 0.125403
## exam1          0.22437    0.06954   3.226 0.001410 **
## project        0.00885    0.04804   0.184 0.853973
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 14.59 on 269 degrees of freedom
## Multiple R-squared:  0.3249, Adjusted R-squared:  0.3124
## F-statistic:  25.9 on 5 and 269 DF,  p-value: < 2.2e-16
```

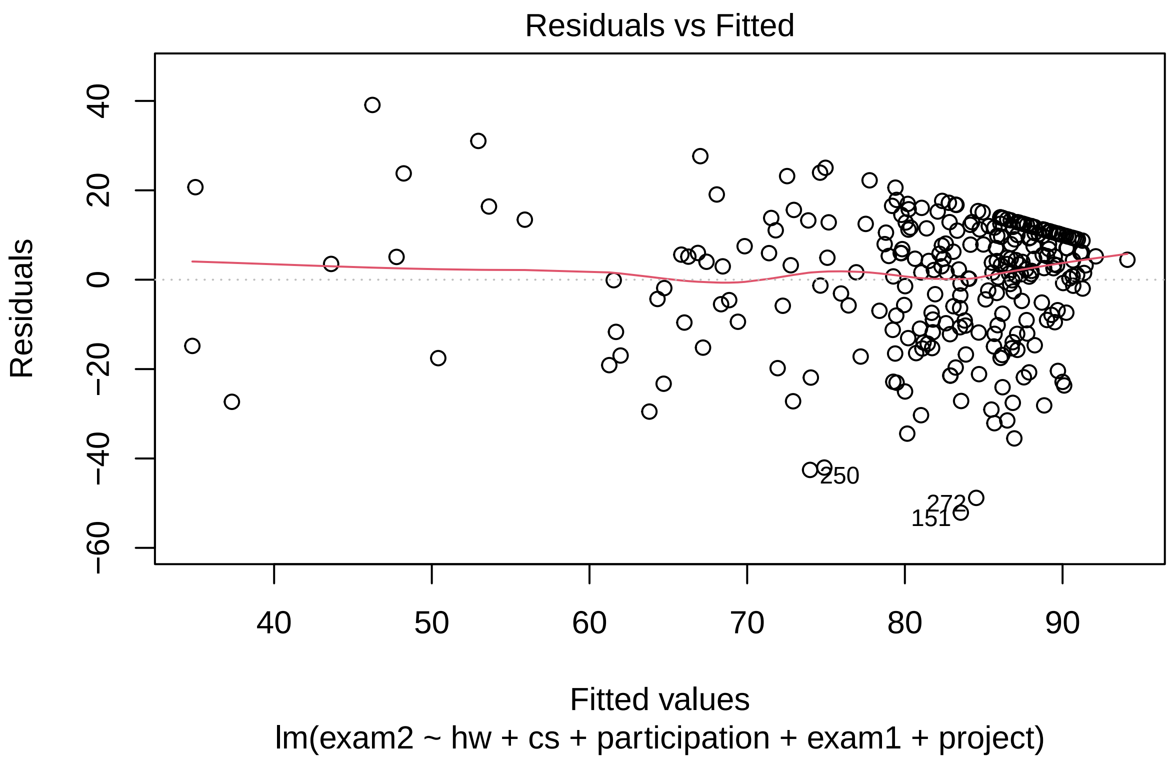
```
hist(grades.mlr$residuals)
```

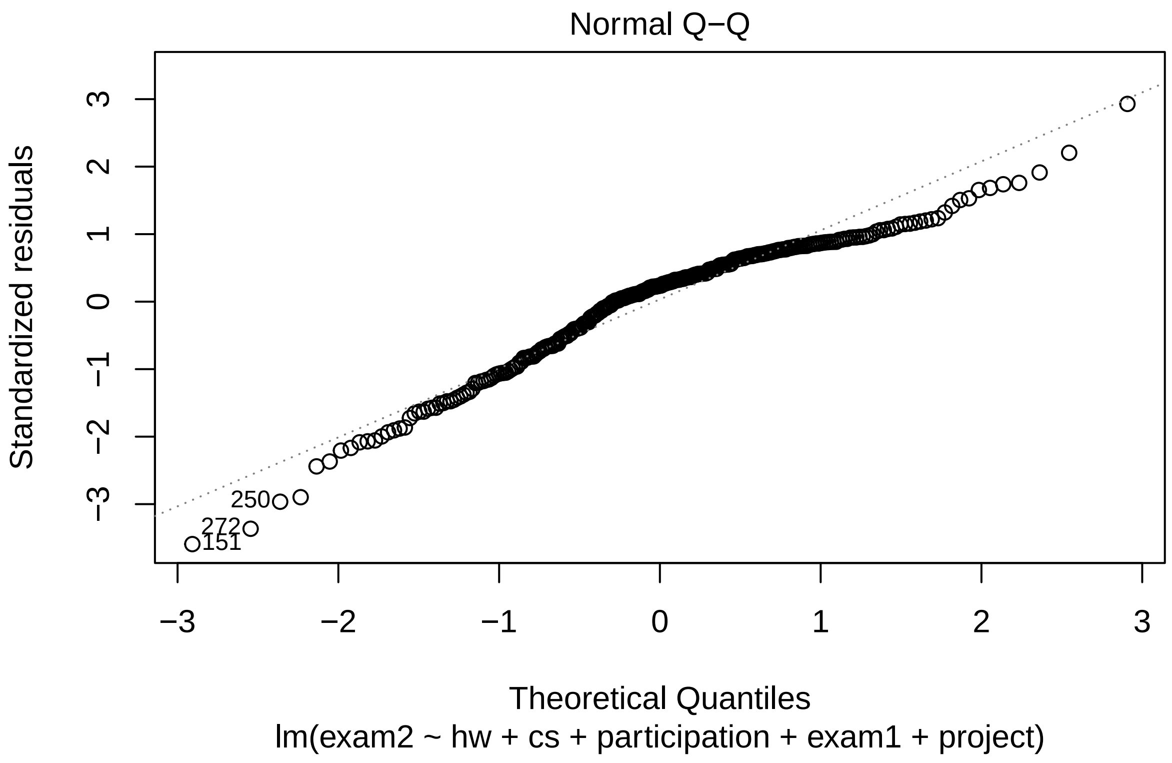


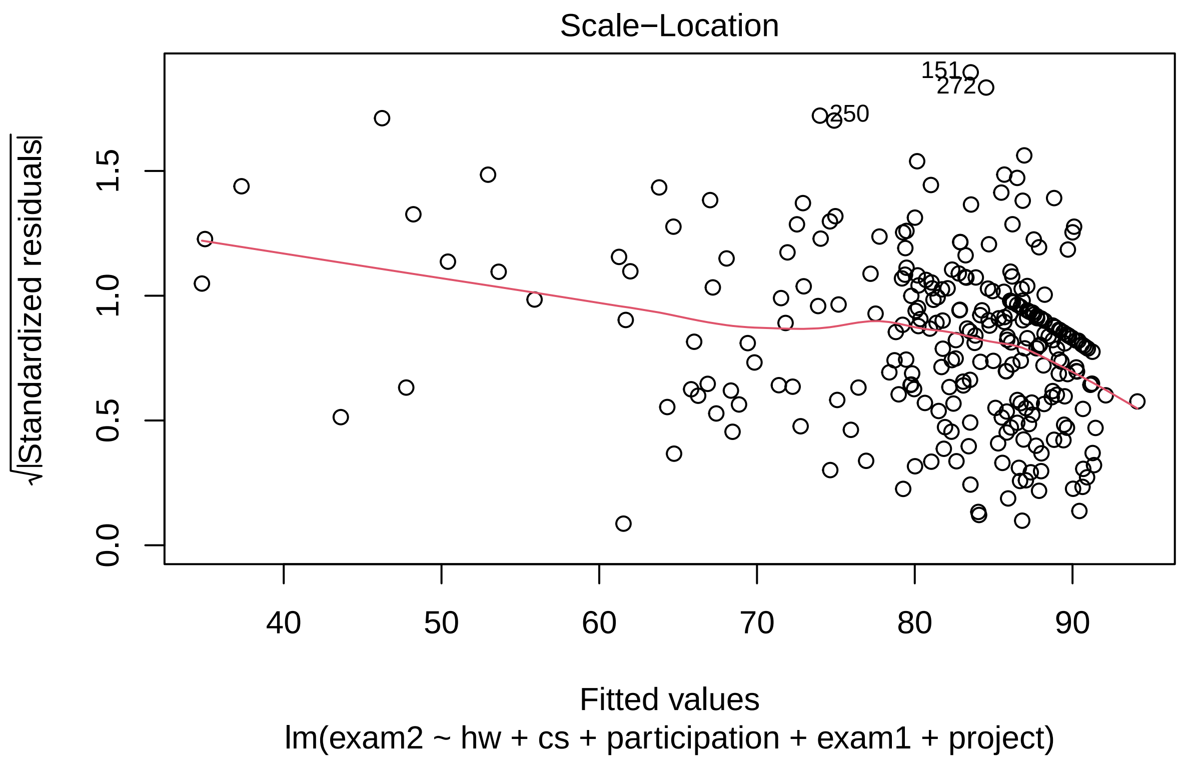
```
predicted_values <- predict(grades.mlr)
plot(x = predicted_values, y = residuals(grades.mlr),
     xlab = "Predicted values", ylab = "Residuals",
     main = "Residual plot for heteroscedasticity check")
```



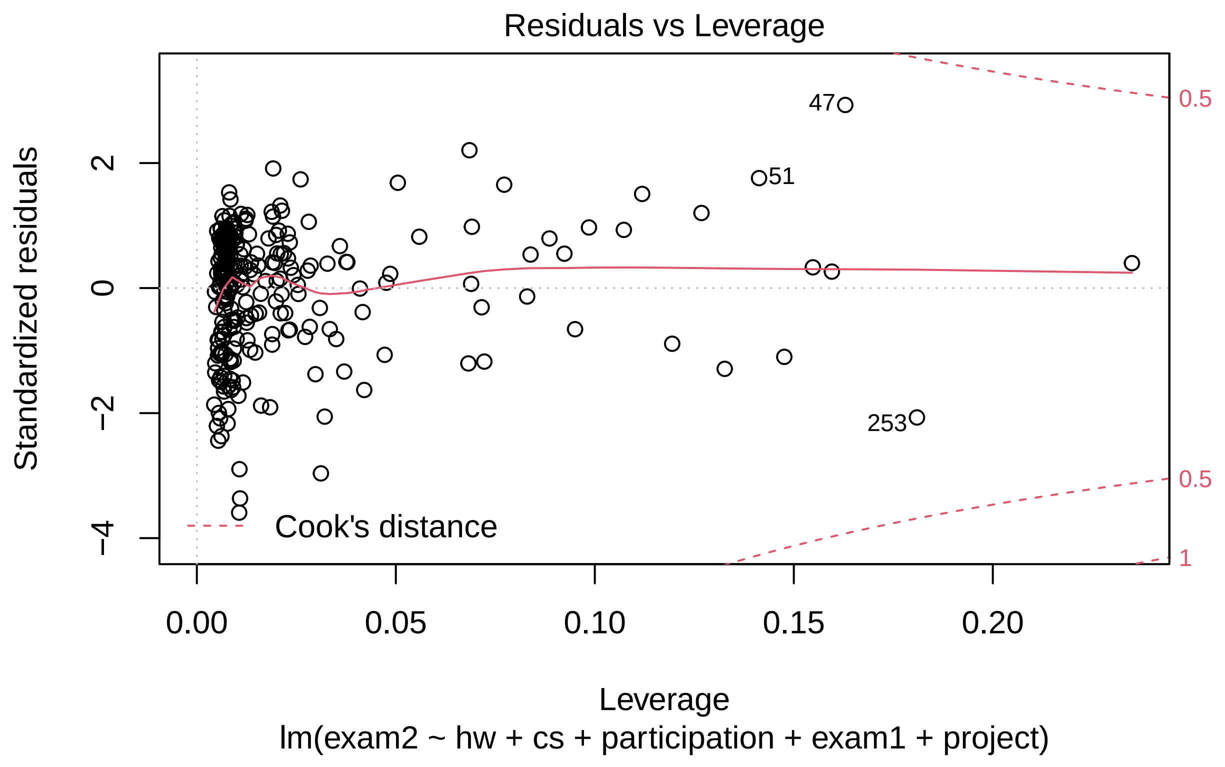
```
plot(grades.mlr)
```


Residuals vs Fitted
Residuals
40
20
0
−20
−40
−60
40
50
60
70
80
90
250
272
151
Fitted values
lm(exam2 ~ hw + cs + participation + exam1 + project)


Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(exam2 ~ hw + cs + participation + exam1 + project)
250
272
151
−3
−2
−1
0
1
2
3



Scale−Location
151
272
250
√|Standardized residuals|
0.0
0.5
1.0
1.5
40
50
60
70
80
90
Fitted values
lm(exam2 ~ hw + cs + participation + exam1 + project)



Based on the full model summary above, we may want to look into dropping project, cs, and participation from the dataset since the t-values in the summary output for project, cs, and participation are all small, meaning that they're likely up to chance.

However, the individual t-tests do not tell us enough information to drop multiple predictors from our model at a time.

So, we can start by dropping an individual predictor from our model. We will check `project`.

Our null and alternative hypothesis are as follows.

$$\begin{cases} H_0, & \beta_{project} = 0 \\ H_A, & \beta_{project} \neq 0 \end{cases}$$

By conducting an individual t-test (which can be found in our summary output), we can see that the t-test statistics for project is 0.397. ## TODO PLEASE CHECK IF WE NEED TO BE THOROUGH AND MENTION WHICH DISTRIBUTION THESE ARE FROM This comes from a . Thus, we can see that the p-value for project is 0.692. $p = 0.692 > 0.05 = \alpha$. Thus, we fail to reject the null hypothesis, meaning that it is likely that $\beta_{project} = 0$. In other words, we can drop project from our model.

This leaves us with the following reduced model:

