Moderation Assignment Instructions

Assignment Overview

Moderation occurs when the relationship between two variables depends on a third variable.

- The third variable is referred to as the moderating variable or simply the moderator.
- The moderator affects the direction and/or strength of the relation between your explanatory and response variable.
- When testing a potential moderator, we are asking the question whether there is an association between two constructs, **but separately for different subgroups within the sample.**
  - This is also called a *stratified* model, or a *subgroup analysis.*

> *This assignment file demonstrates some advanced graphic adjustments, as well as uses the package `pander` to present model output in nicely formatted code (similar to `knitr` for tables). These are highly desirable, but not mandatory. If you are having difficulty with the plots and/or tables, remove the code and just include raw R output.*
>
> *It is **not** recommended that you copy the graph code that I present below directly, but instead start with the code used in the bivariate inference assignment and adjust from there*

Submission Guidelines

- Use the template provided: [RMD]
- This is an individual assignment. I expect you to work with your team/partner on this, but each person must submit their own work, and own writing.
- Upload to the corresponding assignment on Blackboard by the due date.
  - A copy of your assignment will be uploaded to the corresponding graded Google Drive Folder for you to see and learn from the work of other classmates.

Instructions

0. Copy relevant content and code from Step 1-4 for the ANOVA, Chi-Squared, and Regression inferences from your bivariate inference assignment into the appropriate location in the moderation assignment template file.
   - We are not doing the full 5 step analysis in this document.
1. For each analyses, decide on a third variable to test as a moderating variable.
   - The potential moderator can be different for each analyses. You need to decide what variables are most appropriate for your research question.
   - This third variable must be categorical and the fewer number of levels it has the easier it is to interpret.
   - Add this variable declaration into your Step 1 for each analysis.
2. Adjust your bivariate visualization to account for this third variable.
   - Typical methods for plotting a third variable include paneling or coloring by the third variable.
   - State your thoughts about how the relationship changed with the moderator variable. You should talk about differences between the original analysis and EACH level of your moderator variable (i.e., both males and females). For instance, with the ANOVA, discuss changes in the p-value, means, and graph for males in comparison to the original analysis AND for females in comparison to the original analysis.
3. Adjust your Research Question to include this third variable.
   - Is the relationship between X and Y the same for all levels of Z?

4. For each analysis, run the original model, and stratified model.
   - See examples below for how to do this in R.
5. Determine if the third variable is a moderator or not.
   - You should state what the original analysis shows regarding the relationship you are testing.
   - State based on your previous explanation if the third variable moderates the Bivariate Relationship.

How to determine if a variable is a moderator (Used in step 4)

- What you are looking for first depends on which of the 3 scenarios below describe your original analysis (i.e., your original ANOVA test).
- Whether your third variable is a moderator depends on what you see happening in your moderator analysis (i.e., the second ANOVA test split by your third variable).

- If ANY of the 3 scenarios explained below occur in your analysis then your Third Variable IS a Moderator of the Bivariate Relationship.

Scenario 1 - Significant relationship at bivariate level (i.e., ANOVA, Chi-Square, Correlation) (saying expect the effect to exist in the entire population) then when test for moderation the third variable is a moderator if the strength (i.e., p-value is Non-Significant) of the relationship changes. Could just change strength for one level of third variable, not necessarily all levels of the third variable.

Scenario 2 - Non-significant relationship at bivariate level (i.e., ANOVA, Chi-Square, Correlation) (saying do not expect the effect to exist in the entire population) then when test for moderation the third variable is a moderator if the relationship becomes significant (saying expect to see it in at least one of the sub-groups or levels of third variable, but not in entire population because was not significant before tested for moderation). Could just become significant in one level of the third variable, not necessarily all levels of the third variable.

