Practical 6060: Factorial ANOVA

1 ANOVA: Ensure R Results Match SPSS Results

Three steps are needed to ensure R results match SPSS results:

Step 1. Each independent variable is a factor in R (recall the as.factor function)

Step 2. Set the contrasts correctly (critical in multi-factor ANOVA designs)

Step 3. Use Type III Sums of Squares (typically using the car package Anova function)

When all three of these steps are done correctly, the ANOVA values in R will match those from SPSS.

Here is an example of how you would proceed with an one-way ANOVA.

2 Load the data,

```
library(tidyverse)
crf.data<-read_csv("crfData.csv")
```

2.1 Set Factors (Match SPSS Step 1)

```
crf.data$anxiety     <- as.factor(crf.data$anxiety)
crf.data$preparation <- as.factor(crf.data$preparation)

levels(crf.data$anxiety) <- list("Low Anxiety"=1, "High Anxiety"=2)
levels(crf.data$preparation) <- list("Low Preparation"=1,
                                     "Medium Preparation"=2,
                                     "High Preparation"=3)
```

2.2 Set Contrasts (Match SPSS Step 2)

```
options(contrasts = c("contr.sum", "contr.poly"))
```

3 Determining presence of main effects and interaction(s)

We proceed just like before creating a linear model using anxiety and preparation predicting mark. In regression we would have expressed this as: mark ~ anxiety + preparation + I(anxiety*mark).

In ANOVA we can use a shorter form for the model: mark ~ anxiety * preparation This shorter form tests the main effects and the interaction.

```
crf.lm<-lm(mark ~ anxiety * preparation, data=crf.data)
```

3.1 Easy way: apaTables (Match SPSS Step 3)

```
library(apaTables)
apa.aov.table(crf.lm, filename="Table1.doc")
```

```
##
##
## ANOVA results using mark as the dependent variable
##
##
##              Predictor        SS df        MS       F    p partial_eta2
##            (Intercept) 132933.63  1 132933.63 2215.56 .000
##                anxiety   3477.63  1   3477.63   57.96 .000          .71
##            preparation    434.47  2    217.24    3.62 .042          .23
##  anxiety x preparation    539.27  2    269.63    4.49 .022          .27
##                  Error   1440.00 24     60.00
##  CI_90_partial_eta2
##
##          [.50, .79]
##          [.00, .40]
##          [.02, .44]
##
##
## Note: Values in square brackets indicate the bounds of the 90% confidence interval for partial eta-s
```

3.2 Old-school way: CAR package (Match SPSS Step 3)

apaTables uses the car package to create the output displayed. You can use the car package directly to see the output it provides.

```
car::Anova(crf.lm, type=3)
```

```
## Anova Table (Type III tests)
##
## Response: mark
##                     Sum Sq Df   F value    Pr(>F)
## (Intercept)         132934  1 2215.5606 < 2.2e-16 ***
## anxiety               3478  1   57.9606 7.501e-08 ***
## preparation            434  2    3.6206   0.04225 *
## anxiety:preparation    539  2    4.4939   0.02199 *
## Residuals             1440 24
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4 Display Descriptive Statistics Using apaTables

```
library(apaTables)
apa.2way.table(iv1=preparation, iv2=anxiety, dv=mark, data=crf.data,
               show.marginal.means = TRUE, filename="Table2.doc")
```

