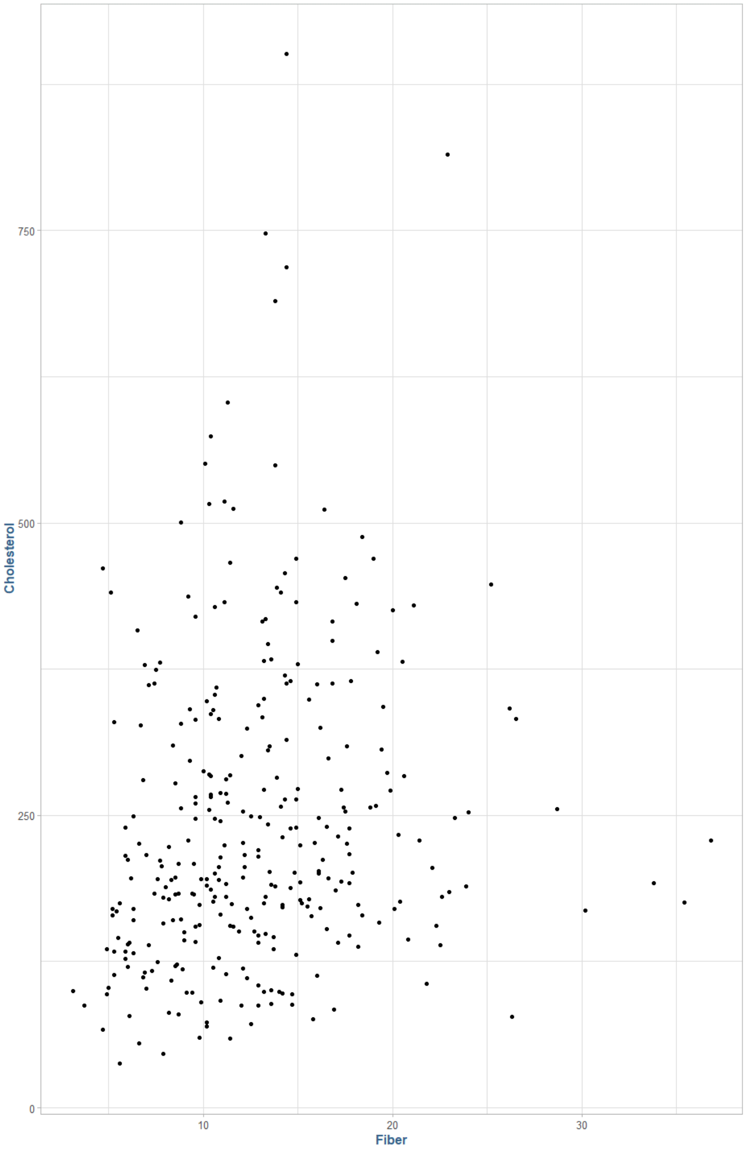
COMPUTATIONAL ASSIGMENT #4
BRANDON MORETZ

INTRODUCTION

1) *Consider the continuous variable, FIBER. Is this variable correlated with Cholesterol? Obtain a scatterplot and appropriate statistics to address this question.*

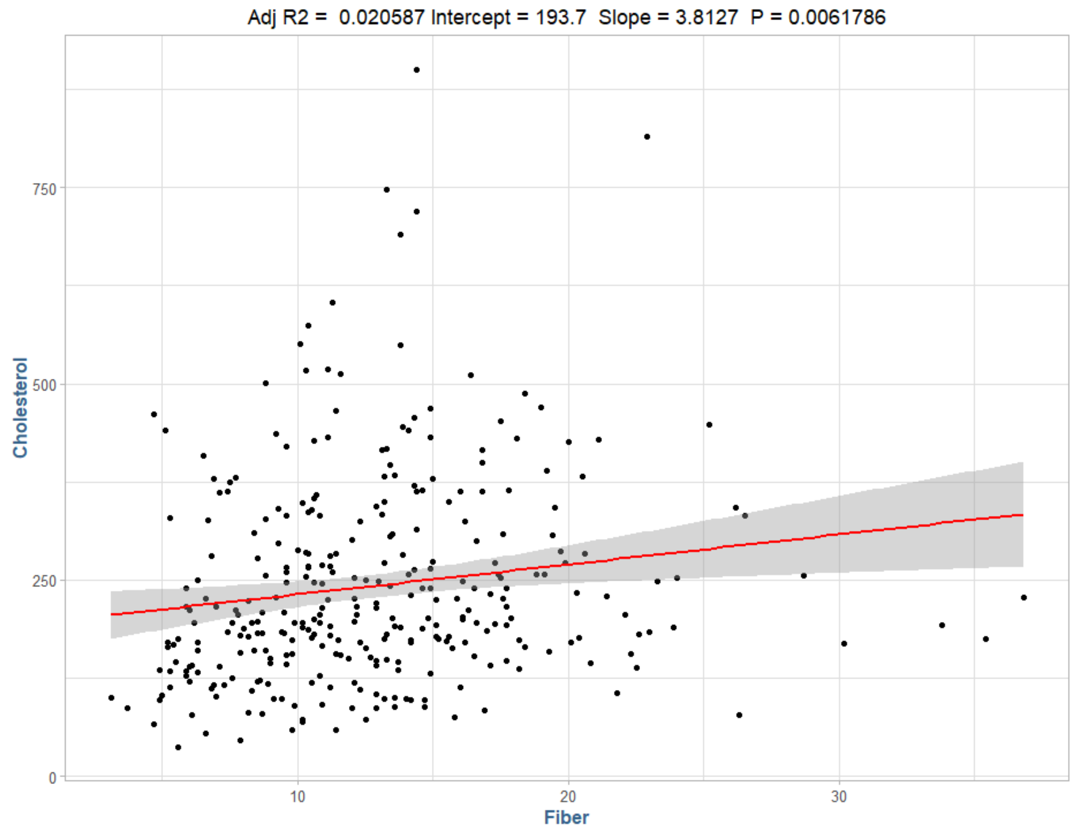
   In the following diagram we see a lot of variance in the following scatterplot of Cholesterol ~ Fiber.

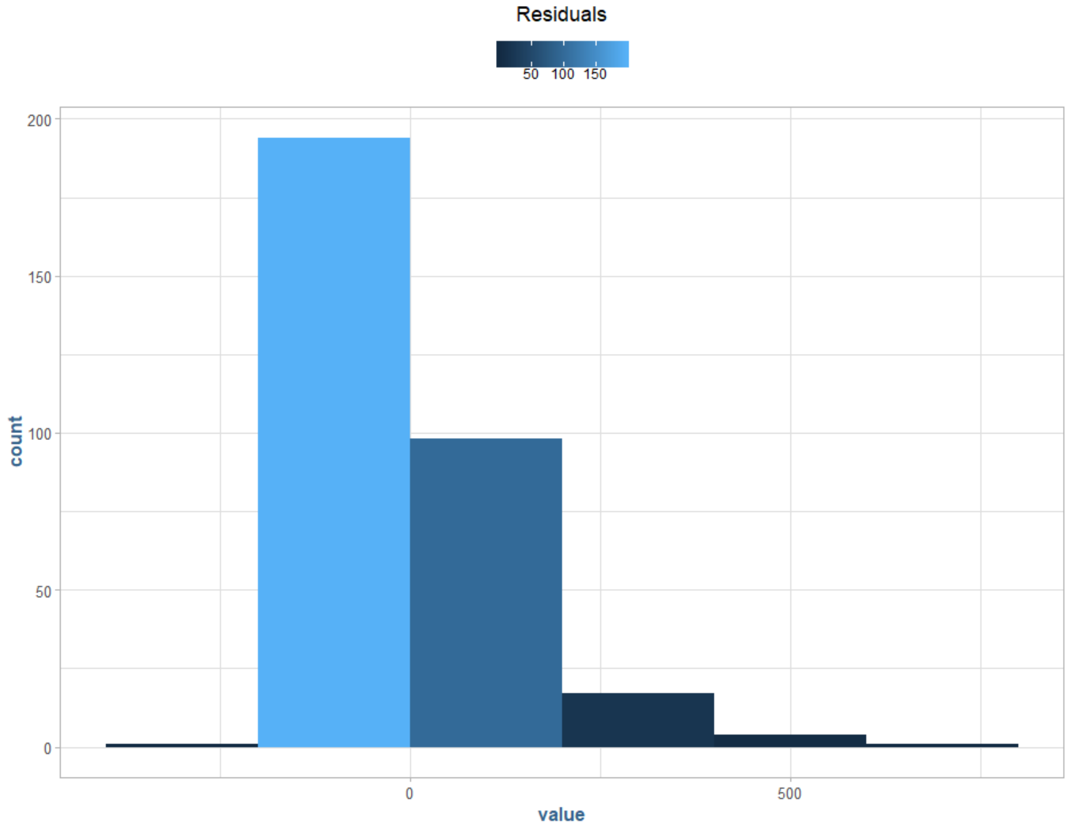


There is a liner correlation of .1539 between Cholesterol and Fiber.

