PSYC 6380 Psychological Applications of Multivariate Analysis

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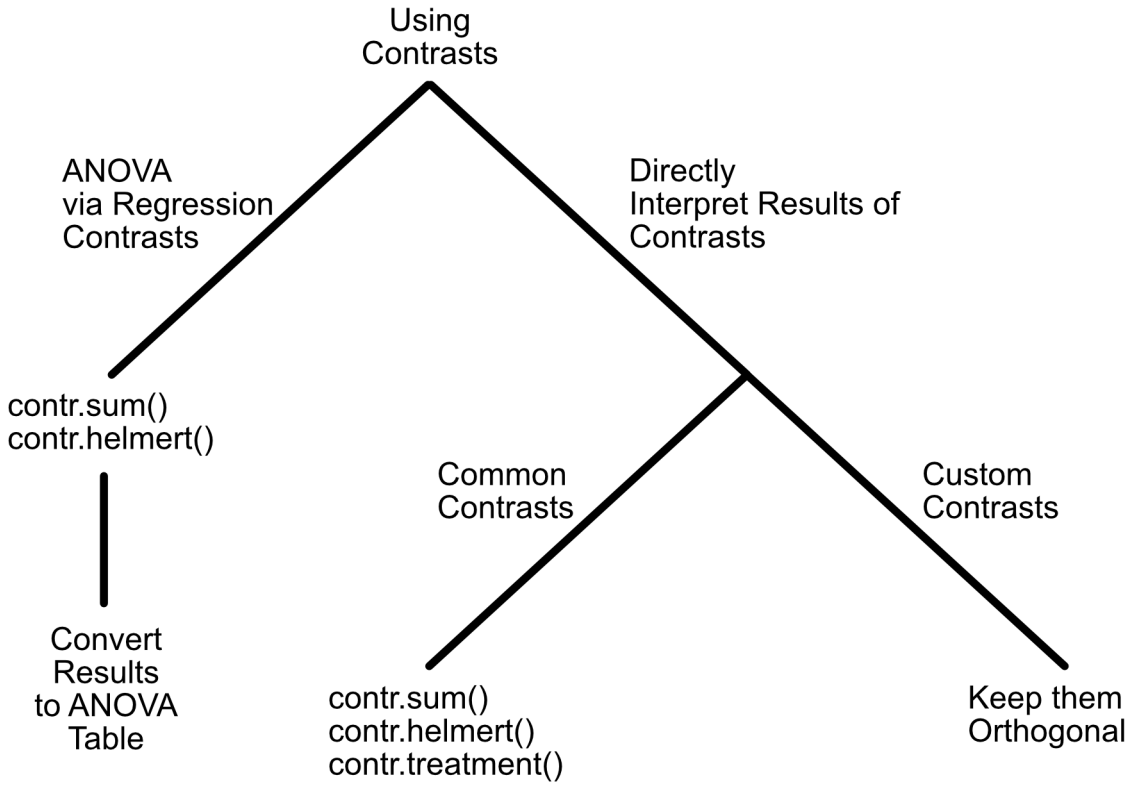
Preface

This is a Quarto book designed to supplement PSYC 6380.

1 One-way ANOVA via Regression

1.1 Using Contrasts



1.2 Treatement/Dummy Coding

Use the Treatment contrast ONLY when you are interested in the contrast itself. DO NOT use if you are interested in typical ANOVA results (main effect, main effect, interaction, etc.).

This approach is the default appraoch in R unless you specify otherwise. In most cases, this is NOT what you want in Psychology analyses.

Comparisons are to one specific level of the Independent Variables that we call the reference group.