Scenario 3 - Significant relationship at bivariate level (i.e., ANOVA, Chi-Square, Correlation) (saying expect the effect to exist in the entire population) then when test for moderation the third variable is a moderator if the direction (i.e., means change order/direction) of the relationship changes. Could just change direction for one level of third variable, not necessarily all levels of the third variable.

What to look for in each type of analysis.

ANOVA - look at the p-value, r-squared, means, and the graph of the ANOVA and compare to those values in the Moderation (i.e., each level of third variable) output to determine if third variable is a moderator or not.

Chi-Square - look at the p-value, the percents for the columns in the cross tabs table, and the graph for the Chi-Square and compare to those values in the Moderation (i.e., each level of third variable) output to determine if third variable is a moderator or not.

Correlation - look at the correlation coefficient (r), p-value, calculate the r-squared, and the graph for the Correlation and compare to those values in the Moderation (i.e., each level of third variable) output to determine if third variable is a moderator or not.

Example Submission

```r
library(knitr)
opts_chunk$set(warning=FALSE, message=FALSE)
library(dplyr)
library(ggplot2); library(gridExtra)
library(pander) # Used for printing nice linear model tables
panderOptions("digits", 3)
iris<-iris # only used to run sample code
load("C:/Box Sync/Data/AddHealth/addhealth_clean.Rdata")
```

ANOVA

1. **Identify response, explanatory, and moderating variables**

- Categorical explanatory variable = Perceived General Health (variable `genhealth`)
- Quantitative response variable = Body Mass Index (variable `BMI`)
- Categorical Potential Moderator = Ever smoked (variable `eversmoke_c`)

2. **Visualize and summarise the potential effect of the moderator**

These plots are modified for readability in several ways. These modifications may not apply to your situation. When running into trouble start taking off the fancy layers.

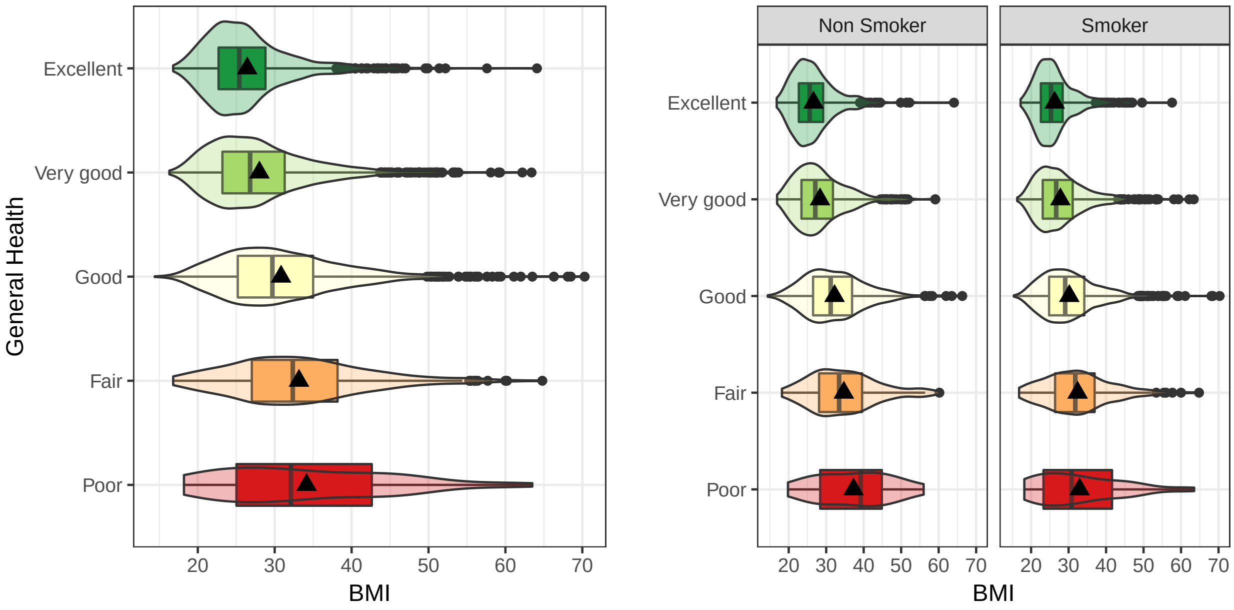
1. `scale_x_discrete` is used to reverse the display order of the limits on general health.
2. `coord_flip` is used to turn the boxplots horizontal, thereby removing the overlapping category labels.
3. `scale_fill_brewer` is used to apply a red-yellow-green color palette to the categories of general health. This is applicable because general health is an ordinal variable that has an interpretation of "good" to "bad".

```r
bmi.plot <- addhealth %>% select(genhealth, BMI, eversmoke_c) %>% na.omit()

twoway.boxplot <- ggplot(bmi.plot, aes(x=genhealth, y=BMI, fill=genhealth)) +
                  geom_boxplot(width=.4) + geom_violin(alpha=.3) +
                  stat_summary(fun.y="mean", geom="point", size=3, pch=17,
                  position=position_dodge(width=0.75)) + theme_bw() +
                  labs(x="General Health", y="BMI") +
                  scale_x_discrete(limits=rev(levels(bmi.plot$genhealth)))+
                  scale_fill_brewer(guide=FALSE, palette="RdYlGn", direction=-1) +
                  theme(legend.position = "top")+ coord_flip()

threeway.boxplot <- ggplot(bmi.plot, aes(x=genhealth, y=BMI, fill=genhealth)) +
                  geom_boxplot(width=.4) + geom_violin(alpha=.3) +
                  stat_summary(fun.y="mean", geom="point", size=3, pch=17,
                  position=position_dodge(width=0.75)) + theme_bw() +
                  facet_wrap(~eversmoke_c)+
                  labs(x="", y="BMI") +
                  scale_x_discrete(limits=rev(levels(bmi.plot$genhealth)))+
                  scale_fill_brewer(guide=FALSE, palette="RdYlGn", direction=-1) +
                  theme(legend.position = "top")+ coord_flip()

grid.arrange(twoway.boxplot, threeway.boxplot, ncol=2)
```