2) *Fit a simple linear regression model that uses FIBER to predict CHOLESTEROL(Y). Report the model, interpret the coefficients, discuss the goodness of fit.*

   The Fiber variable appears to be a relatively poor indicator of cholesterol. In the graphic below, we can see an R^2 value of 0.0237, indicating that approximately 2% of the variance in the data is explained by the Fiber variable.

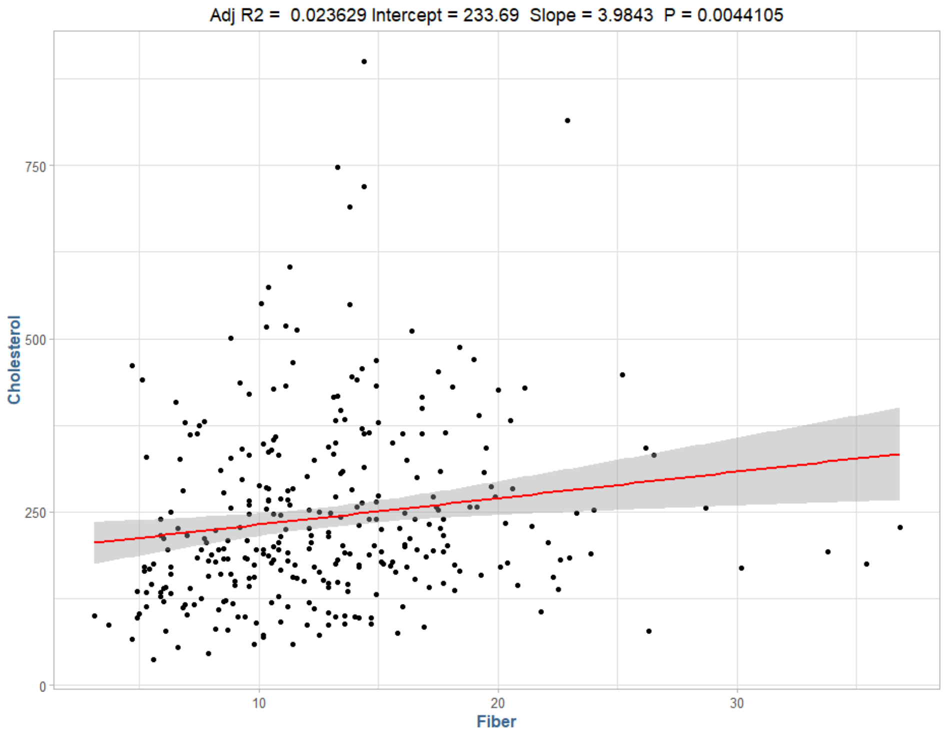


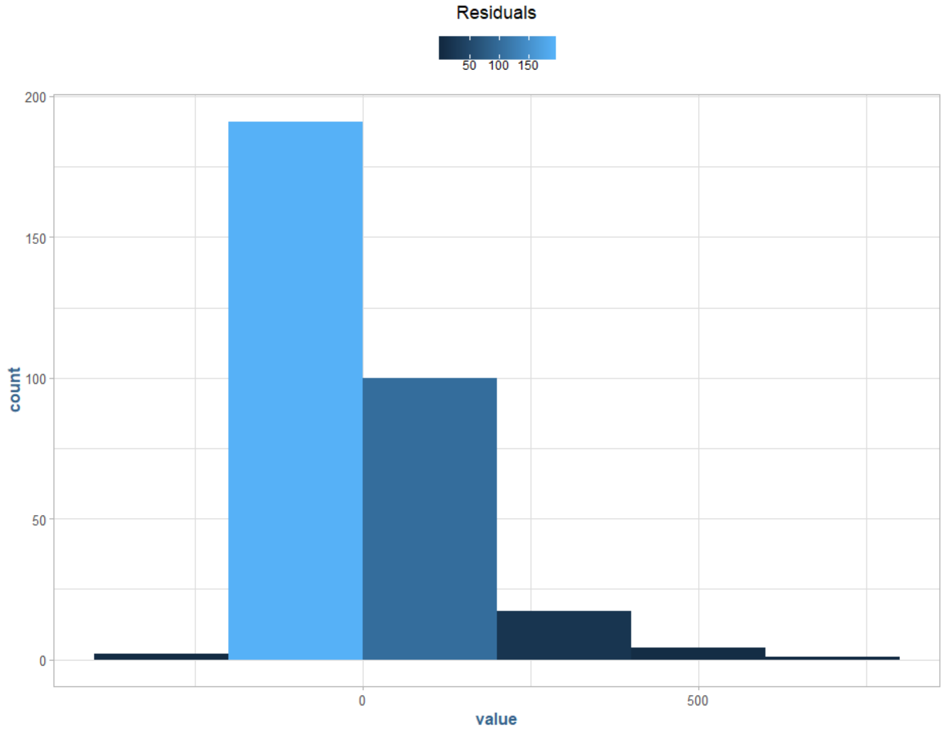


Model: 193.7014 + 3.8127 β_1, where β_1 is fiber.

The intercept term here, 193.701, is the baseline cholesterol level for an individual, and for every 1 unit increase in fiber consumed it should account for an approximate 3.8 unit increase in an individual's cholesterol level.

3.) *For the ALCOHOL categorical variable, create a set of dummy coded (0/1) indicator variables. Fit a multiple linear model that uses the FIBER continuous variable and the ALCOHOL dummy coded variables to predict the response variable Y=CHOLESTEROL. Remember to leave one of the dummy coded variables out of the model so that you have a basis of interpretation for the constant term. Report the model, interpret the coefficients, discuss hypothesis test results, goodness of fit statistics, diagnostic graphs, and leverage, influence and Outlier statistics. This is called an Analysis of Covariance Model (ANCOVA).*



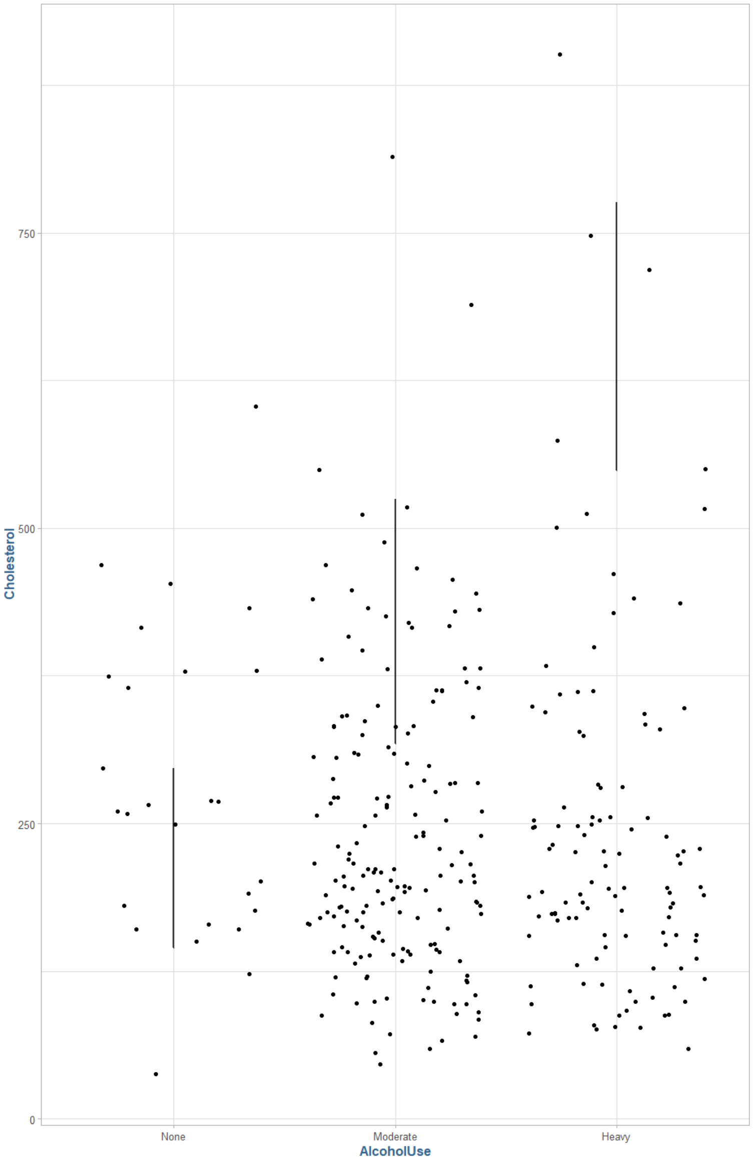


Model 2: $233.6946 + 3.9543\beta_1 - 46.9518\ \beta_2 - 44.4289\beta_3$

Where β_1 = Fiber, β_2 = Alcohol (Moderate), β_3 = Alcohol (Heavy)

