

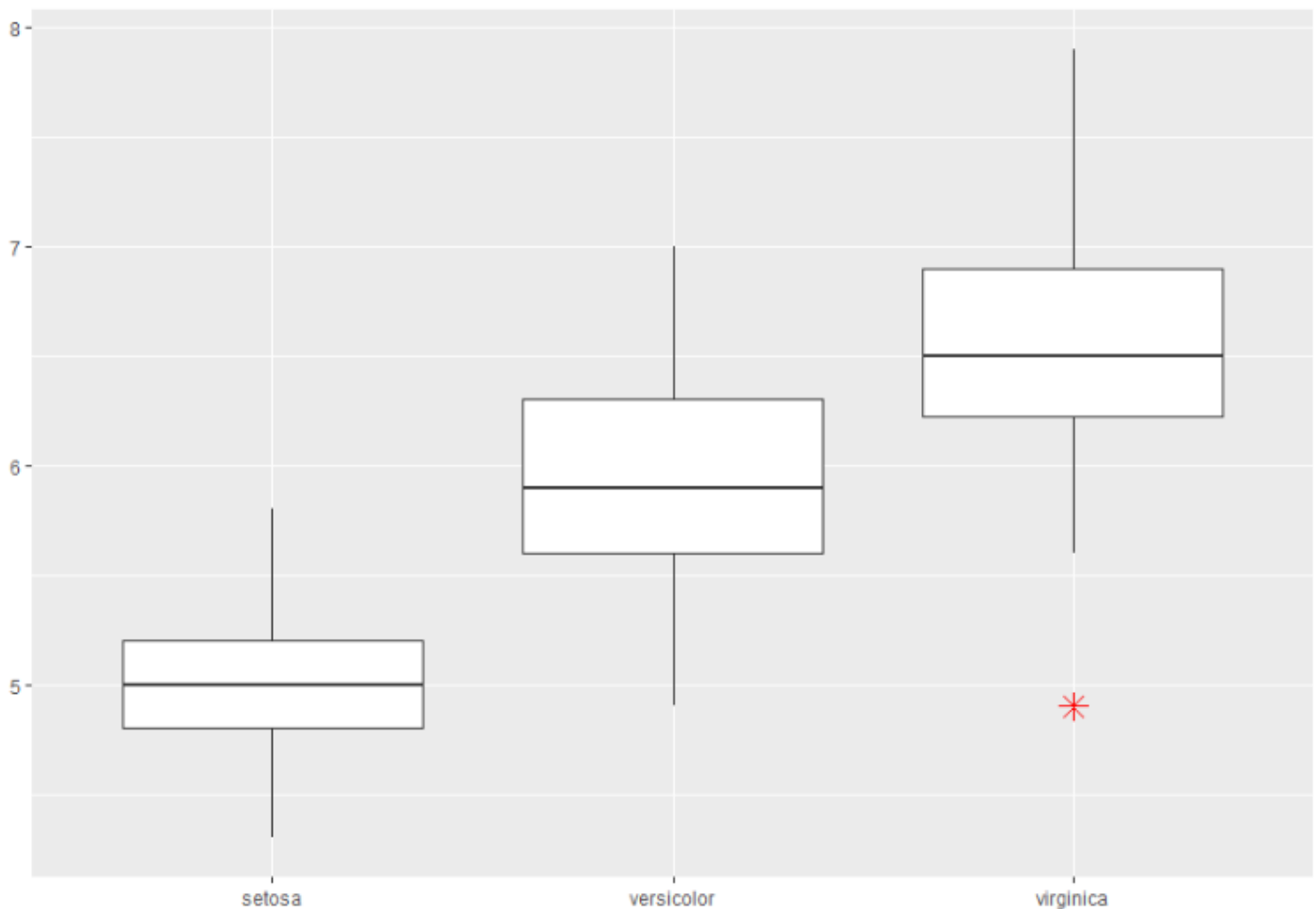
In this lab, we will test whether there is a difference in the mean sepal length among all three iris species.

To start, let's do some exploratory data analysis.

```
> library(ggplot2)
> iris_boxplot <- ggplot(iris, aes(x = Species, y = Sepal.Length)) +
  labs(title = "", x = "", y = "") + # You finish the code! Optional to add
  + coord_flip() to make horizontal boxplots instead
```

**Question #1** Insert the final set of boxplots below.

---



**Question #2** Write the (null) hypothesis for a one-way ANOVA test of the claim that the three species have the same mean sepal length. Recall that this is a Fisher-type test and so only a null hypothesis is specified.

There is no difference in the mean lengths between the 3 species (setosa, versicolor, virginica)

Now let's check our variability.

```
> library(dplyr)
> iris %>% group_by(Species) %>% summarize(mean = mean(Sepal.Length), sd =
sd(Sepal.Length)) # No need to store in a variable - just output it
directly to console
```

**Question #3** What are the three sample standard deviations? Is our rule of thumb about the population standard deviation satisfied?

The three standard deviations are:

setosa: 0.352

versicolor: 0.516

virginica: 0.636

Our population rule of thumb is satisfied.

We will now do the one-way ANOVA test in R:

```
> iris_anova <- aov(Sepal.Length ~ Species, data = iris)
> summary(iris_anova)
```

**Question #4** Copy and paste the output from the summary function below. Note that this table does not include the "Total" row shown in lecture (we can derive all numbers in that row from the values in the table).

```
      Df Sum Sq Mean Sq F value Pr(>F)
Species      2   63.21   31.606   119.3 <2e-16 ***
Residuals   147   38.96    0.265
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

**Question #5** From the output in **Question #4**, identify the test statistic, the sampling distribution it comes from (don't forget to include all relevant degrees of freedom parameters), and its observed value in this sample of 150 flowers.

The test-statistic is F and the sampling distribution is 2 DfG, 147 DfE, and 119.3 as the number of observed values.

**Question #6** What is the p-value for this one-way ANOVA F test? At the 5% significance level, is the model assumption "all three populations have the same mean sepal length" reasonable?

The p-value is <2e-16 which is significantly less than 0.05, so we reject the null hypothesis that we came up with in question 2 and say that all three pops. don't have the same mean sepal length.

Your answer to **Question #6** should be that the model assumption is not reasonable. In this case, we want to do *post hoc* tests to determine *which* means are different. Let's perform the Tukey Honestly Significant Difference post hoc test:

```
> TukeyHSD(iris_anova)
```

**Question #7** Copy and paste below the part of the output starting at **Fit: aov(formula = Sepal.Length ~ Species, data = iris).**

```
Fit: aov(formula = Sepal.Length ~ Species, data = iris)
```

```
$Species
```

	diff	lwr	upr	p adj
versicolor-setosa	0.930	0.6862273	1.1737727	0
virginica-setosa	1.582	1.3382273	1.8257727	0
virginica-versicolor	0.652	0.4082273	0.8957727	0

**Question #8** This output reports the results of three two-tailed hypothesis tests (one for each pairwise difference of two species) with the p-values “adjusted” to reflect that three tests are being done knowing that at least one pair of means is different. At the 5% significance level, which pairs of means appear to be different?

They all appear to be different considering that their p adj value is so low