The `grid.arrange` code takes each of the plots above, and places them side by side. Remove this line, and the `<-` object assignment for each plot above if the resulting plot for your analysis is too crammed and difficult to read.

The `scale_x_discrete` and `scale_fill_brewer` code are specific to this analysis. Do not copy/paste this code to use in your analysis unless you can confirm that it is appropriate for your research question.

```
bmi.plot %>% group_by(eversmoke_c, genhealth) %>%
             summarise(mean=mean(BMI)) %>%
             tidyr::spread(genhealth, mean) %>%
              kable(digits=1, caption = "Average BMI per general health category, for smokers and non s
```

Table 1: Average BMI per general health category, for smokers and non smokers separately

eversmoke_c	Excellent	Very good	Good	Fair	Poor
Non Smoker	26.6	28.4	32.2	34.7	37.3
Smoker	26.3	27.8	30.2	32.4	32.9

note the code above uses the `spread` function in `tidyr` package to turn the table of means on it's side

The average BMI for those reporting excellent health is basically the same between smokers and non-smokers. As perceived general health decreases, the average BMI increases, but it seems to do so at a faster rate in non-smokers compare to smokers. There seems to be more high end outlying points that are smokers compared to non-smokers. Otherwise the relationship between BMI and general health appears the same within each smoking group.

3. **Write the relationship you want to examine in the form of a research question - including a statement about the modifier**

Does ever smoking change the relationship between perceived general health and BMI? Is the distribution of BMI the same across perceived general health status, for both smokers and non-smokers?