1.2.1 Original Data

```
print(viagra)
```

```
   libido      dose
1       3   placebo
2       2   placebo
3       1   placebo
4       1   placebo
5       4   placebo
6       5  low_dose
7       2  low_dose
8       4  low_dose
9       2  low_dose
10      3  low_dose
11      7 high_dose
12      4 high_dose
13      5 high_dose
14      3 high_dose
15      6 high_dose
```

Note the means for the three groups are:

```
viagra %>% group_by(dose) %>% summarise(group_mean = mean(libido))
```

```
# A tibble: 3 x 2
  dose      group_mean
  <fct>          <dbl>
1 placebo          2.2
2 low_dose         3.2
3 high_dose        5
```

1.2.2 Set Factor with Reference Group

```
viagra <- viagra %>%
  mutate(dose = as_factor(dose)) %>%
  mutate(dose = relevel(dose, ref = "placebo"))
```

1.2.3 Regression with Treatment Contrast

The computer will always use contrasts when there are categorical variables. So you should set the contrast you want. Here we set the contrast as Treatment (or Dummy) Coding. In most cases you will not want Treatment Coding. You will want Sum Coding we cover that in the next section. But we start with Treament Coding because it is easier to understand.

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

lm_viagra <- lm(libido ~ dose + 1, data = viagra)
```

```
tidy(lm_viagra)
```

term	estimate	std.error	statistic	p.value
(Intercept)	2.2	0.6271629	3.507860	0.0043189
doselow_dose	1.0	0.8869423	1.127469	0.2815839
dosehigh_dose	2.8	0.8869423	3.156913	0.0082681

What is going on here? The single dose column has disappeared. Instead we get b-weights for doselow_dose and dosehigh_dose. How do you interpret that information?

1.2.4 Treatment Contrasts Explained

In the above analysis, we take a categorical variable and indicate it's factor with the code below. With this code we are telling the computer it as a factor (i.e., a categorical variable) and indicating, with ref = "placebo", that all the group means should be compared to the placebo group mean - **if a treatment contrast is used**.

```
viagra <- viagra %>%
  mutate(dose = as_factor(dose)) %>%
  mutate(dose = relevel(dose, ref = "placebo"))
```

In conjuction with the above "as_factor" commmand, we specify the rule for turning the factor (i.e., categorical variables) into "contrast columns" that will be used for the actual analysis. We do that with the line below that indicates we want to use treatment coding also known as dummy coding. It is CRITICAL that you set the contrast used for your regression if you have categorical variables.

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

A contrast will ALWAYS be used if you have categorical variables - you want to make sure it's the one you want. Treatment Contrast is probably not the one you want in most cases - but we start with this one because it is common and easy to understand.

The combination of the two code blocks above (creating a factor, setting the contrast) results in the computer creating a data set like the one below when you conduct the regression.

```
print(viagra_dummy_coded)
```

```
# A tibble: 15 x 3
   libido dose_low_dose dose_high_dose
    <int>         <dbl>          <dbl>
 1      3             0              0
 2      2             0              0
 3      1             0              0
 4      1             0              0
 5      4             0              0
 6      5             1              0
 7      2             1              0
 8      4             1              0
 9      2             1              0
10      3             1              0
11      7             0              1
12      4             0              1
13      5             0              1
14      3             0              1
15      6             0              1
```

Then, when we specified this:

```
lm_viagra <- lm(libido ~ dose + 1, data = viagra)
```

The computer actually ran the code below. Notice how the predictors are the contrast columns dose_low_dose and dose_high_dose. That's how the computer handles categorical variables in a regression.

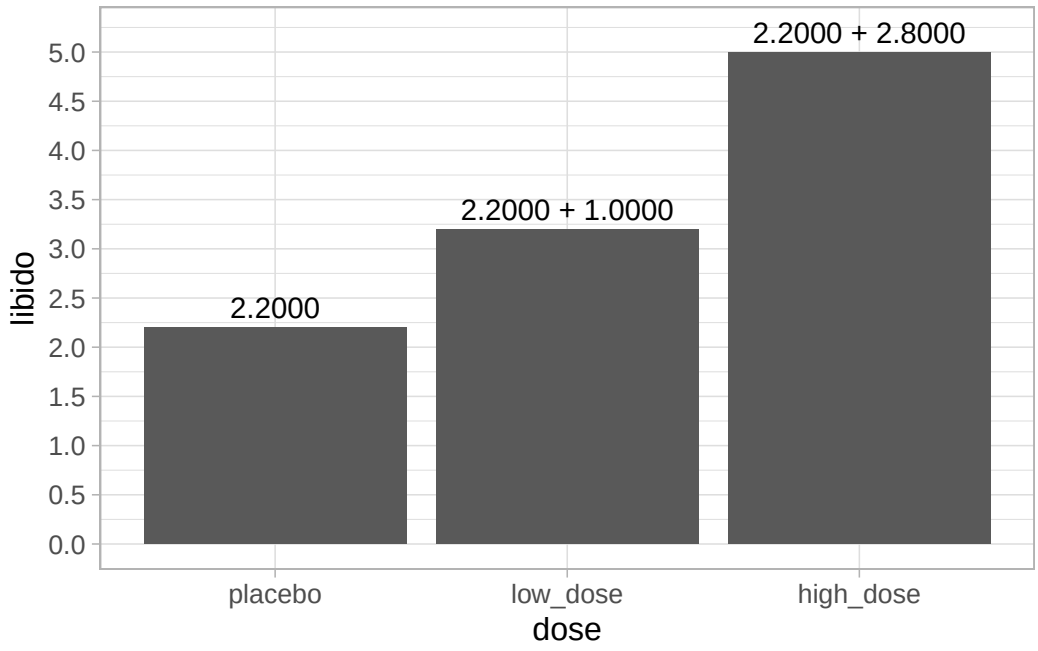
```r
lm_viagra <- lm(libido ~ dose_low_dose + dose_high_dose + 1,
                data = viagra_dummy_coded)
```

```r
tidy(lm_viagra)
```

term	estimate	std.error	statistic	p.value
(Intercept)	2.2	0.6271629	3.507860	0.0043189
dose_low_dose	1.0	0.8869423	1.127469	0.2815839
dose_high_dose	2.8	0.8869423	3.156913	0.0082681

The p-values for the b-weights assess the statistical difference between each group and the reference group (i.e., placebo). So Treatment (Dummy) Contrasts are a great way to compare each group mean to the reference group.

Examine the weights in the above table and see how they can be used to recreate the group means.



1.2.5 ANOVA Summary Information

With a one-way ANOVA, it's easy to exact ANOVA information from the Regression output.

```
glance(lm_viagra)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	nobs
0.4603659	0.3704268	1.402379	5.118644	0.0246943	2	-24.68305	57.36616	60.1983	23.6	12	15

From this output you can see that for this one-way ANOVA, $F(2, 12) = 5.119$, $p = .025$. In a one-way ANOVA the effect size is $\eta^2 = \eta^2_{partial} = R^2 = .46$. Note that in a one-way ANOVA, $\eta^2 = \eta^2_{partial}$ but this is not the case when you move to N-way ANOVA.

```
summary(lm_viagra)
```

```
Call:
lm(formula = libido ~ dose_low_dose + dose_high_dose + 1, data = viagra_dummy_coded)

Residuals:
   Min     1Q Median     3Q    Max
  -2.0   -1.2   -0.2    0.9    2.0

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)      2.2000     0.6272   3.508  0.00432 **
dose_low_dose    1.0000     0.8869   1.127  0.28158
dose_high_dose   2.8000     0.8869   3.157  0.00827 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.402 on 12 degrees of freedom
Multiple R-squared:  0.4604,    Adjusted R-squared:  0.3704
F-statistic: 5.119 on 2 and 12 DF,  p-value: 0.02469
```

From this output you can (AGAIN) see that for this one-way ANOVA, $F(2, 12) = 5.119$, $p = .025$. In a one-way ANOVA the effect size is $\eta^2 = \eta^2_{partial} = R^2 = .46$.

Note: A good exam question would be to present a table like this an then ask you the mean for each group. With treatment/dummy coding the regression weight indicate for the reference group the mean of that group. For the other groups, the regression weights indicate the difference from the reference group.