```
grades.reducedmlr1 = lm(exam2~exam1 + hw + cs + participation, data=grades)
summary(grades.reducedmlr1)
```

```
##
## Call:
```

```
## lm(formula = exam2 ~ exam1 + hw + cs + participation, data = grades)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -52.129  -9.371   3.396  10.476  39.564
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)   25.36389    6.46413   3.924 0.000111 ***
## exam1          0.22444    0.06942   3.233 0.001377 **
## hw             0.50605    0.07216   7.013 1.88e-11 ***
## cs             0.02568    0.06535   0.393 0.694589
## participation -0.09430    0.06161  -1.531 0.127027
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.56 on 270 degrees of freedom
## Multiple R-squared:  0.3249, Adjusted R-squared:  0.3148
## F-statistic: 32.48 on 4 and 270 DF,  p-value: < 2.2e-16
```

```
anova(grades.mlr, grades.reducedmlr1)
```

```
## Analysis of Variance Table
##
## Model 1: exam2 ~ hw + cs + participation + exam1 + project
## Model 2: exam2 ~ exam1 + hw + cs + participation
##   Res.Df   RSS Df Sum of Sq      F Pr(>F)
## 1    269 57240
## 2    270 57247 -1   -7.2221 0.0339  0.854
```

## Can we reference the overall summary and p-values to give us guidance on where to look next?

From the summary, We can see that the p-values for cs and participation have changed. They are still high, so we can conduct a different test.

$$\begin{cases} H_0, & \beta_{participation} = \beta_{cs} = 0 \\ H_A, & \text{Either } \beta_{participation} \text{ or } \beta_{cs} \text{ is not equal to zero} \end{cases}$$

