## DailyCheck#6

## 2025-04-16

## R Markdown

Please answer the following questions in your R Markdown file:

1) In the calculation of the F statistic, what do the numerator and denominator represent in very general terms? (this was answered on the board when discussing Slide 7 in today's slide deck, but can also be found throughout the slides and in the textbook).

Answer: 1. Numerator: Measure of variability across treatment groups; that is how different are the group means from each other? Denominator: Measure of variability within the groups, that is, we calculate this by using the variances within each group representing natural or random variation.

2) If the denominator of the F statistic (also called MSE and is the Residuals value of Mean Sq in the R output) is large, why will this make it more difficult to reject H0, generally speaking? (This was discussed on Slide 18 and can also be found in the textbook).

Answer: 2. If the MSE is large, meaning the denominator of the F statistic also large. It indicates a high level of variability within the groups, which can make it difficult to detect differences between the groups means are significantly different, making it harder to reject the null hypothesis.

3) Why will the numerator of the F statistic (also called MSTreatments by our textbook, and is the method value of Mean Sq in the R output) be small if the treatment of interest has no impact, and large if the treatment DOES have an impact? (This was discussed on Slides 19-21 and can also be found in the textbook)

Answer: 3. If the treatment has no impact, all the group means will be close together so the variability between them will be small. If the treatment does have an impact, the group means will be more spread out, making the numerator larger.

```
google <- c(46,49,51,42)
waze <- c(44,47,47,43)
gut <- c(50,51,45,43)

MSE <- (3*var(google) + 3*var(waze) +
3*var(gut)) / (12-3)
print(MSE)</pre>
```

```
## [1] 11.5
```

## [1] 9.5

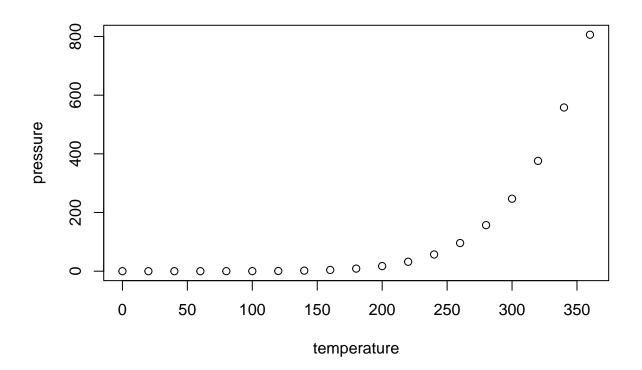
```
#Calculate MST
MST <- SST / (3-1)

#Calculate F0 and get p-value
F0 <- MST/MSE
p.val <- pf(F0,df1 =2, df2=9,lower.tail=FALSE)
print(p.val)</pre>
```

## [1] 0.6735636

## **Including Plots**

You can also embed plots, for example:



Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated the plot.