4. **Fit both the original, and stratified models.**

The pander() function prints these as nice tables. This is not required, just recommended.

```r
twoway.anova <- summary(aov(BMI ~ genhealth, data=addhealth))
pander(twoway.anova, caption="Original model")
```

Table 2: Original model

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
genhealth	4	22563	5641	109	2.05e-89
Residuals	5037	260096	51.6	NA	NA

```r
pander(summary(aov(BMI ~ genhealth,
                   data=filter(addhealth, eversmoke_c=="Smoker"))),
       caption="Model for Smokers")
```

Table 3: Model for Smokers

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
genhealth	4	11364	2841	56.6	2.99e-46
Residuals	3271	164117	50.2	NA	NA

```r
pander(summary(aov(BMI ~ genhealth,
                   data=filter(addhealth, eversmoke_c=="Non Smoker"))),
       caption="Model for Non-Smokers")
```

Table 4: Model for Non-Smokers

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
genhealth	4	12565	3141	59	8.72e-47
Residuals	1745	92873	53.2	NA	NA

5. **Determine if the Third Variable is a moderator or not.**

Both the original ANOVA and the stratified ANOVA models for smokers and non-smokers separately are highly significant. There is not a clear difference in the relationship between BMI and general health status between smokers and non-smokers, so ever being a smoker is not a moderating variable for this relationship.

Chi-Square

1. **Identify response and explanatory variables**

- Categorical explanatory variable = Gender (variable `female_c`)
- Categorical response variable = General Health (variable `genhealth`)
- Categorical Potential Moderator = Ever smoked (variable `eversmoke_c`)

2. **Visualize and summarise the potential effect of the moderator**

Set up the two and three way tables for printing, and as a data frame for plotting.

For the two way table, I put `female_c` as rows and `genhealth` as columns. So when calculating proportions of females within each general health category, I want the column margins (`margin=2`).

```
crosstab.gender.genhealth <- table(addhealth$female_c, addhealth$genhealth)
proptab.gender.genhealth  <- prop.table(crosstab.gender.genhealth, margin=2)
plot.crostab <- data.frame(proptab.gender.genhealth)
kable(proptab.gender.genhealth, digits=2)
```

	Excellent	Very good	Good	Fair	Poor
Male	0.52	0.46	0.45	0.4	0.31
Female	0.48	0.54	0.55	0.6	0.69

Here I create a three way table: `female_c` as rows (1), `genhealth` as columns (2), and then stratified by `eversmoke_c` (3).

```
freq.gend.health.smoke <- table(addhealth$female_c, addhealth$genhealth, addhealth$eversmoke_c)
```

To get the correct column proportions within each level of `eversmoke_c`, I put `c(3,2)` for the margin argument: calculate the proportions within variable (3), and then across (2).

```
prop.gend.health.smoke <- prop.table(freq.gend.health.smoke, margin=c(3,2))
plot.threeway <- data.frame(prop.gend.health.smoke)
kable(prop.gend.health.smoke[,,1], digits=2, caption="General Health by Gender - for Non Smokers")
```

Table 6: General Health by Gender - for Non Smokers

	Excellent	Very good	Good	Fair	Poor
Male	0.44	0.39	0.36	0.29	0.27
Female	0.56	0.61	0.64	0.71	0.73

```
kable(prop.gend.health.smoke[,,2], digits=2, caption="General Health by Gender - for Smokers")
```

