excercises_week_5

Lindsey Greenhill

2/24/2021

excercises 4.4 and 4.8

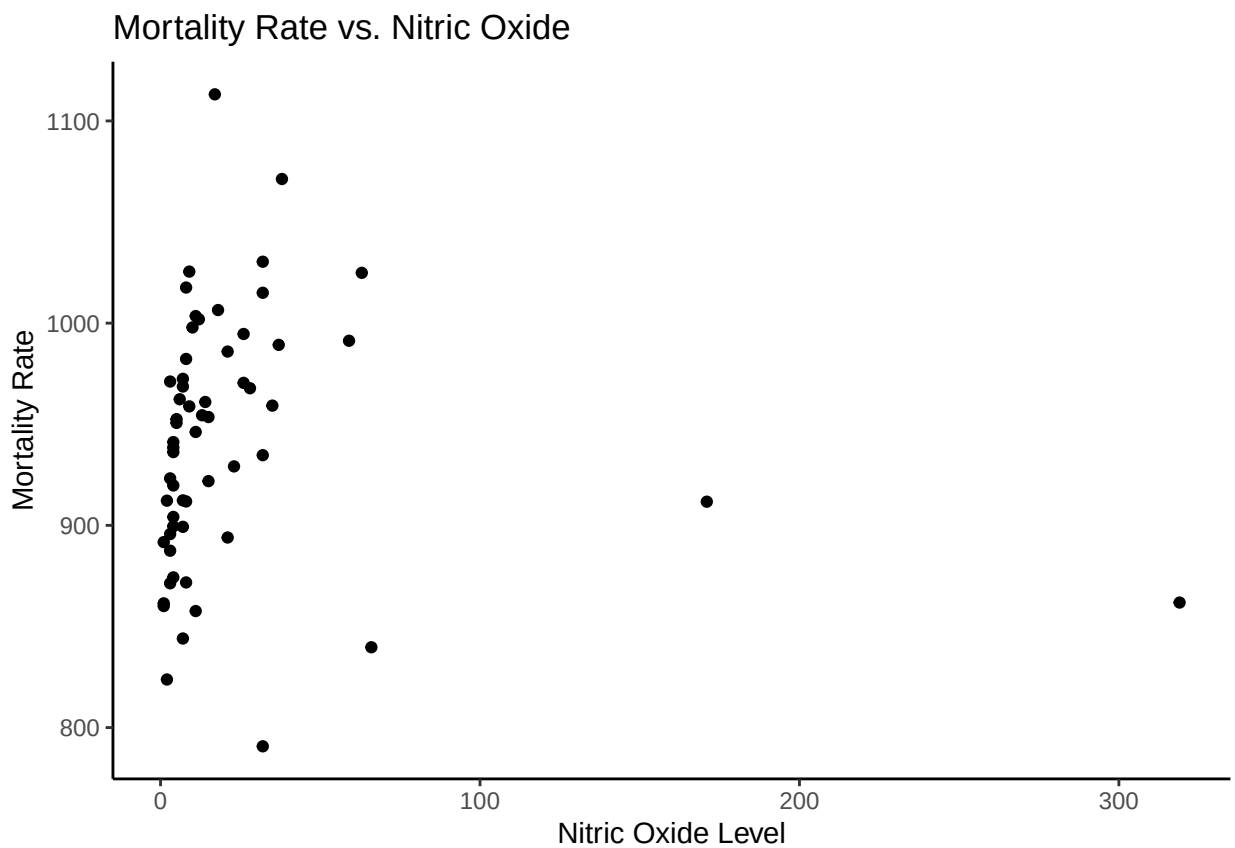
Question 3

Part a

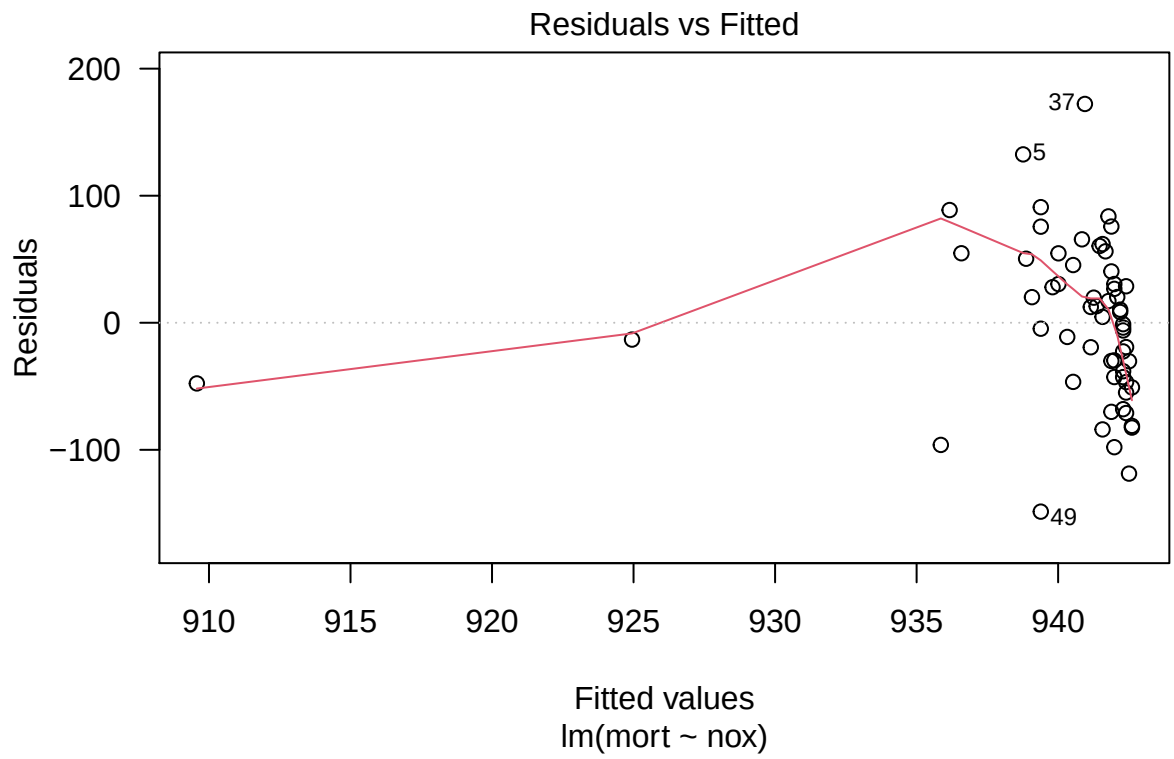
The scatterplot we created of Mortality rate vs. Nitric Oxide suggests that a linear regression without any transformations will not fit the data very well, as many of the data points are clustered around the start of the range and only a few data points appear around the end of the range.

Fitting a linear regression (fit_1) and looking at its residuals confirms that a linear regression may not be the best fit for this data. The residuals are not randomly distributed and are clustered at the end of the range, telling us that the linear regression is not a good fit.

```
# creating scatterplot. Data looks like a lot of the data is very clustered
# around 0 with some values much further away.

pollution %>%
  ggplot(aes(x = nox, y = mort)) +
  geom_point() +
  labs(title = "Mortality Rate vs. Nitric Oxide",
       x =  "Nitric Oxide Level",
       y =  "Mortality Rate") +
  theme_classic()
```



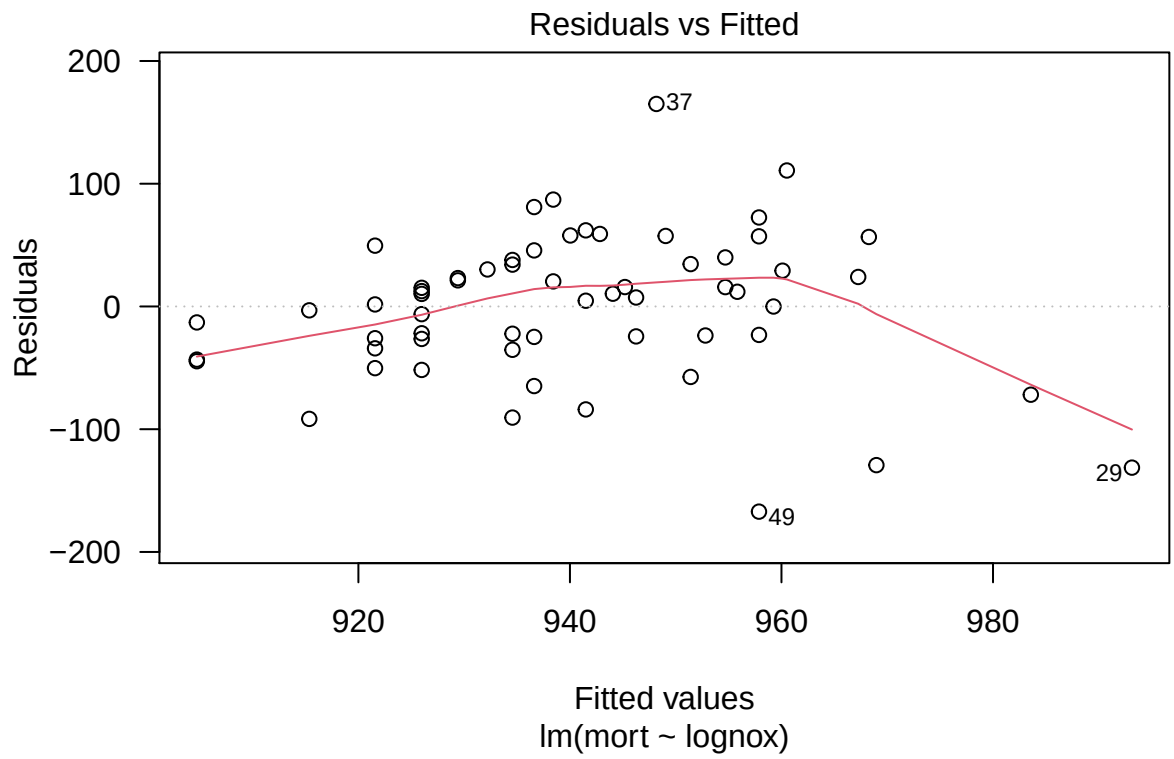

```r
# fitting the linear regression

fit_1 <- lm(mort ~ nox, data = pollution)

# creating the residuals

plot(fit_1, which = 1, las = 1, )
```



Part b

I chose to do a logarithmic transformation of the data, meaning that I ran a regression on mortality rate vs. log(nox), where nox is our nitric oxide variable from part a. The residuals for this regression look much better than the linear regression from part a. They are relatively randomly distributed and aren't clustered around any one point, telling us that the model is not a bad fit.

```
# creating a log version of nox

pollution <- pollution %>%
  mutate(lognox = log(nox))


fit_2 <- lm(mort ~ lognox, data = pollution)

# creating the residuals. This residual plots look a lot better than the other
# residuals. They are more randomly distributed and not clustered.

plot(fit_2, which = 1, las = 1, )
```



Part c

The slope coefficient from the model in b is 15.34. The interpretation of this coefficient is a difference of 1% in nitric oxide levels is associated with an (approximate) positive difference of .1534% in mortality rate on average.