1.3 Sum Contrast / Effect Contrast

With sum coding, the contrasts create b-weight represent comparisons of each group mean to the to the grand mean. The contrasts we use for each group are presented below:

```
contr.sum(3)
```

```
  [,1] [,2]
1    1    0
2    0    1
3   -1   -1
```

We run the regression with the code below. Notice we take care to set the contrast to sum before the regression.

```
# Check levels
levels(viagra$dose)
```

```
[1] "placebo"   "low_dose"  "high_dose"
```

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

lm_viagra_sum_coded <- lm(libido ~ dose + 1,
                          data = viagra)
```

We see the results are below. We use as.data.frame() just to see all the decimals.

```
tidy(lm_viagra_sum_coded) %>% as.data.frame()
```

```
         term   estimate std.error  statistic      p.value
1 (Intercept)  3.4666667 0.3620927  9.5739760 5.720565e-07
2       dose1 -1.2666667 0.5120764 -2.4735893 2.930022e-02
3       dose2 -0.2666667 0.5120764 -0.5207556 6.120112e-01
```

In the results above the intercept corresponds to the grand mean.

Recall the sum contrast below:

```
contr.sum(3)
```

```
  [,1] [,2]
1    1    0
2    0    1
3   -1   -1
```

- The first contrast row (1 0) indicates the mean group 1 (placebo) is the intercept plus the 1 times first slope and 0 times the second slope.

$$placebo - mean = 3.4666667 + 1(-1.2666667) + 0(-0.2666667) = 2.20$$

- The second contrast row (0 1) indicates the mean group 2 (low dose) is the intercept plus the 0 times first slope and 1 times the second slope.

$$low - dose - mean = 3.4666667 + 0(-1.2666667) + 1(-0.2666667) = 3.20$$

- The third contrast row (-1 -1) indicates the mean group 3 (high dose) is the intercept plus the -1 times first slope and -1 times the second slope.

$$low - dose - mean = 3.4666667 + (-1)(-1.2666667) + (-1)(-0.2666667) = 5.00$$

1.3.1 Behind the scenes

What is the grand mean? It's just the mean of the dependent variable column across all conditions.

```
summary_stat = viagra %>%
  summarise(grand_mean = mean(libido))

print(summary_stat)
```

```
  grand_mean
1   3.466667
```

In the above analysis, when we used this code block:

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

lm_viagra_sum_coded <- lm(libido ~ dose + 1,
                          data = viagra)
```

We were doing a regression with the predictors below:

libido	intercept	dose1	dose2
3	1	1	0
2	1	1	0
1	1	1	0
1	1	1	0
4	1	1	0
5	1	0	1
2	1	0	1
4	1	0	1
2	1	0	1
3	1	0	1
7	1	-1	-1
4	1	-1	-1
5	1	-1	-1
3	1	-1	-1
6	1	-1	-1

That is, when we specified this:

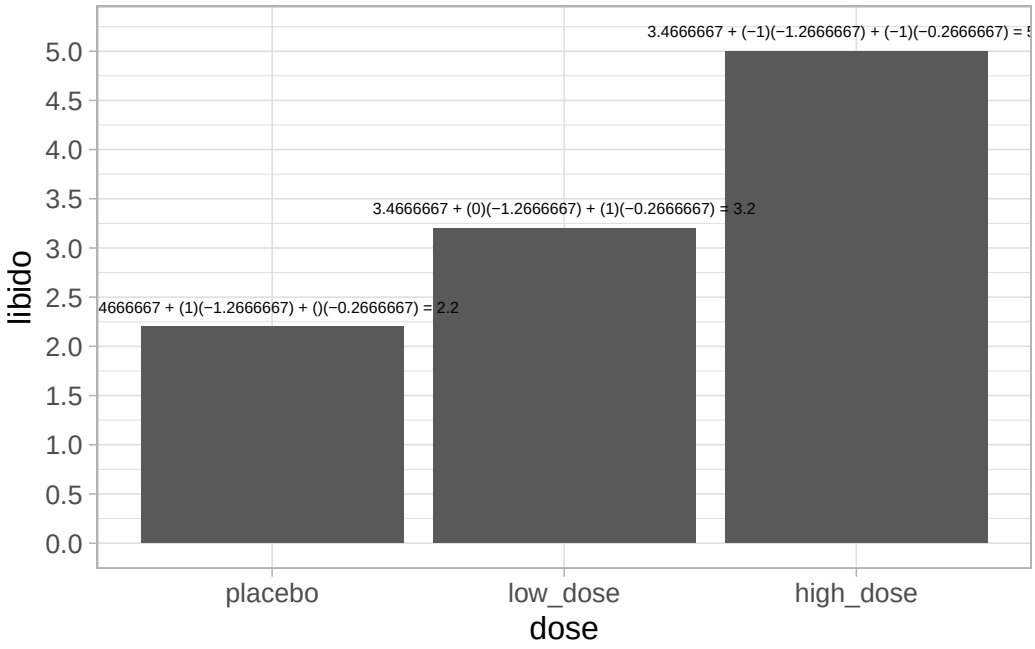
```
lm_viagra <- lm(libido ~ dose + 1, data = viagra)
```