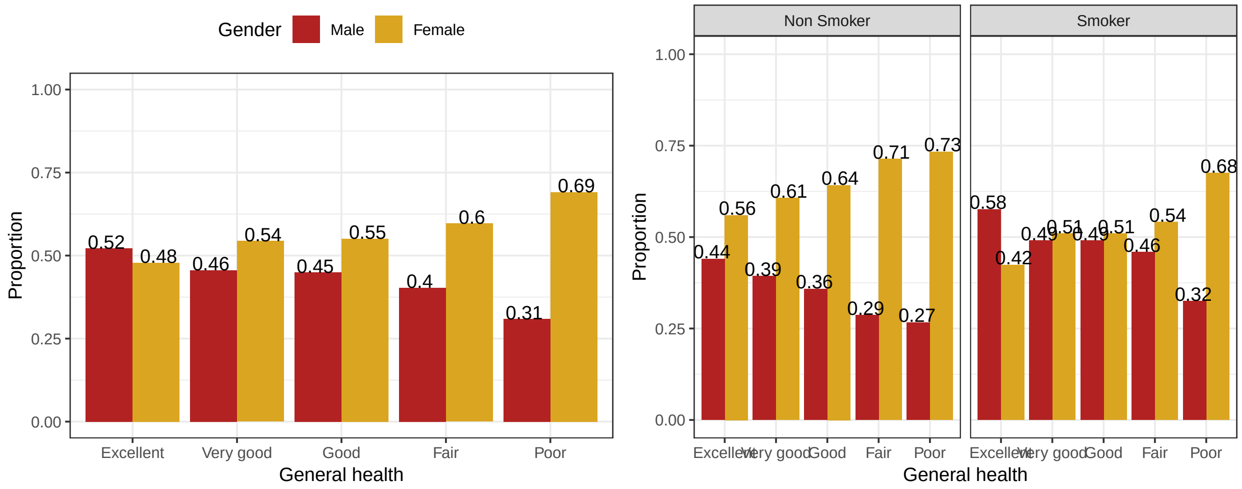
Table 7: General Health by Gender - for Smokers

	Excellent	Very good	Good	Fair	Poor
Male	0.58	0.49	0.49	0.46	0.32
Female	0.42	0.51	0.51	0.54	0.68

```
biv.crosstab <- ggplot(plot.crostab, aes(x=Var2, y=Freq, fill=Var1)) +
              geom_col(position = position_dodge()) + theme_bw() +
              geom_text(aes(y=Freq+.02, label=round(Freq,2)),
                        position = position_dodge(width=1)) +
              labs(x="General health", y="Proportion") +
               scale_fill_manual(name="Gender",
                                 values=c("firebrick", "goldenrod")) +
              theme(legend.position = "top") +
              scale_y_continuous(limits=c(0,1))

threeway.crosstab <- ggplot(plot.threeway, aes(x=Var2, y=Freq, fill=Var1)) +
              geom_col(position = position_dodge()) + theme_bw() + facet_wrap(~Var3) +
              geom_text(aes(y=Freq+.02, label=round(Freq,2)), position = position_dodge(width=1)) +
              labs(x="General health", y="Proportion") +
               scale_fill_manual(guide=FALSE, values=c("firebrick", "goldenrod")) +
              scale_y_continuous(limits=c(0,1))

grid.arrange(biv.crosstab,threeway.crosstab, ncol=2)
```



The gender difference across levels of general health seems to be due to the non-smokers. With the exception of those reporting excellent, or poor health, the proportions of male and females seem equal within each general health category for the smokers. For the non-smokers, as perceived general health worsens, the proportion of females in that category increases.

There is likely reason to believe that smokers have a different view on their general health compared to non-smokers, and this viewpoint is pretty similar between males and females.

Optional way of plotting a binary grouping variable

Since this our explanatory variable is only two levels we can plot the proportion of "yes" values - here it would be females only. This makes for a more easily understood plot. Additional color names can be found here: http://www.stat.columbia.edu/~tzheng/files/Rcolor.pdf