```
##
##
## Means and standard deviations for mark as a function of a 3(preparation) X 2(anxiety) design
##
##                         anxiety
##                    Low Anxiety       High Anxiety       Marginal
##         preparation           M    SD            M    SD        M    SD
##     Low Preparation       71.40  5.50        59.40  3.13    65.40  7.60
##  Medium Preparation       72.60  8.88        52.60  7.64    62.60 13.12
##    High Preparation       88.00  8.15        55.40 10.78    71.70 19.40
##            Marginal       77.33 10.55        55.80  7.81
##
## Note. M and SD represent mean and standard deviation, respectively.
## Marginal indicates the means and standard deviations pertaining to main effects.
```

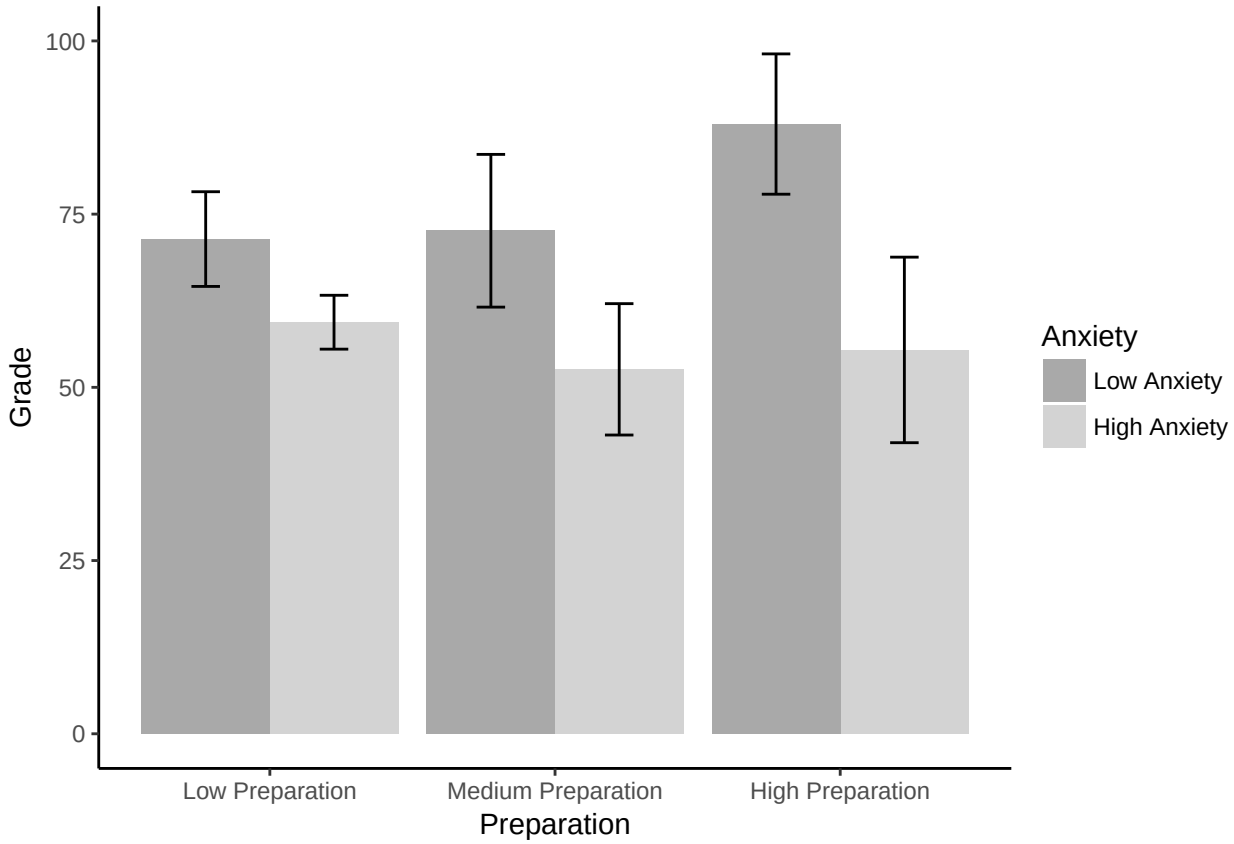
5 Graphing cell means (i.e., graphing the interaction, if there is one)

```
#order matter, preparation (the IV) must be first. Fill (anxiety) is the the other IV.
myBar<-ggplot(crf.data,aes(preparation,mark,fill=anxiety))

 #bars
myBar<-myBar + stat_summary(fun.y =mean,geom="bar",position="dodge")

#CI
myBar<-myBar + stat_summary(fun.data =mean_cl_normal, geom="errorbar",
                            position=position_dodge(width=0.9), width=0.2)

#bar coloring and legend label "Anxiety"
myBar<-myBar + scale_fill_manual("Anxiety",values=c("Dark Grey","Light Grey"))
myBar<-myBar + coord_cartesian(ylim=c(0, 100)) #axes
myBar<-myBar + labs(x="Preparation",y="Grade")  #labels
myBar<-myBar + theme_classic()
print(myBar)
```



6 Homogeneity of Variance Assumption

Testing the homogeneity of variance assumption is somewhat different in a multi-factor ANOVA. This test requires that you compare the cell variances for all cells in the 2 by 3 design. To do this, you first need to create a column in the data frame that identifies each of the 6 cells. The name for each cell is a combination of the IV levels that created that cell. Thus there will be 6 unique values in the cell column we create below.

