# Module 9 Notes

*Justin Millar*

*2018-10-25*

## Upcoming Assignments/Quizzes

| Assignments | Open Time | Due Time |
|---|---|---|
| ANOVA Article Analysis Activity | October 22nd (1:00 am EST) | October 28th (11:55 pm EST) |
| Module 8 Data Quiz | October 26th (1:00 am EST) | October 28th (11:55 pm EST) |
| Module 9 Conceptual Quiz | October 26th (1:00 am EST) | October 28th (11:55 pm EST) |

## Notes from Discussion Board/Office Hours

### Relationship between the $F$-statistic, p-value, and null hypothesis

In sub-module 9.3, Dr. Baiser covers how to test hypotheses using ANOVA. To do this, we calculate our observed $F$-statistic using the mean square among groups and mean square within group from our observed data, and compare that to the distribution of possible $F$-statistics (i.e. the $F$ distribution) based on the degrees of freedom (df) in the numeration and denominator of our $F$-statistic to determine how significance of our observed value.

Let's make some plots to visualize this comparison step-by-step. I'll use the same example from the sub-module 9.3 lecture. Let's start from when we calculate our observed $F$-statistics (pg. 15 from 9.3 notes), which I'll call `f_obs`. Based on our calculations of the mean squares we determined that $F_{obs} = 5.11$.

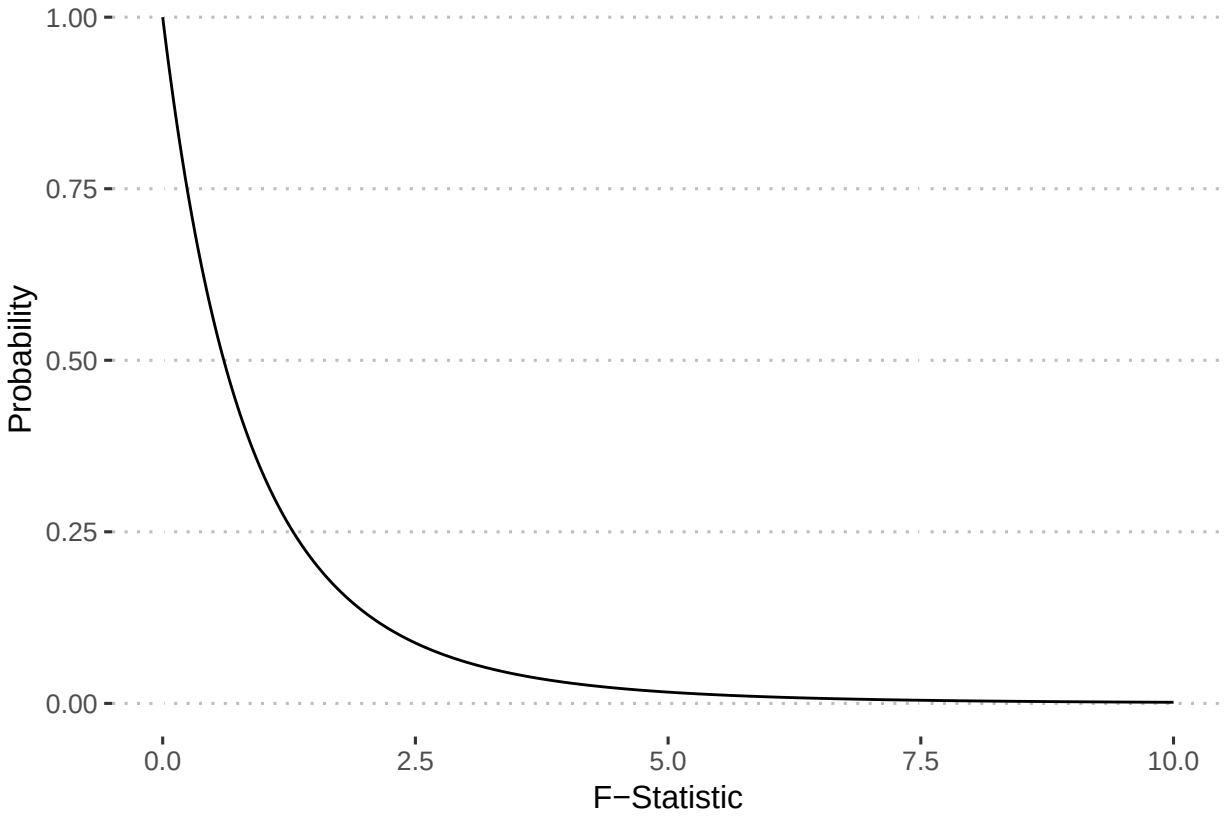
Now let's draw our $F$-distribution. Recall that this is determined by the dfs in the numerator ($df_{num}$) and the denominator ($df_{den}$) of our $F$-statistic. If we have $a$ number of treatments and $n$ number of replicates, than $df_{num} = a - 1$ and $df_{den} = n(a - 1)$. In our example, $a = 3$ and $n = 3$ (pg. 8), therefore $df_{num} = 2$ and $df_{num} = 9$. With this information we can draw our $F$-distribution by creating a vector of possible values of $F$ and passing those into the `df()` function in .

```
library(tidyverse)
library(ggpubr)

# Possible values of F-stat:
x = seq(from = 0, to = 10, by = 0.01)

# Probability of possible values of F-stat
y = df(x = x, df1 = 2, df2 = 9)

ggplot() +
  geom_line(aes(x, y)) +
  labs(x = "F-Statistic", y = "Probability") +
  theme_pubclean()
```



