

Copter ANOVAs I

Experimental design and analysis must match. If they don't match we risk making wrong conclusions about the results. This occurs more often in science than we wish to admit. Today we run various analyses that do not *fully* match our experimental design – next week, we will analyze the results in the full, correct way and compare those results to today's results.

So save your results today – you will need to look at them again next week.

A reminder: we evaluated two treatments that potentially affect helicopter flight times: wing length and whether wings included a fold or not.

Today we treat each of these as separate treatments – *in reality* we designed an experiment to investigate the interaction of those two treatments. We ignore interactions today.

1. Import and attach the copter data from

```
https://sciences.ucf.edu/biology/d4lab/wp-content/uploads/sites/125/2019/09/helicopter-data.txt
```

It may also be helpful to remove all NAs with a command like this:

```
data <- na.omit(data)
```

You have already examined normality of these data. To save time right now, let's assume that normality is not too far out of whack. But you also should already expect the other key assumption (homogeneous variance) to be a big problem. This is more critical for ANOVAs than normality so let's revisit:

2. First make a factor for ID, Wing Length (WL) and Body Width (BW):

```
fid <- factor(ID)
fwl <- factor(WL)
fbw <- factor(BW)
```

3. then run a Levene's test by first loading the package “car” and then running:

```
leveneTest(Time~fid)
```

This is a shortcut – using IDs for all combinations of wing length, fold, and body width. Are the variances among each design about the same? If so, then we can use ANOVA with confidence. *If not, then all we do below is on shaky ground.* And iterative attempts to transform data may not help. ***This should be a big red flag to you! Beware of analyses with bad assumptions!***

3. Let's stumble ahead anyway to conduct an ANOVA on just Wing Length (WL). We will

do this two ways. Both are linear models (i.e., assume linear responses); the first reports results as a simple ANOVA (with the expectation that treatments are categorical), and the second produces regression output, with the expectation that treatments are quantitative:

```
model1 <- aov(Time ~ fwl) # an ANOVA on factored WL
model2 <- lm(Time ~ WL) # a linear model on quant WL
summary(model1)
summary(model2)
```

4. What does the aov command show you that the lm command does not? Vice versa - What does the lm command show you that the aov command does not?
5. And do you get different answers? [Hint: look at F statistics] Notice that the ANOVA (aov) uses factored WL, but the regression uses quantitative WL.
6. Now rename and repeat those analyses but use Fold in place of WL (I assume you call those model3 & model4). How does this compare to WL outcomes?
7. Now rename and repeat those analyses but use BW in place of Fold (I assume you call those model5 & model6). How does this compare to above outcomes? *Do you see a problem with evaluating these effects (WL, Fold, BW) separately? You should!*
8. How much of the variation in flight times is explained by WL, Fold, or BW? How can you tell? Is this satisfactory?
9. Now let's try a factorial statement that *starts* to represent the complex experiment – so far we have only analyzed pieces that do not fully represent the whole. A factorial design allows us to examine the effects of one factor on the effects of a second factor. Our factorial experiment answers the question: “Does the effect of wing length on flight time depend on whether wings are folded?” You could flip that as “Does the effect of folded wings on flight time depend on wing length?”

```
model5 <- aov(Time ~ fwl*Fold)
model6 <- lm(Time ~ WL*Fold)
summary(model5)
summary(model6)
```

NOTE: R knows when you enter WL*Fold that you mean this: [WL + Fold + WL X Fold]. So you will be able to evaluate each effect and the interaction.

10. Look at the ANOVA results first: Did both treatments affect flight time, and did treatments affect each other's flight time? This answers the italicized question in #7 above. Which effect seems most important?

11. Now let's examine the linear model (lm) results: notice that the rows are named differently? This takes a moment's thought because now we see an intercept – what is this?

And what do the WL, Fold, and WL:FoldY lines tell you?

Let's make an interaction graph to help interpret this. Enter this command:

```
interaction.plot(Fold, trace.factor=fwl, response=Time,  
fun=mean, type="b")
```

Do longer Wings make copters stay in the air longer? How do you know?

Do folded Wings alter that effect of Wings? How do you know?

How would you explain this in a few sentences that would convince your advisor?

So what have we accomplished? We computed a factorial ANOVA to find out if there was an interaction between two treatments. We can compare SS & MS in the ANOVA table to see which treatment had a greater effect. But that basic ANOVA leaves us wishing for more details. And lm output gave us that.

The lm output and the interaction plot allow us to tease apart what happened, **and to quantify those effects**. We will refine this later.

One final conclusion to make: how much variation in helicopter flight times did we account for with our most recent model? Does this seem like enough?

Next week we more fully account for Body Width & Group effects and the covariate of Stairs to complete our over-analyses of little pieces of paper falling down.