```
library(ellipse)
```

```
## Warning: package 'ellipse' was built under R version 4.1.3
```

```
##
## Attaching package: 'ellipse'
```

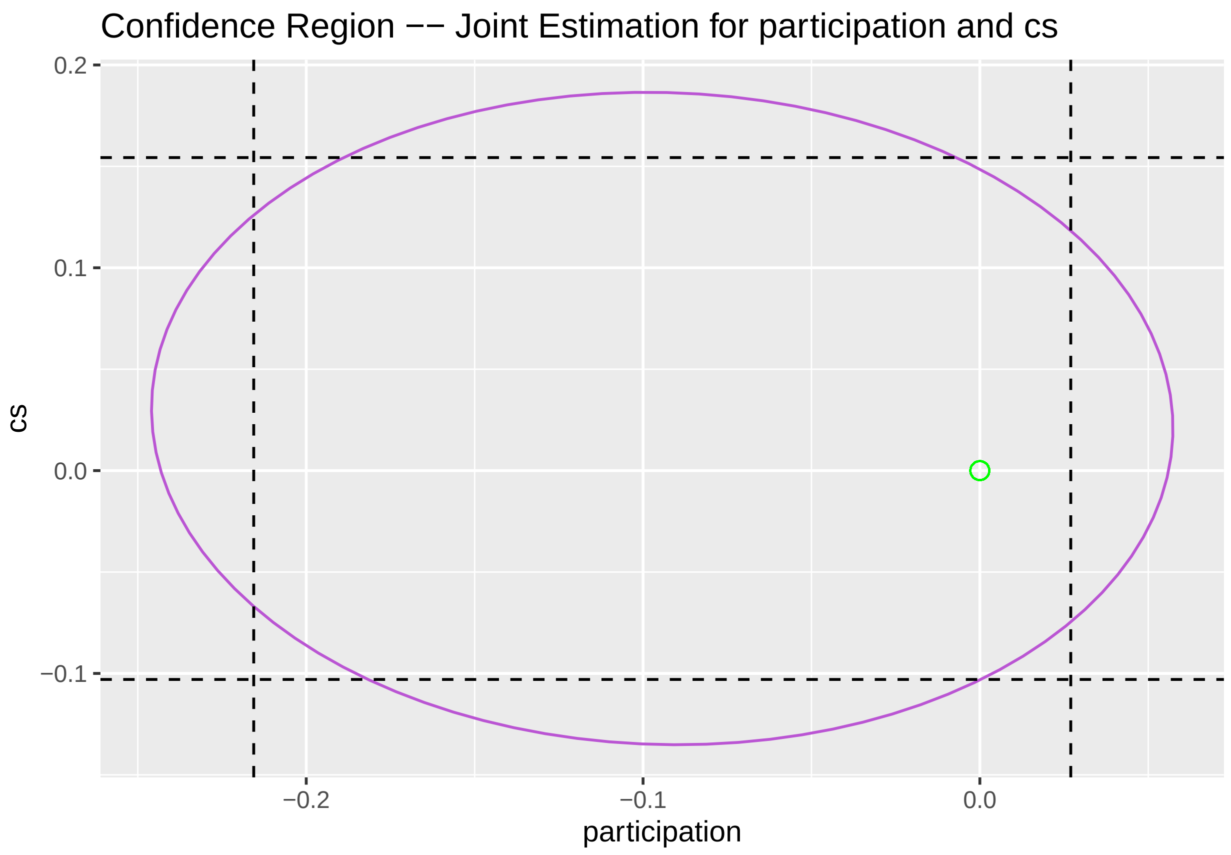
```
## The following object is masked from 'package:graphics':
##
##     pairs
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.1.3
```

We can draw the confidence region (as an ellipse) for both participation and for cs. If the point (0,0) falls inside of our confidence region, then it is likely that both the coefficients $\beta_{cs}$ and $\beta_{participation}$ are zero—as according to the null hypothesis.

```
intervals <-confint(grades.reducedmlr1)
cr_ellipse <- ellipse(grades.reducedmlr1, c(4,5), level=0.95)

par_interval <- confint(grades.reducedmlr1, level = 0.95, 'participation')
cs_interval <- confint(grades.reducedmlr1, level = 0.95, 'cs')

cr_df <- as.data.frame(cr_ellipse)
cr_plot <-
ggplot(data=cr_df, aes(x=participation, y=cs)) +
  ggtitle("Confidence Region -- Joint Estimation for participation and cs") +
  geom_path(aes(x=participation,y=cs), colour='mediumorchid') +
  geom_point(x=coef(grades.reducedmlr1)[2], y=coef(grades.reducedmlr1)[3],
             shape=3, size=3, colour='mediumorchid') +
  geom_hline(yintercept = cs_interval[1], lty=2) +
  geom_hline(yintercept = cs_interval[2], lty=2) +
  geom_vline(xintercept = par_interval[1], lty=2) +
  geom_vline(xintercept = par_interval[2], lty=2)+
  geom_point(x=0, y=0, shape=1, size=3, colour='green')

plot(cr_plot)
```



As we can see, the origin—which is the green dot—falls inside the confidence region. Thus, it is likely enough that both $\beta_{cs}$ and $\beta_{participation}$ are zero. Therefore, we can drop them both from our model.

Since the p-value in the full model is the same as the reduced model, this confirms that the dropped variables were not significant in our model. The sample size is quite small, therefore dropping variables may lead to insignificant changes in p value.

So, our final model (before diagonistcs) is the following:

```
grades.reducedmlr = lm(exam2 ~ exam1 + hw, data=grades)
summary(grades.reducedmlr)
```

```
##
## Call:
## lm(formula = exam2 ~ exam1 + hw, data = grades)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -51.150  -9.195   3.301  10.349  40.987
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 24.64208    5.61643   4.387 1.64e-05 ***
## exam1        0.20858    0.06780   3.077  0.00231 **
## hw           0.46396    0.05768   8.044 2.69e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 14.57 on 272 degrees of freedom
## Multiple R-squared:  0.3187, Adjusted R-squared:  0.3137
## F-statistic: 63.62 on 2 and 272 DF,  p-value: < 2.2e-16
```

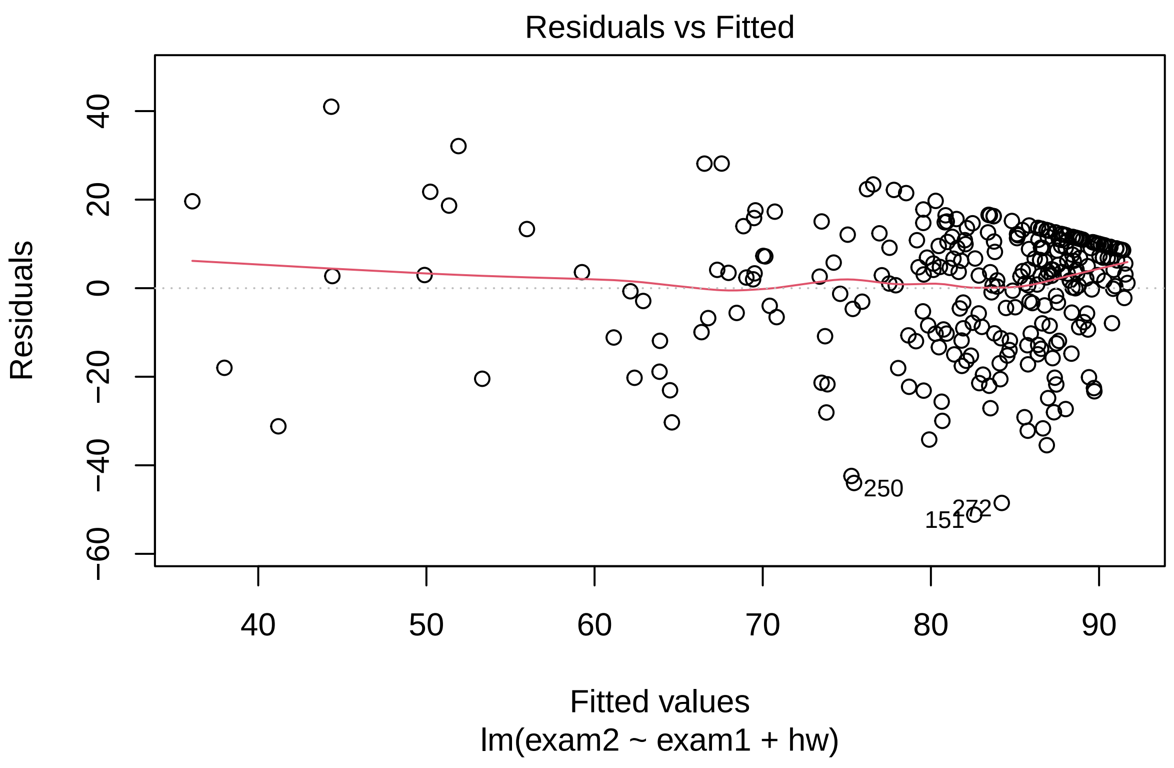
## Unusual Observations and Model Assumptions

Now we can analyze the final model for unusual observations and check for deviations from the model assumptions.

### Constant variances

First, we can check the model assumption for constant variances by checking the residual vs. fitted plot.