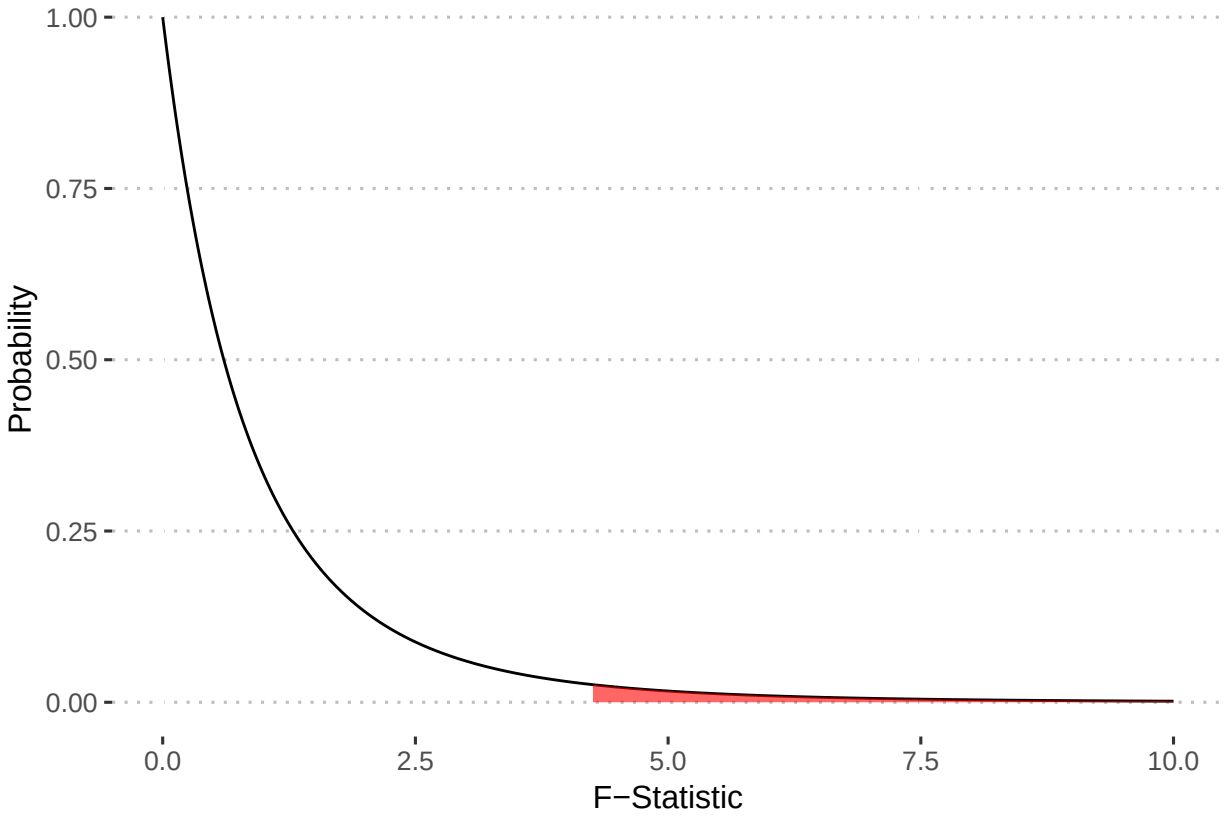

This curve shows the possible values for the $F$-statistic (shown on the x-axis) and the probability of observing those values (y-axis) *if the null hypothesis were true* (based on the dfs we specified). We can use this to determine if we should reject or fail to reject the null hypothesis by comparing `f_obs` to a theoretical $F$-statistic based on a critical value $\alpha$, which you'll recall is often set to $\alpha = 0.05$. This $F$-statistic, which we will call `f_crit`, will correspond to having a p-value of exactly 0.05.

