

# Assign. 1 STA 445

YOUR NAME HERE

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## Directions:

This assignment covers chapter 5. Please show all work in this document and knit your final draft into a pdf. This assignment is about statistical models, which will be helpful if you plan on taking STA 570, STA 371, or STA 571.

```
library(tidyverse)
```

## Problem 1: Two Sample t-test

- Load the `iris` dataset.

```
data(iris)
```

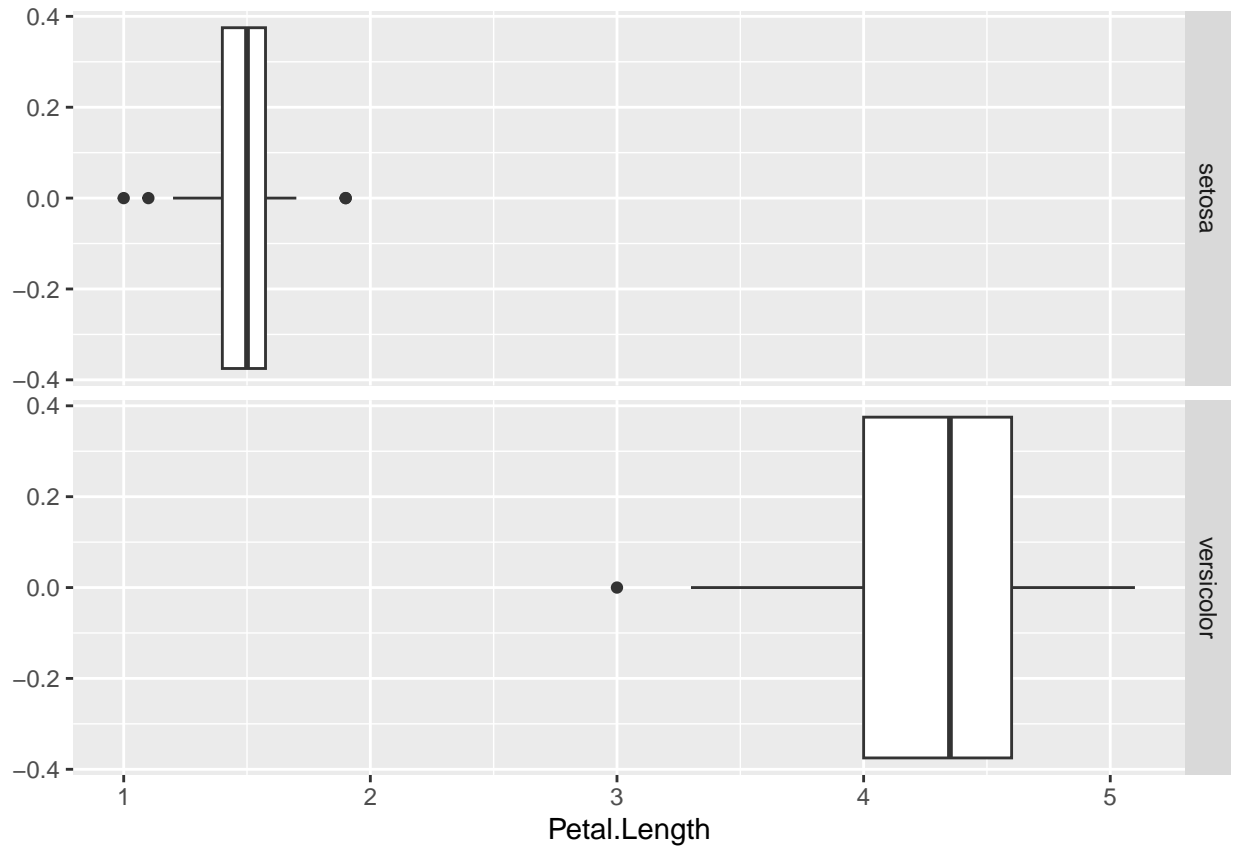
- Create a subset of the data that just contains rows for the two species `setosa` and `versicolor` using `filter`. Use `slice_sample` to print out 20 random rows of the dataset.

```
iris.filter <- iris %>% filter(Species == "setosa" | Species == "versicolor")
slice_sample(iris.filter, n = 20)
```