```
plot(grades.reducedmlr, which=1)
```

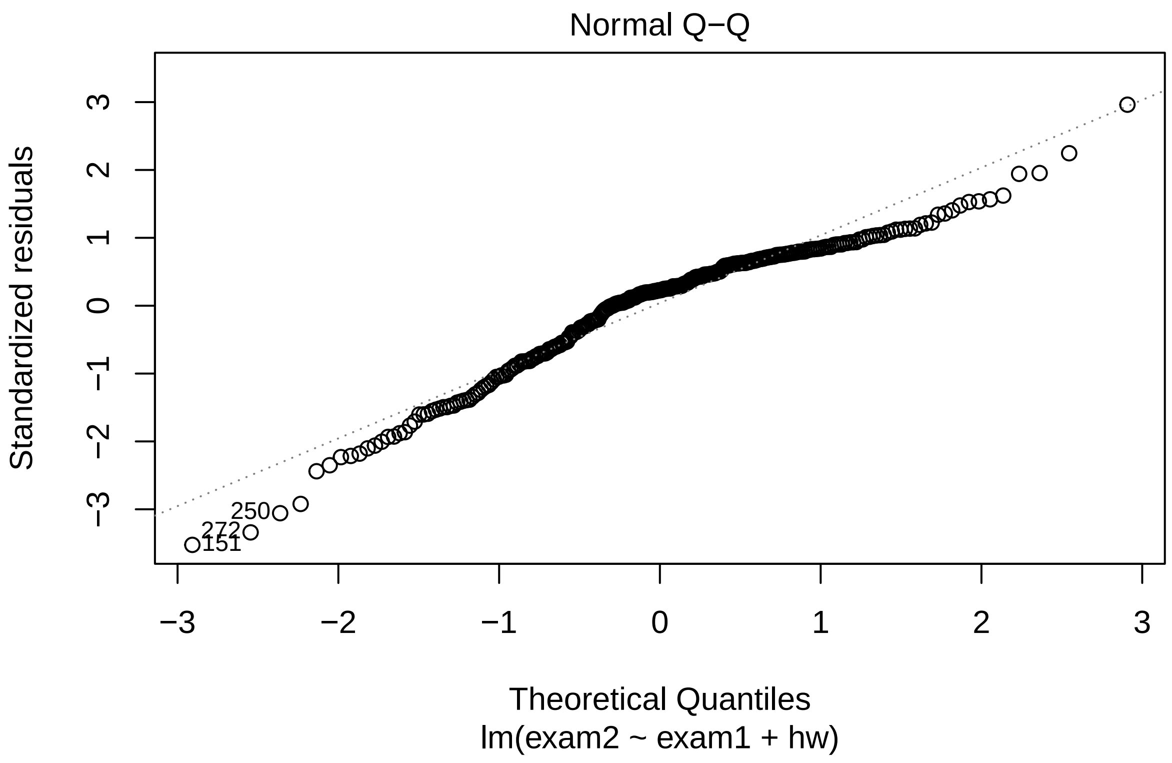


From the residuals vs. fitted plots, we can see the the assumptions for constant variance are not met because the residuals are not evenly disributed around the 0 line, and seem to decrease in magnitude as the residuals increase.

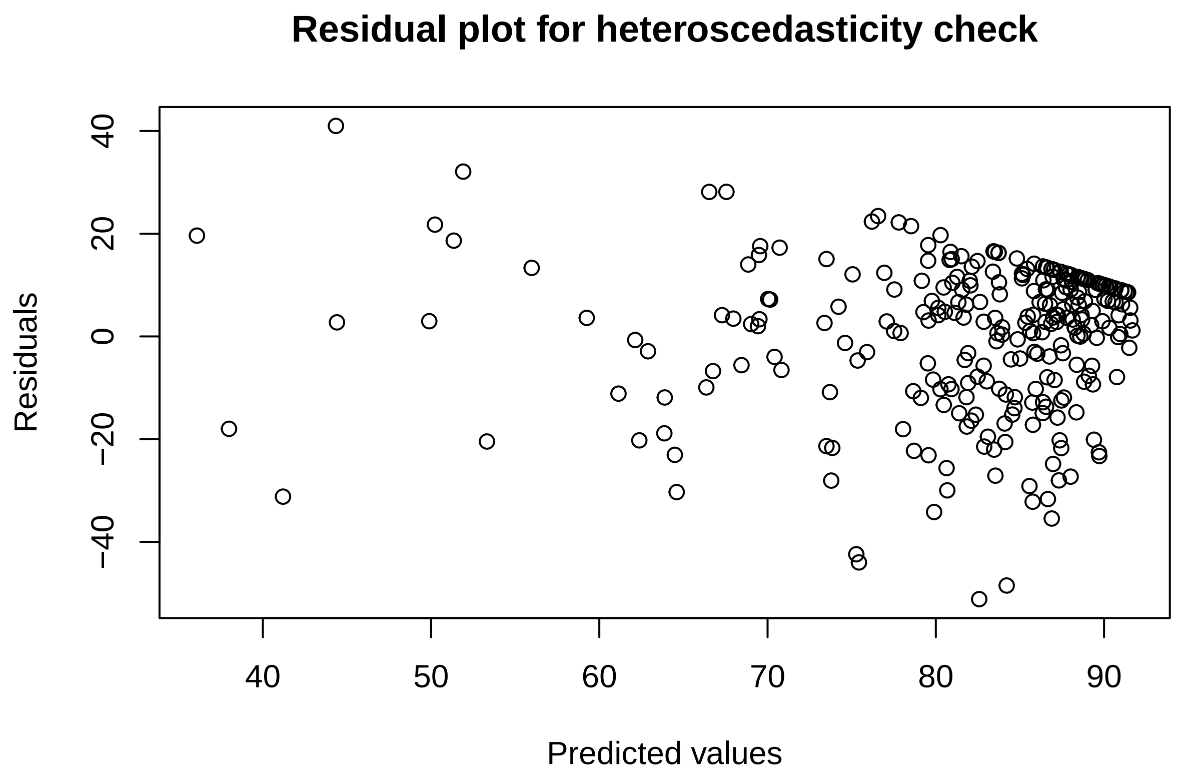
### Normality

Next, we can chck for normaltiy of the residuals by creating a QQ plot.

```r
plot(grades.reducedmlr, which=2)
```



```r
predicted_values <- predict(grades.reducedmlr)
plot(x = predicted_values, y = residuals(grades.reducedmlr),
     xlab = "Predicted values", ylab = "Residuals",
     main = "Residual plot for heteroscedasticity check")
```

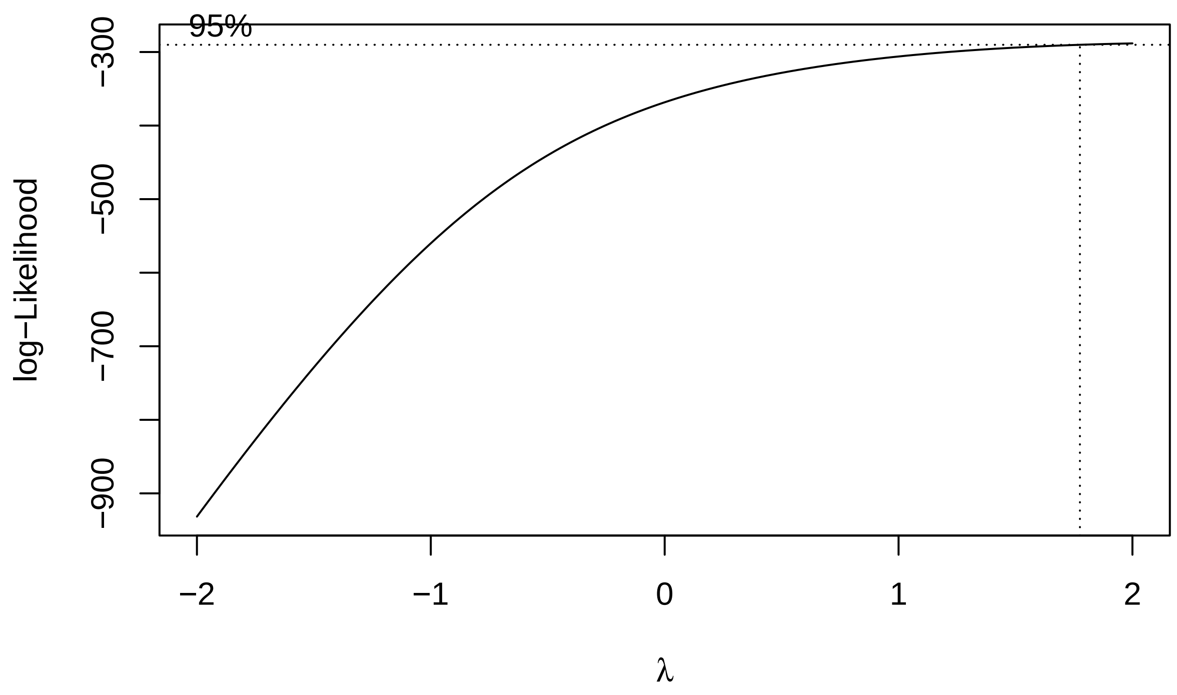


From the QQ plot, we can see that we seem to have departures from the normality assumption as points along the edges of the plot don't follow the straight line. We can attempt to remedy this and reduce the non-normality of the errors by performing a Box-Cox transformation.