This model will output a predicted value of cholesterol for an individual given their self-reported fiber intake and alcohol consumption, where each unit of fiber consumption increases their cholesterol by 3.6 points per unit, and alcohol will reduce the predicted cholesterol by either 46.96 points or 44.43 points depending on if they consume moderate or heavy amounts of alcohol, respectively. The R^2 denotes that about 3.3% of the total variance in the data is explained by the model.

We should note that there is an uneven distribution of subjects reported with no alcohol consumption (26), relative to those who report either moderate (178) or heavy (111) consumption. Additionally, there is a great deal of variance in the cholesterol levels by alcohol use:



The null hypothesis in this case would be,

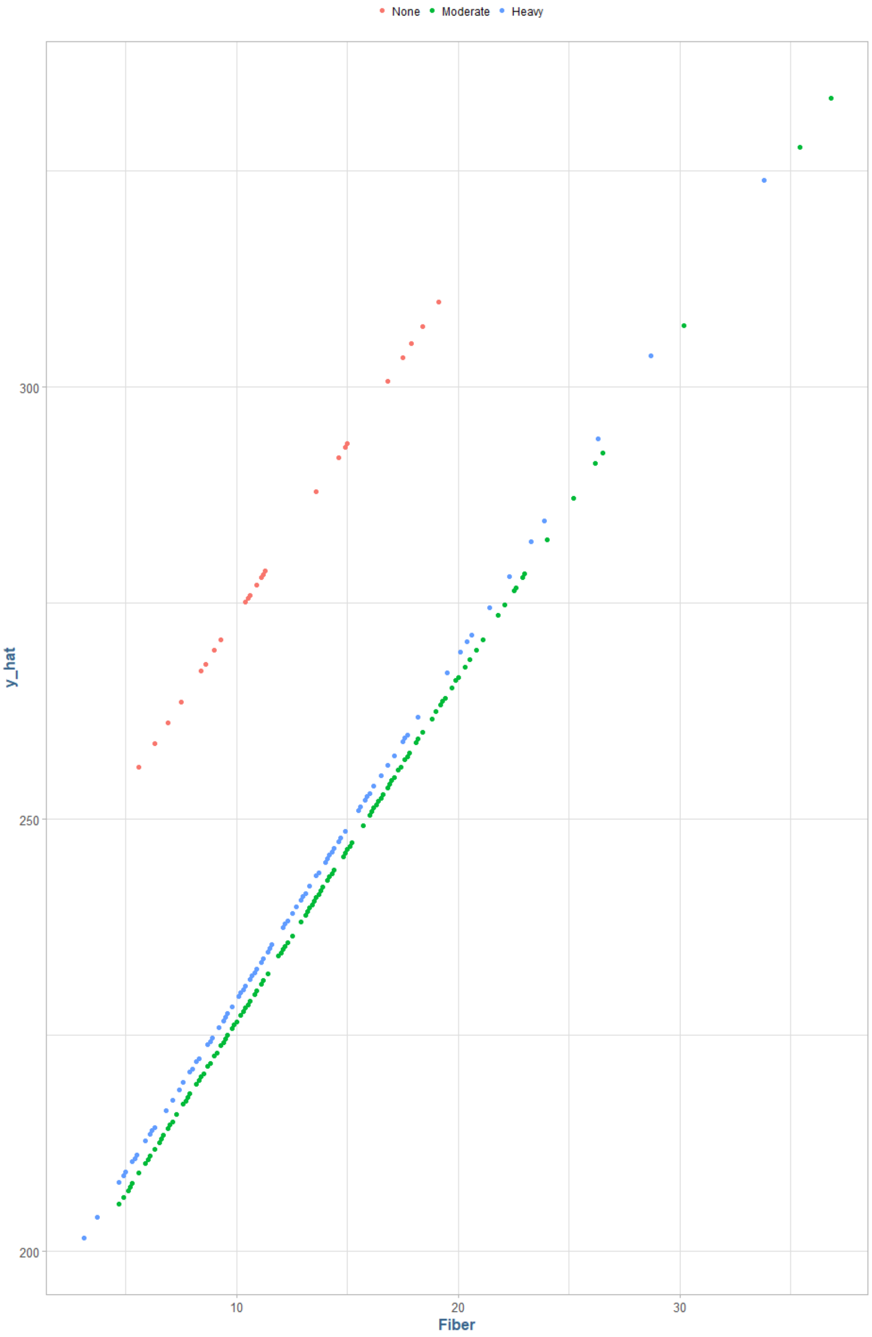
$$H_0 : \beta_1 = \beta_2 = \beta_3 = 0$$

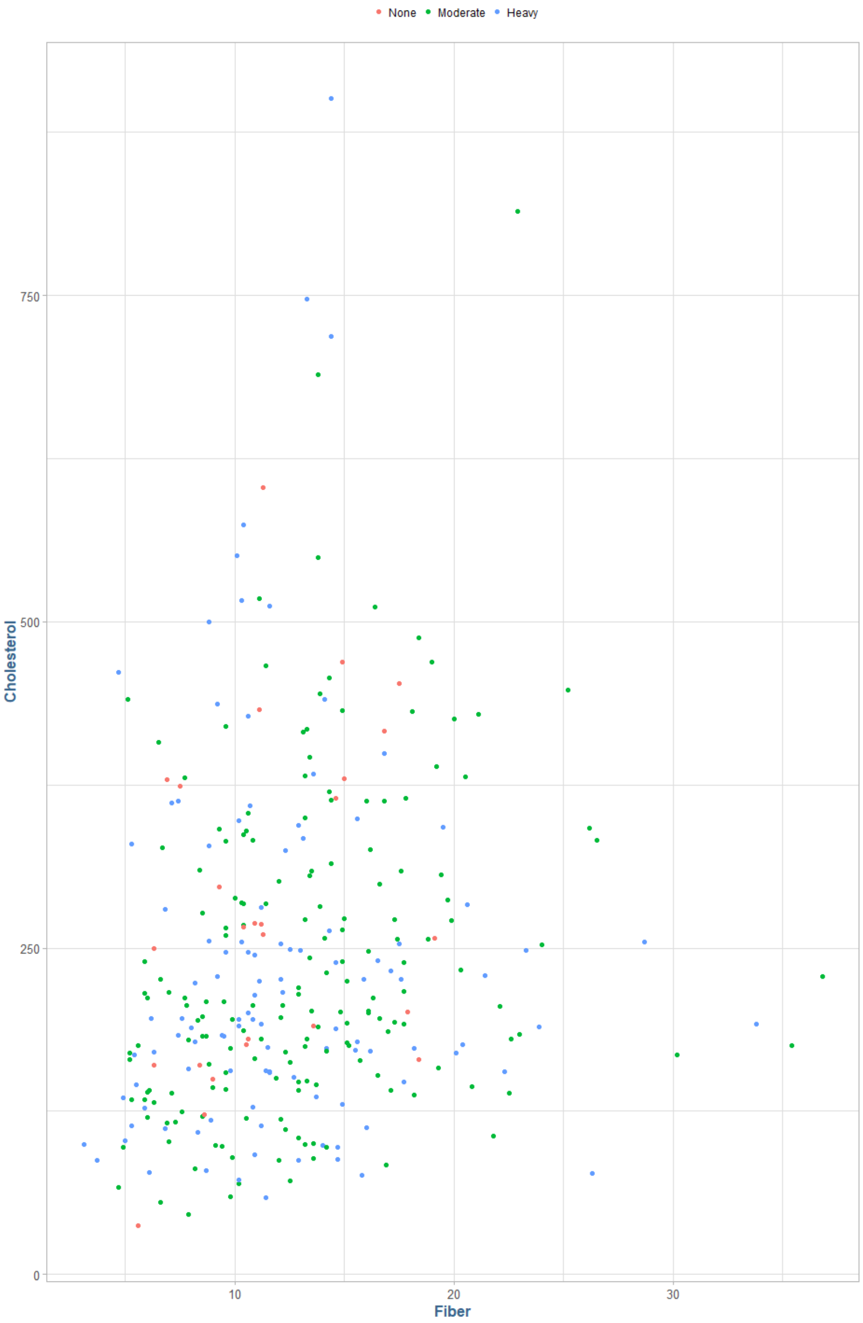
Or that there is no effect on the model using the beta coefficient derived from fiber consumption and the coded variables for alcohol consumption, against the alternative hypothesis that:

$$H_a : \beta_1 = \beta_2 = \beta_3 \neq 0$$

Or that there is additional variance explained in the data by including the beta coefficients. In our model summary, the p-value of < 0.05 for our fiber variable suggests that there is statistically significant difference when using the beta1 coefficient. However, the alcohol variables have p-values > 0.5, which suggests that they are not statistically significant.

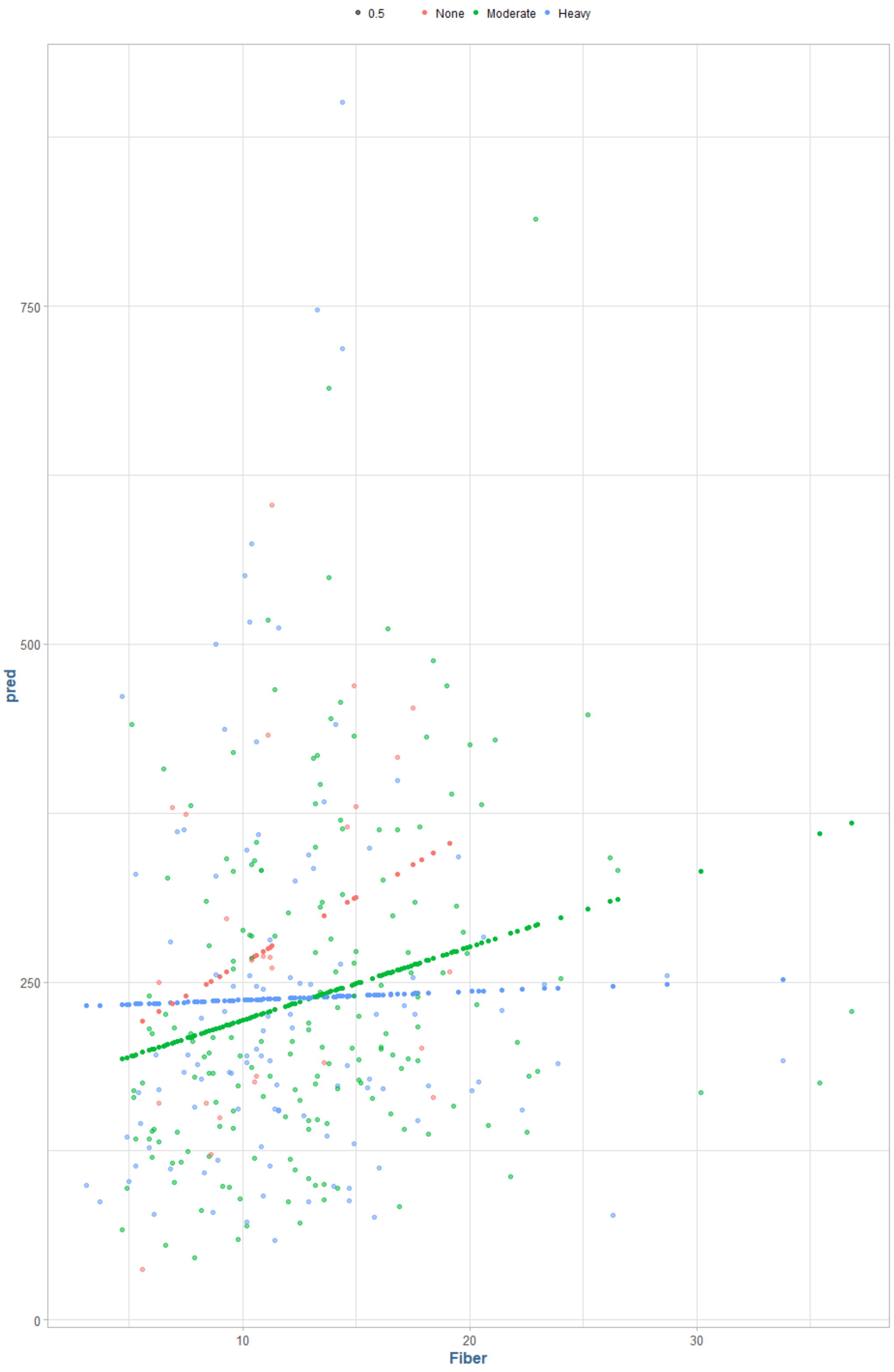
4.) *Use the ANCOVA model from task 3) to obtain predicted values for CHOLESTEROL(Y). Now, make a scatterplot of the Predicted Values for Y (y-axis) by FIBER (X), but color code the records for the different groups of ALCOHOL. What do you notice about the patterns in the predicted values of Y? Now, make a scatterplot of the actual values of CHOLESTEROL(Y) by FIBER (X), but color code by the different groups of the ALCOHOL variable. If you compare the two scatterplots, does the ANCOVA model appear to fit the observed data very well? Or, is a more complex model needed?*





The predicted values of cholesterol all fill in parallel straight lines separated by alcohol consumption, whereas the actual values are clustered together in pockets in the lower left quadrant of the graph. It does not appear that a linear model is reflective enough of the actual data to provide meaningful predictions.

5.) *Create new interaction variables by multiplying the dummy coded variables for ALCOHOL by the continuous FIBER(X) variable. Save these product variables to your dataset. Now, to build the model, start with variables in your ANCOVA model from task 4) and add the interaction variables you just created into the multiple regression model. Don't forget, there is one category that is the basis of interpretation. DO NOT include any interaction term that is associated with that category. This is called an Unequal Slopes Model. Fit this model, and save the predicted values. Plot the predicted values for CHOLESTEROL (Y) by FIBER(X). Discuss what you see in this graph. In addition, report the model, interpret the coefficients, discuss hypothesis test results, goodness of fit statistics, diagnostic graphs, and leverage, influence and Outlier statistics.*



Model 3: $166.9620 + 9.7105\beta_{1\,+}\ 0.5333\beta_2 + 63.3814\beta_3 - 4.2737\beta_4 – 9.0742\beta_5$

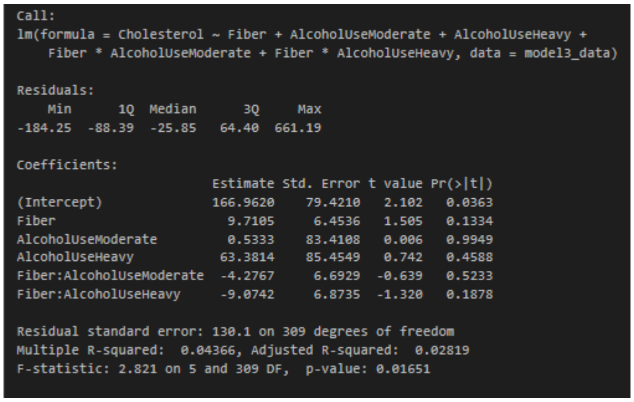
Where β_1 = Fiber, β_2 = Alcohol (Moderate) β_3 = Alcohol (Heavy) β_4 = Fiber + Moderate Alcohol interaction, β_5 = Fiber + Heavy alcohol interaction. This model has an R^2 of 0.0437 denoting that it accounts for approximately 4.3% of the overall variance in the data. We can see in the graph above the predicted model values (straight lines) plotted over the actual values, both of which are color coded to indicate the level of alcohol use per individual. Heavy alcohol use appears to have an unequal slope to that of the non/moderate users.