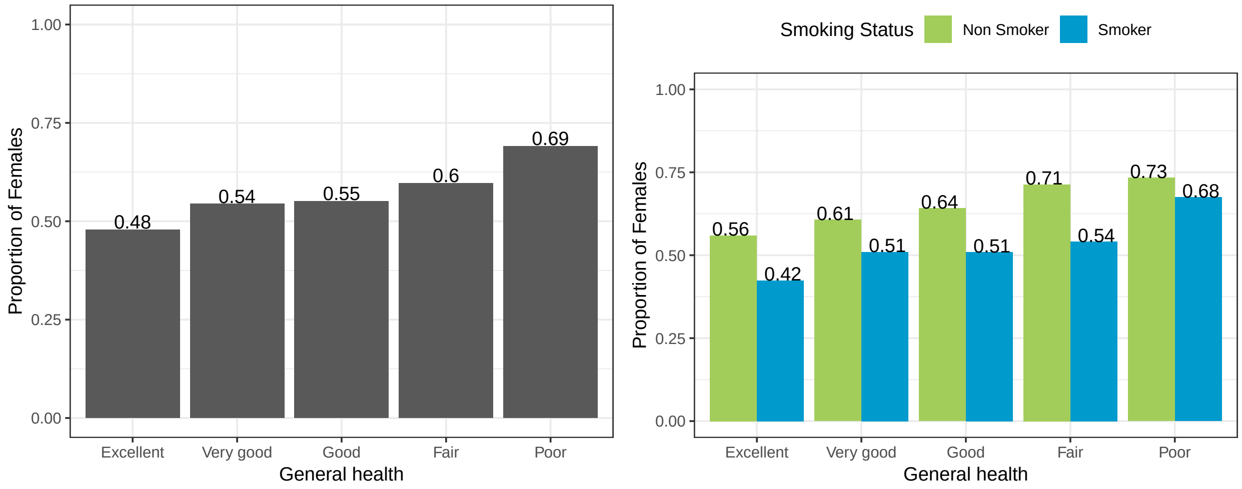
```
female.only_2 <- filter(plot.crostab, Var1=="Female")

plot2 <- ggplot(female.only_2, aes(x=Var2, y=Freq)) +
              geom_col(position = position_dodge()) + theme_bw() +
              geom_text(aes(y=Freq+.02, label=round(Freq,2)),
                        position = position_dodge(width=1)) +
              labs(x="General health", y="Proportion of Females") +
              scale_y_continuous(limits=c(0,1))

female.only_3 <- filter(plot.threeway, Var1=="Female")

plot3 <- ggplot(female.only_3, aes(x=Var2, y=Freq, fill=Var3)) +
              geom_col(position = position_dodge()) + theme_bw() +
              geom_text(aes(y=Freq+.02, label=round(Freq,2)), position = position_dodge(width=1)) +
              labs(x="General health", y="Proportion of Females") +
              theme(legend.position = "top") +
              scale_fill_manual(name="Smoking Status", values=c("darkolivegreen3", "deepskyblue3")) +
              scale_y_continuous(limits=c(0,1))
```

```r
grid.arrange(plot2,plot3, ncol=2)
```



3. **Write the relationship you want to examine in the form of a research question - including a statement about the modifier**

Does ever smoking change the relationship between gender and general health? Is the distribution of gender (proportion of females) equal across all levels of general health, for both smokers and non smokers?

4. **Fit both the original, and stratified models.**

```r
chisq.test(addhealth$female_c, addhealth$genhealth)
```

```
##
##  Pearson's Chi-squared test
##
## data:  addhealth$female_c and addhealth$genhealth
## X-squared = 26.471, df = 4, p-value = 2.543e-05
```

```r
by(addhealth, addhealth$eversmoke_c, function(x) chisq.test(x$female_c, x$genhealth))
```

```
## addhealth$eversmoke_c: Non Smoker
##
##  Pearson's Chi-squared test
##
## data:  x$female_c and x$genhealth
## X-squared = 13.438, df = 4, p-value = 0.009324
##
## ----------------------------------------------------------
## addhealth$eversmoke_c: Smoker
##
##  Pearson's Chi-squared test
##
## data:  x$female_c and x$genhealth
## X-squared = 20.994, df = 4, p-value = 0.0003175
```

5. **Determine if the Third Variable is a moderator or not.**

The relationship between gender and general health is significant in both the main effects and the stratified model. The distribution of females across general health categories differs greatly between smokers and non-smokers. One could argue that the smoking status of an individual does not modify the relationship between gender and reported general health status *enough* to warrent controlling for. However one could argue that the effect of gender on general health *is* modified by smoking status since the strength of the relationship has been attenuated for the non-smoking group. The p-value in the stratified model is 10-100 magnitudes larger than in the overall model (.000025 vs .009 and .0003).