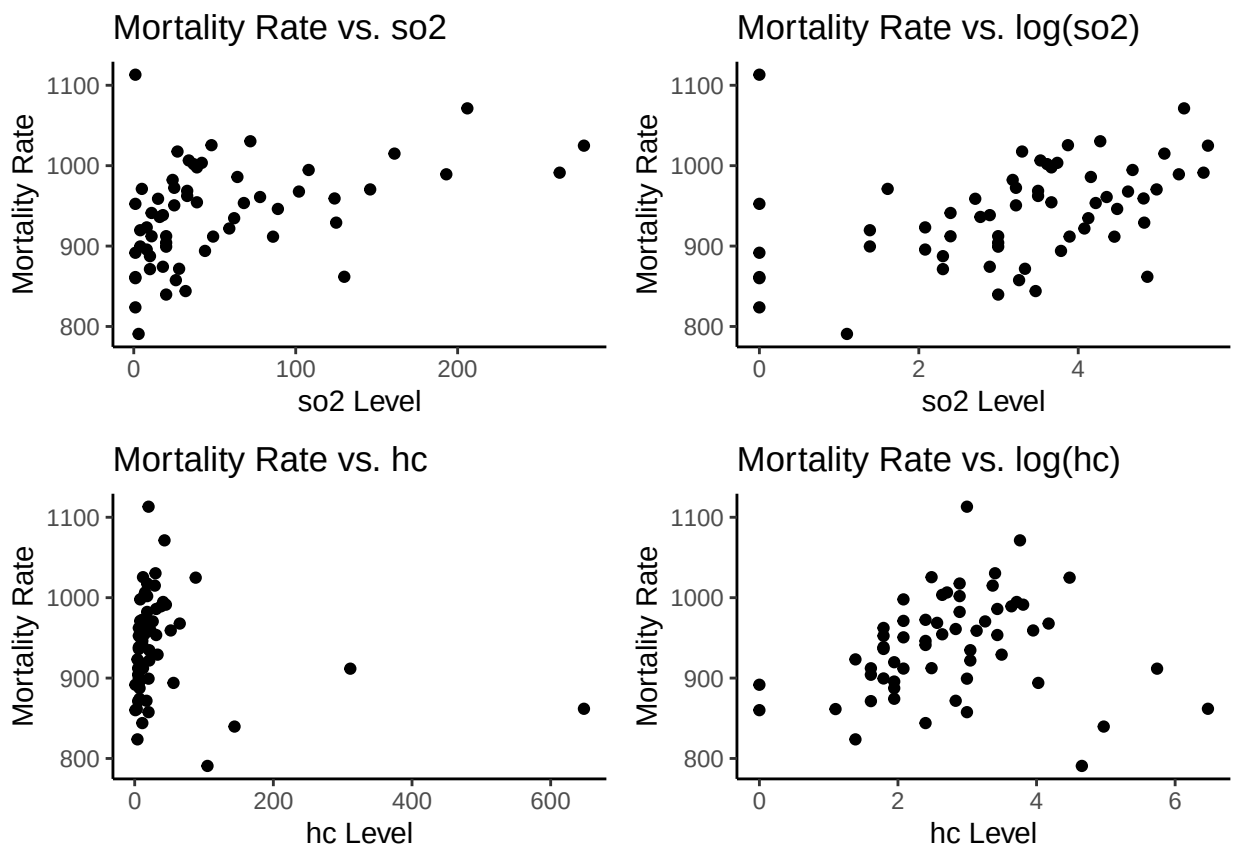
Part d

To determine whether or not I should use logarithmic transformations for sulfur dioxide and hydrocarbons, I ran a linear regression on mortality rate vs. each variable and mortality rate vs. each log variable and compared the scatter plots and residual plots.

The graphs below show the scatter plots for both the non log so2 and hc variables as well as the log verison of each variable. It looks like a logarithmic transformation might be a better fit for for both of these variables based on their scatterplots. I will confirm this by looking at the residual plots for each variable.

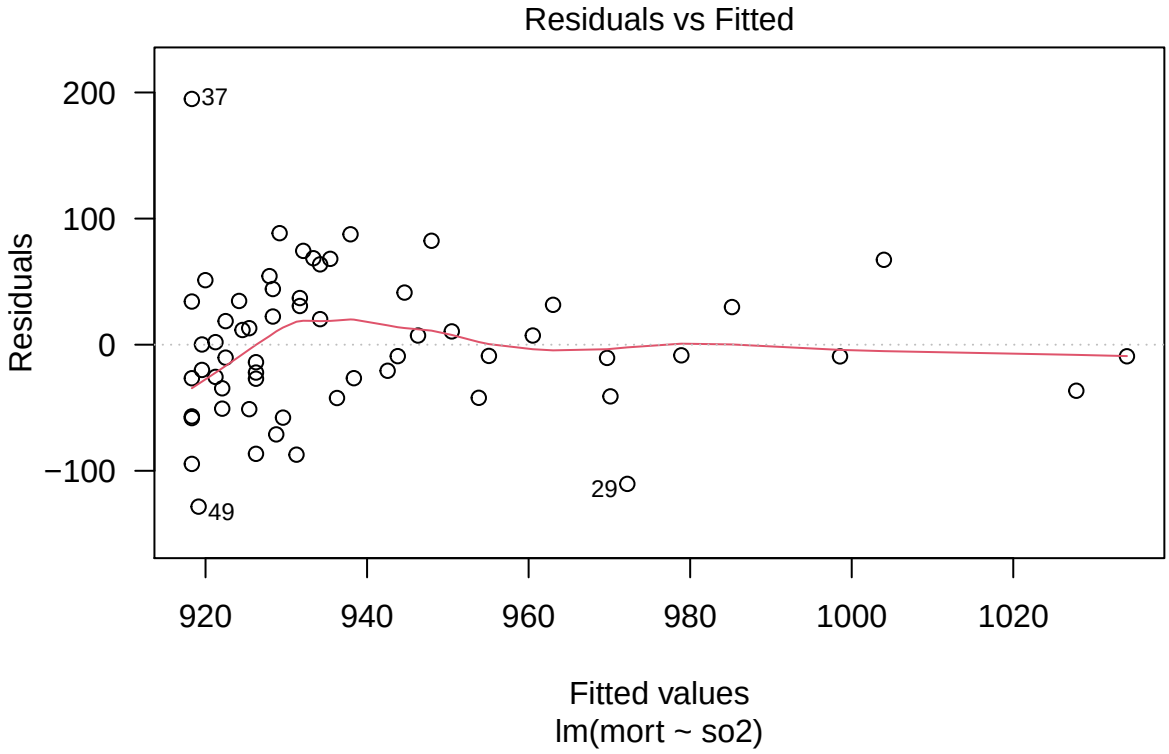
```
# creating logged versions of the variables

pollution <- pollution %>%
  mutate(logso2 = log(so2),
         loghc = log(hc),
         logmort = log(mort))

# maybe want to do the log of so2
```

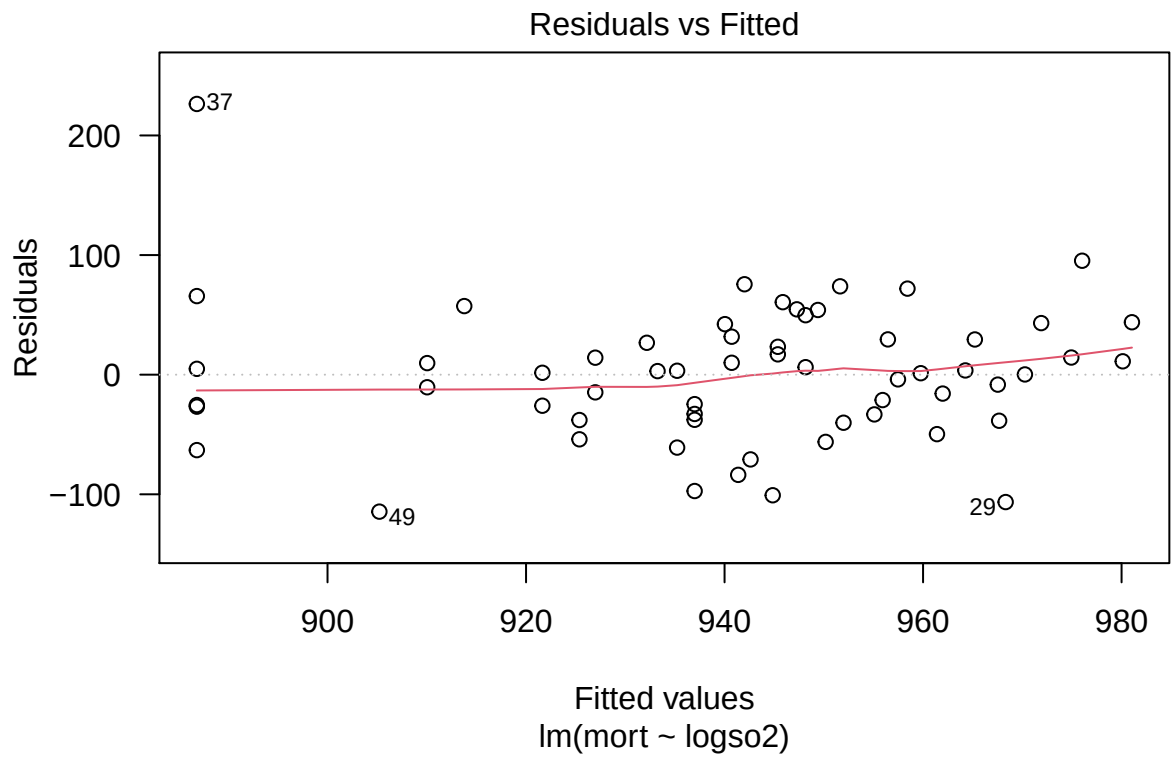
```r
so2_plot <- pollution %>%
  ggplot(aes(x = so2, y = mort)) +
  geom_point() +
  labs(title = "Mortality Rate vs. so2",
       x =  "so2 Level",
       y =  "Mortality Rate") +
  theme_classic()

# definitely want to do the log of hc

hc_plot <- pollution %>%
  ggplot(aes(x = hc, y = mort)) +
  geom_point() +
  labs(title = "Mortality Rate vs. hc",
       x =  "hc Level",
       y =  "Mortality Rate") +
  theme_classic()

logso2_plot <- pollution %>%
  ggplot(aes(x = logso2, y = mort)) +
  geom_point() +
  labs(title = "Mortality Rate vs. log(so2)",
       x =  "so2 Level",
       y =  "Mortality Rate") +
  theme_classic()

# definitely want to do the log of hc

loghc_plot <- pollution %>%
  ggplot(aes(x = loghc, y = mort)) +
  geom_point() +
  labs(title = "Mortality Rate vs. log(hc)",
       x =  "hc Level",
       y =  "Mortality Rate") +
  theme_classic()

ggarrange(so2_plot, logso2_plot,
          hc_plot, loghc_plot)
```