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.7	2.8	4.1	1.3	versicolor
## 2	6.1	2.9	4.7	1.4	versicolor
## 3	5.6	3.0	4.5	1.5	versicolor
## 4	5.1	3.8	1.5	0.3	setosa
## 5	5.0	2.3	3.3	1.0	versicolor
## 6	5.2	3.4	1.4	0.2	setosa
## 7	4.8	3.4	1.6	0.2	setosa
## 8	5.5	2.6	4.4	1.2	versicolor
## 9	6.4	2.9	4.3	1.3	versicolor
## 10	6.8	2.8	4.8	1.4	versicolor
## 11	4.9	3.1	1.5	0.2	setosa
## 12	6.2	2.2	4.5	1.5	versicolor
## 13	5.5	4.2	1.4	0.2	setosa
## 14	6.1	2.8	4.7	1.2	versicolor
## 15	5.1	3.8	1.6	0.2	setosa
## 16	5.1	3.5	1.4	0.2	setosa
## 17	4.8	3.0	1.4	0.1	setosa
## 18	5.2	3.5	1.5	0.2	setosa
## 19	4.8	3.1	1.6	0.2	setosa
## 20	4.6	3.6	1.0	0.2	setosa

- c. Create a box plot of the petal lengths for these two species using ggplot. Does it look like the mean petal length varies by species?

```
ggplot(iris.filter, aes(x = Petal.Length)) +  
  geom_boxplot() + facet_grid(Species~.)
```



Yes it does look like the species plays a role in the mean petal length

- d. Do a two sample t-test using `t.test` to determine formally if the petal lengths differ. Note: The book uses the `tidy` function in the `broom` package to make the output “nice”. I hate it! Please don’t use `tidy`.

```
t.test(Petal.Length ~ Species, iris.filter)
```

```
##  
## Welch Two Sample t-test  
##  
## data: Petal.Length by Species  
## t = -39.493, df = 62.14, p-value < 2.2e-16  
## alternative hypothesis: true difference in means between group setosa and group versicolor is not eq  
## 95 percent confidence interval:  
## -2.939618 -2.656382  
## sample estimates:  
## mean in group setosa mean in group versicolor  
## 1.462 4.260
```

d. What is the p-value for the test? What do you conclude?

$P = 2.2e-16$  which is about 0. from this test we can conclude that there is a difference in petal sizes depending on the species

e. Give a 95% confidence interval for the difference in the mean petal lengths.

We are 95% confident that the true mean difference between the two species is in the interval (-2.94, -2.66)

f. Give a 99% confidence interval for the difference in mean petal lengths. (Hint: type `?t.test`. See that you can change the confidence level using the option `conf.level`)

```
t.test(Petal.Length ~ Species, iris.filter, conf.level = 0.99)

##
##  Welch Two Sample t-test
##
## data:  Petal.Length by Species
## t = -39.493, df = 62.14, p-value < 2.2e-16
## alternative hypothesis: true difference in means between group setosa and group versicolor is not equal to 0
## 99 percent confidence interval:
##  -2.986265 -2.609735
## sample estimates:
##      mean in group setosa mean in group versicolor
##                1.462                4.260
```

We are 99% confident that the mean difference is within the interval (-2.99, -2.61)

g. What is the mean petal length for setosa?

The mean for setosa is 1.462

h. What is the mean petal length for versicolor?