Either way you decide if a variable is a moderator or not, you must justify your choice by talking about changes in the sample statistics and inferential test results.

Linear Regression

1. **Identify response, explanatory, and moderating variables**

- Quantitative explanatory variable = Sepal Length (variable `Sepal.Length`)
- Quantitative response variable = Petal Length (variable `Petal.Length`)
- Categorical Potential Moderator = Species (variable `Species`)

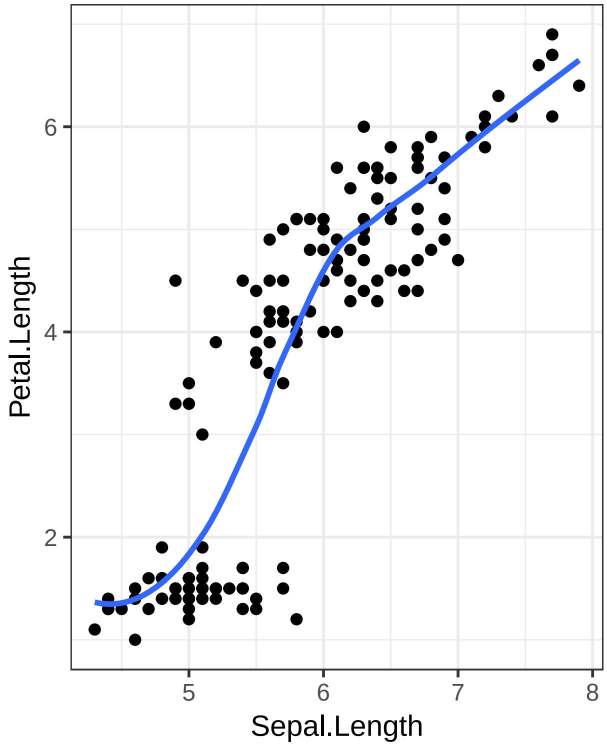
2. **Visualize and summarise the potential effect of the moderator**

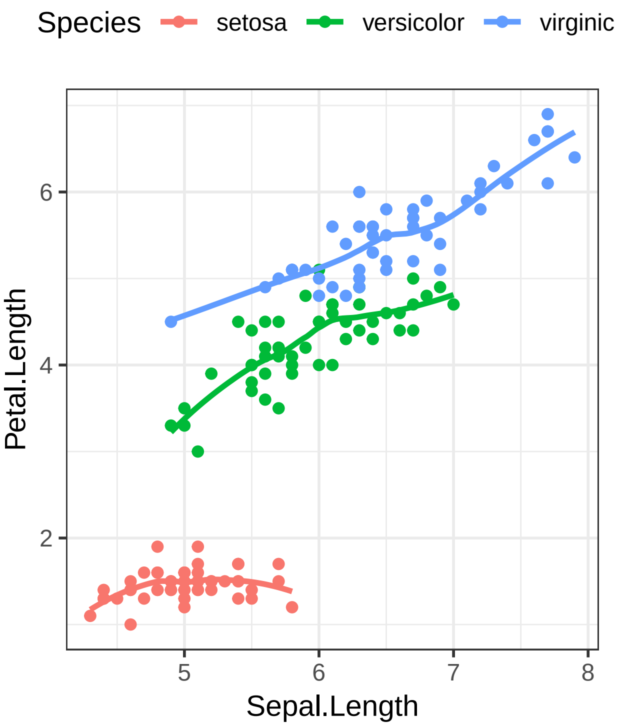
Plot your original bivariate plot on the left,

```
linreg.plot <- ggplot(iris, aes(x=Sepal.Length, y=Petal.Length)) +
                geom_point() + geom_smooth(se=FALSE) +
                theme_bw()

linreg.modifier.plot <- ggplot(iris,
                               aes(x=Sepal.Length, y=Petal.Length, col=Species)) +
                          geom_point() + geom_smooth(se=FALSE) +
                          theme_bw() + theme(legend.position="top")

grid.arrange(linreg.plot, linreg.modifier.plot , ncol=2)
```





```r
cor(iris$Sepal.Length, iris$Petal.Length)
```

```
## [1] 0.8717538
```

```r
by(iris, iris$Species, function(x) cor(x$Sepal.Length, x$Petal.Length))
```

```
## iris$Species: setosa
## [1] 0.2671758
## --------------------------------------------------------
## iris$Species: versicolor
## [1] 0.754049
## --------------------------------------------------------
## iris$Species: virginica
## [1] 0.8642247
```