The plots below show the residuals for the so2 model and the log(so2) model. The residuals for the log model look more randomly distributed than the residuals for the non log model, so I am inclined to use the logso2 variable in my final model.

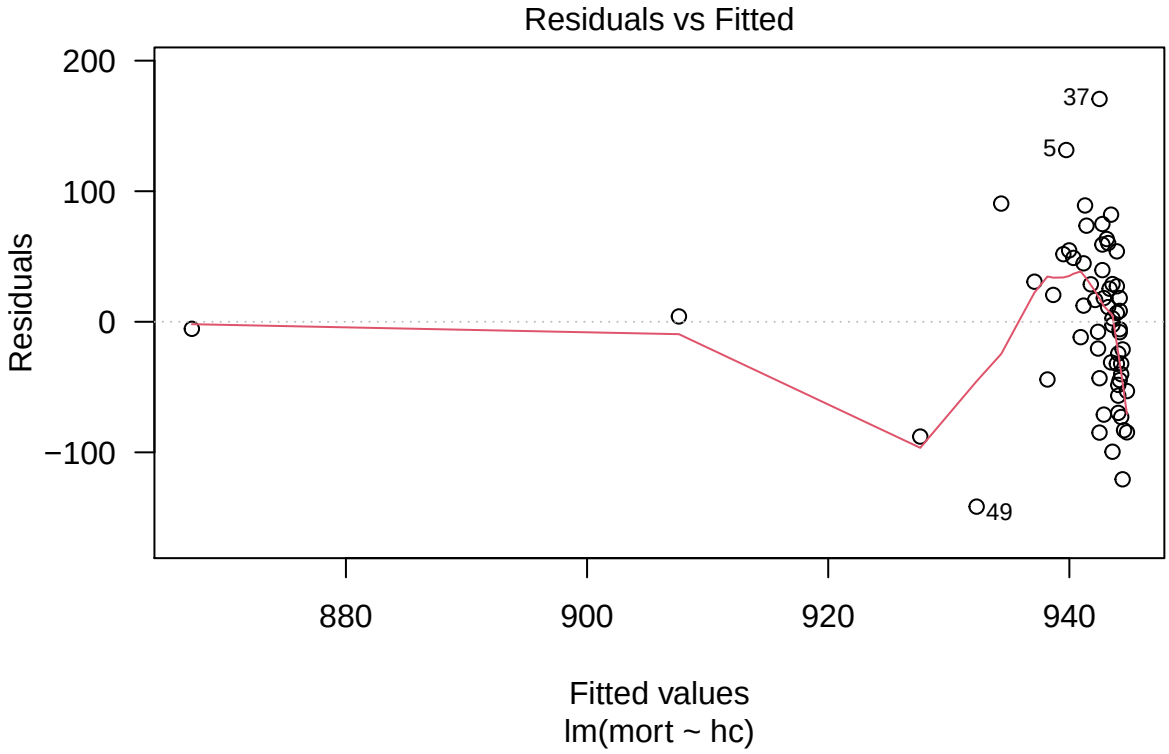
```
# creating models and residual plots for so2 and hc for log and non log

fit_so2 <- lm(mort ~ so2, data = pollution)
fit_logso2 <- lm(mort ~ logso2, data = pollution)

fit_hc <- lm(mort ~ hc, data = pollution)
fit_loghc <- lm(mort ~ loghc, data = pollution)

# using par to display all of them together
{
plot(fit_so2, which = 1, las = 1, )
plot(fit_logso2, which = 1, las = 1, )
}
```

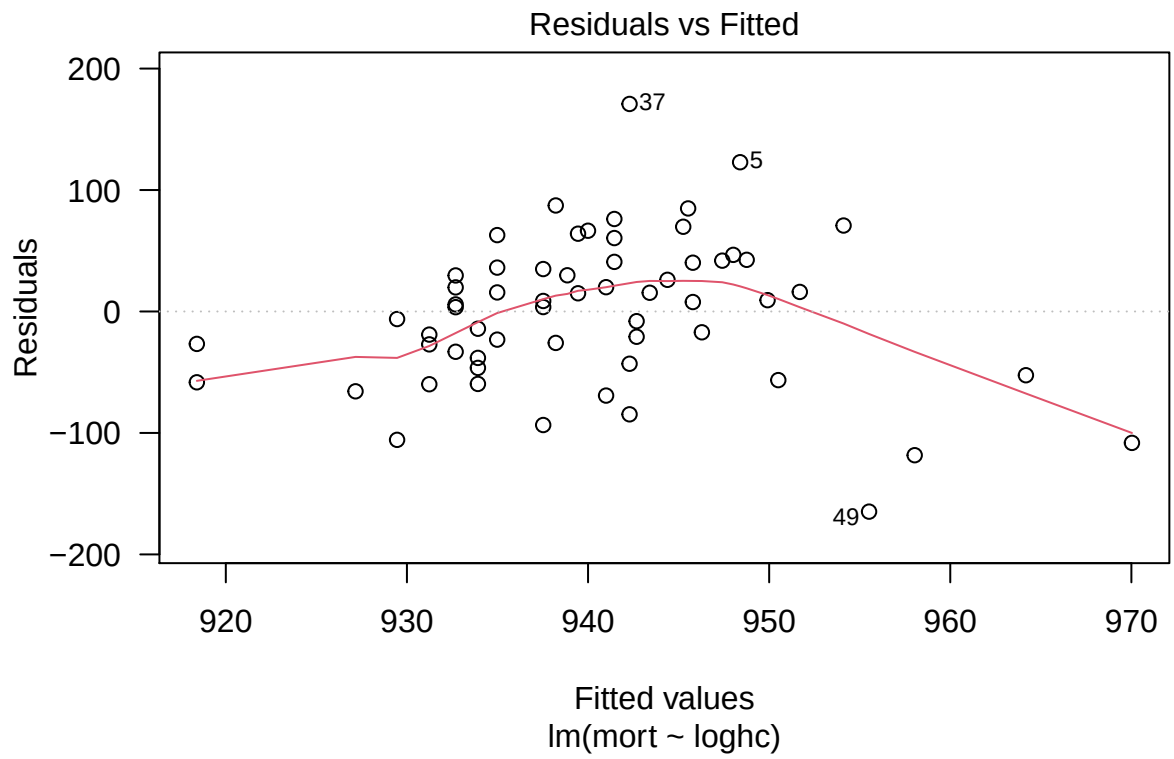

Residuals vs Fitted
Residuals
Fitted values
lm(mort ~ so2)
200
100
0
−100
920
940
960
980
1000
1020
37
49
29



The plots below show the residuals for the hc model and the log(hc) model. The residuals for the log model look dramatically more randomly distributed than the residuals for the non log model, so I am inclined to use the loghc variable in my final model.

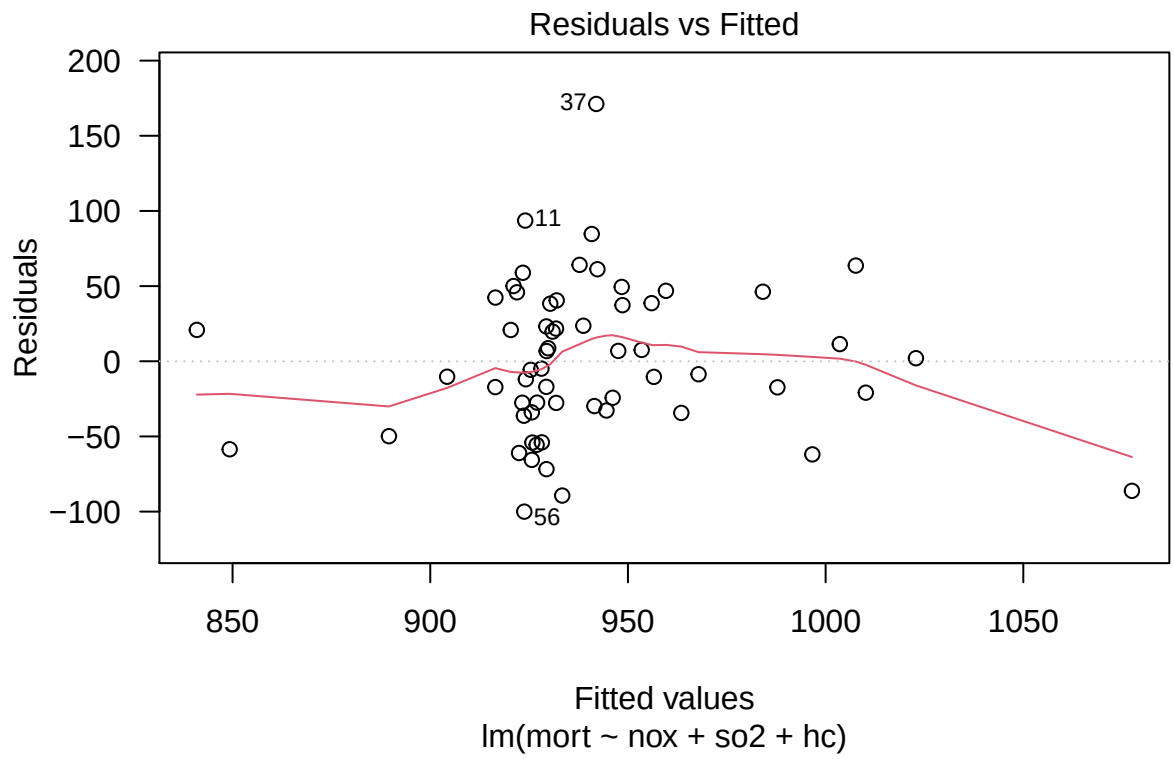
```
{
plot(fit_hc, which = 1, las = 1, )
plot(fit_loghc, which = 1, las = 1, )
}
```


