**Transcript: Interpreting Factorial ANOVA Output**

In this video, we will go over how to interpret output for factorial ANOVA from R Commander and SPSS.

The first thing we want to look at is our model level statistics, which can be seen here in R Commander, and here in SPSS. These should look familiar from the one-way ANOVA video, but they have a few more rows that we need to look at. Remember that in a two-way ANOVA, we have two predictor variables. We will have two main effects as well as an interaction term.

The first thing we can look at is our main effect of “condition”. We can see in R Commander here that we have an *F* value of 99.2 and a *p* value of less than .001. These values can be found in the row for “conCat” in SPSS. We can see the same *F* value and significance value here. This indicates that there is a significant main effect of “condition”.

Next, we can look at the main effect of “substance”. In R Commander, we can see the *F* value here of 50.4 and the *p* value of less than .001. These same values can be found in the “subCat” row in SPSS. Here, we have the same *F* value and *p* value. From this we can say that there is also a significant main effect of “substance”.

Lastly, we want to look at the interaction between “condition” and “substance”. This is represented in R Commander using a colon and an SPSS using an asterisk. Our *F* value for the interaction term is 37.9 and our *p* value is less than .001. We can see the same *F* value and *p* value here in SPSS.

Because we have a significant interaction, it's important that we look at the interaction first before trying to interpret the main effects. The best way to look at our interaction is to look at the plots that we made. See our plots here side by side. The reason that they look different is because in SPSS we were able to select that the variable we wanted on the x-axis was “condition” and that we wanted separate lines for each substance. In R Commander, we're not able to specify, and so we're getting the opposite, where we have “substance” on the x-axis, and we have different lines for the treatment and control conditions. In this case, the plot produced by SPSS is easier to interpret, so we will look at that first and then see how we can see the same results from R Commander.

On our y-axis, we have our “Estimated Marginal Means”, which is a term for the predicted value of our outcome variable (in this case “bam”) in each condition. We have our control condition here and our treatment condition here. We can see that BAM scores are very similar for all three substances for participants in the control condition (all around 51–53). But if we look at the treatment condition, we can see that there are differences between the different substances that participants are seeking treatment for. For participants who are seeking treatment for opioid use, the BAM scores are very similar between the treatment and control condition. For alcohol, the BAM scores are lower (it looks like around 44 or 45). And for cannabis, they are quite a bit lower at around 32. We can see this significant interaction because we have different slopes for the different substances. For cannabis there is the largest difference between the treatment and control. For alcohol, there's a smaller difference, and for opioids, there is very little difference. Based on this, we could say that the significant interaction is showing the greatest difference between treatment and control for cannabis, followed by alcohol, and then very little difference for opioids.

Within our plot from R Commander, we can see that the black line is showing BAM scores for participants in the control condition across the three substances. We can see again here that they are very similar. Whereas for the treatment condition, we are seeing quite a bit of difference between the three substances, and again, we're seeing cannabis with the lowest BAM scores within the treatment condition, followed by alcohol and opioids.

So, from this from this study, we could say that the treatment appeared to have the greatest effect for participants seeking treatment for cannabis use, a smaller effect for participants seeking treatment for alcohol use, and finally very little effect for participants seeking treatment for opioid use.

The last thing we’re going to look at is the effect size for this model, which again is produced only in SPSS and not in R Commander. Our effect sizes can be found in this column labelled “Partial Eta squared” (*ηp2*). These values have a very similar interpretation to *η2*, which we discussed in the videos on one-way ANOVA. The difference is that in this case they reflect the proportion of variance in the outcome, in this case BAM scores, that is attributable to the predictor once the other terms in the model have been partialed out. This sounds very complicated, and the specific details of it are beyond the scope of this course. But we'll look at one of the *ηp2* as an example, and hopefully that will make things clear.

So, if we look at the “subCat” row, we can see that we have a *ηp2* value of .30. This means that substance accounts for 30% of the variance in BAM scores once the variance is attributable to the other two terms, the main effect of condition and the interaction, have been removed. In other words, we're taking out the variance that's associated with treatment condition and with the interaction between treatment condition and substance, and we're looking at what proportion of the total variance remaining is attributable to “substance”. In this case, that is 30%.

For the main effect of condition, we also have a *ηp2* value of .30. The *ηp2* value of .30 indicates that once the variance that's associated with “substance” and with the interaction are removed, 30% of the remaining variance is associated with “condition”.

Lastly, our *ηp2* for our interaction is .25, indicating that once we remove the variance associated with the main effects, 25% of the remaining variance is attributable to the interaction. Similar to how we didn't interpret our main effects because we had a significant interaction, in this case, the most meaningful value here is the *ηp2* for the interaction. We're seeing a good chunk of the variance being explained by the interaction term after we removed the variance being explained by the main effects.