```
crf.data.temp <- crf.data
crf.data.temp$cells <- interaction(crf.data$anxiety,crf.data$preparation)
print(crf.data.temp)
```

```
## # A tibble: 30 × 4
##        anxiety        preparation  mark                         cells
##         <fctr>             <fctr> <int>                        <fctr>
## 1  Low Anxiety    Low Preparation    79    Low Anxiety.Low Preparation
## 2  Low Anxiety    Low Preparation    66    Low Anxiety.Low Preparation
## 3  Low Anxiety    Low Preparation    70    Low Anxiety.Low Preparation
## 4  Low Anxiety    Low Preparation    75    Low Anxiety.Low Preparation
## 5  Low Anxiety    Low Preparation    67    Low Anxiety.Low Preparation
## 6  Low Anxiety Medium Preparation    62 Low Anxiety.Medium Preparation
## 7  Low Anxiety Medium Preparation    84 Low Anxiety.Medium Preparation
## 8  Low Anxiety Medium Preparation    66 Low Anxiety.Medium Preparation
## 9  Low Anxiety Medium Preparation    73 Low Anxiety.Medium Preparation
## 10 Low Anxiety Medium Preparation    78 Low Anxiety.Medium Preparation
## # ... with 20 more rows
```

Next we need to determine if the variances of all 6 cells are the same. More specifically, we test if the population variances for all 6 cells are the same. If Levene's test is non-significant then the homogeneity of variance assumption is not rejected (i.e., it is assumed to be true).

```
car::leveneTest(y = crf.data.temp$mark,
                group = crf.data.temp$cells,
                center="median") #compares cell variances
```

```
## Levene's Test for Homogeneity of Variance (center = "median")
##       Df F value Pr(>F)
## group  5  0.5556 0.7327
##       24
```

We would report $F(5, 24) = 0.56$, $p = .73$ and indicate that the homogeneity of variance assumption was not violated.

6.1 What did we find

These analyses revealed a main effect for anxiety (i.e., anxiety marginal means are different), a main effect for preparation (i.e., preparation marginal means are different), and an interaction (i.e., the effect of preparation on mark depends on anxiety).

7 Exploring the Interaction: post hoc Analyses with Common Pooled Variance Approach

Sometimes it is helpful to explore an interaction by looking at the effect of one predictor on the criterion by holding the effects of the other predictors constant.

Consider, for example, a two-predictor case with preparation and anxiety. What is the effect of preparation on grades for low anxiety participants (i.e., holding anxiety constant at low anxiety)? Likewise, what is the effect of preparation on grades for high anxiety participants? These types of analyses are called simple main effects.

Simple main effects examine whether a set of cell means are the same or not; specifically the set of cell means for one level of an independent variable. This differs from a main effect, which examines marginal means.

7.1 Simple Main Effects

7.1.1 F-values

Simple main effects are easy to do in R using the phia library (post hoc interaction analysis).

```
library(phia)
```

```
## Loading required package: car
```

```
##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:dplyr':
##
##     recode
```

```
## The following object is masked from 'package:purrr':
##
##     some
```

```
testInteractions(crf.lm, fixed="anxiety", across="preparation",adjustment="none")
```

```
## F Test:
## P-value adjustment method: none
##               preparation1 preparation2 Df Sum of Sq      F   Pr(>F)
##  Low Anxiety         -16.6        -15.4  2    856.93 7.1411 0.003686 **
## High Anxiety           4.0         -2.8  2    116.80 0.9733 0.392244
## Residuals                             24   1440.00
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The output from this code will provide an F-value and p-value for the two simple main effects described above. Specifically, it will indicate the cell means for low anxiety participants across low, medium, and high preparation are different. As well, it will indicate the cell means for high anxiety participants across low, medium, and high preparation are all the same. Note that this **is similar** to doing two one-way ANOVAs but not **the same** as doing two one-way ANOVAs. The reason it is different than doing two one-way ANOVAs is that the error variance term in the denominator in the F-ratio (i.e., Mean Squared Error) is based on all six cells not just the three involved in a particular simple main effect (as it would be in a one-way ANOVA).

The chance of making a Type I Error for this set of analysis is .05 per simple main effect. Thus, it is .10 for the two simple main effects in this example. You could potentially control the Type I Error to .05 for the set of simple main effects by specifying "bonferroni" in the adjustment argument. Other adjustments are possible see phia Documentation: Controlling for Type I Errors later in this document.