The computer actually ran this:

```
lm_viagra_sum <- lm(libido ~ dose1 + dose2 + 1,
                    data = viagra_sum_coded)
```

```
tidy(lm_viagra_sum)
```

term	estimate	std.error	statistic	p.value
(Intercept)	3.4666667	0.3620927	9.5739760	0.0000006
dose1	-1.2666667	0.5120764	-2.4735893	0.0293002
dose2	-0.2666667	0.5120764	-0.5207556	0.6120112



1.3.2 ANOVA values

```
glance(lm_viagra_sum)
```

r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik	AIC	BIC	deviance	df.residual	nobs
0.4603659	0.3704268	1.402379	5.118644	0.0246943	2	-24.68305	57.36616	60.1983	23.6	12	15

From this output you can see that for this one-way ANOVA, F(2,12) = 5.118644, p = 0.0246943.

```
summary(lm_viagra_sum)
```

```
Call:
lm(formula = libido ~ dose1 + dose2 + 1, data = viagra_sum_coded)

Residuals:
   Min     1Q Median     3Q    Max
```

```
  -2.0   -1.2   -0.2    0.9    2.0

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   3.4667     0.3621   9.574 5.72e-07 ***
dose1        -1.2667     0.5121  -2.474   0.0293 *
dose2        -0.2667     0.5121  -0.521   0.6120
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.402 on 12 degrees of freedom
Multiple R-squared:  0.4604,    Adjusted R-squared:  0.3704
F-statistic: 5.119 on 2 and 12 DF,  p-value: 0.02469
```

From this output you can (again) see that for this one-way ANOVA, F(2,12) = 5.118644, p = 0.0246943.

Note: A good exam question would be to present a table like this an then ask you the mean for each group. With treatment/dummy coding the regression weight indicate for the reference group the mean of that group. For the other groups, the regression weights indicate the difference from the reference group.

1.4 Helmert Contrast

Use the Helmert Contrast if you are interested in typical ANOVA results (main effect, main effect, interaction, etc.).

1.5 Summary: Contrast Types

Name/Synonym	R command Example	Nature of Comparison	Note

Treatment Contrast / Dummy Contrast	`> contr.treatment(4)`
	`  2 3 4`
	`1 0 0 0`
	`2 1 0 0`
	`3 0 1 0`
	`4 0 0 1`
		Intercept is the reference group mean. Unstandardized weights indicate difference between a group's mean and reference group mean. In this example, group 1 is the reference group. Notice the first contrast column is for the second group - because group 1 is the intercept.	Default in R. **Do NOT use for ANOVA.**

Sum Contrast / Effect Contrast	`> contr.sum(4)`
	`  [,1] [,2] [,3]`
	`1  1  0  0`
	`2  0  1  0`
	`3  0  0  1`
	`4 -1 -1 -1`
		Intercept is the grand mean. Unstandardized weights indicate difference between a group's mean and last group's mean (Group 4 here).	**USE for ANOVA.** This works because the intercept is the grand mean.