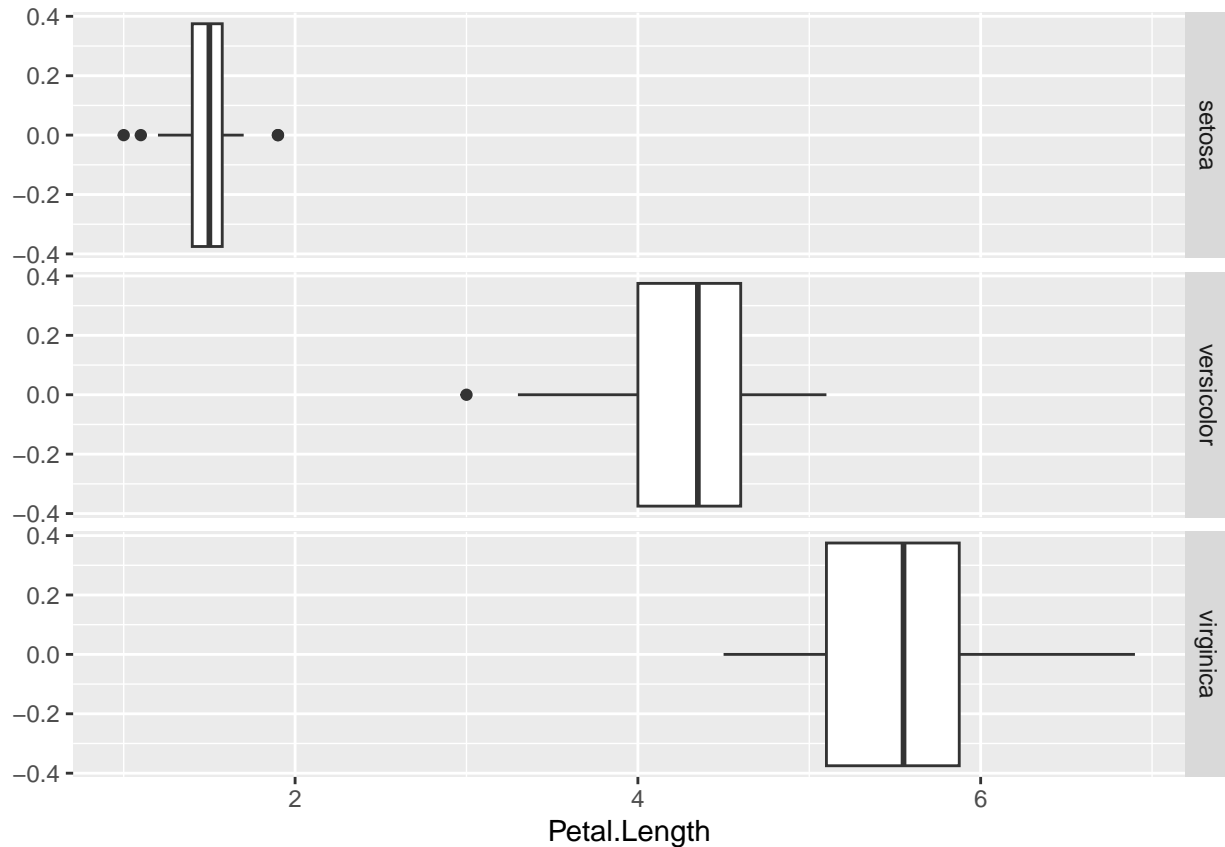
The mean for versicolor is 4.260

## Problem 2: ANOVA

Use the iris data with all three species.

a. Create a box plot of the petal lengths for all three species using `ggplot`. Does it look like there are differences in the mean petal lengths?

```
ggplot(iris, aes(x = Petal.Length)) +
  geom_boxplot() + facet_grid(Species~.)
```



Yes it does look like there is a difference with the mean for each species

b. Create a linear model where sepal length is modeled by species. Give it an appropriate name.

```
iris.lm <- lm(Sepal.Length~Species-1, iris)
```

c. Type anova(your model name) in a code chunk.

```
anova(iris.lm)
```

```
## Analysis of Variance Table
##
## Response: Sepal.Length
##          Df Sum Sq Mean Sq F value    Pr(>F)
## Species    3  5184.9  1728.30   6521.7 < 2.2e-16 ***
## Residuals 147    39.0    0.27
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

d. What is the p-value for the test? What do you conclude.

The p-value is 2.2e-16. This shows that there is a significance in the difference between species.

e. Type summary(your model name) in a code chunk.

