Lab 8: Reaction Times

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General information

This lab is due November 4th by 11:59 pm. This lab is worth 10 points. You must upload your .rmd file and knitted file to the dropbox on Canvas. You are welcome and encouraged to talk with classmates and ask for help. However, each student should turn in their own lab assignment and all answers, including all code, needs to be solely your own.

Objective

The goal of this lab is to design an experiment and collect data to test what factors influence reaction times. You will be collecting data during class time and investigating your hypotheses using the statistical tests you have used in the past. This lab should help prepare you for your independent project, in which you will be choosing appropriate statistical analyses on your own.

Experimental design

In class on Tuesday, you will decide what variables may be associated with increased or decreased reaction time. Come up with 2 continuous variables and 2 categorical variables as a class. We will brainstorm these during class time.

Data Collection

Each person will use the reaction timer at: https://www.humanbenchmark.com/tests/reactiontime. Conduct 5 trial per person and record the average (the website will calculate this for you). We will also collect information on the covariates that you come up with as a class on Tuesday. These will be entered in a Google Sheet and we will make the csv file available before Thursday's lab.

Notes on assumptions

Since we are collecting brand-new data today, it's possible we will collect data that violate some assumptions of statistical tests. For today, and for the purposes of completing this lab, assume that the tests will be robust to these violations. Run them, but if you notice serious errors with the data, discuss these in your interpretations.

For your own independent project, don't take this same approach! Rigorously examine whether assumptions are met before proceeding with a given statistical test!

Example two-way ANOVA

Before you analyze the class' dataset, explore the two-way ANOVA, using a built-in dataset in R, called crabs. The crabs data frame has 200 rows and 8 columns, describing 5 morphological measurements on 50 crabs each of two species and both sexes. The researchers want to know if sexual dimorphism depends on species.

Let's use the response variable "FL" which is the frontal lobe size in mm. We will test (1) whether sex affects lobe size, (2) whether species (sp) affects lobe size and (3) whether there is an interaction between the two.

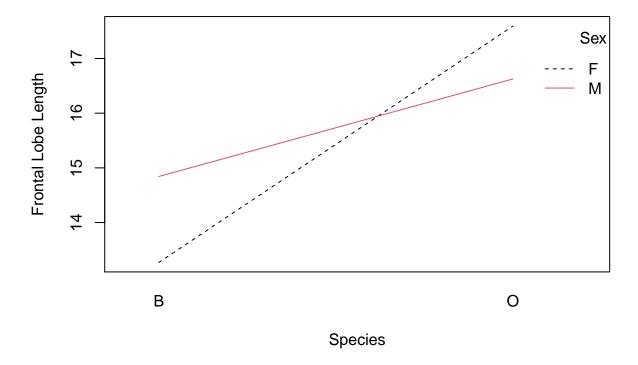
crabdat <- read.csv("https://raw.githubusercontent.com/vincentarelbundock/Rdatasets/master/csv/MASS/crabdat)</pre>

```
##
     X sp sex index
                      FL
                          RW
                               CL
## 1 1 B
                  1
                    8.1 6.7 16.1 19.0 7.0
            М
## 2 2
       В
            М
                  2
                     8.8 7.7 18.1 20.8 7.4
## 3 3
       В
            М
                  3
                     9.2 7.8 19.0 22.4 7.7
## 4 4
       В
            М
                  4
                    9.6 7.9 20.1 23.1 8.2
## 5 5 B
                  5 9.8 8.0 20.3 23.0 8.2
## 6 6 B
                  6 10.8 9.0 23.0 26.5 9.8
            М
# run the ANOVA
crab.2.way.anova <- aov(FL ~ sp * sex, data = crabdat)</pre>
# explore output
summary(crab.2.way.anova)
##
                Df Sum Sq Mean Sq F value
                                            Pr(>F)
## sp
                    466.3
                            466.3 48.627 4.63e-11 ***
                      4.6
                              4.6
                                    0.476 0.49128
## sex
## sp:sex
                 1
                     80.6
                             80.6
                                    8.409 0.00416 **
## Residuals
               196 1879.7
                              9.6
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
# run post-hoc tests to understand group comparisons
TukeyHSD(crab.2.way.anova)
##
     Tukey multiple comparisons of means
##
       95% family-wise confidence level
##
## Fit: aov(formula = FL ~ sp * sex, data = crabdat)
##
## $sp
##
        diff
                  lwr
## O-B 3.054 2.190289 3.917711
##
## $sex
##
        diff
                    lwr
                             upr
## M-F 0.302 -0.5617106 1.165711 0.4912819
##
## $`sp:sex`
             diff
                                             p adj
##
                          lwr
                                     upr
## 0:F-B:F 4.324 2.71910212
                               5.9288979 0.0000000
## B:M-B:F
            1.572 -0.03289788
                               3.1768979 0.0572712
## 0:M-B:F 3.356 1.75110212 4.9608979 0.0000010
## B:M-O:F -2.752 -4.35689788 -1.1471021 0.0000868
```

