

## Dealing with Treatment\*Block Interactions

When there is only one experimental unit per treatment-block combination in an RCBD, there are not enough degrees of freedom to include the interaction in the model; therefore, the interaction SS is necessarily merged into the error SS. There's nothing you can do about this except probe the data using the Tukey 1-df Test for Nonadditivity and see if the interaction term is significant. If there is non-additivity, it's an indicator that there is something going on in your system that you need to better understand. For the data in hand, it may be possible to address the problem of non-additivity with a data transformation; and you'll hear that story later.

But what if you have more than one experimental unit per treatment-block combination? In this case, you don't need to use the 1-df test because you can directly include the interaction in your model statement, like this:

```
explore.mod<-lm(Response ~ Trtmt + Block + Trtmt:Block, data = X.dat)
```

Some call this an "exploratory model," because you have the degrees of freedom required to explore directly the Block\*Treatment interaction.

If you find this interaction to be NS (e.g. see below), great. Blocks are behaving additively, as you expect. You should note this result, and then **use the interaction MS as the proper error term for testing treatment effects**.

Example ANOVA table:

Source	DF	SS	Mean Square	F Value	Pr > F	
Block	2	44.92026857	14.15337810	109.80	<.0001	
Treatment	3	40.00007429	13.33335810	103.44	<.0001	
Block*Treatment	6	1.42600000	0.23766666	1.84	0.1335	NS

If these were the results of your ANOVA, you would note this NS result ( $p = 0.1335$ ) and then test Treatment by calculating  $F = 13.3334/0.2377$ , with  $df_{\text{num}} = 3$  and  $df_{\text{den}} = 6$ .

Now, if the interaction *were* significant, you would note this because it's signalling to you some unexpected (and potentially very interesting) behavior of your blocks. That is, there is something lurking within your blocking variable that warrants investigation. You would then proceed with your analysis as above, leaving the significant interaction in the model and **using that interaction as the proper error term for testing treatment effects**.