```
summary(iris.lm)
```

```
##
## Call:
## lm(formula = Sepal.Length ~ Species - 1, data = iris)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.6880 -0.3285 -0.0060  0.3120  1.3120
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## Speciessetosa      5.0060     0.0728   68.76  <2e-16 ***
## Speciesversicolor  5.9360     0.0728   81.54  <2e-16 ***
## Speciesvirginica   6.5880     0.0728   90.49  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5148 on 147 degrees of freedom
## Multiple R-squared:  0.9925, Adjusted R-squared:  0.9924
## F-statistic: 6522 on 3 and 147 DF,  p-value: < 2.2e-16
```

f. What is the mean sepal length for the species setosa?

The mean sepal length for Setosa is 5.0060.

g. What is the mean sepal length for the species versicolor?

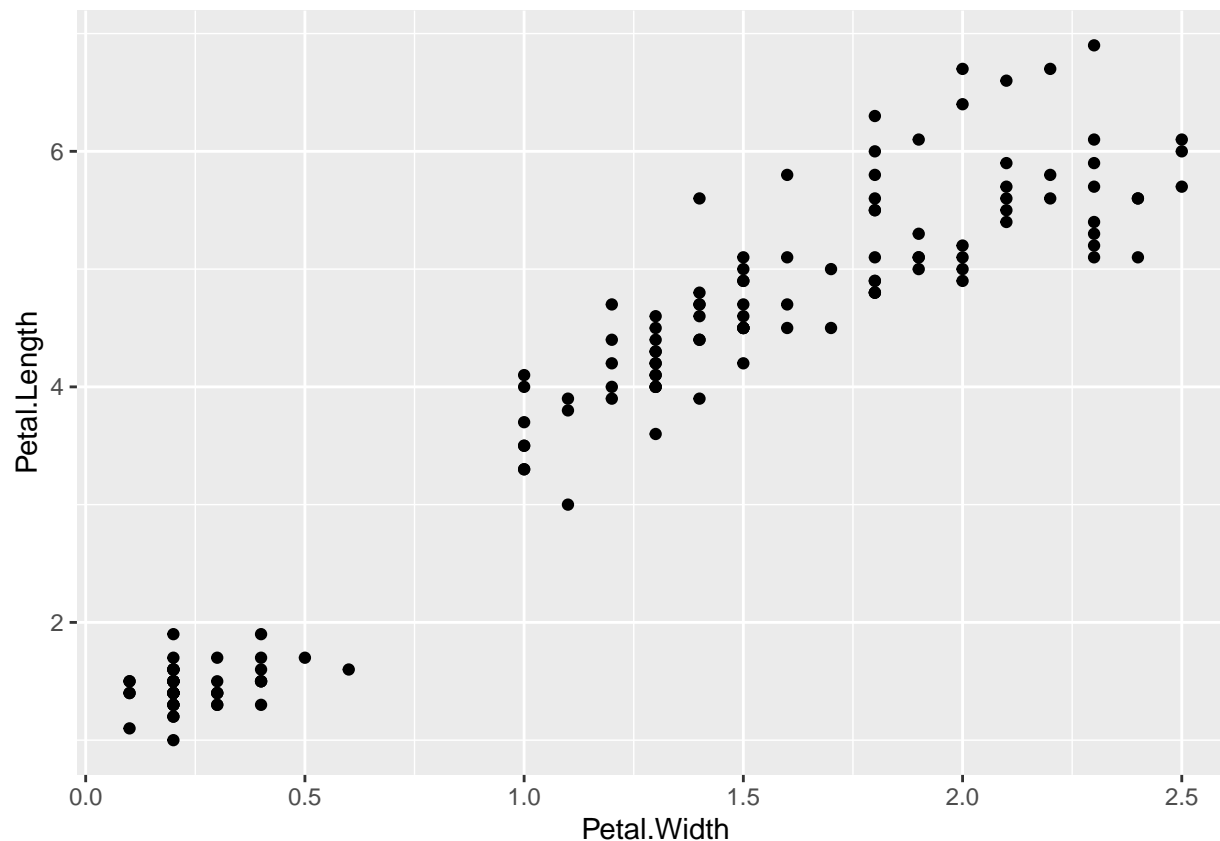
The mean sepal length for versicolor is 6.59880.

### Problem 3: Regression

Can we describe the relationship between petal length and petal width?

a. Create a scatterplot with petal length on the y-axis and petal width on the x-axis using ggplot.

```
ggplot(iris, aes(x = Petal.Width, y = Petal.Length)) +
  geom_point()
```



- b. Create a linear model to model petal length with petal width (length is the response variable and width is the explanatory variable) using `lm`.

```
iris.petal.lm <- lm(Petal.Length ~ Petal.Width, data = iris)
iris.petal.lm
```

```
##
## Call:
## lm(formula = Petal.Length ~ Petal.Width, data = iris)
##
## Coefficients:
## (Intercept)  Petal.Width
##          1.084          2.230
```

- c. What is the estimate of the slope parameter?

The estimate of the slope is 2.23.

- d. What is the estimate of the intercept parameter?

The estimate of the intercept is 1.084.

- e. Use `summary()` to get additional information.