Name/Synonym	R command Example	Nature of Comparison	Note

Helmert Contrast	`> contr.helmert(4)`
	`  [,1] [,2] [,3]`
	`1   -1   -1   -1`
	`2    1   -1   -1`
	`3    0    2   -1`
	`4    0    0    3`
		Intercept is the grand mean. First contrast, unstandardized weight indicate difference between Group 2 and Group 1 means. Second contrast, unstandardized weight indicate difference between Group 3 mean and the average of the Group 1 and Group 2 means. Third contrast, unstandardized weight indicate difference between Group 4 mean and the average of the Group 1, Group 2, and Group 3 means. And so on.	**USE for ANOVA.** This works because the intercept is the grand mean.

2 Two-way ANOVA via Regression

2.1 Conducting a 2-way ANOVA

2.1.1 Activate Packages

```
library(tidyverse)
library(janitor)
library(pracma)
library(recipes)
library(forcats)
library(tidymodels)
library(apaTables)
```

2.1.2 Load Data

```
gdata = read_csv("gdata.csv")
```

2.1.3 Inspect Data

This example is from the Andy Field book. The example uses alcohol(0, 2 pints, 4 pints) and sex(male,female) as predictors of attractiveness. See the Discovering Statistics Using R (2012) for the complete example. We use this example to illustrate sum contrasts in an ANOVA context.

```
glimpse(gdata)
```

```
Rows: 41
Columns: 3
$ attractiveness <dbl> 60, 60, 55, 60, 55, 70, 65, 60, 70, 65, 60, 60, 50, 55,~
$ gender         <chr> "female", "female", "female", "female", "female", "fema~
$ alcohol        <chr> "none", "none", "none", "none", "none", "pint2", "pint2~
```

```r
print(gdata)
```

```
   attractiveness gender alcohol
1              60 female    none
2              60 female    none
3              55 female    none
4              60 female    none
5              55 female    none
6              70 female   pint2
7              65 female   pint2
8              60 female   pint2
9              70 female   pint2
10             65 female   pint2
11             60 female   pint2
12             60 female   pint2
13             50 female   pint2
14             55 female   pint4
15             65 female   pint4
16             70 female   pint4
17             55 female   pint4
18             55 female   pint4
19             60 female   pint4
20             50 female   pint4
21             50 female   pint4
22             50   male    none
23             55   male    none
24             80   male    none
25             65   male    none
26             70   male    none
27             75   male    none
28             75   male    none
29             65   male    none
30             45   male   pint2
31             60   male   pint2
32             85   male   pint2
33             65   male   pint2
34             70   male   pint2
35             70   male   pint2
36             80   male   pint2
37             60   male   pint2
38             30   male   pint4
39             30   male   pint4
```

```
40              30   male   pint4
41              55   male   pint4
```

2.1.4 Make Factors

```
gdata <- gdata %>%
  mutate(gender = as_factor(gender)) %>%
  mutate(alcohol = as_factor(alcohol))

glimpse(gdata)
```

```
Rows: 41
Columns: 3
$ attractiveness <dbl> 60, 60, 55, 60, 55, 70, 65, 60, 70, 65, 60, 60, 50, 55,~
$ gender         <fct> female, female, female, female, female, female, female,~
$ alcohol        <fct> none, none, none, none, none, pint2, pint2, pint2, pint~
```

2.1.5 Linear Model

```
options(contrasts = c("contr.sum", "contr.poly"))
lm_output <- lm(attractiveness ~ gender*alcohol, data = gdata)
```

```
table1 <- apa.aov.table(lm_output, table.number = 1)
apa.save("table1aov.doc", table1)
```

Predictor	*SS*	*df*	*MS*	*F*	*p*	$\eta^2_{partial}$	90% CI
(Intercept)	127477.89	1	127477.89	1490.97	<.001		
gender	67.37	1	67.37	0.79	.381	.02	[.00, .15]
alcohol	2230.76	2	1115.38	13.05	<.001	.43	[.19, .56]
gender x alcohol	1508.65	2	754.33	8.82	.001	.34	[.11, .48]
Error	2992.50	35	85.50				