```
library(MASS)
```

```
## Warning: package 'MASS' was built under R version 4.1.3
```

```
grades.transformation = boxcox(grades.reducedmlr, lambda=seq(-2, 2, length=400))
```

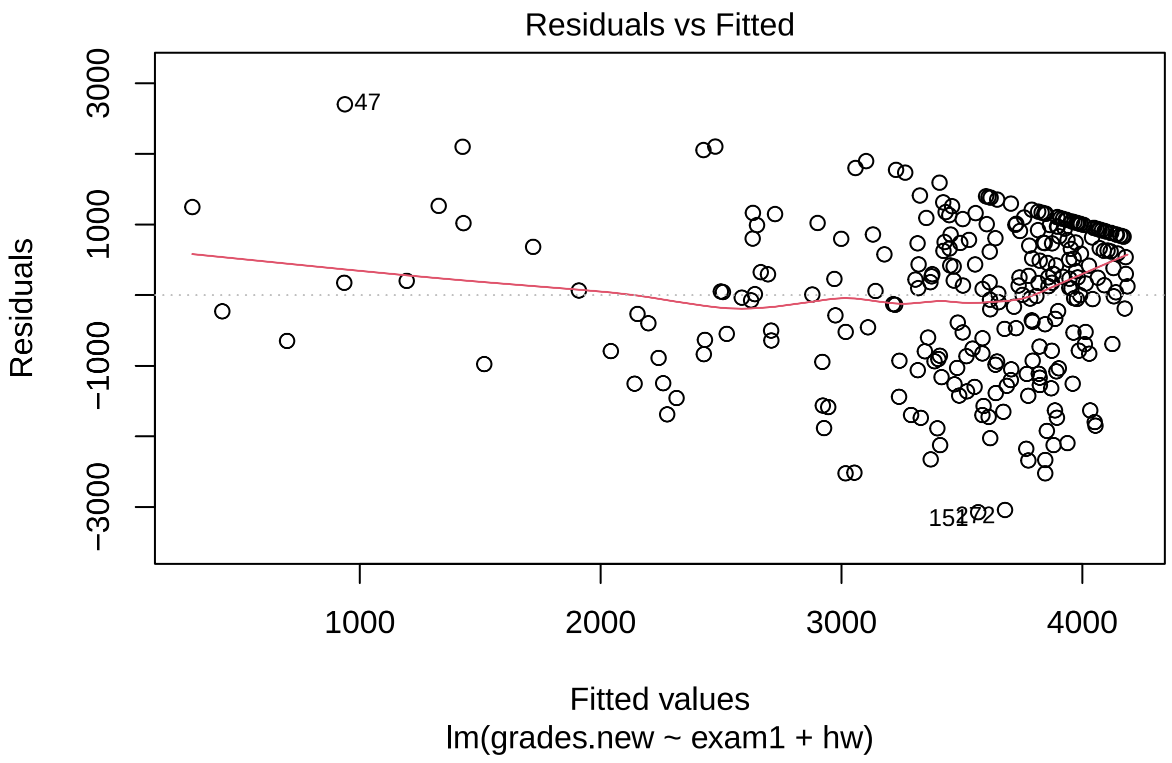


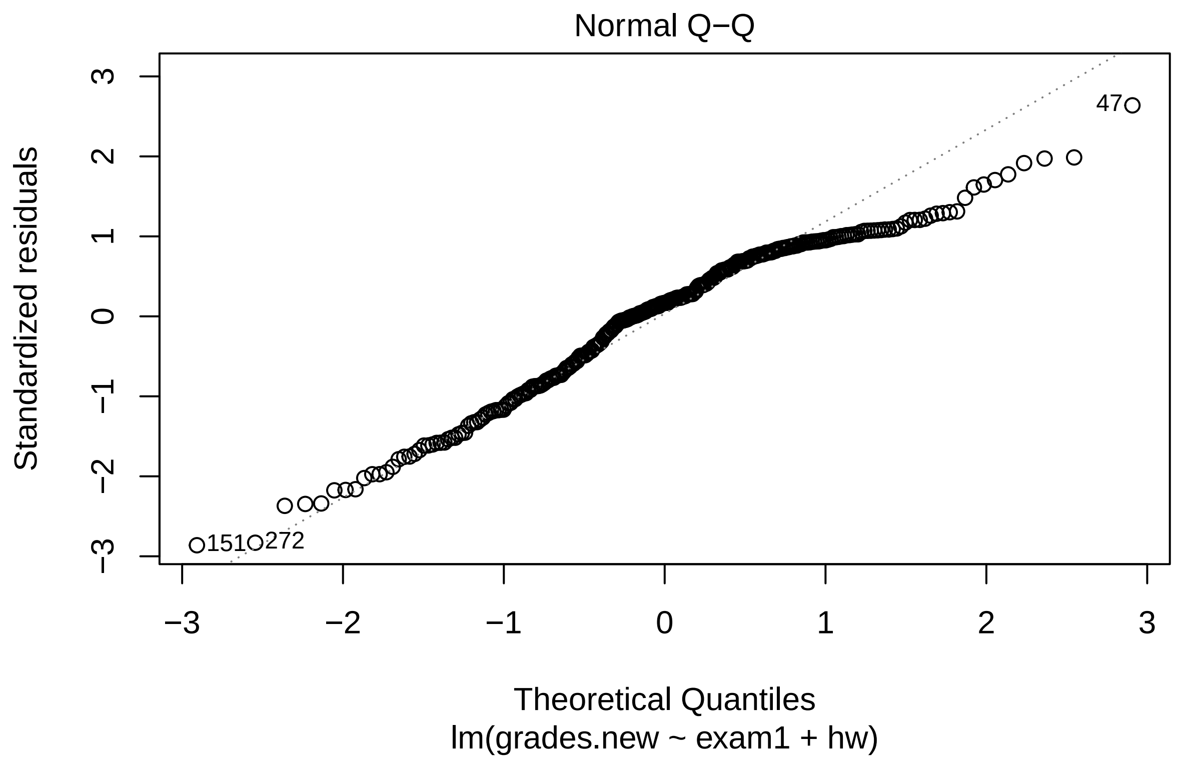
Looking at the Box-Cox plot, the optimal $\lambda$ is somewhere between 1.5 and 2. We can try both to see which provides better results.

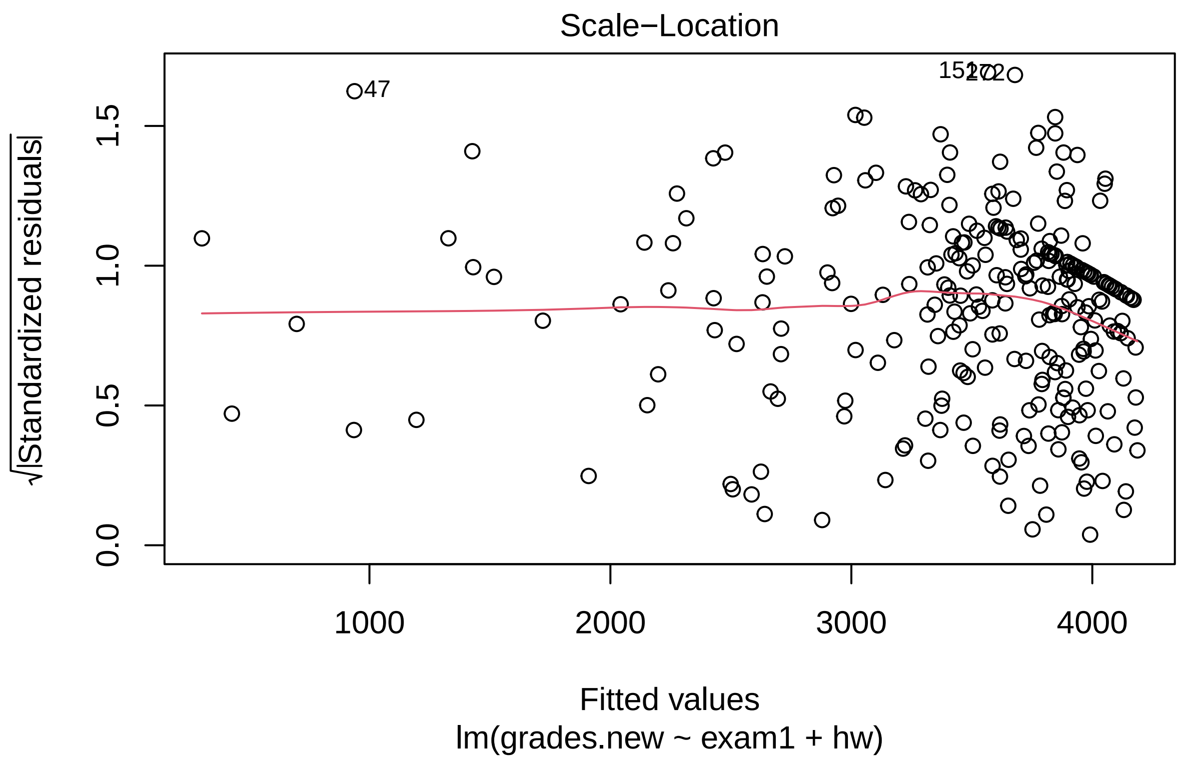
```
grades2 = grades
grades2$grades.new = ('^'(grades2$exam2,2)-1) / 2
grades.mlr.tr = lm(grades.new ~ exam1 + hw, data=grades2[])
summary(grades.mlr.tr)
```

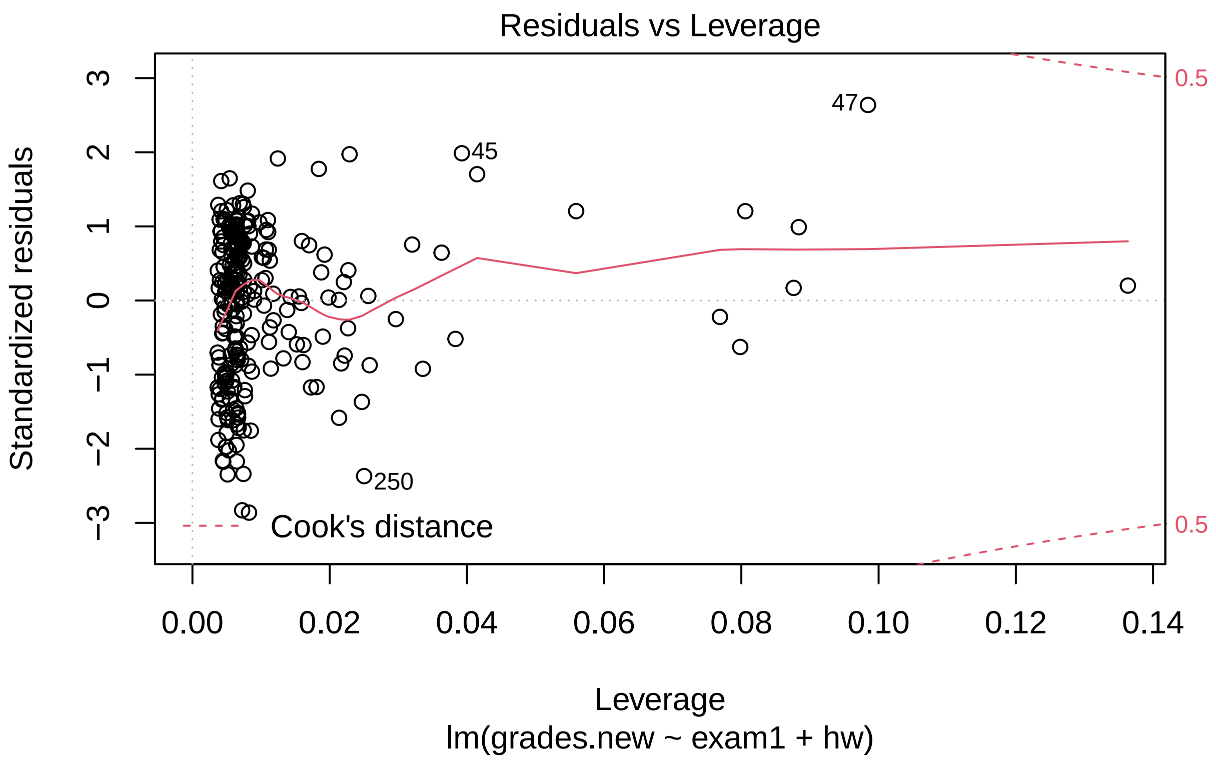
```
##
## Call:
## lm(formula = grades.new ~ exam1 + hw, data = grades2[])
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3074.2  -794.3   175.5   869.6  2702.0
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -526.872    415.703  -1.267    0.206
## exam1         15.659      5.018   3.120    0.002 **
## hw            31.640      4.269   7.412 1.58e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1079 on 272 degrees of freedom
## Multiple R-squared:  0.2932, Adjusted R-squared:  0.2881
## F-statistic: 56.43 on 2 and 272 DF,  p-value: < 2.2e-16
```