```
summary(iris.petal.lm)
```

```
##
## Call:
## lm(formula = Petal.Length ~ Petal.Width, data = iris)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.33542 -0.30347 -0.02955  0.25776  1.39453
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.08356    0.07297   14.85  <2e-16 ***
## Petal.Width  2.22994    0.05140   43.39  <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4782 on 148 degrees of freedom
## Multiple R-squared:  0.9271, Adjusted R-squared:  0.9266
## F-statistic: 1882 on 1 and 148 DF,  p-value: < 2.2e-16
```

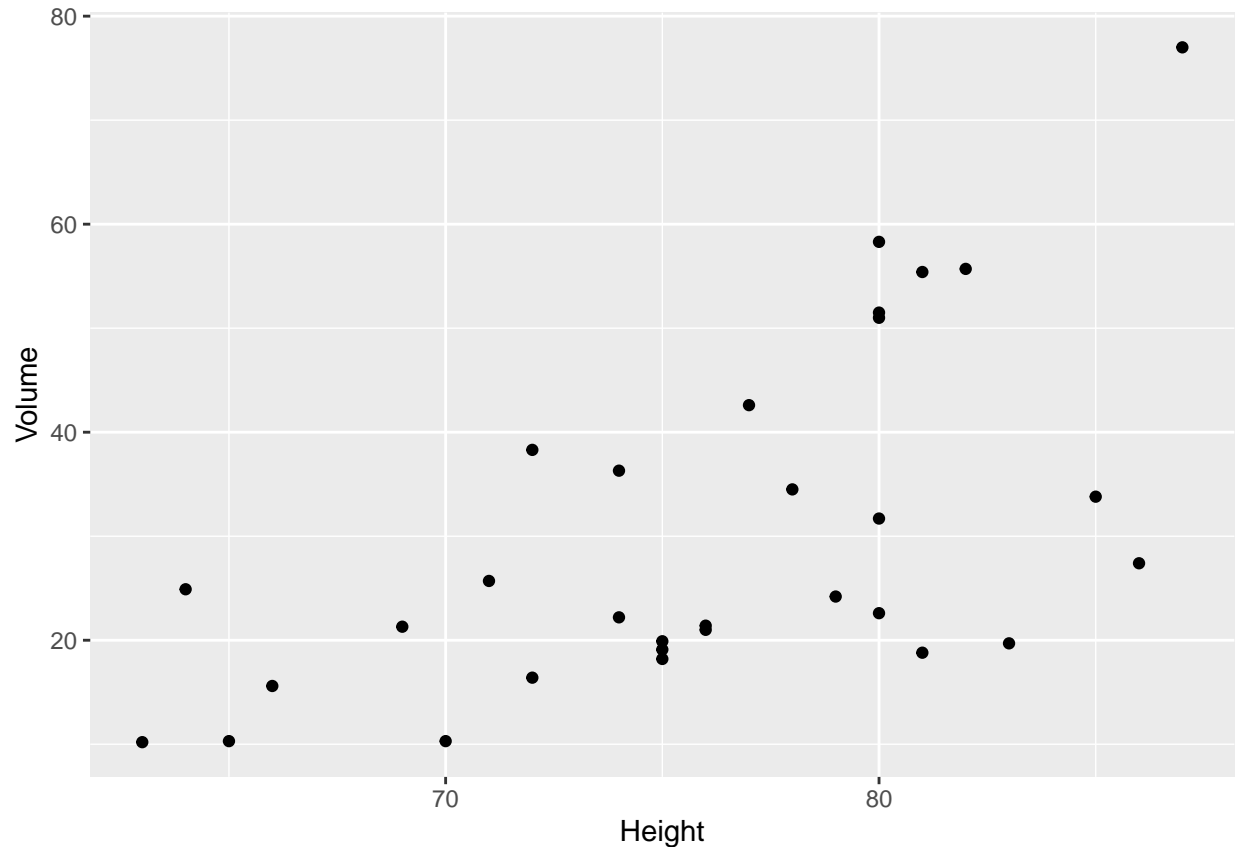
## Problem 4: Modeling Trees

Using the `trees` data frame that comes pre-installed in R, follow the steps below to fit the regression model that uses the tree `Height` to explain the `Volume` of wood harvested from the tree.

- a. Create a scatterplot of the data using `ggplot`.

```
data(trees)

ggplot(trees, aes(x = Height, y = Volume)) +
  geom_point()
```



b. Fit a lm model using the command `model <- lm(Volume ~ Height, data=trees)`.

```
trees.lm <- lm(Volume ~ Height - 1, data=trees)
```

c. Print out the table of coefficients with estimate names, estimated value, standard error, and upper and lower 95% confidence intervals.

