# Research Methods and Statistics with R 3

# Week 5 – All ANOVA, All the time (Mock Exam I)

## Introduction to the session

In this session, you will have the opportunity to practice all that you have learned thus far with regards to ANOVA.

Below is an **exam-style question** that you are to attempt during this in-person session. Please note: *it is not expected that you will finish the entire question during this session*; at least not at this stage. Use this opportunity to become familiar with how questions will be asked on the exam and develop strategies to deconstruct and ultimately tackle the question.

You are free to consult your lecture material and previous R scripts. **Do NOT use generative AI (i.e., ChatGPT; not permitted during the exam).** You can work with other students if you wish, and you are welcome to ask for assistance from the teaching staff.

## Learning Outcomes

By the end of this session, you will:

1. Be familiar with how questions will appear on the final exam
2. Apply one or more statistical methods *largely unprompted* to a noveldataset

## The Setup

A picture containing arthropod, invertebrate, spider

Description automatically generatedIn 2013, Ryan et al. compared the results of a survey conducted online (via Facebook, n=1500) vs. one conducted in person (n=100). The survey examined the effect of “frightfulness” (low vs. high) and “disgustingness” (low vs. high) on participants’ desire to kill various insects (hostility, scale from 0-10). Briefly, each participant was shown pictures of various insects that had been previously rated (by an independent group of observers) as inducing low vs. high levels of fright and low vs. high levels of disgust. For each image, the participant had to assign a rating from 0-10 indicating their desire to kill the insect.

Figure - An insect rated as inducing "low" levels of disgust but "high" levels of fright.

The researchers found that the results from the study conducted using Facebook yielded additional information compared to the study conducted in-person. Specifically, in addition to the two significant main effects observed in the in-person study, they also found a significant interaction effect that was not observed in the in-person study.

Fast forward to the year 2022. No one uses Facebook anymore: everything is now on TikTok. You saw the potential of this new modality, and you wished to determine whether the same trend can be seen with data collected via TikTok (data found on KEATS). It is now time to analyse the data and because you are a modern scientist - skilled in all the latest techniques - you prefer to use Bayesian methods. However, to protect yourself against ignorant reviewers who don't understand Bayesian methods, you have decided to *also* include an equivalent analysis based on null-hypothesis significance testing.

The dataset is found on KEATS. It is a \*.csv file with the following fields:

1. **subjectID**: participant number
2. **gender**: gender of the participant (male/female)
3. **hostility**: score from 1-10 indicating the participant’s desire to kill the insect
4. **frightening**: whether the image of the insect was (independently) rated as evoking a “low” or “high” level of fright.
5. **disgusting**: whether the image of the insect was (independently) rated as evoking a “low” or “high” level of disgust.

## Procedure

1. **List research question, hypotheses, and analysis plan appropriate for this dataset and objective. This section can be in bullet-point form or complete sentences**

Research Question: *What is a sensible research question given these data?*

Hypotheses: *What are some reasonable hypotheses given these data? How many hypotheses do you need to identify? Are these guided by your particular analysis strategy?*

Analysis Plan: *Of the tools you have learned thus far, what is/are the most appropriate method(s) to analyse these data?*

1. **Using R, write a program to produce:**

* At least one figure displaying the data in a manner appropriate for the analysis and the research question
* Relevant descriptive statistics
* An analysis appropriate to the data and research question
* Your code should be annotated to be understood by an R-coder naïve to the study

*Have you properly annotated your code?*

*What is an appropriate figure(s) to visualise these data? Is it/are they properly labelled?*

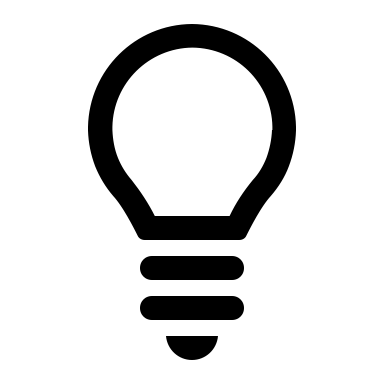
1. **Summarise your findings as if for a results section of a paper. Include any figures or tables in this section. Bullet-point form is not acceptable for this section.**

*What information must you include in this section?*

*Have you presented your results in proper APA format?*

## Suggested Procedure

1. Before you proceed to the exploration and analysis of your data, write down your **research question, hypotheses**, and consider if you need to plan some **contrasts**. *Note: at minimum, you should have a set of null/alternative hypotheses for each IV plus the interaction.*
2. Start a new script applying the heading and commenting practices you have developed. Include your research question, hypotheses and – if relevant – planned contrasts in your script as comments.
3. Download the dataset from KEATS and load it into your R environment. The data will be available as a \*.csv, so the **read\_csv()** or **rio::import()** should both work..
4. You should always inspect your data to determine e.g., if there are missing data, missing fields, etc. This can be done in a similar way to how you did it for the independent factorial ANOVA (i.e., using **psych::describeBy()**, **summary()**, **xtabs()**, **skimr::skim()**, etc.).
5. It is also recommended (and in the case of an exam question, ***required***) that you visualise the data in a figure or figures. There are many suitable options to visualize factorial data: you can use boxplots, swarm/violin plots, bar graphs, etc. Try out several different types of graphs to see which you feel best informs the reader.