Residuals vs Fitted
Residuals
Fitted values
lm(mort ~ hc)
200
100
0
−100
880
900
920
940
37
5
49

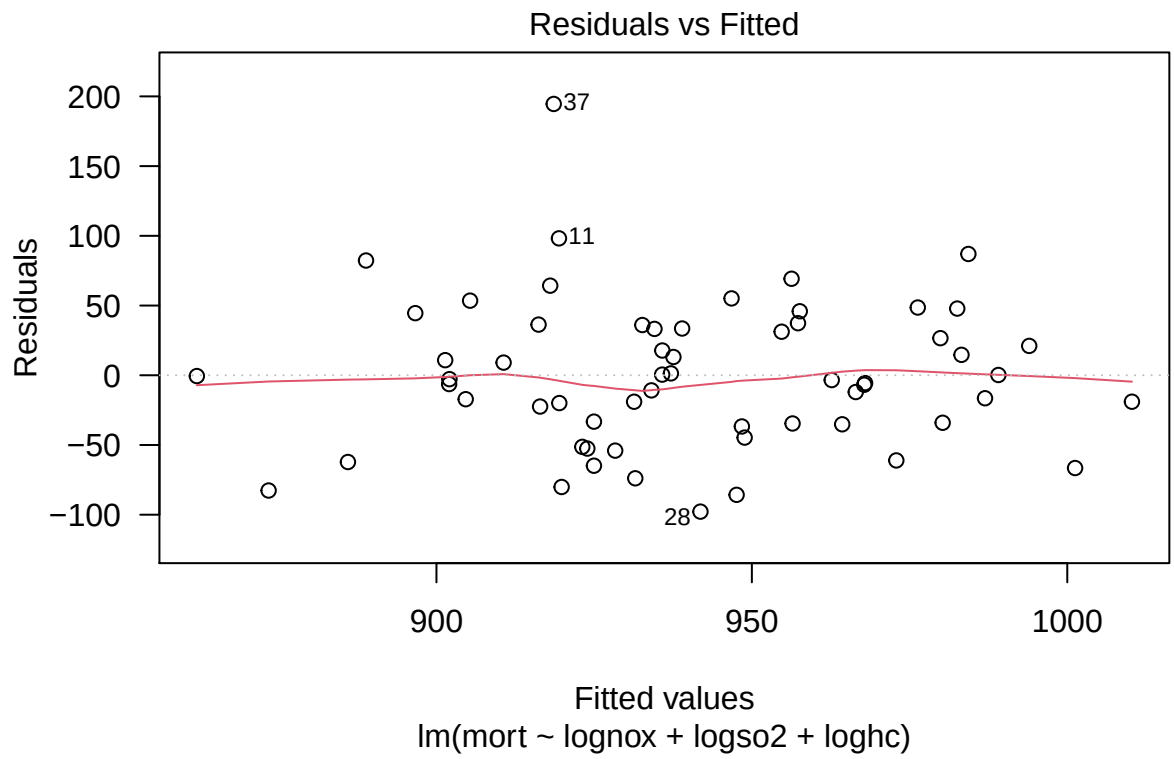


The plots below compare the residuals for the non log and log regressions including nox, so2, and hc (at this point, y is still not in log form). The residuals for the log regression are more evenly distributed and random, confirming my decision above to use the log version of both so2 and hc.

```
# creating two regression to compare

fit_all <- lm(mort ~ nox + so2 + hc, data = pollution)

fit_all_log <- lm(mort ~ lognox + logso2 + loghc, data = pollution)

# the residuals look better for the logged model

plot(fit_all, which = 1, las = 1, )
```



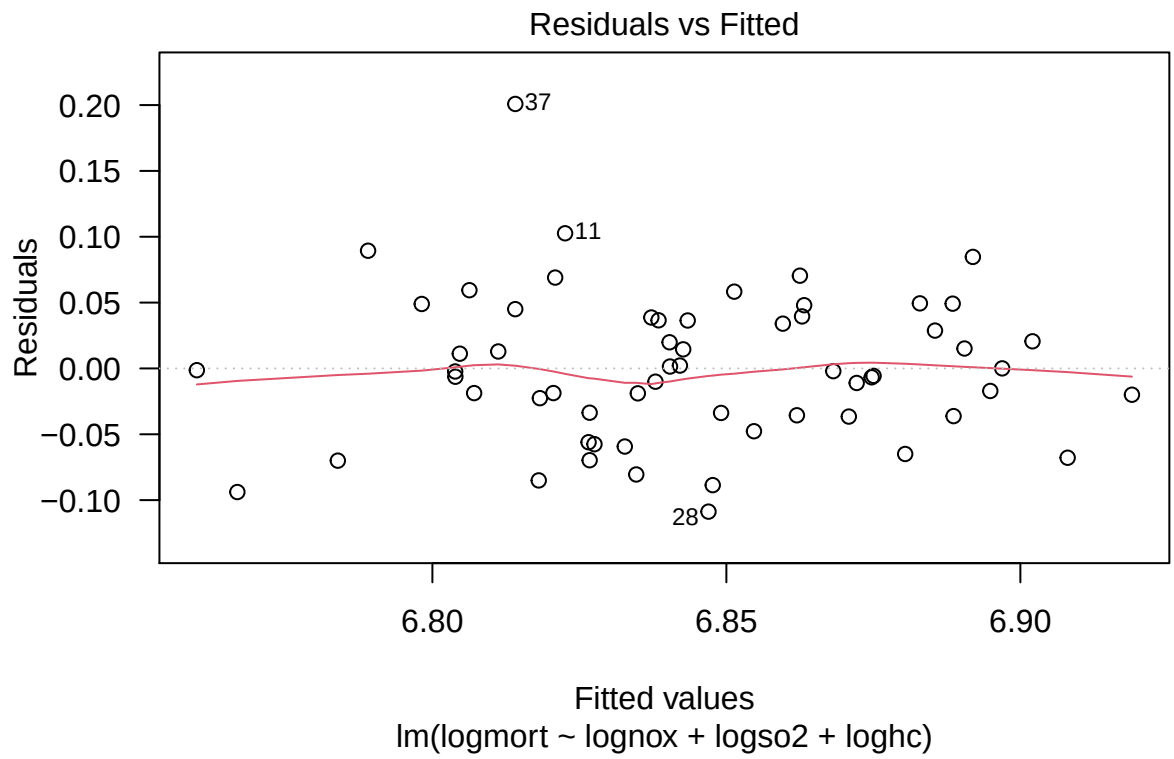

```r
plot(fit_all_log, which = 1, las = 1, )
```




```
# log level.
# level log: 1% change in x is associated with a beta/100 change in y, on average
# log log: 1% change in x is associated with a beta % change in y
```

I also decided to see how running a regression on log mortality rate vs the log other variables affected the model. I would prefer to have both sides of the regression be logged, so the interpretation of the coefficients is simpler. Looking at the residual plot below, using log y in the regression doesn't appear to make the residuals any less random, so I will use log mortality in my model.

```
# benefit of also logging y: the coefficients become easier to interpret

fit_all_log_y <- lm(logmort ~ lognox + logso2 + loghc, data = pollution)

# logging the y doesn't seem to make the residuals less random

plot(fit_all_log_y, which = 1, las = 1, )
```