```
summary(trees.lm)
```

```
##
## Call:
## lm(formula = Volume ~ Height - 1, data = trees)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -18.031 -11.184  -7.407   7.755  41.788
##
## Coefficients:
##           Estimate Std. Error t value Pr(>|t|)
## Height  0.40473    0.03545   11.42 1.91e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.05 on 30 degrees of freedom
```



```
## Multiple R-squared:  0.8129, Adjusted R-squared:  0.8067
## F-statistic: 130.4 on 1 and 30 DF,  p-value: 1.91e-12
```

```
anova(trees.lm)
```

```
## Analysis of Variance Table
##
## Response: Volume
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Height      1 29530.3  29530.3   130.38 1.91e-12 ***
## Residuals   30  6794.7    226.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

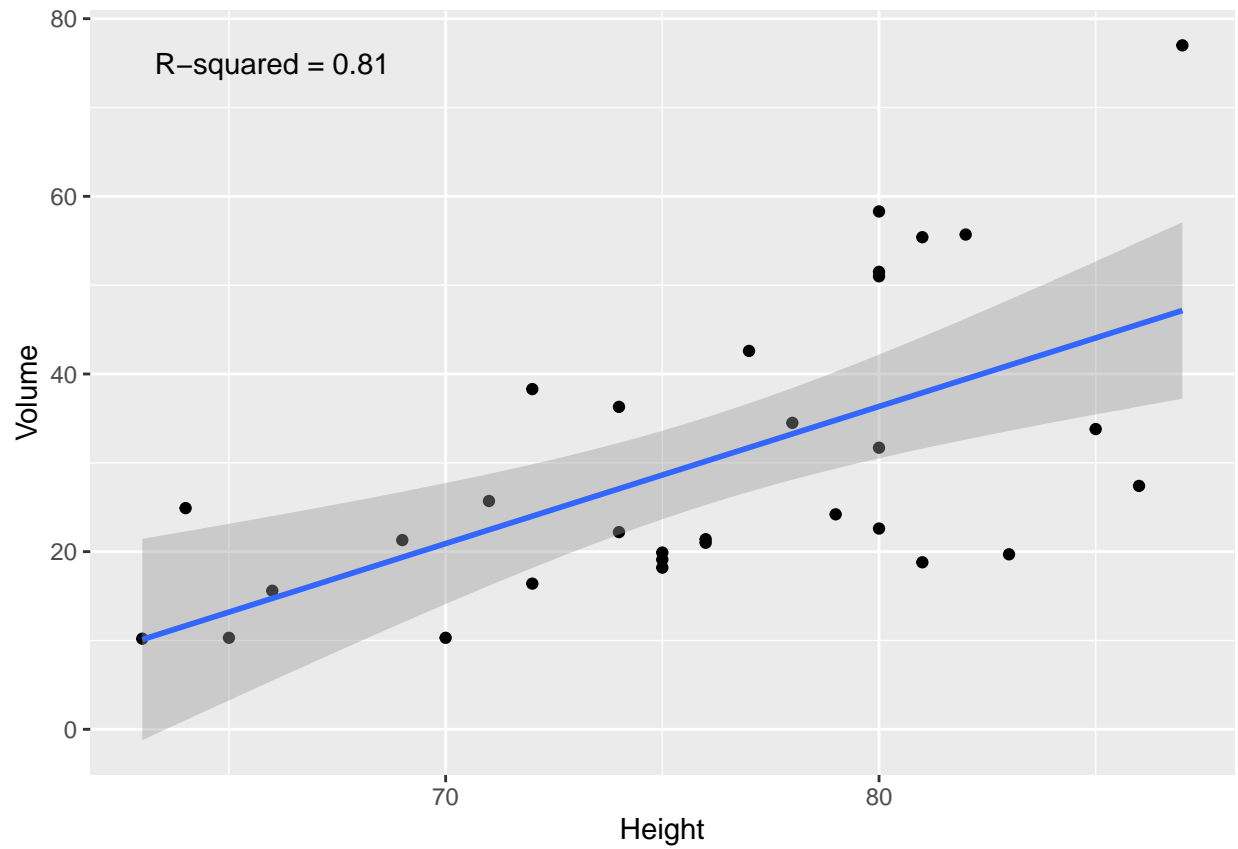
d. Add the model fitted values to the `trees` data frame along with the regression model confidence intervals. Note: the book does this in a super convoluted way. Don't follow the model in the book. Instead try `cbind`.

```
trees.bound <- cbind(trees, trees.lm$fitted.values)
```

e. Graph the data and fitted regression line and uncertainty ribbon.

```
ggplot(trees.bound, aes(x = Height, y = Volume)) +
  geom_point() +
  geom_smooth(method = lm) +
  annotate('text', x = 66, y = 75, size = 4, color = 'gray1',
          label = 'R-squared = 0.81')
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```



f. Add the R-squared value as an annotation to the graph using `annotate`.

$$r\text{-squared} = 29530.3 / (29530.3 + 6794.7) = 0.81294700619$$