7.1.2 Effect size with CI

To get partial eta-squared for these effects, you need to calculate it by hand using the Sum of Squares Effect and Sum of Squares Error using the formula:

$\eta^2_{partial} = \frac{SS_{effect}}{SS_{effect}+SS_{error}}$.

In the output above the Sum of Squares Error is 1440.00. The Sum of Squares for the Low Anxiety an High Anxiety Simple Main Effects, are 856.93 and 116.80, respectively.

Low Anxiety: $\eta^2_{partial} = \frac{856.93}{856.93+1440} = 0.3730762$

High Anxiety: $\eta^2_{partial} = \frac{116.80}{116.80+1440} = 0.07502569$

We can get the confidence intervals for these $\eta^2_{partial}$ values using a command from apaTables:

```
#Low Anxiety
get.ci.partial.eta.squared(F.value=7.1411, df1=2, df2=24, conf.level = .90)
```

```
## $LL
## [1] 0.09227443
##
## $UL
## [1] 0.529424
```

```
#High Anxiety
get.ci.partial.eta.squared(F.value=0.9733, df1=2, df2=24, conf.level = .90)
```

```
## $LL
## [1] 0
##
## $UL
## [1] 0.2250462
```

Thus, we have the following:

Low Anxiety Simple Main Effect: $\eta^2_{partial} = .37$, 95% CI[.09, .53], $F(2, 24) = 7.14$, $p = .004$

High Anxiety Simple Main Effect: $\eta^2_{partial} = .08$, 95% CI[.00, .23], $F(2, 24) = 0.97$, $p = .392$

7.2 Simple Main Effects: Paired Comparisons, Bonferroni and Others

If a simple main effect is significant, then it makes sense to see which particular means are different from each other. If the simple main effect is non-significant, there is no need to examine particular pairs of mean for differences – you have already established the means are all the same.

In the current data, the simple main effect for high anxiety participants was non-significant. Consequently, there is no need to further examine those means (despite the fact we will continue to see results pertaining to those means below). In contrast, the simple main effect for low anxiety participants was significant. Therefore, we want to know where the differences are among the means for low anxiety participants. We do this using paired comparisons:

```
testInteractions(crf.lm, fixed="anxiety", pairwise="preparation", adjustment="none")
```

Of course, we would still have the Type I Error problem if we used this approach. A better approach would be to control for Type I Errors using the Bonferroni method.

```
testInteractions(crf.lm, fixed="anxiety", pairwise="preparation", adjustment="bonferroni")
```

```
## F Test:
## P-value adjustment method: bonferroni
##                                                        Value Df Sum of Sq
##  Low Preparation-Medium Preparation :  Low Anxiety  -1.2  1       3.6
##    Low Preparation-High Preparation :  Low Anxiety -16.6  1     688.9
## Medium Preparation-High Preparation :  Low Anxiety -15.4  1     592.9
##  Low Preparation-Medium Preparation : High Anxiety   6.8  1     115.6
##    Low Preparation-High Preparation : High Anxiety   4.0  1      40.0
## Medium Preparation-High Preparation : High Anxiety  -2.8  1      19.6
## Residuals                                                   24    1440.0
##                                                             F  Pr(>F)
##  Low Preparation-Medium Preparation :  Low Anxiety  0.0600 1.00000
##    Low Preparation-High Preparation :  Low Anxiety 11.4817 0.01455 *
## Medium Preparation-High Preparation :  Low Anxiety  9.8817 0.02641 *
##  Low Preparation-Medium Preparation : High Anxiety  1.9267 1.00000
##    Low Preparation-High Preparation : High Anxiety  0.6667 1.00000
## Medium Preparation-High Preparation : High Anxiety  0.3267 1.00000
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We are only interested in the comparisons for the Low Anxiety level in the output above.

7.3 Getting d-value effect sizes with confidence intervals:

7.3.1 apaTables d-values

You could use apaTables to get the *d*-values. Note that the significance (i.e., stars) used in the apa.d.table command does not take into account Type I Error like your post hoc calculations. Therefore, you should disregard the stars indicating significance in this table for post hoc purpose. You can just manually delete them or change them to match the significance values from the above calculations.

In this case, we create two separate tables - but we would might want to combine these into one large table manually.