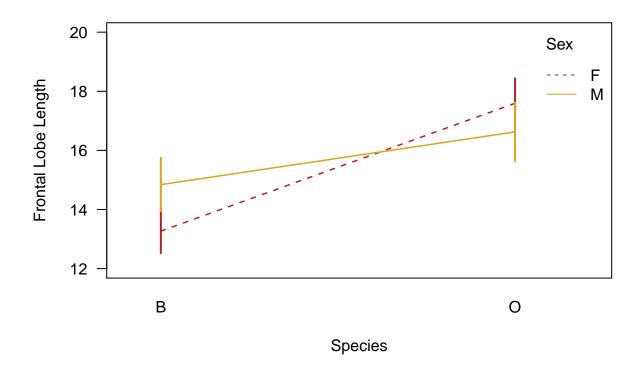
0:M-0:F -0.968 -2.57289788 0.6368979 0.4022824

0:M-B:M 1.784 0.17910212 3.3888979 0.0227162

The output of this test indicates that frontal lobe size significantly differs between species, and that differences between sexes depend on species. If we look at the below quick-n-dirty plot we see that there is little-to-no difference between males and females in the "O" species, but there is a greater difference in the "B" species. This is why the interaction term is significant (P = 0.004) but the fixed effect of sex on its own is not. You could run a one-way ANOVA to confirm that sex, on its own, does not influence frontal lobe size.



Below is the same plot, but with the addition of SE bars. Feel free to explore the code below for making an interaction plot. You may be interested in making a similar plot for your independent project, but it will not be tested in this lab assignment.



Analyzing the class data

Start by reading in our class data (download the csv from the Canvas assignment page, NOT from the google drive directly). Take a look at the object in R using the str() or head() functions to make sure the data look correct.

```
library(tidyverse)
## -- Attaching packages
                                                                                              - tidyverse 1
## v ggplot2 3.3.2
                        v purrr
                                  0.3.4
## v tibble 3.0.3
                        v dplyr
                                  1.0.1
             1.1.1
## v tidyr
                        v stringr 1.4.0
## v readr
             1.3.1
                        v forcats 0.5.0
## -- Conflicts -----
                                                                                        - tidyverse_conflic
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                     masks stats::lag()
reactDat <- read_csv("~/Repos/School/BioStats/Lab8/reaction_time.csv")</pre>
## Warning: Missing column names filled in: 'X1' [1]
## Parsed with column specification:
## cols(
##
     X1 = col_double(),
##
     mean_reaction_time = col_double(),
```

```
## mouse_type = col_character(),
## gamer = col_character(),
## minutes_awake = col_double(),
## body_temp = col_double()
## )
```

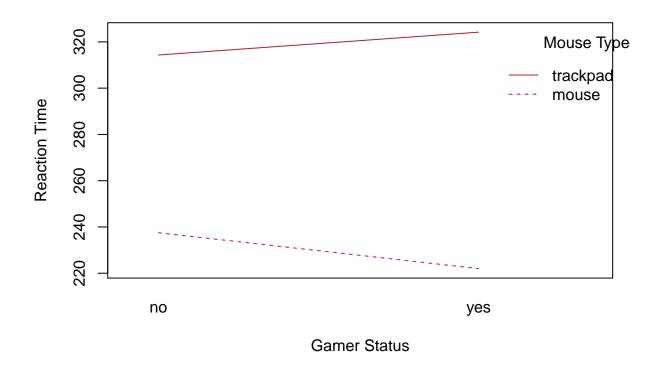
Analysis 1

In this analysis, you will use a two-way ANOVA to determine whether *each* categorical variable individually, or interactively, influences reaction time. See the Crab example above for how to run this test.