```
plot(grades.mlr.tr)
```




Normal Q−Q
Standardized residuals
Theoretical Quantiles
lm(grades.new ~ exam1 + hw)
151
272
47
−3
−2
−1
0
1
2
3


Scale−Location
√|Standardized residuals|
0.0
0.5
1.0
1.5
1000
2000
3000
4000
47
1517
272
Fitted values
lm(grades.new ~ exam1 + hw)



**Serial Dependence**

It is not possible to check serial dependence for this model because there is no order or time value associated with the data points.

**Unusual Observations**

```
grades.leverages = lm.influence(grades.reducedmlr)$hat
head(grades.leverages)
```

**High Leverage points**

```
##           1           2           3           4           5           6
## 0.007424924 0.007274227 0.006206353 0.006622878 0.005729212 0.005620944
```

```
n = dim(grades)[1]
p = length(variable.names(grades.reducedmlr))

grades.leverages.high = grades.leverages[grades.leverages>2*p/n]
grades.leverages.high
```

```
##         33         34         39         45         47         50         51 
## 0.02272018 0.02206615 0.02583001 0.03926475 0.09845203 0.03631088 0.05592355 
##        138        153        159        160        162        164        165 
## 0.04149202 0.02290199 0.03202090 0.03833443 0.02218738 0.02563467 0.02268266 
##        166        167        168        169        250        253        254 
## 0.08057361 0.03358242 0.08762130 0.07687729 0.02502428 0.07983386 0.13633458 
##        273        274        275 
## 0.02469497 0.02964430 0.08837007
```

There are 23 high leverage points within our reduced model versus 50 in our full model. These points have the potential of increasing variability, so having less in our reduced is ideal. This also shows how the dropped variables contributed to high leverage points in the full model.

```r
grades.leverages = lm.influence(grades.reducedmlr)$hat
head(grades.leverages)
```

### Outliers

```
##           1           2           3           4           5           6 
## 0.007424924 0.007274227 0.006206353 0.006622878 0.005729212 0.005620944
```

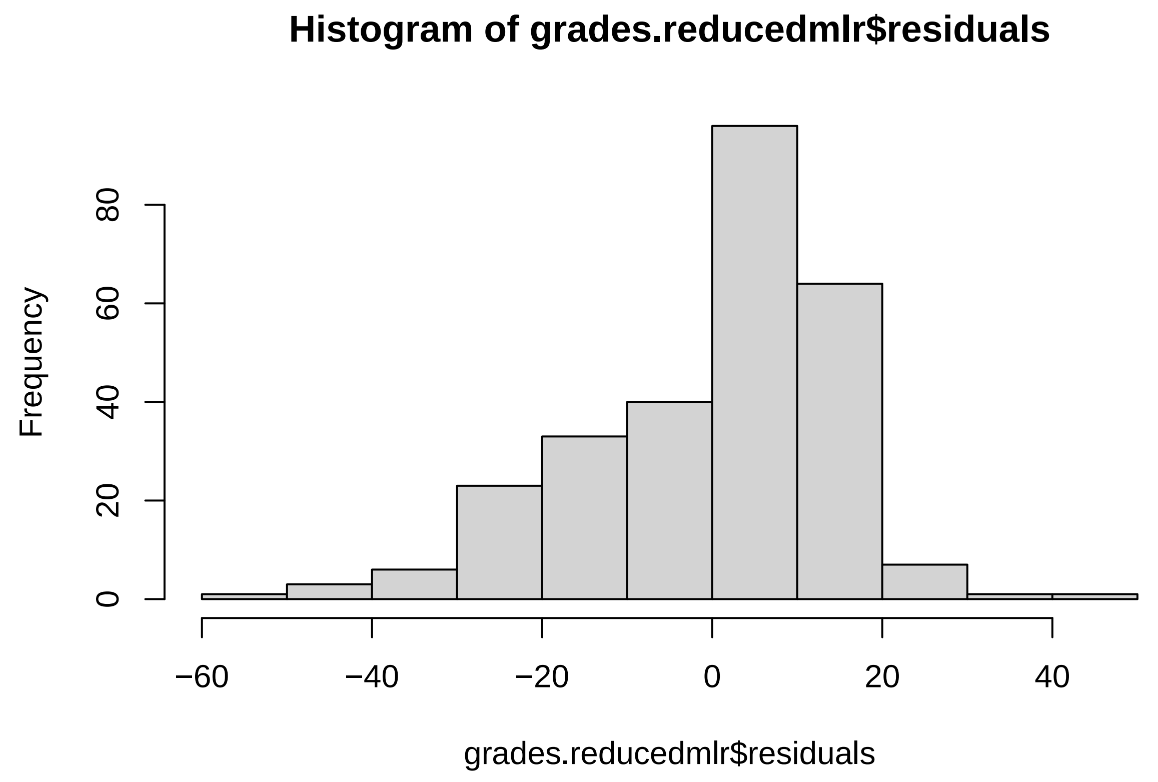
```r
n = dim(grades)[1]
p = length(variable.names(grades.reducedmlr))