```
low.anx.people  <- crf.data %>% filter(anxiety=="Low Anxiety")
apa.d.table(iv=preparation, dv=mark, data=low.anx.people,filename="Table3a.doc")
```

```
##
##
## Means, standard deviations, and d-values with confidence intervals
##
##
##   Variable              M     SD   1             2
##   1. Low Preparation    71.40 5.50
##
##   2. Medium Preparation 72.60 8.88 0.16
##                                    [-1.08, 1.40]
##
##   3. High Preparation   88.00 8.15 2.39**        1.81*
##                                    [0.66, 4.04]  [0.26, 3.28]
##
##
## Note. * indicates p < .05; ** indicates p < .01.
## M and SD are used to represent mean and standard deviation, respectively.
## Values in square brackets indicate the 95% confidence interval for each d-value.
## The confidence interval is a plausible range of population d-values
## that could have caused the sample d-value (Cumming, 2014).
## d-values are unbiased estimates calculated using formulas 4.18 and 4.19
## from Borenstein, Hedges, Higgins, & Rothstein (2009).
## d-values not calculated if unequal variances prevented pooling.
##
```

```
high.anx.people <- crf.data %>% filter(anxiety=="High Anxiety")
apa.d.table(iv=preparation, dv=mark, data=high.anx.people,filename="Table3b.doc")
```

```
##
##
## Means, standard deviations, and d-values with confidence intervals
##
##
##   Variable              M     SD    1             2
##   1. Low Preparation    59.40 3.13
##
##   2. Medium Preparation 52.60 7.64  1.17
##                                     [-0.23, 2.50]
##
##   3. High Preparation   55.40 10.78 0.50          0.30
##                                     [-0.77, 1.75] [-0.96, 1.54]
##
##
## Note. * indicates p < .05; ** indicates p < .01.
## M and SD are used to represent mean and standard deviation, respectively.
## Values in square brackets indicate the 95% confidence interval for each d-value.
## The confidence interval is a plausible range of population d-values
## that could have caused the sample d-value (Cumming, 2014).
## d-values are unbiased estimates calculated using formulas 4.18 and 4.19
## from Borenstein, Hedges, Higgins, & Rothstein (2009).
## d-values not calculated if unequal variances prevented pooling.
##
```

7.3.2 Old-school d-values

Comparison 1 Low Anxiety: Low Preparation vs High Preparation (smd is the *d*-value)

We begin by getting the scores for each cell. The easiest way to do this is using the dplyr library. However, as you see below, the dplyr library returns a subset of the entire data frame, not just the column we are interested in.

```
group1.rows <- crf.data %>% filter(anxiety=="Low Anxiety",preparation=="Low Preparation")
print(group1.rows)
```

```
## # A tibble: 5 × 3
##       anxiety     preparation  mark
##        <fctr>          <fctr> <int>
## 1 Low Anxiety Low Preparation    79
## 2 Low Anxiety Low Preparation    66
## 3 Low Anxiety Low Preparation    70
## 4 Low Anxiety Low Preparation    75
## 5 Low Anxiety Low Preparation    67
```

```
group2.rows <- crf.data %>% filter(anxiety=="Low Anxiety",preparation=="High Preparation")
print(group2.rows)
```

```
## # A tibble: 5 × 3
##       anxiety      preparation  mark
##        <fctr>           <fctr> <int>
## 1 Low Anxiety High Preparation    76
```

```
## 2 Low Anxiety High Preparation    94
## 3 Low Anxiety High Preparation    83
## 4 Low Anxiety High Preparation    94
## 5 Low Anxiety High Preparation    93
```

Now that we have the contents of the cells we can compute the d-value and corresponding confidence interval.

```
library(MBESS)
d.value <- smd(Group.1=group1.rows$mark, Group.2=group2.rows$mark)

ci.smd(smd=d.value,n.1=length(group1.rows$mark),
       n.2=length(group2.rows$mark))
```

```
## $Lower.Conf.Limit.smd
## [1] -4.037633
##
## $smd
## [1] -2.386082
##
## $Upper.Conf.Limit.smd
## [1] -0.6578413
```

Comparison 2 Low Anxiety: Low Preparation vs Medium Preparation (smd is the *d*-value)

```
group1.rows <- crf.data %>% filter(anxiety=="Low Anxiety",preparation=="Low Preparation")
group2.rows <- crf.data %>% filter(anxiety=="Low Anxiety",preparation=="Medium Preparation")

d.value <- smd(Group.1=group1.rows$mark, Group.2=group2.rows$mark)

ci.smd(smd=d.value,n.1=length(group1.rows$mark),
       n.2=length(group2.rows$mark))
```