**Tip: Do you spot any indication of an interaction between the two independent variables?**

1. Next, you should calculate your **cell means, marginal means, and grand mean.** An easy way to do this is to use the following R commands: **mean ()** [to calculate the grand mean]**, tapply()** [to calculate the marginal means],and **aggregate()** [to calculate the individual “cell” means]. Copy these into a table somewhere for later use.
2. The next step is to test for our assumptions. However, the easiest way to do so is to first generate your ANOVA object,so now is a good time to run the command of your choice. Remember that you can use, at least, **rstatix::anova\_test()**, **ez::ezANOVA()** or **afex::aov\_ez()**, but the *ez* and *afex* function will allow you to test for the assumptions more readily. Consult the lecture material if you are unsure of the proper syntax. **Also remember that if you want to set contrasts, you should do so before you build the ANOVA object.** These can be bound to your factor using the same method as for the between-subject factorial ANOVA.
3. Once you have produced your ANOVA, you can check the assumption of sphericity and the assumption of normality. For the latter, the function **stats::residuals()** will be handy.
4. Once you have checked the assumptions and made a decision about how to proceed based on the results of these checks, you can inspect your ANOVA object. Identify whether there are any significant **main effects** and/or a significant **interaction.**

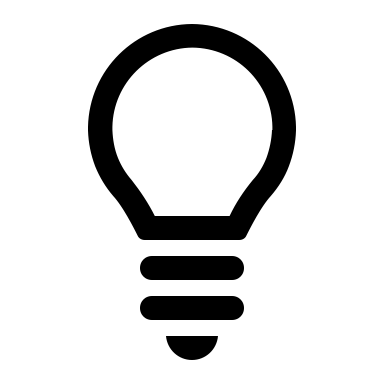
***No Planned Contrasts***

1. The ANOVA output will tell you if there is a significant main effect for one or more of your factors, and if there is a significant interaction. However, it does not tell you which differences are driving that significant main effects/interaction. That is, which pair(s)[[1]](#footnote-1) of conditions are significantly different from each other. To determine this, you will need to run **post-hoc comparisons.**

**However - Recall from Week 3: You should only do post-hoc comparisons on your data if your main effects/interaction is significant!**

If none of your main effects/interaction are significant, do not conduct any pairwise comparisons on those data - Just walk away. If some but not all of your effects *are* significant, you can restrict your post-hoc comparisons to the significant effects [Note: the one exception is if you are using Tukey’s HSD, in which case you should always include all data].

1. To run **post-hoc comparisons**, you have several options:
   1. You could use a function that automatically calculates all pairwise comparisons, such as “pairwise.t.test()” or “lsr::posthocPairwiseT()” (from Danielle Navarro’s package)
   2. You could use individual t.tests() between relevant pairs, being sure to correct your p-value accordingly.
   3. You can use Tukey’s HSD
   4. Many others…

**Note:** several functions that automatically calculate pairwise comparisons (e.g., pairwise.t.test(), lsr::posthocPairwiseT, etc.) do not work with factorial designs. Therefore, you either need to “****fool” the function into thinking that you have run a one-way ANOVA (e.g., by *actually running a separate one-way ANOVA*) or run your tests manually using t.test(). Even **TukeyHSD()** does not work with the ANOVA objects produced by the three methods discussed this week.

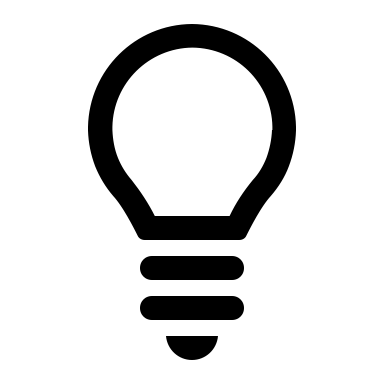
***Planned Contrasts***

1. If you have planned contrasts at the start of the workshop, you should have done this at step 7; if not, you need to create a **contrasts** object to run your contrasts. Consult the lecture material on how to construct and include contrasts in factorial designs.

***Effect Sizes***

1. The effect size commonly reported for factorial ANOVAs is ηp2 (partial eta-squared), although η2 (eta-squared) is arguably a more interpretable measure of effect size as it is simply a measure of the variance explained by a factor or an interaction (i.e., the same as *r*2). Unfortunately the {*lsr*} package does not accept ANOVA objects produced with any of the three methods discussed this week. However, **effectsize::eta\_squared()** will accept an afex ANOVA object and provide you with ηp2. **rstatix::** **eta\_squared()** and **rstatix::** **partial\_eta\_squared()** will accept an aov or a rstatix ANOVA object.

That being said, *afex* calculates effect sizes already within the ANOVA, but does not report them when you run **summary()** on your afex ANOVA object; to access these, you can use **my\_afex\_ANOVA$anova\_table**, which will give you the F-ratios etc as well as the generalized eta-squared values (ηG2), which controls for the variance from the other factors.



**Tip:** inserting the dollar symbol after an object name will reveal to you what objects, lists, tables, etc, are saved into that object by whichever function you have just used, often helping you narrow down where to find the precise information you are looking for. It is worth placing a dollar symbol after an object name just to explore all the objects they contain.

1. Note: if you have a significant main effect for an independent variable with only two levels, the ANOVA does in fact tell you where the differences are (they cannot be anywhere else than between these two levels) and a post-hoc test, or a contrast, would be an overkill. Simply look at the means to understand the direction of the difference. [↑](#footnote-ref-1)