# Computing Studentized Residuals
grades.resid = rstudent(grades.reducedmlr);

# Critical value WITH Bonferroni correction
bonferroni_cv = qt(.05/(2*n), n-p-1)

grades.resid.sorted = sort(abs(grades.resid), decreasing=TRUE)[1:10]
print(grades.resid.sorted)
```

```
##      151      272      250       47      247      227      241       45 
## 3.601063 3.404720 3.105902 3.005424 2.962759 2.462233 2.371182 2.263594 
##      253      226 
## 2.248131 2.229855
```

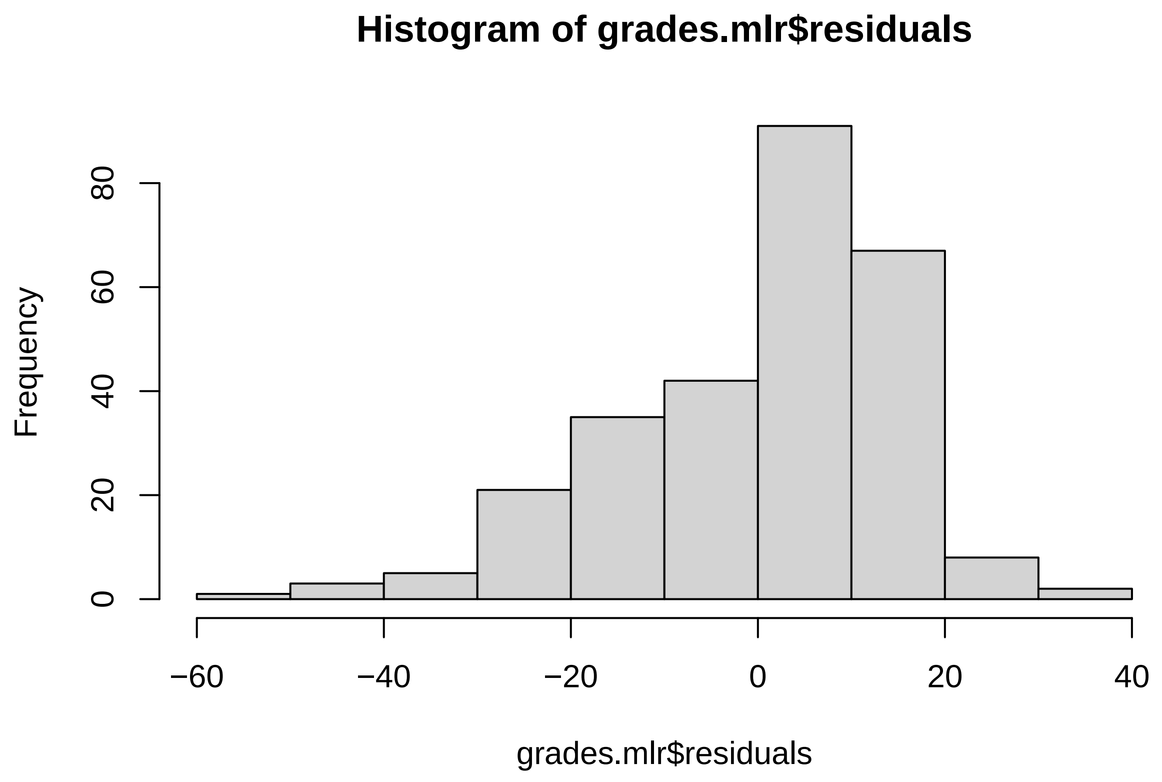
```r
grades.outliers = grades.resid.sorted[abs(grades.resid.sorted) > abs(bonferroni_cv)]
print(grades.outliers)
```

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

```r
hist(grades.reducedmlr$residuals)
```



```
hist(grades.mlr$residuals)
```

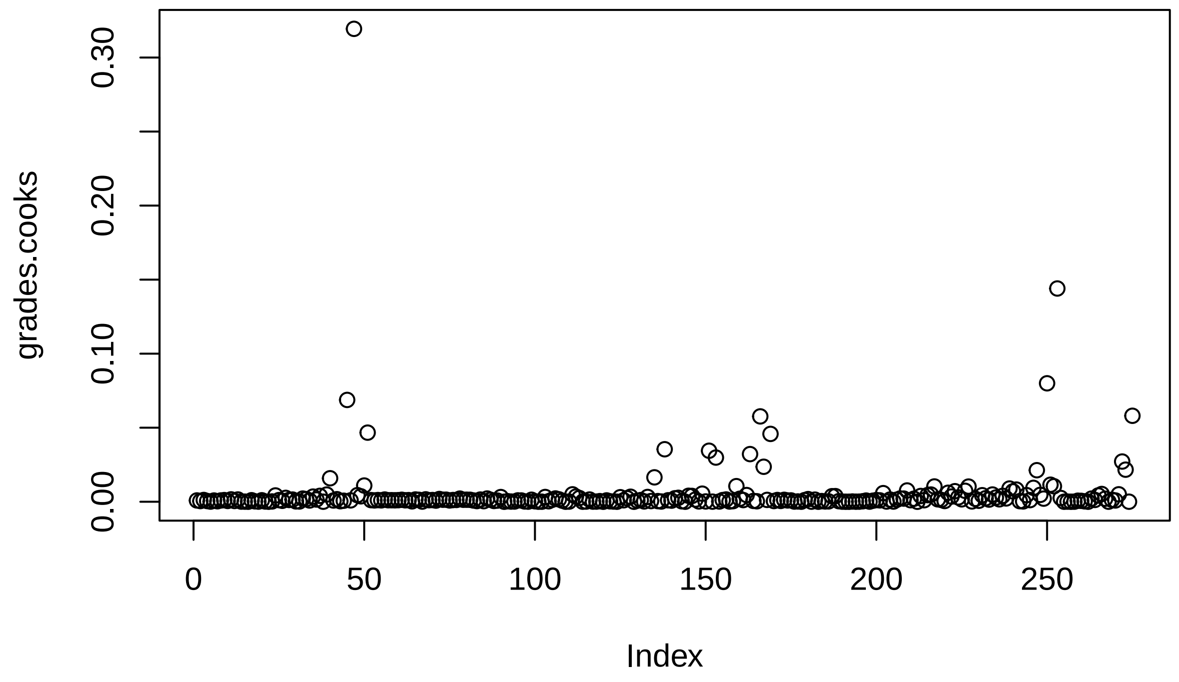


```
grades.cooks = cooks.distance(grades.reducedmlr)
sort(grades.cooks, decreasing = TRUE)[1:10]
```

**Influential Observations**