It is important to note that we working with a density function, which means that we are interested in the **area under the curve**. We *can not* simply draw a line with a y-intercept of 0.05 to find `f_crit`. Instead we need to find the "quantile" of our area of interest (5% or 0.05). Luckily the `qf()` can calculate quantile for the $F$-distribution:

```
f_crit <- qf(p = 0.05, df1 = 2, df2 = 9, lower.tail = F)
```

Which determines that `f_crit` is equal to 4.26. Note that we set `lower.tail = F` because were are using a one-way test on the high end. Now we can draw the area under the curve that represents the "rejection region":

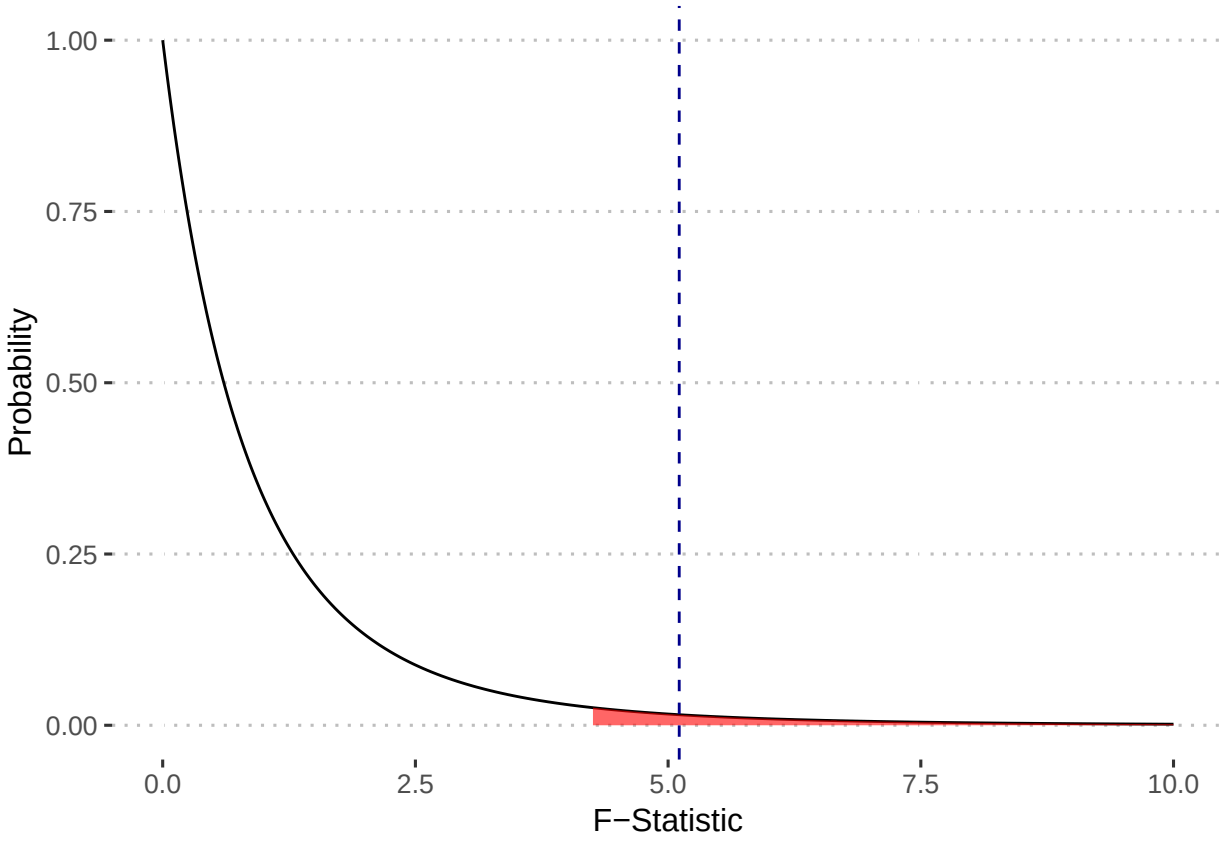
```
ggplot(data.frame(x,y)) +
  geom_line(aes(x, y)) +
  stat_function(fun = df,
                args = list(df1 = 2, df2 = 9),
                xlim = c(f_crit, 10),
                geom = "area",
                fill = "red",
                alpha = 0.6) +
  labs(x = "F-Statistic", y = "Probability") +
  theme_pubclean()
```




Finally, let's add `f_obs` to our plot:

```
f_obs = 5.11

ggplot(data.frame(x,y)) +
  geom_line(aes(x, y)) +
  stat_function(fun = df,
                args = list(df1 = 2, df2 = 9),
                xlim = c(f_crit, 10),
                geom = "area",
                fill = "red",
                alpha = 0.6) +
  geom_vline(aes(xintercept = f_obs), color = "darkblue", linetype = 2) +
  labs(x = "F-Statistic", y = "Probability") +
  theme_pubclean()
```




As you can see, `f_obs` falls in the rejection region, and therefore we will reject the null hypothesis that there is no difference between our treatments. As a final note, we can also calculate the p-value associated with `f_obs` using the `pf()` function:

```
p_value <- pf(f_obs, df1 = 2, df2 = 9, lower.tail = F)
round(p_value, 3)
```

```
## [1] 0.033
```