```
## $Lower.Conf.Limit.smd
## [1] -1.399568
##
## $smd
## [1] -0.162474
##
## $Upper.Conf.Limit.smd
## [1] 1.084552
```

Comparison 3 Low Anxiety: Medium Preparation vs High Preparation (smd is the *d*-value)

```
group1.rows <- crf.data %>% filter(anxiety=="Low Anxiety",preparation=="Medium Preparation")
group2.rows <- crf.data %>% filter(anxiety=="Low Anxiety",preparation=="High Preparation")

d.value <- smd(Group.1=group1.rows$mark, Group.2=group2.rows$mark)

ci.smd(smd=d.value,n.1=length(group1.rows$mark),
       n.2=length(group2.rows$mark))
```

```
## $Lower.Conf.Limit.smd
## [1] -3.284666
##
## $smd
## [1] -1.80677
##
## $Upper.Conf.Limit.smd
```

```
## [1] -0.2556158
```

7.4 Write-up

I examined the effects of preparation (low, medium, or high) and anxiety (low, high) on exam grades (0-not at all to 100-extremely) using a 3x2 between-participants ANOVA. Levene's test was non-significant, $F(5, 24) = 0.56$, $p = .733$, indicating that the CRF ANOVA homogeneity of variance assumption was fulfilled. There was an interaction between preparation and juggling, $\eta^2_{partial} = .27$, 95% CI[.02, .44], $F(2, 24) = 4.49$, $p = .022$, (see Figure 1 and Tables 1 and 2) and I explored this interaction using simple main effect posthocs. For students with high anxiety, there appeared to be little effect of preparation on grades, $\eta^2_{partial} = .08$, 95% CI[.00, .23], $F(2, 24) = 0.97$, $p = .392$. In contrast, for students with low anxiety, there appeared to be a moderate to very strong effect of preparation on grades $\eta^2_{partial} = .37$, 95% CI[.09, .53], $F(2, 24) = 7.14$, $p = .004$. Specifically, as per Table 3a, among low anxiety students those who prepared extensively were calmer than students who prepared for a medium, $d = 1.81$, 95% CI[0.26, 3.28], $p = .026$, or low amount of time, $d = 2.39$, 95% CI[0.66, 4.04], $p = 0.015$. As well, among among low anxiety students, those who prepared for a moderate amount of time did not differ meaninfully in grades from those of students who prepared a minimal amount of time, $d = 0.16$, 95% CI[-1.08, 1.40], $p = 1.00$. Paired comparison p-values used a Bonferroni correction for three comparisons.

(Note: You might also report the main effects but indicate that they were qualified by the interaction).

7.5 phia Documentation Excerpt: Controlling for Type I Errors

The adjustment methods include the Bonferroni correction ("bonferroni") in which the p-values are multiplied by the number of comparisons. Less conservative corrections are also included by Holm (1979) ("holm"), Hochberg (1988) ("hochberg"), Hommel (1988) ("hommel"), Benjamini & Hochberg (1995) ("BH" or its alias "fdr"), and Benjamini & Yekutieli (2001) ("BY"), respectively. A pass-through option ("none") is also included. The set of methods are contained in the p.adjust.methods vector for the benefit of methods that need to have the method as an option and pass it on to p.adjust.

The first four methods are designed to give strong control of the family-wise error rate. There seems no reason to use the unmodified Bonferroni correction because it is dominated by Holm's method, which is also valid under arbitrary assumptions. Hochberg's and Hommel's methods are valid when the hypothesis tests are independent or when they are non-negatively associated (Sarkar, 1998; Sarkar and Chang, 1997). Hommel's method is more powerful than Hochberg's, but the difference is usually small and the Hochberg p-values are faster to compute.

The "BH" (aka "fdr") and "BY" method of Benjamini, Hochberg, and Yekutieli control the false discovery rate, the expected proportion of false discoveries amongst the rejected hypotheses. The false discovery rate is a less stringent condition than the family-wise error rate, so these methods are more powerful than the others.

8 For your records: 3-way ANOVA

8.1 Loading Data and Setting Contrasts

Note that the as_factor command below uses an underscore (_) not a period (.).