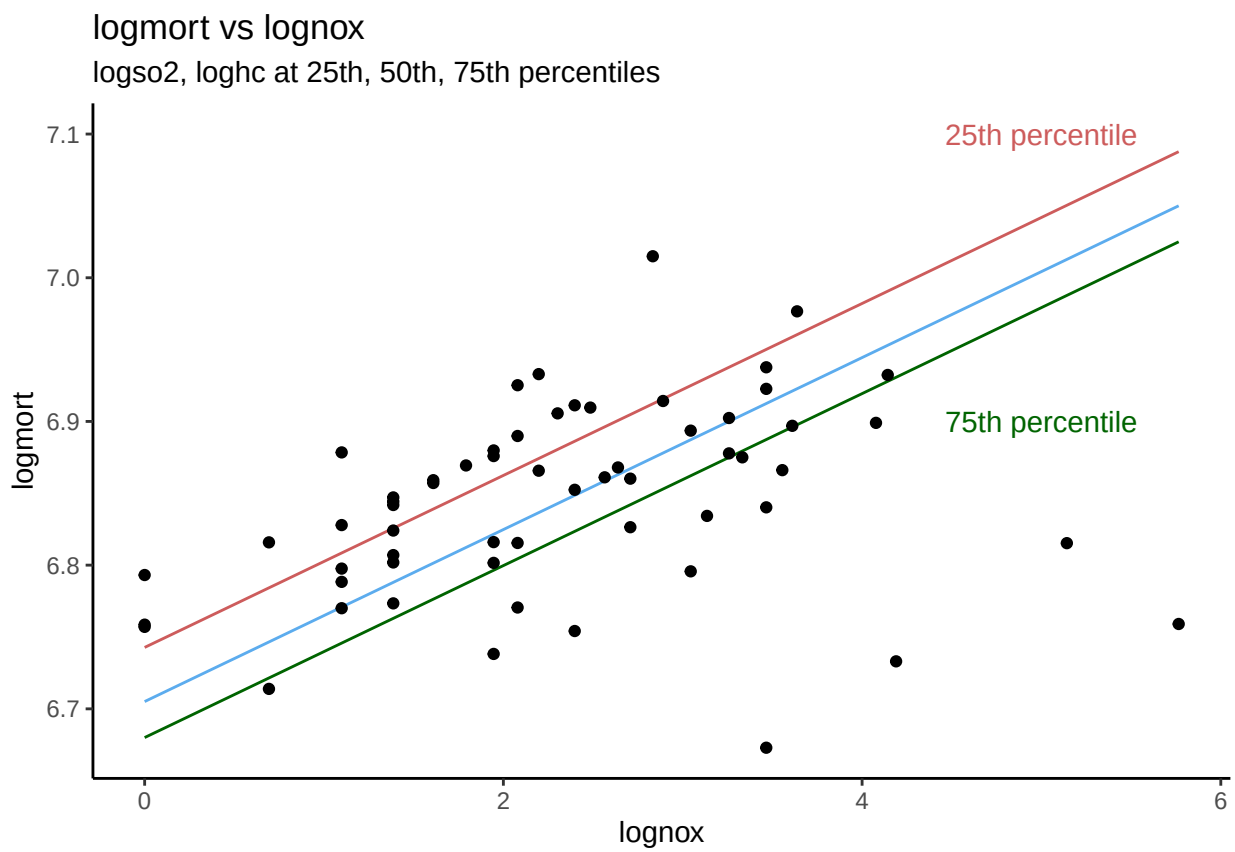


The plot below shows the fitted regression model. Because I couldn't include all 3 IV's, I displayed logmort vs lognox with loghc and logso2 held constant at their 25th, 50th, and 75th quantiles.

The table below shows the regression results for the model.

```
# showing plot of fitted model

pollution %>%
  ggplot(aes(y = logmort)) +
  stat_function(fun = function(.x) 6.82675
                + .05984*.x +
                  (.01431*mean(pollution$logso2)) +
                  (-.06081*mean(pollution$loghc)),
                col  = "steelblue2") +
    stat_function(fun = function(.x) 6.82675
                + .05984*.x +
                  (.01431*quantile(pollution$logso2, probs = .25)) +
                  (-.06081*quantile(pollution$loghc, probs = .25)),
                col  = "indianred") +
      stat_function(fun = function(.x) 6.82675
                + .05984*.x +
                  (.01431*quantile(pollution$logso2, probs = .75)) +
                  (-.06081*quantile(pollution$loghc, probs = .75)),
                col  = "darkgreen") +
  annotate("text", x = 5, y = 6.9, label = "75th percentile",
           col = "darkgreen") +
    annotate("text", x = 5, y = 7.1, label = "25th percentile",
```

```
          col = "indianred") +
  geom_point(aes(x = pollution$lognox)) +
  labs(title = "logmort vs lognox",
       subtitle = "logso2, loghc at 25th, 50th, 75th percentiles",
       x = "lognox") +
  theme_classic()
```




```
# showing regression table

stargazer(fit_all_log_y, type = "latex",
          title = "Regression Results Log Model")
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Tue, Mar 02, 2021 - 19:58:30

The coefficient for lognox is .06. In context, this means that a 1% increase in nitric oxide levels is associated with a .06% increase in mortality rate, on average.

The coefficient for logso2 is .014. In context, this means that a 1% increase in so2 levels is associated with a .014% increase in mortality rate, on average.

the coefficient for loghc is -.061. In context, this means that a 1% increase in hc levels is associated with a .061% decrease in mortality rate, on average.

Table 1: Regression Results Log Model

	Dependent variable:
	logmort
lognox	0.060**
	(0.023)
logso2	0.014*
	(0.008)
loghc	−0.061***
	(0.021)
Constant	6.827***
	(0.023)
Observations	60
R^2	0.285
Adjusted R^2	0.247
Residual Std. Error	0.058 (df = 56)
F Statistic	7.449*** (df = 3; 56)
Note:	*p<0.1; **p<0.05; ***p<0.01

Part e

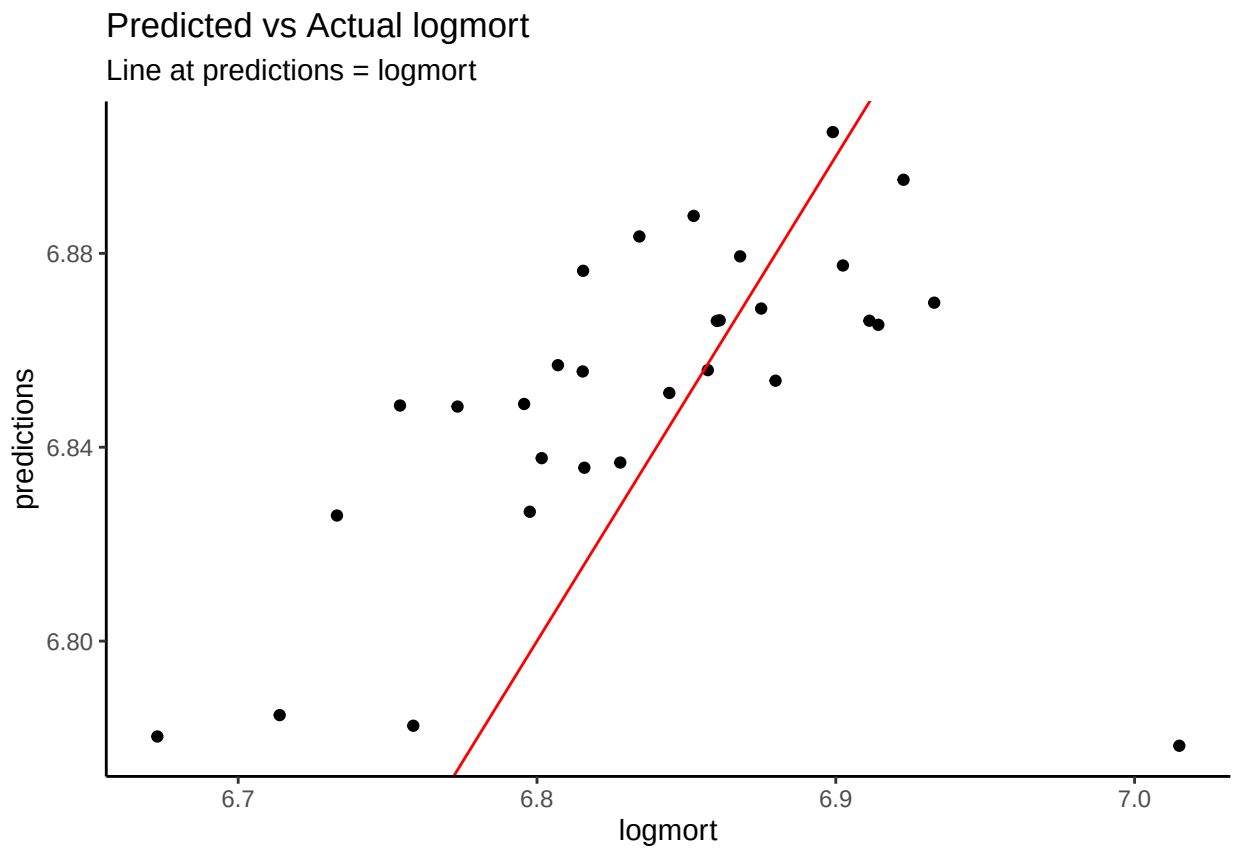
```
# taking first 30 rows of data

pol_train <- pollution %>%
  head(30)

# taking last 30 rows of data

pol_test <- pollution %>%
  tail(30)

# fitting the training model

fit_all_log_y_train <- lm(logmort ~ lognox + logso2 + loghc, data = pol_train)

# creating predictions with test data

predictions <- predict(fit_all_log_y_train, newdata = pol_test)

pred_df <- cbind(predictions, pol_test)
```

The plot below shows the predicted values of logmort vs. the actual values of logmort from the second half of the data frame. The points to the left of the line are overpredictions and the points to the right of the line are underpredictions. From this plot, it appears that the predictions are relatively close to their true values, but the model overestimated more points than underestimated.

Additionally, the Mean Squared Error of the predictions is .004, which is hard to interpret on its own without

conparisonns to other models, but also seems very small to me. Thus, I think the model performed well cross-validation wise.

```
# plot of yhat vs y

pred_df %>%
  ggplot(aes(x = logmort, y = predictions)) +
  geom_point() +
  geom_abline(slope = 1, intercept = 0, col = "red") +
  labs(title = "Predicted vs Actual logmort",
       subtitle = "Line at predictions = logmort") +
  theme_classic()
```

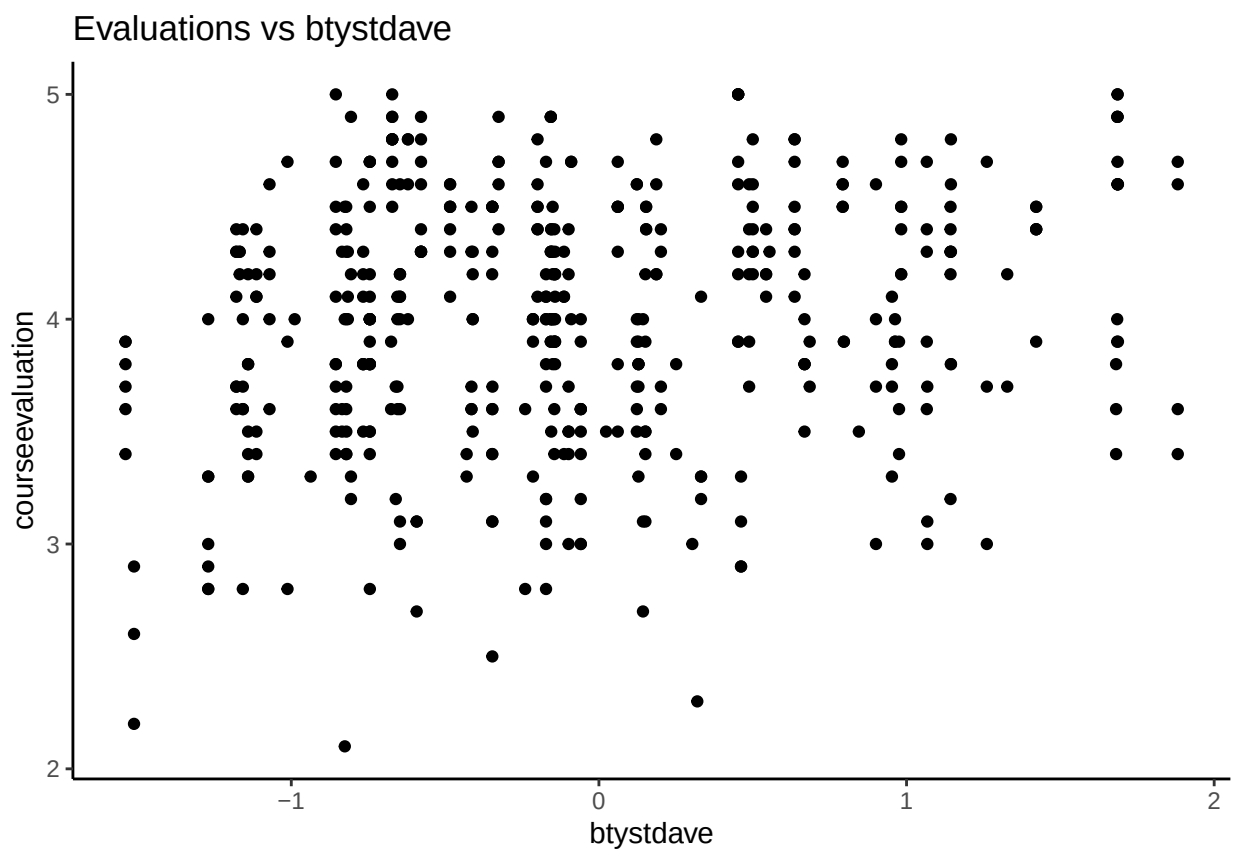



