R code: F tests for ANOVA (Sleuth3 Section 5.3)

We will refine this R code next class

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Iris Flowers Example

Conduct a claim of the test that the population mean sepal width is the same for all three species.

```
H_0: \mu_1 = \mu_2 = \mu_3
```

 H_A : it is not the case that all three means are equal.

Any approach will start off by fitting the full model

```
full_fit <- lm(Sepal.Width ~ Species, data = iris)</pre>
```

Option 1: F statistic and p-value at bottom of model summary

```
summary(full_fit)
```

```
##
## Call:
## lm(formula = Sepal.Width ~ Species, data = iris)
##
## Residuals:
   Min 1Q Median
                        3Q
                             Max
## -1.128 -0.228 0.026 0.226 0.972
## Coefficients:
##
                 Estimate Std. Error t value Pr(>|t|)
## (Intercept) 3.42800 0.04804 71.359 < 2e-16 ***
## Speciesvirginica -0.45400 0.06794 -6.683 4.54e-10 ***
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.3397 on 147 degrees of freedom
## Multiple R-squared: 0.4008, Adjusted R-squared: 0.3926
## F-statistic: 49.16 on 2 and 147 DF, p-value: < 2.2e-16
```

Option 2: Call anova on your model fit

```
anova(full_fit)
```

Option 3: Fit a reduced model and call anova, supplying both the full and reduced models.

For the reduced model, our explanatory variable is "1" – which means, include only an intercept.

```
reduced_fit <- lm(Sepal.Width ~ 1, data = iris)
anova(reduced_fit, full_fit)</pre>
```

```
## Analysis of Variance Table
##
## Model 1: Sepal.Width ~ 1
## Model 2: Sepal.Width ~ Species
## Res.Df RSS Df Sum of Sq F Pr(>F)
## 1 149 28.307
## 2 147 16.962 2 11.345 49.16 < 2.2e-16 ***
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1</pre>
```

This third approach is too much work for the current example, but it is necessary in the examples we will look at next week.