RMANOVA
=======

This R markdown document provides an example of performing a repeated
measures ANOVA using the jmv::anovaRM() function in the jmv (Jamovi)
package.

Package management in R

``` r
# keep a list of the packages used in this script
packages <- c("tidyverse","rio","jmv")
```

This next code block has eval=FALSE because you don't want to run it
when knitting the file. Installing packages when knitting an R notebook
can be problematic.

``` r
# check each of the packages in the list and install them if they're not
installed already
for (i in packages){
  if(! i %in% installed.packages()){
    install.packages(i,dependencies = TRUE)
  }
  # show each package that is checked
  print(i)
}
```

``` r
# load each package into memory so it can be used in the script
for (i in packages){
  library(i,character.only=TRUE)
  # show each package that is loaded
  print(i)
}
```

    ## -- Attaching packages --------------------------------------- tidyverse
    1.3.0 --

    ## v ggplot2 3.3.3   v purrr   0.3.4
    ## v tibble 3.0.6   v dplyr   1.0.4
    ## v tidyr   1.1.2   v stringr 1.4.0
    ## v readr   1.4.0   v forcats 0.5.1

    ## -- Conflicts --
    tidyverse_conflicts() --
    ## x dplyr::filter() masks stats::filter()
    ## x dplyr::lag()   masks stats::lag()

    ## [1] "tidyverse"
    ## [1] "rio"
    ## [1] "jmv"

RMANOVA is a linear model

The RMANOVA is a type of linear model. However the RMANOVA is a
simplified for with additional constraints which allows us to analyze
data which violate the independence of observations assumption which is
required for the linear models we have used to this point. A nice
explanation is provided in Field chapter 15.4.

Open data file

The rio package works for importing several different types of data
files. We're going to use it in this class. There are other packages
which can be used to open datasets in R. You can see several options by
clicking on the Import Dataset menu under the Environment tab in
RStudio. (For a csv file like we have this week we'd use either From
Text(base) or From Text (readr). Try it out to see the menu dialog.)

``` r
# Using the file.choose() command allows you to select a file to import from
another folder.
dataset <- rio::import(file.choose())
# This command will allow us to import a file included in our project folder.
# dataset <- rio::import("Album Sales.sav")
```


Get R code from Jamovi output

You can get the R code for most of the analyses you do in Jamovi.

1. Click on the three vertical dots at the top right of the Jamovi
    window.
2. Click on the Syndax mode check box at the bottom of the Results
    section.
3. Close the Settings window by clicking on the Hide Settings arrow at
    the top right of the settings menu.
4. you should now see the R code for each of the analyses you just ran.

Visualization with ggplot

``` r
# plots for outcome split by groups
ggplot(dataset, aes(x = stick))+
  geom_histogram(binwidth = 1, color = "black", fill = "white")
```


![](Week-12-RMANOVA-Assignment_files/figure-markdown_github/unnamed-
chunk-5-1.png)

``` r
ggplot(dataset, aes(x = testicle))+
  geom_histogram(binwidth = 1, color = "black", fill = "white")
```



``` r
ggplot(dataset, aes(x = eye))+
  geom_histogram(binwidth = 1, color = "black", fill = "white")
```



``` r
ggplot(dataset, aes(x = witchetty))+
  geom_histogram(binwidth = 1, color = "black", fill = "white")
```


RMANOVA in jmv package

``` r
output = jmv::anovaRM(
    data = dataset,
    rm = list(
        list(
            label="Food",
            levels=c(
                "stick",
                "testicle",
                "eye",
                "witchetty"))),
    rmCells = list(
        list(
            measure="stick",
            cell="stick"),
        list(
            measure="testicle",
            cell="testicle"),
        list(
            measure="eye",
            cell="eye"),
        list(
            measure="witchetty",
            cell="witchetty")),
    effectSize = c("ges", "eta", "partEta"),
    depLabel = "Seconds",
    rmTerms = ~ Food,
    spherTests = TRUE,
    spherCorr = c("none", "GG", "HF"),
    postHoc = list(
        "Food"),
    postHocCorr = c(
        "bonf",
```

```
        "none",
        "tukey",
        "scheffe",
        "holm"),
    emMeans = ~ Food,
    emmTables = TRUE)
```