```
# calculating MSE

pred_df <- pred_df %>%
  mutate(sq_error = (predictions - logmort)^2)

MSE <- sum(pred_df$sq_error) / nrow(pred_df)
```

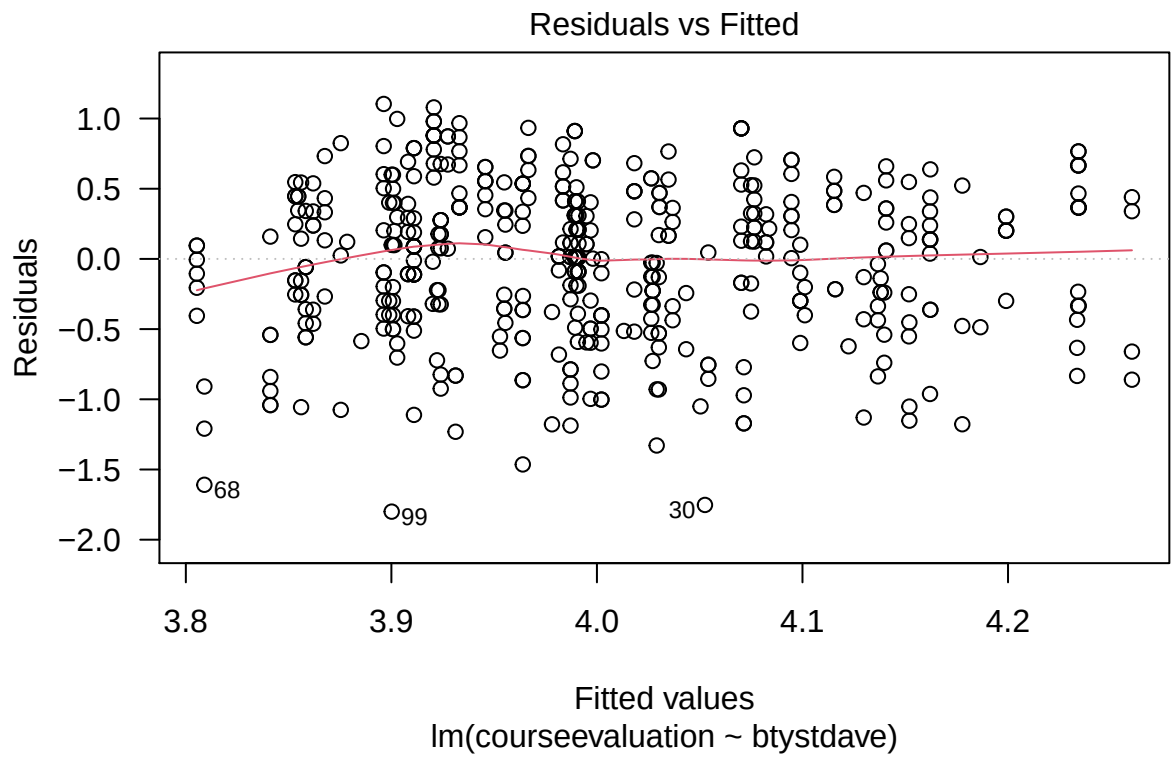
Question 8

For this question, I decided to start by looking at the scatter plot and regression of course evaluations vs the beauty standard deviation score. From the scatter plot and residual plot, it appears than linear regression is a good fit for the data.

```r
# looking at btystdave. The residuals seem to be clustered more toward the
# minimum of the range.

fit_bty <- lm(courseevaluation ~ btystdave, data = beauty)

bty_plot <- ggplot(beauty, aes(x = btystdave, y = courseevaluation)) +
  geom_point() +
  labs(title = "Evaluations vs btystdave") +
  theme_classic()

bty_plot
```




```r
plot(fit_bty, which = 1, las = 1, )
```

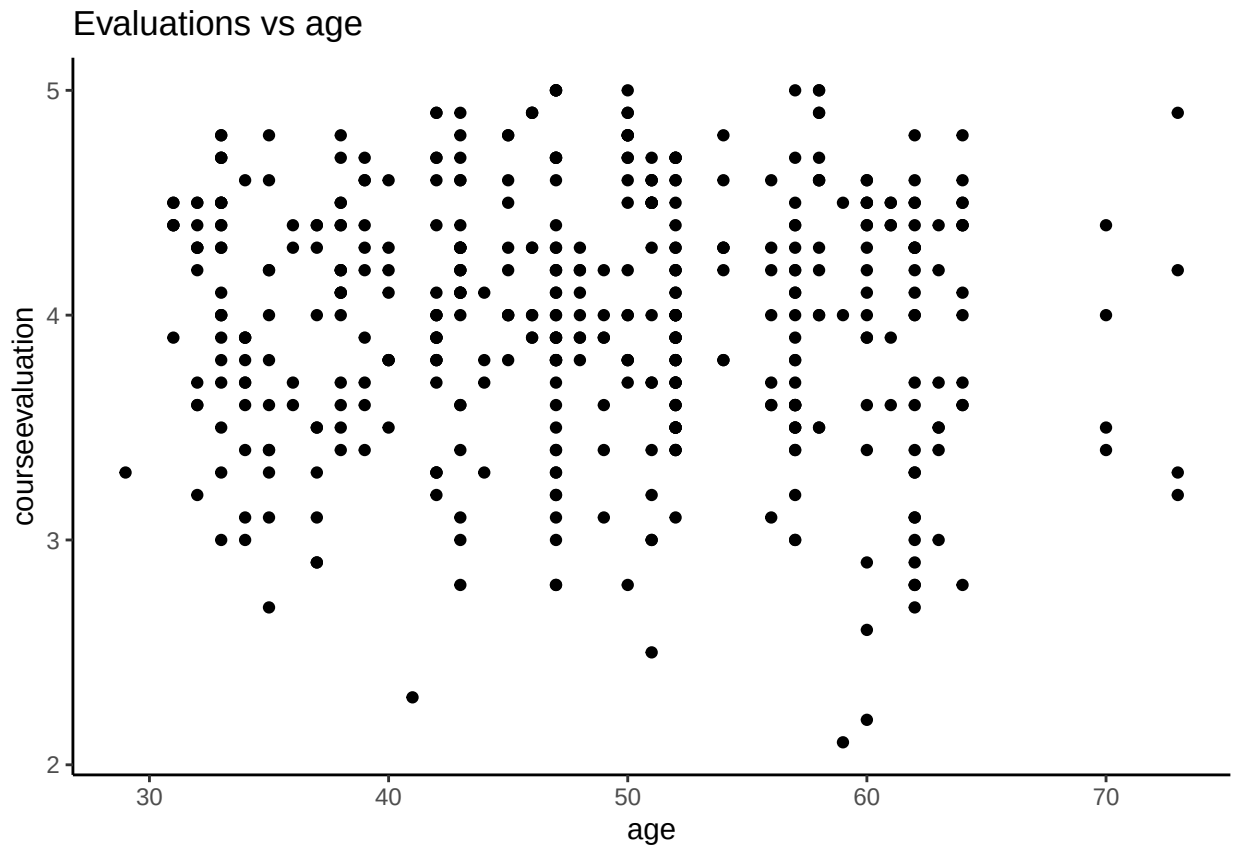


I think decided to look at the age ("age") and class enrollment ("student") variables to add to the model. I looked at the scatter plots and residual plots of course evaluations vs each variable to determine whether or not a linear model would be a good fit.

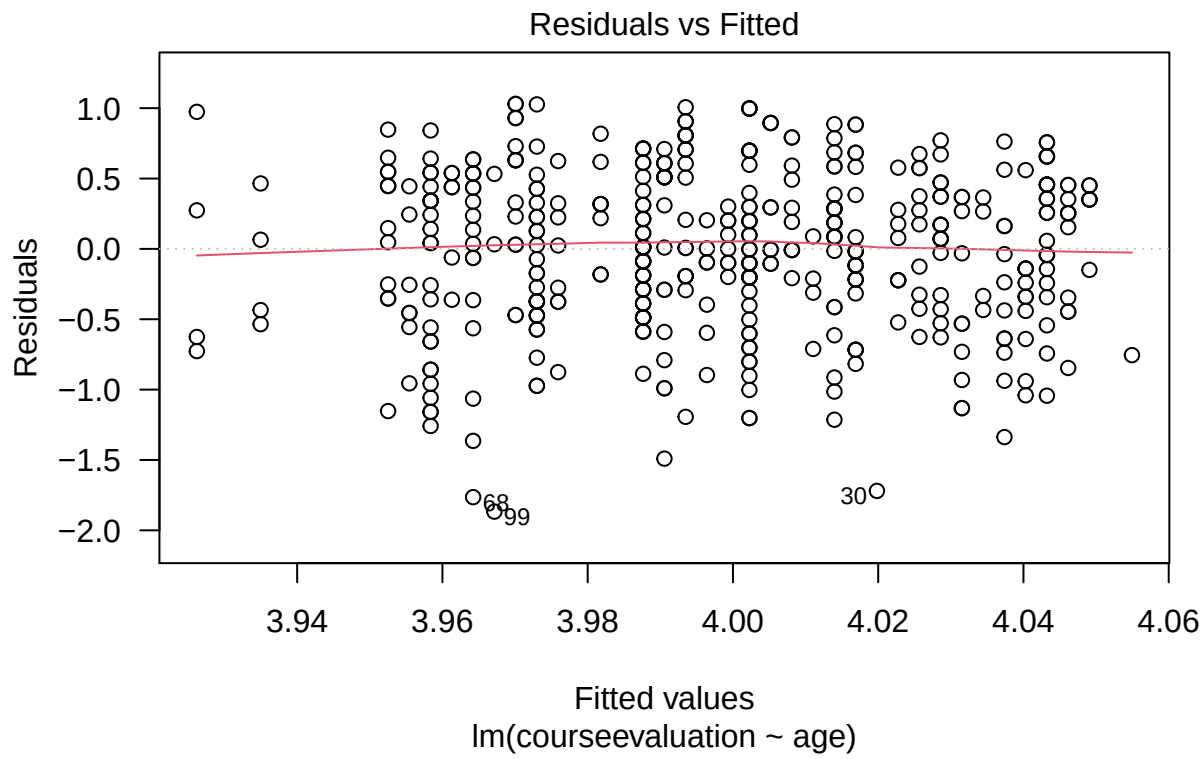
course evaluation vs age

The plots below suggest that the variables may not have any relationship, however, I will still look at the variable in variations of my final model. The data does not appear to need to be transformed.

