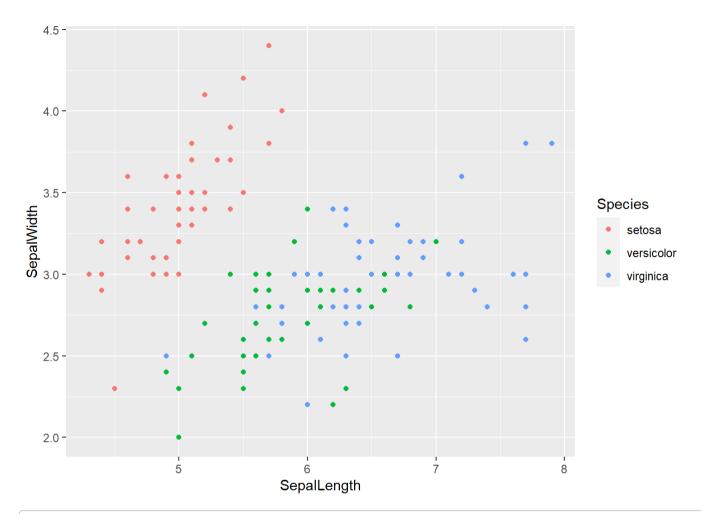
Homework 5

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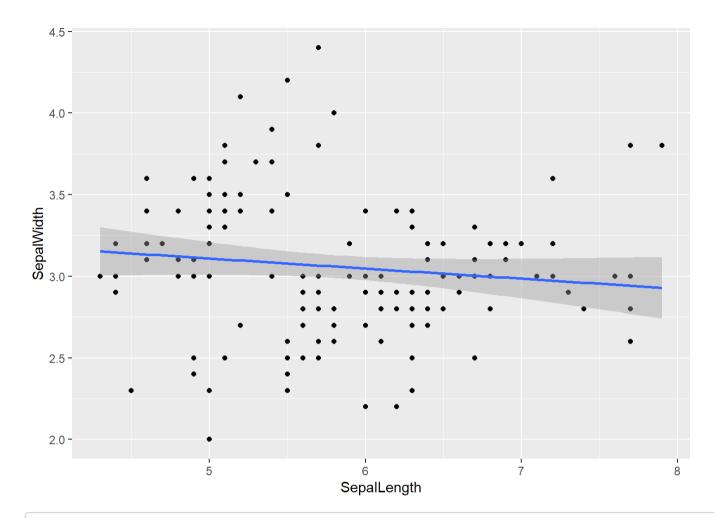
These are my solutions to the homework 5 of the data science course in SS23.

```
summary(iris)
    Sepal.Length
                   Sepal.Width
                                   Petal.Length
                                                  Petal.Width
## Min.
          :4.300 Min.
                        :2.000
                                                        :0.100
                                 Min.
                                         :1.000
                                                 Min.
## 1st Qu.:5.100
                  1st Qu.:2.800
                                 1st Qu.:1.600
                                                 1st Qu.:0.300
   Median :5.800
                  Median :3.000
                                 Median :4.350
                                                 Median :1.300
   Mean :5.843
                  Mean :3.057
                                       :3.758
                                                 Mean :1.199
                                  Mean
   3rd Qu.:6.400
                  3rd Qu.:3.300
                                  3rd Qu.:5.100
                                                 3rd Qu.:1.800
   Max. :7.900
                         :4.400
                                         :6.900
                                                 Max.
                                                      :2.500
                  Max.
                                 Max.
         Species
##
             :50
    setosa
    versicolor:50
   virginica :50
##
##
##
```

```
## make scatter plot with x-axis: Sepal.Length and y-axis: Sepal.Width -> Species should be shown in different colors
SepalLength <- iris$Sepal.Length
SepalWidth <- iris$Sepal.Width
ggplot(iris, aes(x=SepalLength, y=SepalWidth, colour=Species)) + geom_point()</pre>
```