There is a strong, positive, linear relationship between the sepal length of the flower and the petal length when ignoring the species. The correlation coefficient r for *virginica* and *veriscolor* are similar to the overall r value, 0.86 and 0.75 respectively compared to 0.87. However the correlation between sepal and petal length for species *setosa* is only 0.26.

The points are clearly clustered by species, the slope of the lowess line between *virginica* and *versicolor* appear similar in strength, whereas the slope of the line for *setosa* is closer to zero. This would imply that petal length for *Setosa* may not be affected by the length of the sepal.

3. **Write the relationship you want to examine in the form of a research question - including a statement about the modifier**

Does the species of the flower change or modify the linear relationship between the length of the flower's sepal and it's petal?

4. **Fit both the original, and stratified models.**

Fit the Main effects model, print the regression table of coefficients. The `pander()` function prints these as nice tables. This is not required, just recommended.

```r
iris.linear.model <- lm(Petal.Length ~ Sepal.Length, data=iris)
pander(iris.linear.model)
```

Table 8: Fitting linear model: Petal.Length ~ Sepal.Length

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	-7.1	0.507	-14	6.13e-29
Sepal.Length	1.86	0.0859	21.6	1.04e-47

Fit the stratified model, print the regression table of coefficients.

```r
setosa.model     <- lm(Petal.Length ~ Sepal.Length, data=filter(iris, Species=="setosa"))
veriscolor.model <- lm(Petal.Length ~ Sepal.Length, data=filter(iris, Species=="versicolor"))
virginica.model  <- lm(Petal.Length ~ Sepal.Length, data=filter(iris, Species=="virginica"))
pander(setosa.model)
```

Table 9: Fitting linear model: Petal.Length ~ Sepal.Length

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	0.803	0.344	2.34	0.0238
Sepal.Length	0.132	0.0685	1.92	0.0607

```r
pander(veriscolor.model)
```

Table 10: Fitting linear model: Petal.Length ~ Sepal.Length

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	0.185	0.514	0.36	0.72
Sepal.Length	0.686	0.0863	7.95	2.59e-10

```r
pander(virginica.model)
```

Table 11: Fitting linear model: Petal.Length ~ Sepal.Length

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	0.61	0.417	1.46	0.15
Sepal.Length	0.75	0.063	11.9	6.3e-16

5. **Determine if the Third Variable is a moderator or not.**

The estimate for sepal length in the original model is 1.85, p-value <.0001. - For *setosa* the estimate is 0.13, pvalue of 0.06 - For *versicolor* the estimate is 0.69, pvalue <.0001 - For *virginica* the estimate is 0.75, pvalue <.0001

Within the *setosa* species, there is little to no relationship between sepal and petal length. For *veriscolor* and *virginica* the relationship is still signficantly positive. This is **Scenario 1**, so Species moderates the effect of sepal length on petal length.