    ## Warning: attributes are not identical across measure variables; they
will be
    ## dropped

``` r
output
```

    ##
    ## REPEATED MEASURES ANOVA
    ##
    ## Within Subjects Effects
    ##

    ##   Sphericity Correction   Sum of Squares   df
Mean Square   F   p η²-G η²
η²-p
    ##

    ##   Food   None   83.12500   3
27.708333   3.793806   0.0255703   0.3274249   0.3274249   0.3514799
    ##   Greenhouse-Geisser   83.12500   1.598537
52.00068   3.793806   0.0625841   0.3274249   0.3274249   0.3514799
    ##   Huynh-Feldt   83.12500   1.997291
41.61888   3.793806   0.0483306   0.3274249   0.3274249   0.3514799
    ##
    ##   Residual   None   153.37500   21
7.303571
    ##   Greenhouse-Geisser   153.37500   11.189757
13.70673
    ##   Huynh-Feldt   153.37500   13.981036
10.97022
    ##

    ##   Note. Type 3 Sums of Squares
    ##
    ##
    ## Between Subjects Effects
    ##

    ##   Sum of Squares   df   Mean Square   F   p
η²-G η² η²-p
    ##

    ##   Residual   17.37500   7   2.482143
    ##

    ##   Note. Type 3 Sums of Squares
```

```
##
##
##   ASSUMPTIONS
##
##   Tests of Sphericity
##
------------------------------------------------------------------------------
##                 Mauchly's W      p         Greenhouse-Geisser e    Huynh-
Feldt e
##
------------------------------------------------------------------------------
##    Food         0.1362480    0.0468458              0.5328456
0.6657636
##
------------------------------------------------------------------------------
##
##
##   POST HOC TESTS
##
##   Post Hoc Comparisons - Food
##
--------------------------------------------------------------------------------------
##      Food              Food        Mean Difference      SE         df
t            p              p-tukey      p-scheffe     p-bonferroni    p-holm
##
--------------------------------------------------------------------------------------
##     stick       -      testicle          3.8750000     1.351256
21.00000      2.86770228    0.0092136    0.0422912    0.0688661       0.0552818
0.0460681
##                 -      eye               4.0000000     1.351256
21.00000      2.96020881    0.0074701    0.0347801    0.0578305       0.0448205
0.0448205
##                 -      witchetty         2.3750000     1.351256
21.00000      1.75762398    0.0933811    0.3206962    0.3996166       0.5602868
0.3735245
##     testicle    -      eye               0.1250000     1.351256
21.00000      0.09250653    0.9271724    0.9997067    0.9997827       1.0000000
0.9271724
##                 -      witchetty        -1.5000000     1.351256
21.00000     -1.11007830    0.2795153    0.6874563    0.7469435       1.0000000
0.7275647
##     eye         -      witchetty        -1.6250000     1.351256
21.00000     -1.20258483    0.2425216    0.6320079    0.6982714       1.0000000
0.7275647
##
--------------------------------------------------------------------------------------
##
##
##   ESTIMATED MARGINAL MEANS
##
##   FOOD
##
##   Estimated Marginal Means - Food
##   -------------------------------------------------------------
##    Food          Mean          SE          Lower       Upper
##   -------------------------------------------------------------
```

```
##    stick         8.125000    0.8730846    6.327076    9.922924
##    testicle      4.250000    0.8730846    2.452076    6.047924
##    eye           4.125000    0.8730846    2.327076    5.922924
##    witchetty     5.750000    0.8730846    3.952076    7.547924
##    --------------------------------------------------------------
```


Calculate omega squared

Field prefers to use omega squared for the effect size. He shows how to
calculate it using the information from the RMANOVA tables in section
15.11

``` r
omegaSquare = (((4-1)/(8*4))*(27.71 - 7.3))/(7.3 + ((2.48 - 7.3)/4) + (((4-1)/
(8*4))*(27.71 - 7.3)))
omegaSquare
```

```
## [1] 0.2389277
```