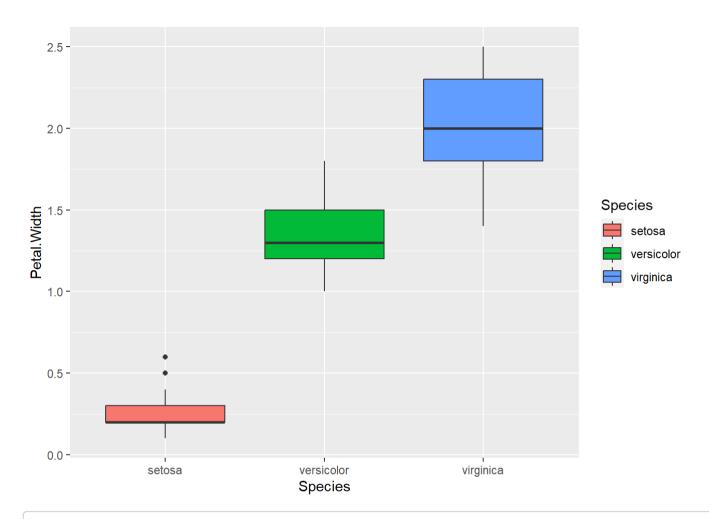


add regression line for the previous plot with the whole dataset (regardless of the species)
reg_plot <- ggplot(iris, aes(x=SepalLength, y=SepalWidth)) + geom_point()
reg_plot + geom_smooth(method='lm', formula= y~x)</pre>

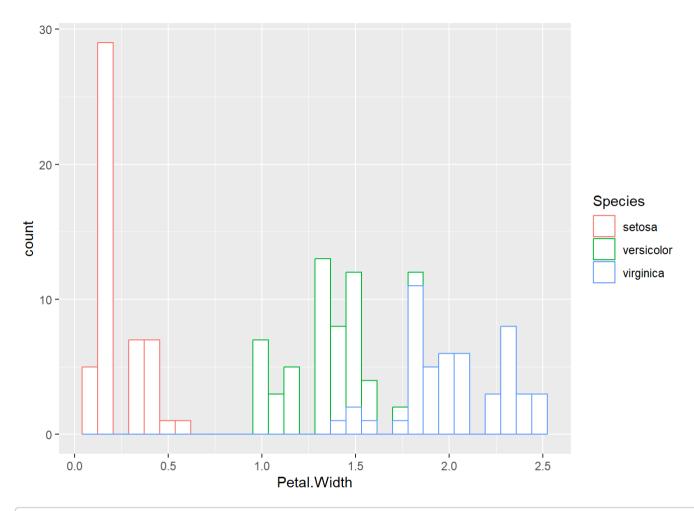


calculate the Pearson correlation for this plot
cor.test(iris\$Sepal.Length, iris\$Sepal.Width, method = "pearson", conf.level = 0.95)

```
## make the box plot for Petal.Width with 3 species separately in the x-axis in different colors
box_plt <- ggplot(iris, aes(x=Species,y=Petal.Width, fill=Species))
box_plt + geom_boxplot()</pre>
```



make the histogram for Petal.Width with 3 species separately in x-axis in different colors
ggplot(iris, aes(x=Petal.Width, color=Species)) + geom_histogram(fill="White", bins = 30)



run the t-test of Petal.Width between setosa and virginica, and give the conclusion if the width is a statistically signi
ficant difference between 2 species
iris = filter(iris, Species != "versicolor") # remove versicolor
#summary(iris)
t.test(Petal.Width~Species, data = iris)

```
##
## Welch Two Sample t-test
##
## data: Petal.Width by Species
## t = -42.786, df = 63.123, p-value < 2.2e-16
## alternative hypothesis: true difference in means between group setosa and group virginica is not equal to 0
## 95 percent confidence interval:
## -1.863133 -1.696867
## sample estimates:
## mean in group setosa mean in group virginica
## 0.246 2.026</pre>
```

p-value < 2.2e-16 which is < 0.05 , it is significant