```
library(haven)
crf.data         <- read_sav("crf6060.sav")
crf.data$prep    <- as_factor(crf.data$prep, labels = "values")
crf.data$anxiety <- as_factor(crf.data$anxiety, labels = "values")
crf.data$univ    <- as_factor(crf.data$univ, labels = "values")

#Match SPSS Step 1: Not needed factors, already factors
glimpse(crf.data)
```

```
## Observations: 60
## Variables: 4
## $ univ    <fctr> Guelph, Guelph, Guelph, Guelph, Guelph, Guelph, Guelp...
## $ anxiety <fctr> low, low, low, low, low, low, low, low, low, low, low...
## $ prep    <fctr> 2-4 hours, 2-4 hours, 2-4 hours, 2-4 hours, 2-4 hours...
## $ mark    <dbl> 79, 66, 70, 75, 67, 80, 84, 78, 75, 78, 76, 94, 83, 94...
```

```
#Match SPSS Step 2
options(contrasts = c("contr.sum", "contr.poly"))
```

8.2 Main Analysis (Match SPSS Step 3)

```
crf.lm <-lm(mark~anxiety*prep*univ,data=crf.data)

apa.aov.table(crf.lm) #match SPSS Step 3
```

8.3 Descriptive Statistics

For the anxiety main effect:

```
psych::describeBy(crf.data$mark,group=list(crf.data$anxiety))
```

For the preparation main effect:

```
psych::describeBy(crf.data$mark,group=list(crf.data$prep))
```

For the university main effect:

```
psyc::describeBy(crf.data$mark,group=list(crf.data$univ))
```

For the interaction effect cell means:

```
psych::describeBy(crf.data$mark,group=list(crf.data$prep,crf.data$anxiety,crf.data$univ))
```

8.4 Graphing

We make a graph for each university separately then combine them.

8.4.1 Guelph Graph

```
crf.data.guelph <- filter(crf.data,univ=="Guelph")

#order matter, prep (the IV) must be first
myBarGuelph<-ggplot(crf.data.guelph,aes(prep,mark,fill=anxiety))

#bars
myBarGuelph<-myBarGuelph + stat_summary(fun.y =mean,geom="bar",position="dodge")

myBarGuelph<-myBarGuelph + stat_summary(fun.data =mean_cl_normal,
                                        geom="errorbar",
                                        position=position_dodge(width=0.9), width=0.2) #CI

#bar coloring and legend label "Anxiety". Replace factor level labels with these
myBarGuelph<-myBarGuelph + scale_fill_manual("Anxiety",values=c("Dark Grey","Light Grey"),
                                             labels=c("Low", "High"))

#replace factor level labels with these ones
myBarGuelph<-myBarGuelph + scale_x_discrete(labels=c("Low", "Medium", "High"))

myBarGuelph<-myBarGuelph + coord_cartesian(ylim=c(0, 100)) #axes
myBarGuelph<-myBarGuelph + labs(title="Guelph",x="Preparation",y="Grade")  #labels
myBarGuelph<-myBarGuelph + theme_classic()

#removes legend from this graph so we only see it once (with the Waterloo graph)
myBarGuelph<-myBarGuelph + theme(legend.position="none")
```

8.4.2 Waterloo Graph

```
crf.data.waterloo <- filter(crf.data,univ=="Waterloo")

#order matter, age (the IV) must be first
myBarWaterloo<-ggplot(crf.data.waterloo,aes(prep,mark,fill=anxiety))

myBarWaterloo<-myBarWaterloo + stat_summary(fun.y =mean,geom="bar",position="dodge") #bars

myBarWaterloo<-myBarWaterloo + stat_summary(fun.data =mean_cl_normal,
                                            geom="errorbar",
                                            position=position_dodge(width=0.9), width=0.2) #CI
#bar coloring and legend label "Anxiety". Replace factor level labels with these
myBarWaterloo<-myBarWaterloo + scale_fill_manual("Anxiety",values=c("Dark Grey","Light Grey"),
                                                 labels=c("Low", "High"))

#replace factor level labels with these ones
myBarWaterloo<-myBarWaterloo + scale_x_discrete(labels=c("Low", "Medium", "High"))

myBarWaterloo<-myBarWaterloo + coord_cartesian(ylim=c(0, 100)) #axes

myBarWaterloo<-myBarWaterloo + labs(title="Waterloo",x="Preparation",y="Grade")  #labels