```
# looking at age. I see quadratic transformations happen with age a lot, so
# maybe I should try it

fit_age <- lm(courseevaluation ~ age, data = beauty)

age_plot <- ggplot(beauty, aes(x = age, y = courseevaluation)) +
  geom_point() +
  labs(title = "Evaluations vs age") +
  theme_classic()

age_plot
```



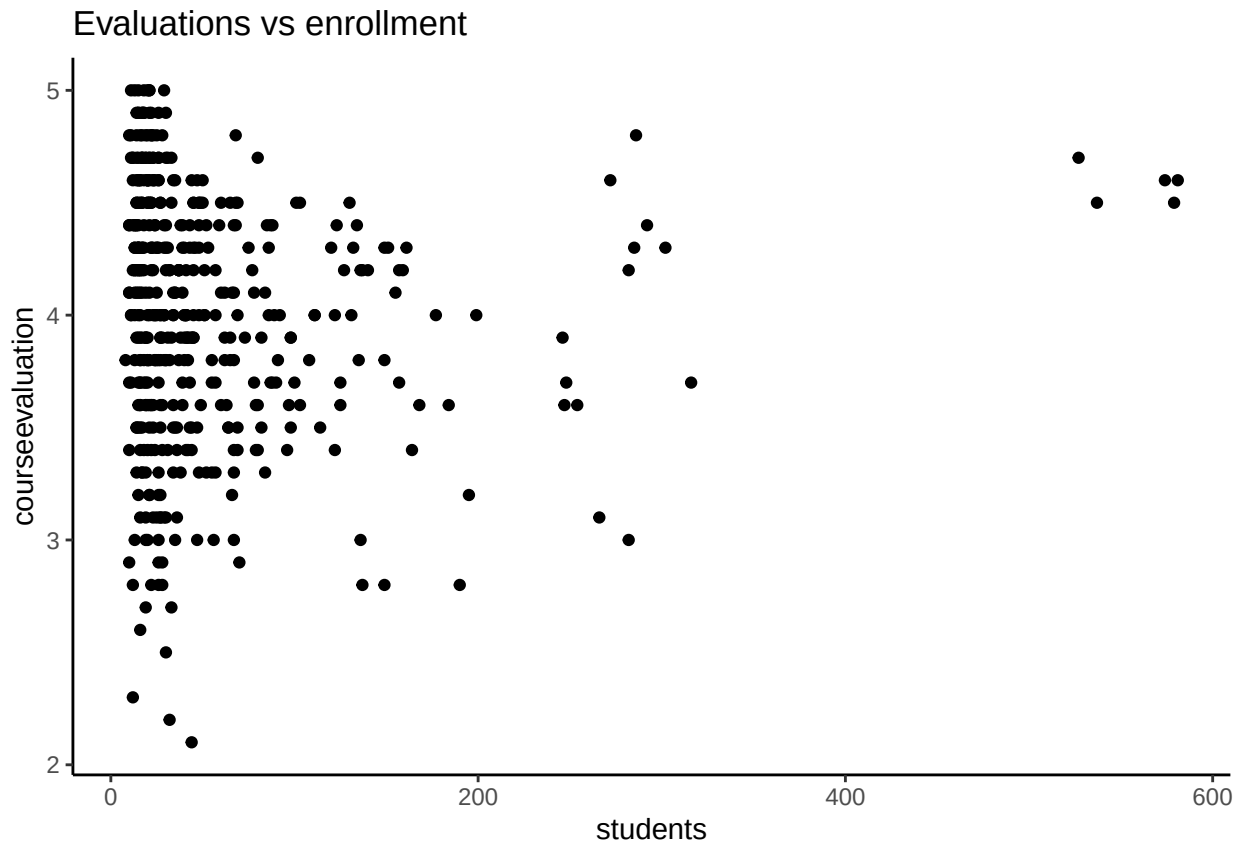

```
plot(fit_age, which = 1, las = 1, )
```



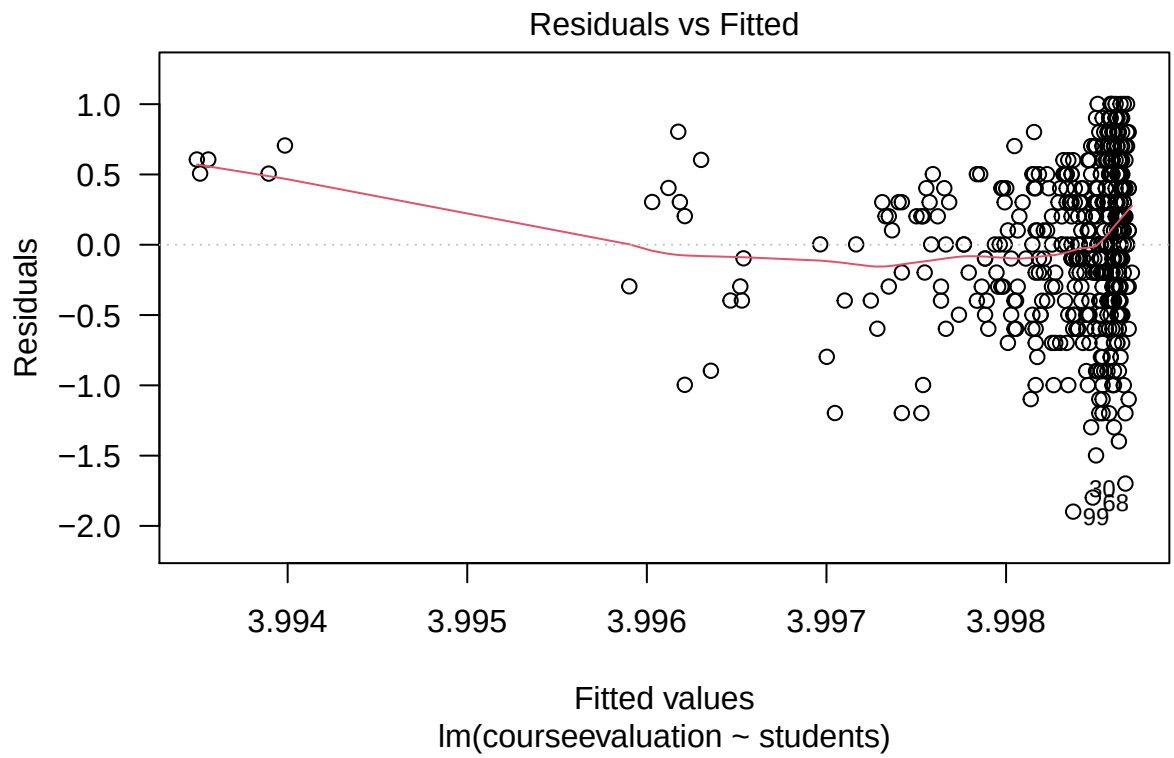
course evaluations vs student

The plots below suggest that a linear model may not be a good fit for the data. The residuals are clustered towards the end of the range and are not random. I will try a logarithmic transformation to see if it is a better fit.