The null hypothesis in this case would be,

$H_o: \beta_1 = \beta_2 = \beta_3 = \beta_4 = \beta_5 = 0$

$H_a: \beta_j \neq 0$, for at least one value of j (for j in 1,2,3,4,5)

Or, simply that at least one of the interaction coefficients in the model is not zero, and that they would help explain the variance in the data greater than the intercept alone.



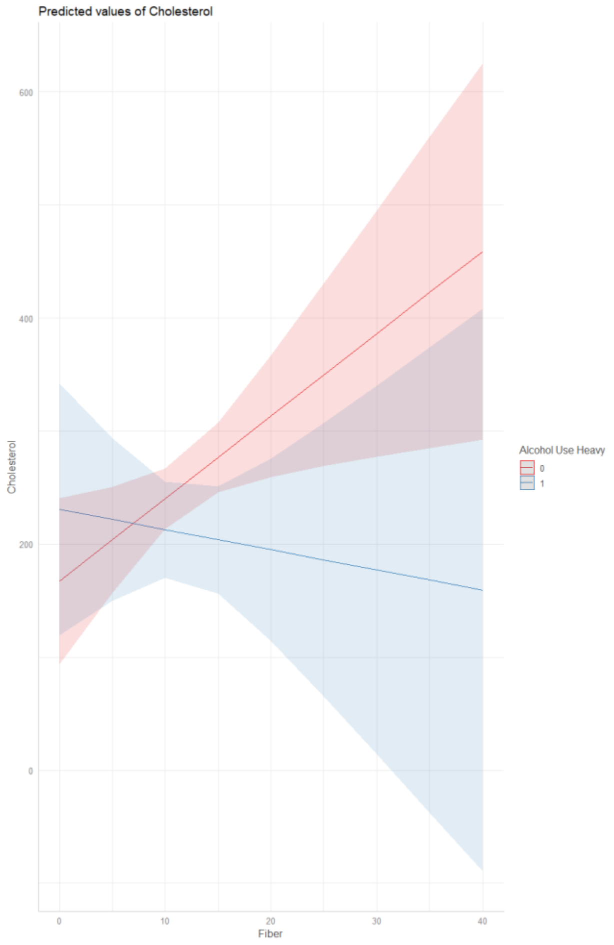
```
Call:
lm(formula = Cholesterol ~ Fiber + AlcoholUseModerate + AlcoholUseHeavy +
    Fiber * AlcoholUseModerate + Fiber * AlcoholUseHeavy, data = model3_data)

Residuals:
    Min      1Q  Median      3Q     Max
-184.25  -88.39  -25.85   64.40  661.19

Coefficients:
                         Estimate Std. Error t value Pr(>|t|)
(Intercept)              166.9620    79.4210   2.102   0.0363
Fiber                      9.7105     6.4536   1.505   0.1334
AlcoholUseModerate         0.5333    83.4108   0.006   0.9949
AlcoholUseHeavy           63.3814    85.4549   0.742   0.4588
Fiber:AlcoholUseModerate  -4.2767     6.6929  -0.639   0.5233
Fiber:AlcoholUseHeavy     -9.0742     6.8735  -1.320   0.1878

Residual standard error: 130.1 on 309 degrees of freedom
Multiple R-squared:  0.04366, Adjusted R-squared:  0.02819
F-statistic: 2.821 on 5 and 309 DF,  p-value: 0.01651
```

Looking at the summary of the model, only the intercept p-value value falls below the standard 0.05 threshold and it does appear that the null hypothesis in this case cannot be rejected. Both of the interaction terms have relatively high p-values; however, it does appear visually that there is some difference with the group of heavy alcohol users and the overall model is significant at $p < 0.5$:



6.) *You should be aware that the models of Task 4) and Task 5) are nested. Which model is the full and which one is the reduced model? Write out the null and alternative hypotheses for the nested F-test in this situation to determine if the slopes are unequal. Use the ANOVA tables from those two models you fit previously to compute the F-statistic for a nested F-test using Full and Reduced models. Conduct and interpret the nested hypothesis test. Are there unequal slopes? Discuss the findings.*

Model 3 (from task 4) with the additional interaction variables is the "full" model, and model 2 (from task 4) is the reduced model. The null and alternative hypothesis in this case would be:

H_o : $\beta_5 = \beta_6 = 0$
H_a : $\beta_j \neq 0$, for at least one value of j (for j in 5, 6)

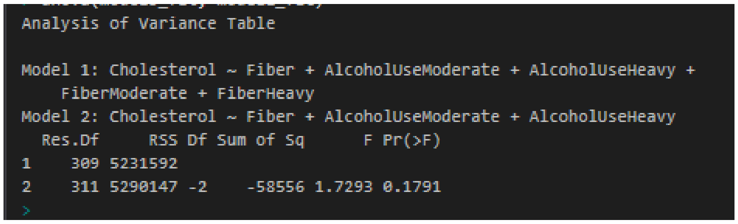
$F = [(SSE_R - SSE_C) / (df2 – df1)] / (SSE_C / df1]$

$F = ((5,290,147 – 5,231,592) / 2) / [5,231,592/ 309]$

$= 29,277.89 / 16,930.72$

$=$ **1.7293**

Which is less than our critical value at 95% confidence, = $F_{95,\ 309}$= **3.0254**, therefore we cannot reject the null hypothesis that fiber and alcohol have no interaction.



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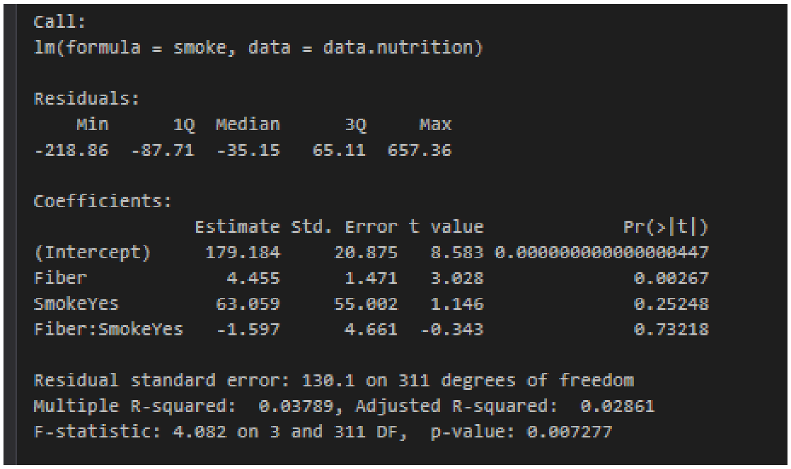
Analysis of Variance Table

Model 1: Cholesterol ~ Fiber + AlcoholUseModerate + AlcoholUseHeavy +
    FiberModerate + FiberHeavy
Model 2: Cholesterol ~ Fiber + AlcoholUseModerate + AlcoholUseHeavy
  Res.Df     RSS Df Sum of Sq      F Pr(>F)
1    309 5231592
2    311 5290147 -2    -58556 1.7293 0.1791
>
```

7.) *Now that you've been exposed to these modeling techniques, it is time for you to use them in practice. Let's examine more of the NutritionStudy data. Use the above practiced techniques to determine if SMOKE, VITAMINS, or GENDER interacts with the FIBER variable and influences the amount of CHOLESTEROL. Formulate hypotheses, construct essential variables (as necessary), conduct the analysis and report on the results. Which categorical variables are most predictive of CHOLESTEROL, in conjunction with FIBER.*

First, let's examine the relationship between cholesterol levels and fiber/smoking.



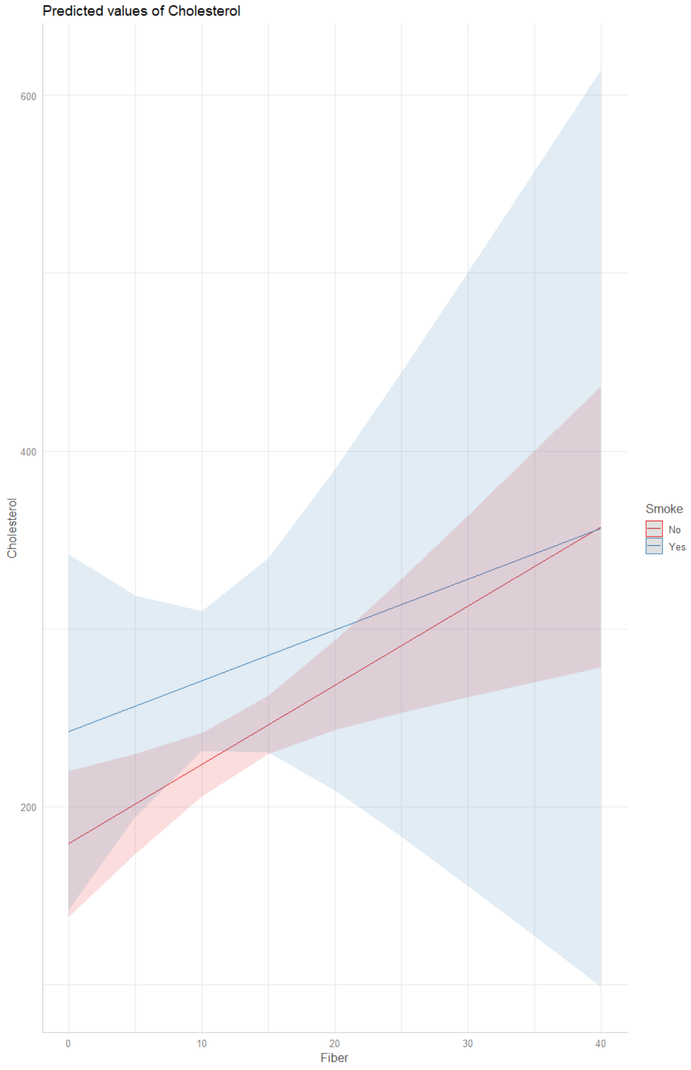
```
Call:
lm(formula = smoke, data = data.nutrition)