myBarWaterloo<-myBarWaterloo + theme_classic()
```

```
myBarWaterloo<-myBarWaterloo + theme(legend.position=c(.9, .9))
#Move legend off side so left/right bar widths are the same.
#Values (.9,.9) indicate x,y position of legend as proportion of graph axes
```

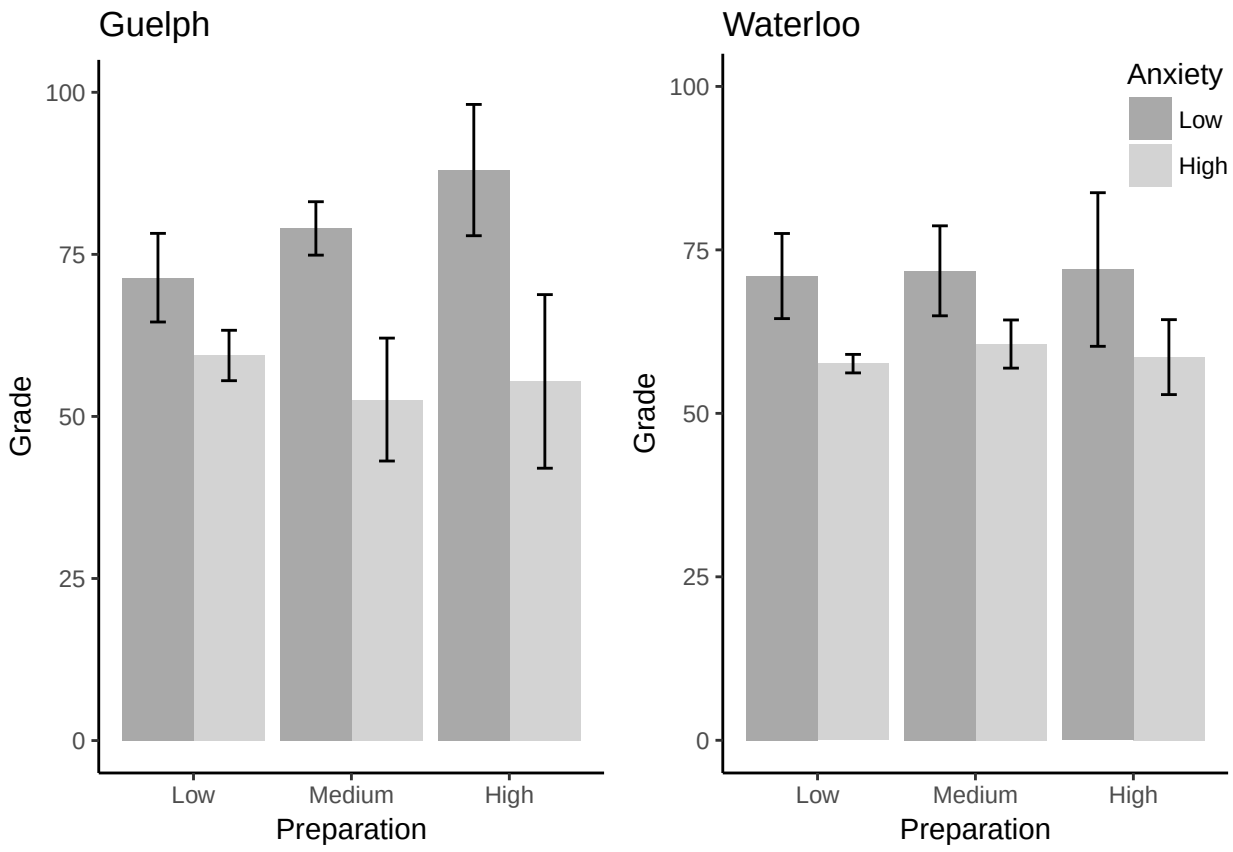
8.4.3 Combine Guelph and Waterloo Graphs

```
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
```

```
## The following object is masked from 'package:dplyr':
##
##     combine
```

```
grid.arrange(myBarGuelph, myBarWaterloo, ncol=2)
```



8.5 Homogeneity of variance assumption

```
crf.data$cells<-interaction(crf.data$anxiety,crf.data$prep,crf.data$univ)
library(car)
leveneTest(crf.data$mark,crf.data$cells,center="median") #compares cell variances
```

8.6 Simple Main Effects and Paired Comparisons

```
library(phia)
#Test 2-way interaction within each university
testInteractions(crf.lm, fixed=c("univ"), across=c("prep","anxiety"),adjustment="none")

#Look at the effect of preparation within each university at a specific anxiety level
testInteractions(crf.lm, fixed=c("univ","anxiety"), across=c("prep"),adjustment="none")


#SME: Low anxiety at Guelph paired comparisons (additional comparisons printed)
testInteractions(crf.lm, fixed=c("univ","anxiety"), pairwise=c("prep"),adjustment="bonferroni")

#Effect sizes as d-value and CI instructions for 2-way above
```