```
# looking at class enrollment with prediction that smaller classes have better
# evaluations. I should definitely try logarithmic transformation here.

fit_students <- lm(courseevaluation ~ students, data = beauty)

students_plot <- ggplot(beauty, aes(x = students, y = courseevaluation)) +
  geom_point() +
  labs(title = "Evaluations vs enrollment") +
  theme_classic()

students_plot
```

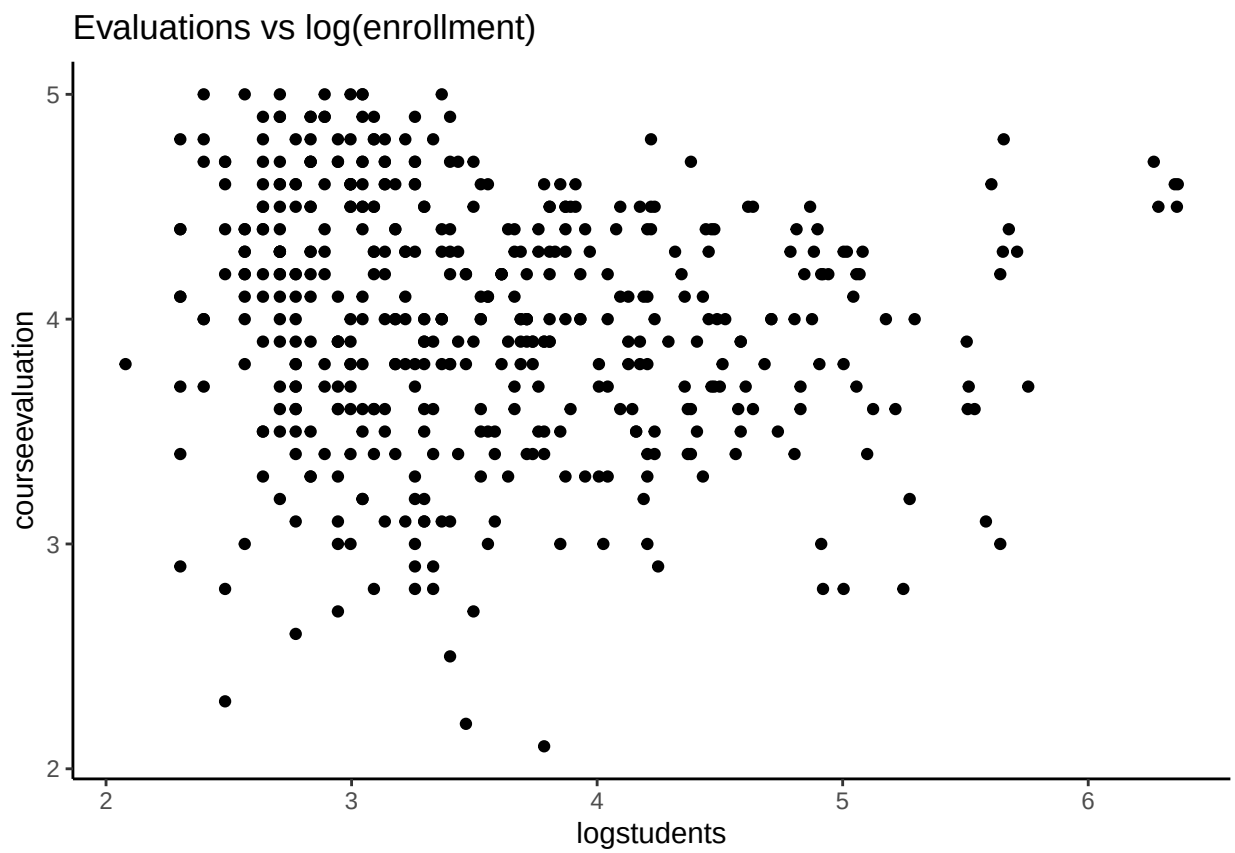



```
plot(fit_students, which = 1, las = 1, )
```

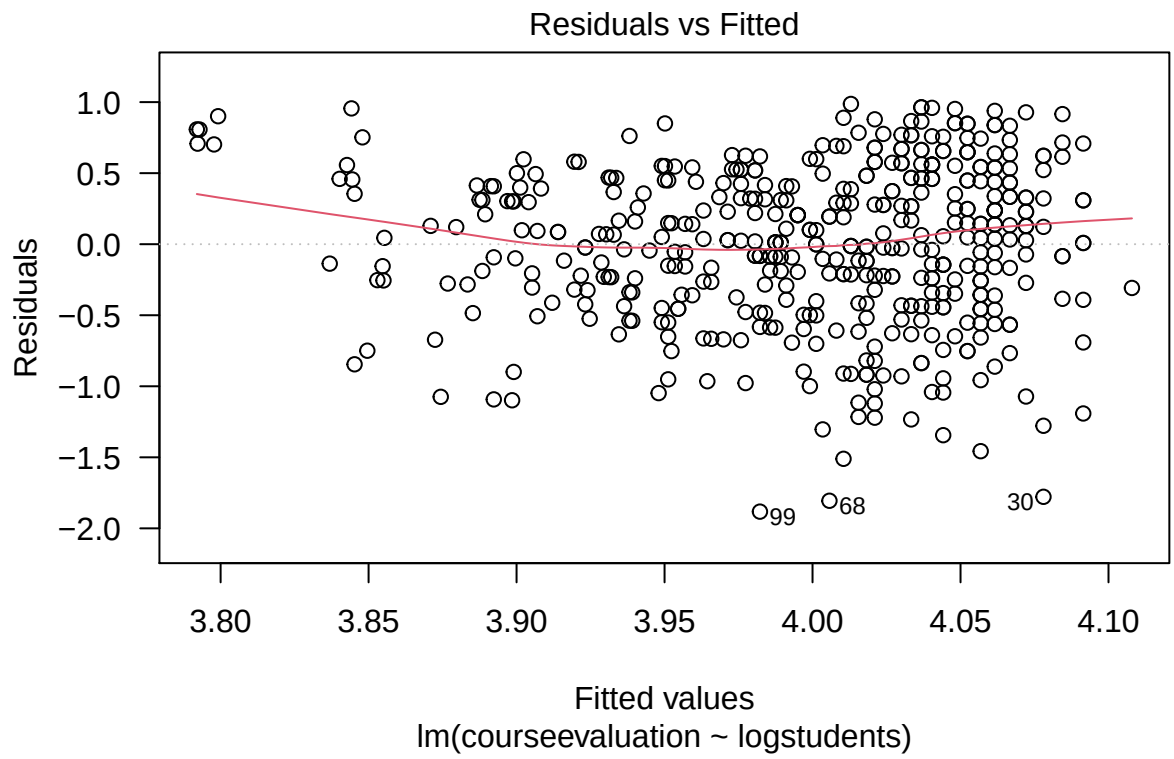


The plots below suggest that the logarithmic model is a fit for the data: the residuals are more randomly distributed and not clustered. So, I will use the log version of student in the variations of my final model.

```
# creating a logged version of beauty

beauty  <- beauty %>%
  mutate(logstudents = log(students))

fit_students_log <- lm(courseevaluation ~ logstudents, data = beauty)

students_plot_log <- ggplot(beauty, aes(x = logstudents, y = courseevaluation)) +
  geom_point() +
  labs(title = "Evaluations vs log(enrollment)") +
  theme_classic()

students_plot_log
```




```
plot(fit_students_log, which = 1, las = 1, )
```



Model variations

In addition to the btysdave, age, and log(student) variables, I will also consider the binary variables of "female" and "minority." The female variable is 1 if the teacher is female and the minority variable is 1 if the teacher is a minority. Both are 0 otherwise.

I considered 3 different models. The first (1) regressed courseevaluation against all of the variables discussed above with no interactions. The second (2) regressed courseevaluation against all of the variables except for age with an interaction between female and btystdave, because, as I noted above, it didn't look like age and courseevaluations had a significant relationship in the plots above. I chose to consider the interaction between female and btystdave because in my mind physical attractiveness is more important for women than it is for men.The last model (3) regressed courseevaluation against btstdave, logstudents, female, and an interaction between btystdave and female. I chose to not include the minority variable because it was not statistically significant in model 2 (see below).

```
# at this point I am going to try an initial model with all of the variables and
# see how it looks. Look at the residuals, etc.

fit_all <- lm(courseevaluation ~ btystdave  + logstudents + age + female + minority,
              data =  beauty)


fit_int <- lm(courseevaluation ~ btystdave*female  + logstudents + female + minority,
              data =  beauty)

fit_int_no_min <- lm(courseevaluation ~ btystdave*female  + logstudents + female,
```

```
              data =  beauty)

stargazer(fit_all, fit_int, fit_int_no_min, type = "latex")
```

% Table created by stargazer v.5.2.2 by Marek Hlavac, Harvard University. E-mail: hlavac at fas.harvard.edu
% Date and time: Tue, Mar 02, 2021 - 19:58:32

Table 2:

	Dependent variable:		
	courseevaluation		
	(1)	(2)	(3)
btystdave	0.144***	0.210***	0.216***
	(0.033)	(0.043)	(0.043)
logstudents	−0.099***	−0.098***	−0.094***
	(0.030)	(0.030)	(0.029)
age	−0.004		
	(0.003)		
female	−0.215***	−0.205***	−0.214***
	(0.053)	(0.051)	(0.051)
minority	−0.137*	−0.106	
	(0.073)	(0.073)	
btystdave:female		−0.116*	−0.131**
		(0.064)	(0.064)
Constant	4.667***	4.469***	4.444***
	(0.189)	(0.113)	(0.112)
Observations	463	463	463
R^2	0.095	0.097	0.093
Adjusted R^2	0.085	0.087	0.085
Residual Std. Error	0.531 (df = 457)	0.530 (df = 457)	0.531 (df = 458)
F Statistic	9.547*** (df = 5; 457)	9.796*** (df = 5; 457)	11.696*** (df = 4; 458)
Note:			*p<0.1; **p<0.05; ***p<0.01

Model choice

Model 1: As I expected, the age variable is not statistically significant. The r squared for the model is .095, meaning that the model accounts for about 9.5% of variation in the response variables

Model 2: All of the coefficients are statistically significant except for the minority coefficient. The r squared is .097, meaning that the model accounts for about 9.7% of the variation in the response variables.

Model 3: All of the coefficients are statistically significant. The r squared is .093, meaning that the model accounts for about 9.3% of the variation in the response variables.

After considering the above factors, I choose Model 2 based on the fact that it has the highest R squared value and it also seems logical to me to include the minority variable even though it wasn't statistically significant. Also, it seems like dropping it in Model 3 decreased the model's explanatory power.

Interpretation of Model 2 coefficients

The slope coefficient for btystdave is .21. In context, this means that an increase in 1 standard deviation in beauty score is associated with a .21 increase in course evaluation score on average, holding all other variables constant. The slope coefficient for logstudents is -.098. In context, this means that an increase in 1% in students is associated with a negative difference of .00098% in course evaluation score on average, holding all other variables constant. The slope coefficient for female is -.205. In context, this means that being female is associated with a negative difference of .205 in course evaluation score on average, holding all other variables constant. The slope coefficient for minority is -.106. In context, this means that being a minority is associated with a negative difference of .106 in course evaluation score on average, holding all other variables constant. The slope coefficient for the interaction between btystdave and female is -.116. In context, this means that an increase in one standard deviation in beauty score has an additional -.116 decrease on course evaluation score when the teacher is female, on average holding all other variables constant. The intercept is 4.469. In context, this means that a teacher who has an average beauty score, has no students, is male and is not a minority has an average course evaluation score of 4.469. However, because all of the students have students, this isn't a logical scenario.