Residuals:
    Min      1Q  Median      3Q     Max
-218.86  -87.71  -35.15   65.11  657.36

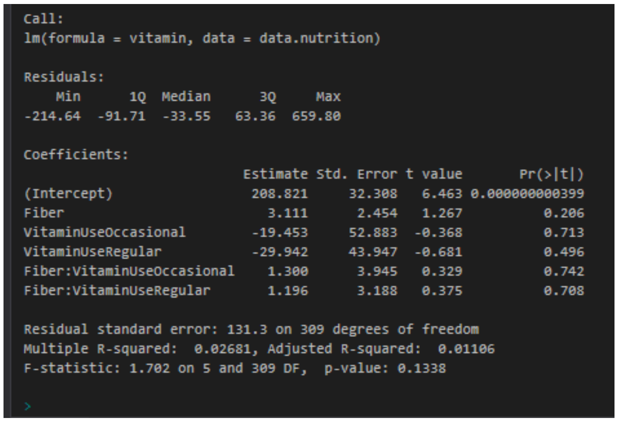
Coefficients:
               Estimate Std. Error t value            Pr(>|t|)
(Intercept)     179.184     20.875   8.583 0.000000000000000447
Fiber             4.455      1.471   3.028             0.00267
SmokeYes         63.059     55.002   1.146             0.25248
Fiber:SmokeYes   -1.597      4.661  -0.343             0.73218

Residual standard error: 130.1 on 311 degrees of freedom
Multiple R-squared:  0.03789, Adjusted R-squared:  0.02861
F-statistic: 4.082 on 3 and 311 DF,  p-value: 0.007277
```

In the preceding model, we note that the significant terms are the intercept and fiber, it appears that smoking and the interaction between fiber and smoking are not statistically significant. We can visualize this interaction in the following graph, noting the roughly equal lines and the large variances.



For vitamin use and fiber, we can the following terms generated from the model.



```
Call:
lm(formula = vitamin, data = data.nutrition)

Residuals:
    Min      1Q  Median      3Q     Max 
-214.64  -91.71  -33.55   63.36  659.80 

Coefficients:
                           Estimate Std. Error t value       Pr(>|t|)    
(Intercept)                 208.821     32.308   6.463 0.000000000399
Fiber                         3.111      2.454   1.267          0.206
VitaminUseOccasional        -19.453     52.883  -0.368          0.713
VitaminUseRegular           -29.942     43.947  -0.681          0.496
Fiber:VitaminUseOccasional    1.300      3.945   0.329          0.742
Fiber:VitaminUseRegular       1.196      3.188   0.375          0.708

Residual standard error: 131.3 on 309 degrees of freedom
Multiple R-squared:  0.02681, Adjusted R-squared:  0.01106 
F-statistic: 1.702 on 5 and 309 DF,  p-value: 0.1338