```
##         47        253        250         45        275        166         51
## 0.31936425 0.14401823 0.07998918 0.06876062 0.05806449 0.05763882 0.04667620
##        169        138        151
## 0.04581583 0.03546309 0.03443911
```

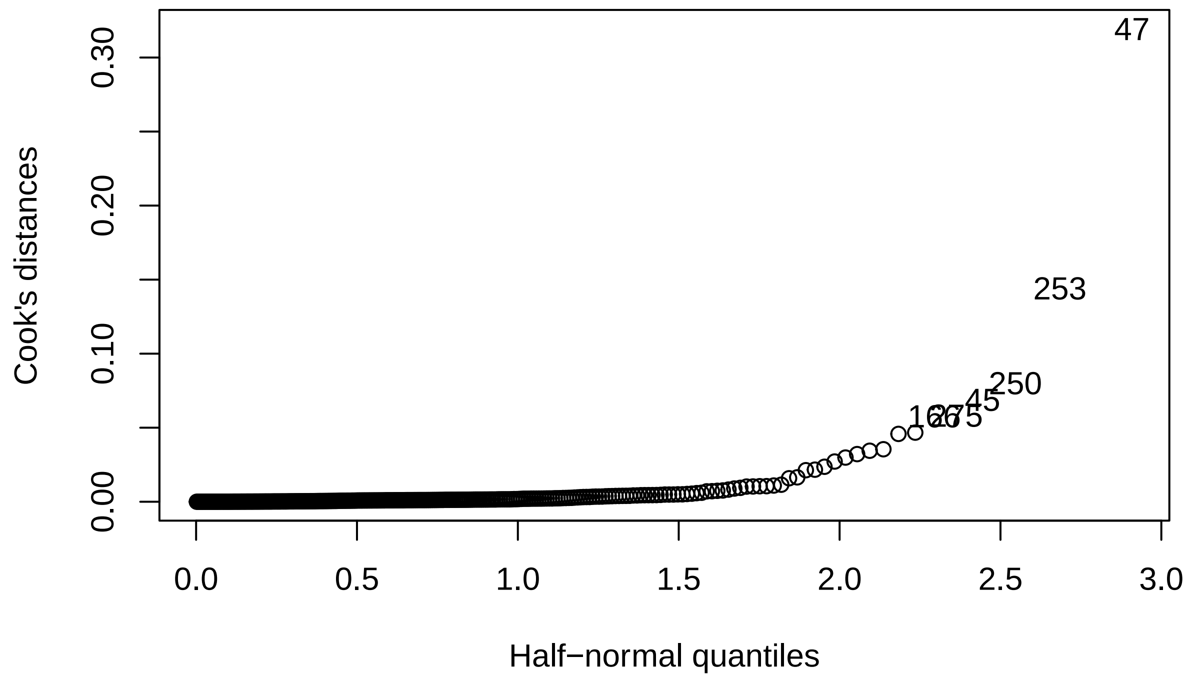
```
plot(grades.cooks)
```



```
library(faraway)
```

```
## Warning: package 'faraway' was built under R version 4.1.3
```

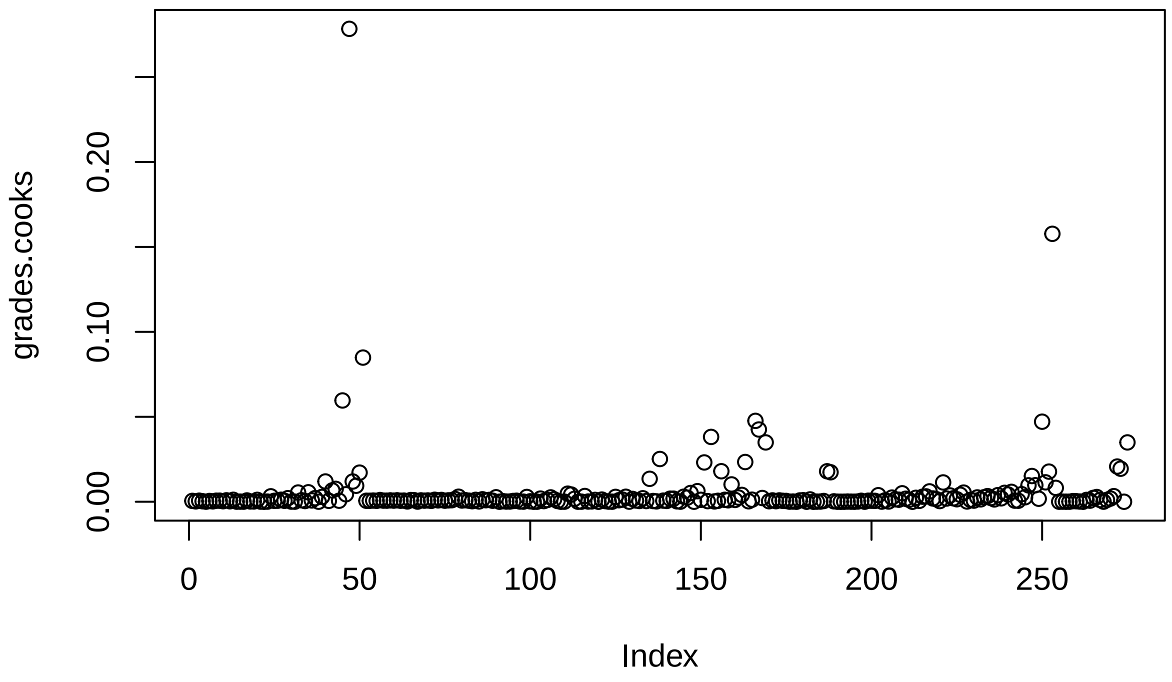
```
halfnorm(grades.cooks, 6, labs=as.character(1:length(grades.cooks)), ylab="Cook's distances")
```



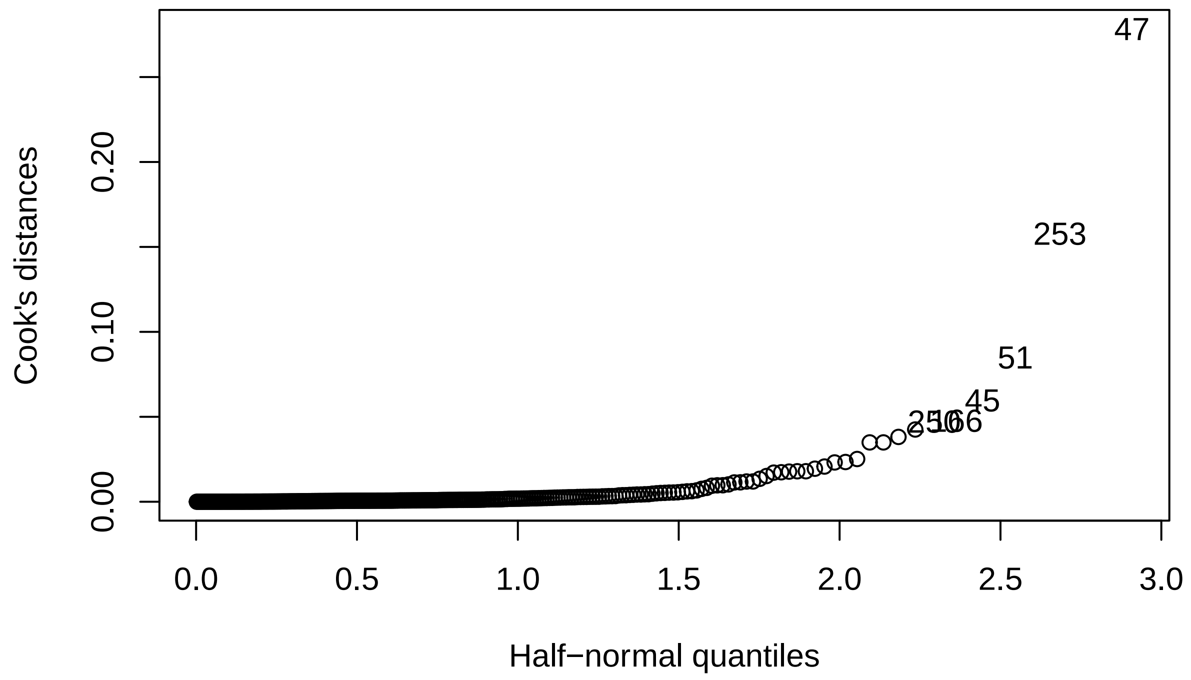
```
grades.cooks = cooks.distance(grades.mlr)
sort(grades.cooks, decreasing = TRUE)[1:10]
```

```
##         47        253         51         45        166        250        167
## 0.27837732 0.15771394 0.08485803 0.05961187 0.04761373 0.04711742 0.04252647
##        153        275        169
## 0.03816061 0.03492719 0.03492200
```

```
plot(grades.cooks)
```



```
library(faraway)
halfnorm(grades.cooks, 6, labs=as.character(1:length(grades.cooks)), ylab="Cook's distances")
```



The number of influential points between the reduced and full model remained the same. It is not bad because the number of points did not increase.