Question 1 (1 point) Before running the test, what are the null hypotheses for your two-way ANOVA? Be specific, i.e. instead of writing "means of the two groups", you'd want to write (for example) "mean reaction times of breakfast eaters vs. breakfast skippers"

Null Hypotheses: 1: reaction times among different mouse type users will not differ significantly 2: reaction times among those that game and those that do not will not differ significantly 3: The effect of mouse type on mean reaction time will not depend on whether or not someone is a gamer and vice versa 5: Reaction times will not depend on the amount of time someone has been awake 6: Reaction times will not depend on the internal body temperature of a person 7: The effect of time awake will on reaction time will not depend on someones internal body temp and vice versa

Question 2 (2 point) Visualize the data using an interaction plot- without error bars is fine. Run a two-way ANOVA on your data. Report the test statistic, and P-value for *each* hypothesis.



```
gamerAOV <- aov(mean_reaction_time ~ gamer * mouse_type, data = reactDat)
summary(gamerAOV)</pre>
```

```
##
                    Df Sum Sq Mean Sq F value Pr(>F)
## gamer
                          633
                                  633
                                        0.120 0.7335
## mouse_type
                                        4.912 0.0398 *
                     1
                        25994
                                25994
                                  420
                                        0.079 0.7815
## gamer:mouse_type
                     1
                          420
                        95252
                                 5292
## Residuals
                    18
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
```

There was no significant effect of gamer status on reaction time (F = 0.12, p > .05) The effect of mouse type on reaction time was significant (F = 4.912, p = .0400) There was no significant interaction effect between gamer status and mouse type on reaction time (F = .079, p > .05)

Question 3 (2 point) Interpret the output from your 2-way ANOVA. If your ANOVA yielded significant results, you might need to use follow-up tests to help you interpret what the results mean; is a Tukey test applicable, here? Why or why not? Write your interpretation of the p value, and interpret the results in relation to the original question.

TukeyHSD(gamerAOV)

```
## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = mean_reaction_time ~ gamer * mouse_type, data = reactDat)
##
## $gamer
```

```
##
              diff
                         lwr
                                   upr
                                           p adi
## yes-no 12.04167 -61.12066 85.20399 0.7335111
##
## $mouse_type
##
                      diff
                                 lwr
                                          upr
                                                  p adj
  trackpad-mouse 81.70196 3.949586 159.4543 0.0404869
##
##
## $`gamer:mouse_type`
##
                                   diff
                                               lwr
                                                        upr
                                                                 p adj
## yes:mouse-no:mouse
                            -15.500000 -245.36539 214.3654 0.9974526
## no:trackpad-no:mouse
                             76.833333
                                        -41.86865 195.5353 0.2924599
                                        -51.21924 224.6192 0.3160067
## yes:trackpad-no:mouse
                             86.700000
## no:trackpad-yes:mouse
                             92.333333 -121.65970 306.3264 0.6229593
## yes:trackpad-yes:mouse
                             102.200000 -123.02117 327.4212 0.5851057
                               9.866667 -99.57115 119.3045 0.9939864
## yes:trackpad-no:trackpad
```

There was no significant effect of gamer status on reaction time (F = 0.12, p > .05) The effect of mouse type on reaction time was significant (F = 4.912, p = .0400) There was no significant interaction effect between gamer status and mouse type on reaction time (F = .079, p > .05) No need for further testing of the mouse type hypothesis, as there were only two levels and no interaction effect TAKEAWAY: Though mean reaction time did not differ significantly between gamer status, it did differ significantly between groups that used different types of mouses. As well, there was no significant interaction effect between our predictor variables

Analysis 2

Next, you will fit a linear model to explore the relationship between one of the continuous predictor variables and the response variable reaction time.