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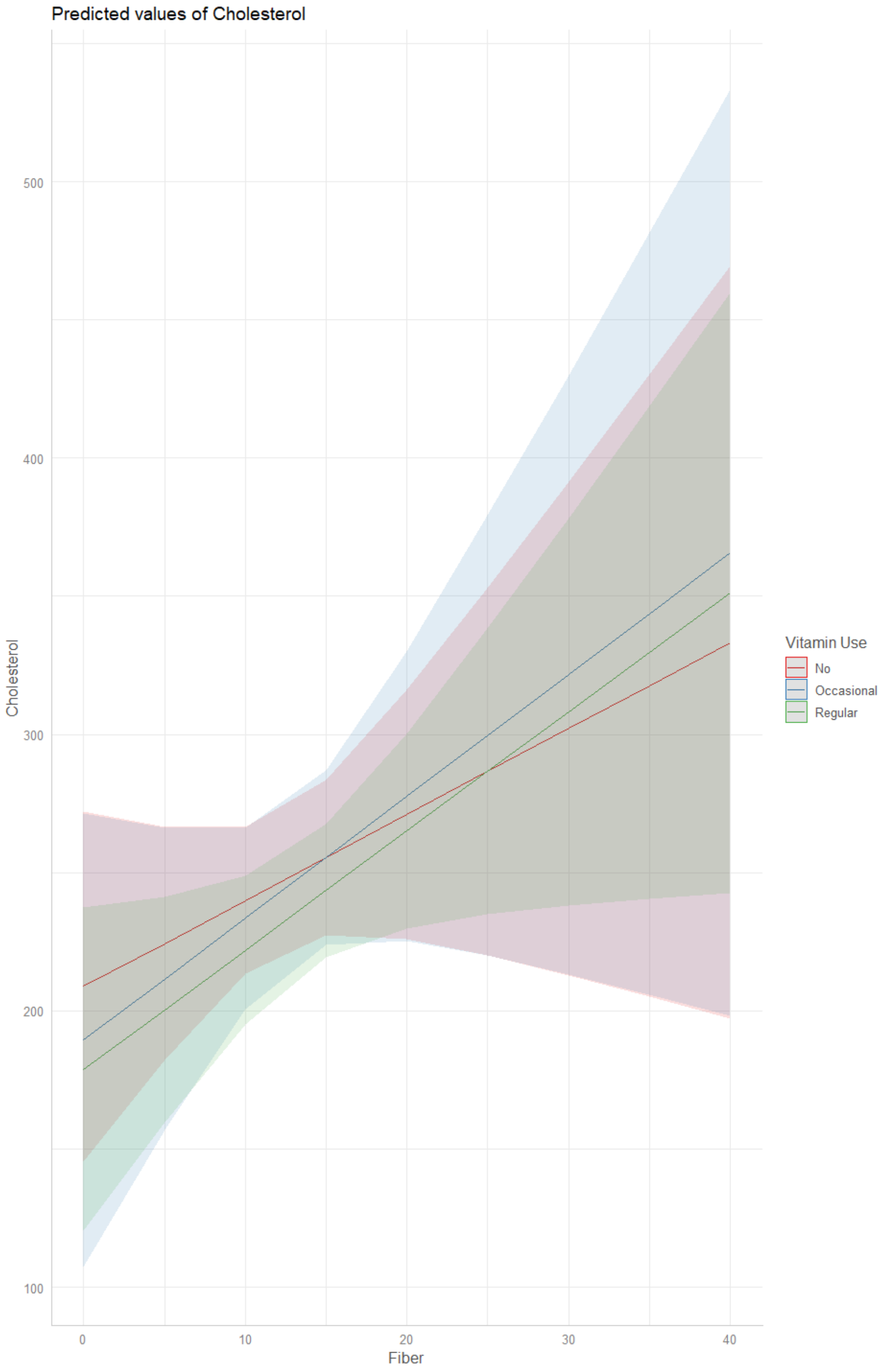
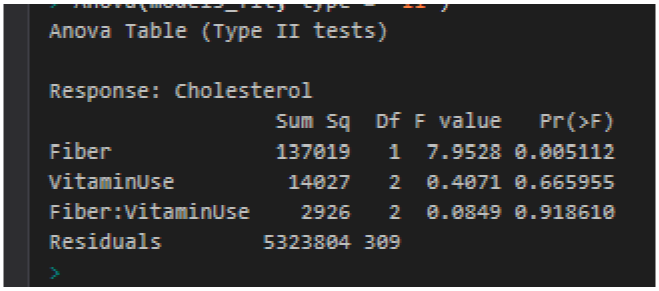
```

When fiber is used in conjunction with the various vitamin usage levels, it does not appear to have any statistically significant effect on cholesterol levels.



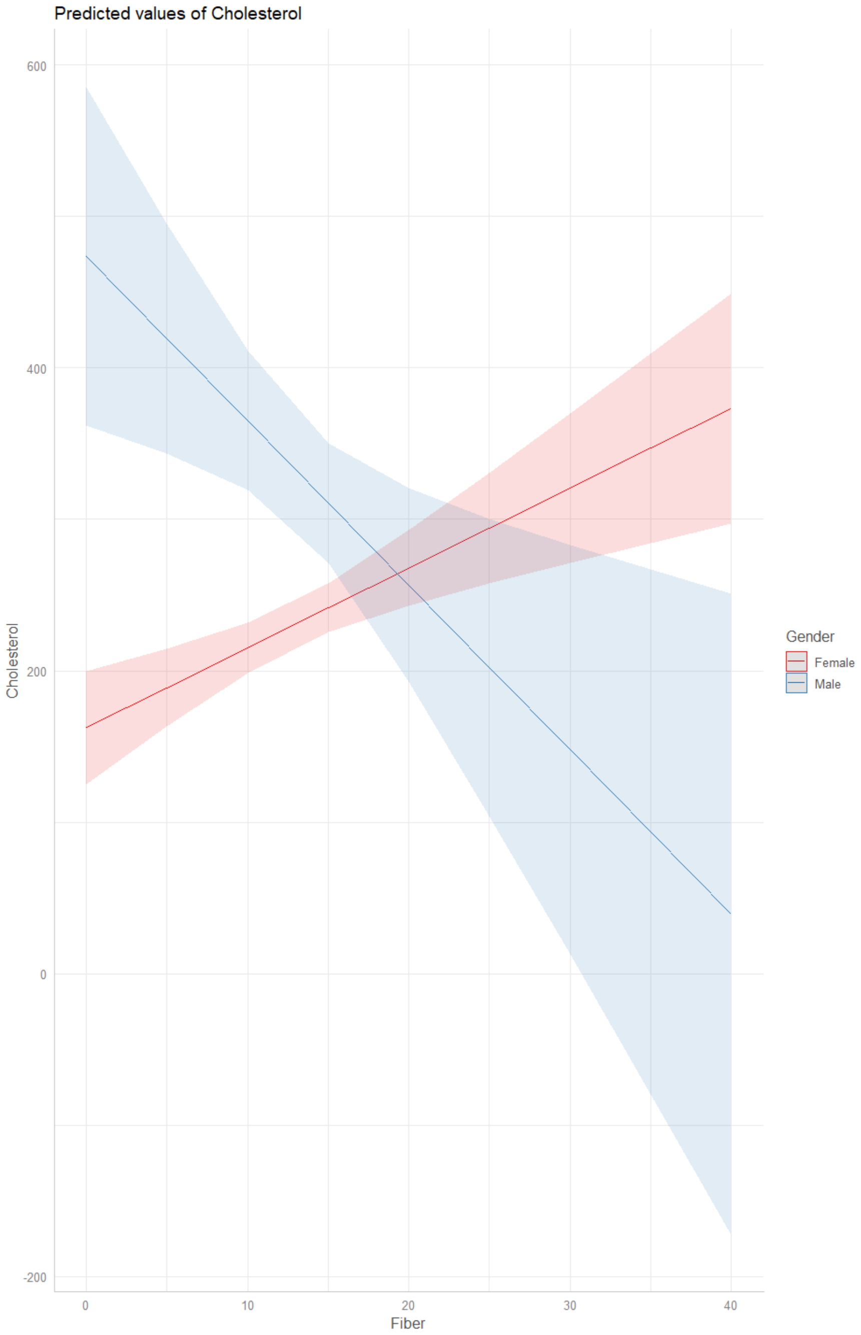
We can also confirm with the results of a type II anova test:



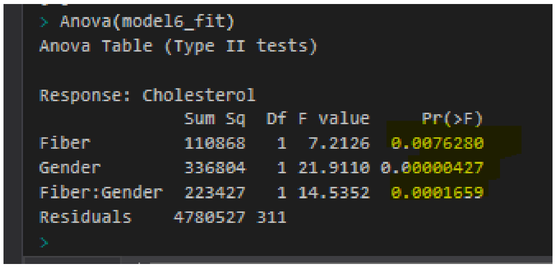
```
> Anova(models_fit, type = "II")
Anova Table (Type II tests)

Response: Cholesterol
                  Sum Sq  Df F value   Pr(>F)
Fiber             137019   1  7.9528 0.005112
VitaminUse         14027   2  0.4071 0.665955
Fiber:VitaminUse    2926   2  0.0849 0.918610
Residuals        5323804 309
>
```

The next variable under consideration is the gender variable in conjunction with the fiber variable. The male and female lines in the following figure clearly exhibit different behavior than the preceding variables.



We can clearly see an effect on the cholesterol levels with this interaction considered. For males, their cholesterol levels decrease sharply with increasing levels of fiber consumption, and a female's cholesterol appear to increase with increasing amounts of fiber. We can also execute a type II ANOVA test to confirm our visual inspection:



```
> Anova(model6_fit)
Anova Table (Type II tests)

Response: Cholesterol
              Sum Sq  Df F value     Pr(>F)
Fiber         110868   1  7.2126  0.0076280
Gender        336804   1 21.9110 0.00000427
Fiber:Gender  223427   1 14.5352  0.0001659
Residuals    4780527 311
>
```

CONCLUSION

In this lab we explore the statistical technique known as ANCOVA, where we assess the impact of categorical values in conjunction with continuous variables. We used the nutritional data collected from an observational study to assess the impacts of both types of variables of predicting an individual's cholesterol levels.

We started by looking at the correlation between fiber and cholesterol, given that one of the underlying assumptions for ANCOVA models is that there is a linear relationship between the dependent variable (cholesterol) and the covariate (fiber), we found a modest colinear association. We then fitted a simple linear model to the fiber variable and confirmed the normality of the residuals from the model.

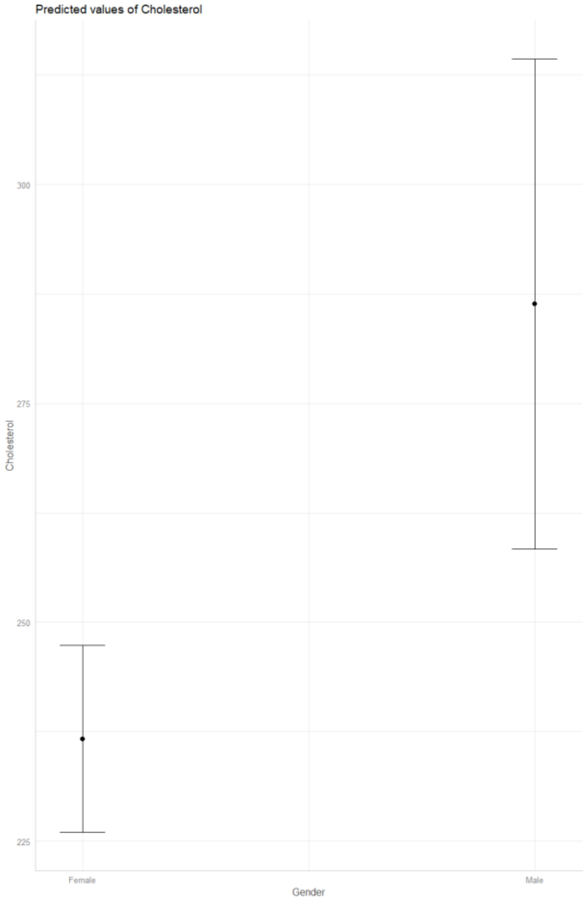
Our first ANCOVA model was generated using cholesterol as the dependent variable, and fiber in conjunction with different predetermined cut-offs in alcohol use which were used to define a categorical variable. This model generated similar slopes for the predicted values and did not exhibit characteristics of having an impact on our dependent variable. Our second model introduced interaction terms between the covariates to help explain individual's cholesterol levels. We noted that the interactions between alcohol and fiber did not appear to be statistically significant, although the heavy alcohol use group did display distinct behavior when examining cholesterol. The nested f-test of these two models did not suggest that the additional interaction terms in the more complex model added significantly to the unexplained variance in the data.

Lastly, we looked at three additional categorical variables: smoking, gender and vitamin usage and their interactions with the fiber variable. Of the three additional variables we considered, only the gender variable appeared to have a statistically significant impact on the individual's cholesterol levels.

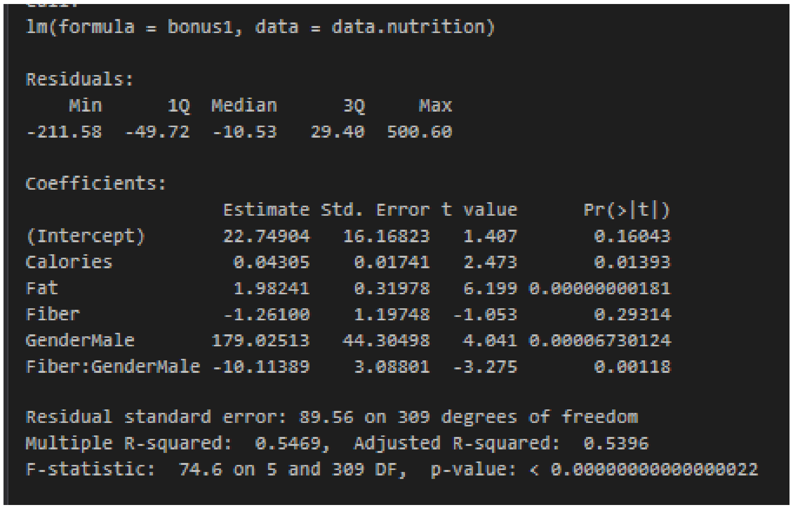
The ANVOCA methods deployed in this lab were both informative and useful, and these techniques will undoubtedly come in useful in further research and analysis.

BONUS

The first model we will explore is based upon the premise of using an individual's diet and sex to predict their cholesterol levels. For this model, we will use the following variables: calories, fat, fiber and gender. From the preceding work, we have a strong indication that sex will have a large influence on an individual's cholesterol.



The model summary can be seen below:



```
lm(formula = bonus1, data = data.nutrition)

Residuals:
    Min      1Q  Median      3Q     Max 
-211.58  -49.72  -10.53   29.40  500.60 

Coefficients:
                  Estimate Std. Error t value      Pr(>|t|)    
(Intercept)       22.74904   16.16823   1.407       0.16043    
Calories           0.04305    0.01741   2.473       0.01393    
Fat                1.98241    0.31978   6.199 0.00000000181    
Fiber             -1.26100    1.19748  -1.053       0.29314    
GenderMale       179.02513   44.30498   4.041 0.00006730124    
Fiber:GenderMale -10.11389    3.08801  -3.275       0.00118    

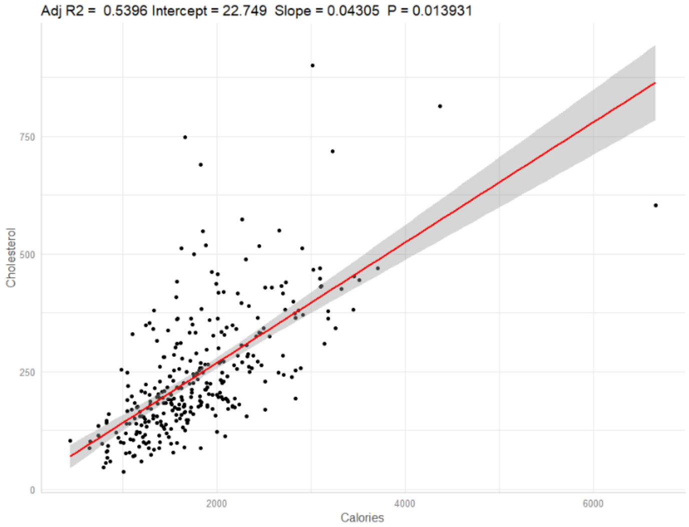
Residual standard error: 89.56 on 309 degrees of freedom
Multiple R-squared:  0.5469,  Adjusted R-squared:  0.5396 
F-statistic:  74.6 on 5 and 309 DF,  p-value: < 0.00000000000000022
```

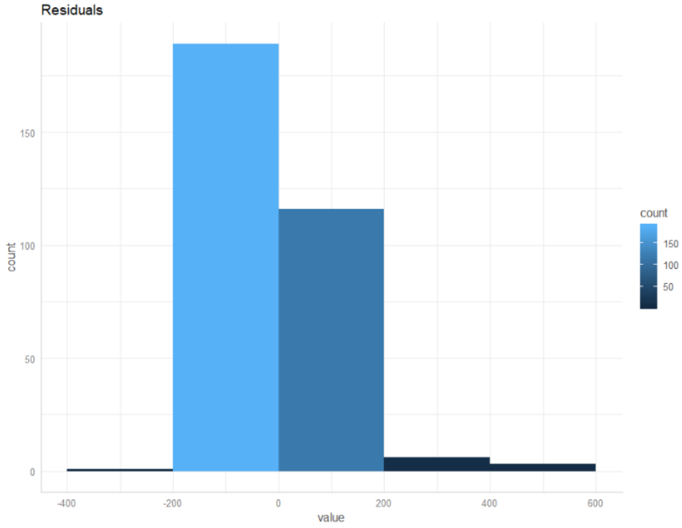
Bonus Model 1: $22.7490 + 0.043\beta_1 + 1.9824\beta_2 – 1.261\beta_3 + 179.0251\beta_4 -10.1139\beta_5$

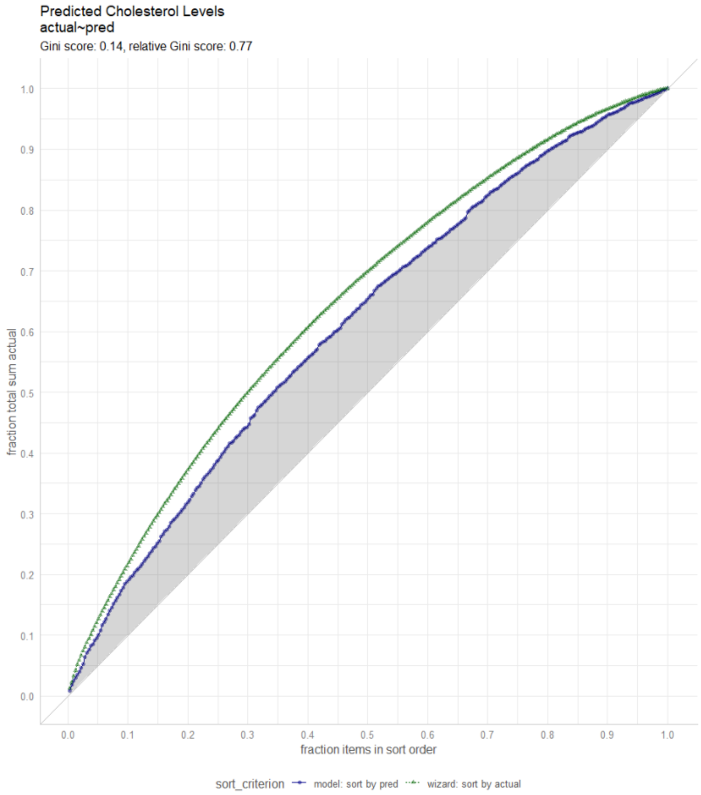
Where, β_1 = calories, β_2 = fat, β_3 = fiber, β_4 = male, β_5 = female

We note the model has a R² value of 0.5469, denoting that approximately 55% of the variance in the data is explained by the model and a Gini score of .77, denoting a relatively high prediction accuracy. We can also look at a gain curve plot, which shows a green curve of a model with 100% prediction accuracy plotted against the area of that curve that our model accounts for with the blue line, of predicted values vs the actual values:

Standard model fit, residuals and gain curve can be seen below:


Adj R2 = 0.5396 Intercept = 22.749 Slope = 0.04305 P = 0.013931
Cholesterol
Calories


Residuals
count
value
count


Predicted Cholesterol Levels
actual~pred
Gini score: 0.14, relative Gini score: 0.77
fraction total sum actual
fraction items in sort order
sort_criterion
model: sort by pred
wizard: sort by actual