Question 4 (1 point) Fit a linear model between one of the continuous variables and reaction time. Report the test statistic, slope with standard error, and P-value.

```
reactLM <- lm(mean_reaction_time ~ minutes_awake * body_temp, data = reactDat)
summary(reactLM)</pre>
```

```
##
## Call:
## lm(formula = mean_reaction_time ~ minutes_awake * body_temp,
       data = reactDat)
##
##
## Residuals:
      Min
              10 Median
                             30
                                   Max
##
  -79.50 -48.57 -19.46
                         34.99 249.51
##
## Coefficients:
##
                             Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                           -2.351e+03
                                        7.764e+03
                                                  -0.303
                                                              0.766
## minutes_awake
                            2.102e+00
                                        3.415e+01
                                                    0.062
                                                              0.952
## body_temp
                            2.708e+01
                                        7.926e+01
                                                    0.342
                                                              0.737
                                        3.489e-01
## minutes_awake:body_temp -2.161e-02
                                                   -0.062
                                                              0.951
##
## Residual standard error: 80.64 on 18 degrees of freedom
## Multiple R-squared: 0.04294,
                                     Adjusted R-squared:
## F-statistic: 0.2692 on 3 and 18 DF, p-value: 0.8467
```

There was no significant effect of minutes awake (p>.05, slope=2.1, std. error=34.15, t=.062) or body

temperature (p>.05, slope = 27.08, std. error = 79.26, t = .342) on reaction time; likewise, there was no interaction effect between the two continuous predictors on reaction time (p>.05, slope = -.022, std. error = 0.4, t = -.062).

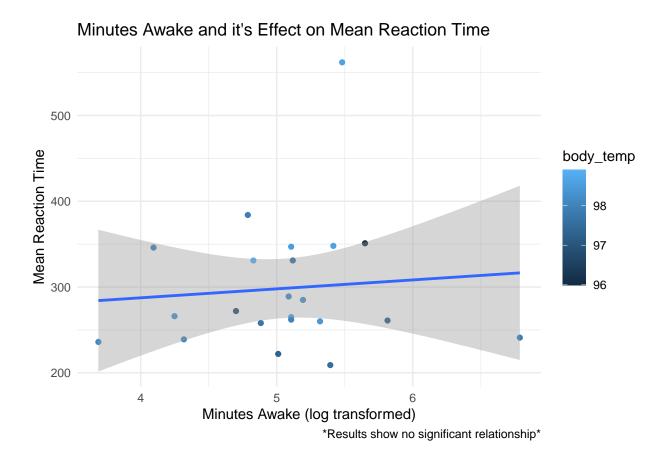
Question 5 (1 point) (a) What was the null hypothesis for the linear regression model? (b) What does the P-value you found represent (e.g. "the probability of...")?

a) Null hypotheses: 1) Body temperature will not have an effect on mean reaction time, 2) Minutes awake will not have an effect on mean reaction time, 3) The effect of body temperature on mean reaction time will not depend on minutes awake, and vice versa.

The p value we found represents the probability of finding our observed t value for any given relationship within a distribution of t values with the appropriate degrees of freedom

Question 6 (2 point) Plot the relationship between the two variables. Even if the linear regression was not significant, for the purpose of this lab, go ahead and add a best fit line to the plot (don't forget that curly braces { } can be useful for running multiple lines as a single code chunk). See example code in Wynne Moss' helpful 'Plotting in R' guide on StatsTree.org (https://static1.squarespace.com/static/5eb33c095018927ea433a883/t/5f7a84444450c5069e7bba9e/1601864778198/Plotting-in-R.pdf) if you are not sure where to begin. You do not need to add uncertainty estimates to your best fit line.

```
## `geom_smooth()` using formula 'y ~ x'
```



Question 7 (1 point) What does the slope tell you about the relationship between your variables? (e.g. "for every 1 unit increase in X, Y increases by..."). Overall, how confident are you in this relationship?

The slope of our line shows us how much "mean reaction time" (Y) changes for every unit increase of log transformed "minutes awake" (X). I am quite confident that there is NO relationship, as our p-vals. were insignificant and our Rsq. value was very small.

Optional BONUS question (1 point) Now, suppose we wanted to test whether yoga improves reaction time. We take the 3 students with the slowest reaction times and have them do 15 minutes of yoga. Then we re-test their reaction times. What would you expect to happen to their reaction times and why? What is the issue with the proposed approach?

Your answer here