2.2 Regression Becoming ANOVA

A bit of magic seems to happen in the above. We conduct a regression and then somehow get an ANOVA table out at the end. How does that work? The key is understanding that when we specify the regression with factors in it - we a really giving the computer a set of instruction and a starting point - rather than an actual analysis. The computer does a few things "under the hood":

1) Factors are turned into contrasts columns
2) Multiple columns be be required for a single factor
3) The number of contrast columns required for a single factor column is equal to the number levels minus one.
4) The "actual analysis" is conducted using the contrast columns - not the factor column from your data set.

2.3 Contrasts for Categorical Variables

Let's load a new data set that has some contrast columns created already.

```
gdata <- read_csv("gdata_contrasts.csv")
```

2.3.1 Gender Contrasts

In R when you use the line:

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

It effectively runs the contr.sum() command on each factor column, when a regression is run, and creates contrasts based on the number of levels of each factor. For example, the sex factor, with levels, causes the command below to be run.

```
contr.sum(2)
```

```
  [,1]
1    1
2   -1
```

These rules are applied to the gender column. We create a new column called sex where this rule has been applied. In the output below, I have already applied this rule and put the result in the sex column. Normally this happens "under the hood" and you don't see it. Notice how every female is coded 1 in the sex column where as males are coded -1 in the sex column; consistent with the contr.sum(2) command.

```
gdata %>%
  select(attractiveness, gender, sex) %>%
  as.data.frame()
```

```
   attractiveness gender sex
1              60 female   1
2              60 female   1
3              55 female   1
4              60 female   1
5              55 female   1
6              70 female   1
7              65 female   1
8              60 female   1
9              70 female   1
10             65 female   1
11             60 female   1
12             60 female   1
13             50 female   1
14             55 female   1
15             65 female   1
16             70 female   1
17             55 female   1
18             55 female   1
19             60 female   1
20             50 female   1
21             50 female   1
22             50   male  -1
23             55   male  -1
24             80   male  -1
25             65   male  -1
26             70   male  -1
27             75   male  -1
28             75   male  -1
29             65   male  -1
30             45   male  -1
31             60   male  -1
32             85   male  -1
33             65   male  -1
34             70   male  -1
35             70   male  -1
36             80   male  -1
37             60   male  -1
38             30   male  -1
39             30   male  -1
40             30   male  -1
41             55   male  -1
```

2.3.2 Alcohol Contrasts

```
contr.sum(3)
```

```
  [,1] [,2]
1    1    0
2    0    1
3   -1   -1
```

In the output below, I have already applied this rule and put the result in the alc1 and alc2 columns. Normally this happens "under the hood" and you don't see it. Notice how every levels of alcohol are coded using this scheme; consistent with the contr.sum(3) command.

```
gdata %>%
  select(attractiveness, alcohol, alc1, alc2) %>%
  as.data.frame()
```

```
   attractiveness alcohol alc1 alc2
1              60    none    1    0
2              60    none    1    0
3              55    none    1    0
4              60    none    1    0
5              55    none    1    0
6              70   pint2    0    1
7              65   pint2    0    1
8              60   pint2    0    1
9              70   pint2    0    1
10             65   pint2    0    1
11             60   pint2    0    1
12             60   pint2    0    1
13             50   pint2    0    1
14             55   pint4   -1   -1
15             65   pint4   -1   -1
16             70   pint4   -1   -1
17             55   pint4   -1   -1
18             55   pint4   -1   -1
19             60   pint4   -1   -1
20             50   pint4   -1   -1
21             50   pint4   -1   -1
22             50    none    1    0
23             55    none    1    0
```

```
24              80    none    1    0
25              65    none    1    0
26              70    none    1    0
27              75    none    1    0
28              75    none    1    0
29              65    none    1    0
30              45   pint2    0    1
31              60   pint2    0    1
32              85   pint2    0    1
33              65   pint2    0    1
34              70   pint2    0    1
35              70   pint2    0    1
36              80   pint2    0    1
37              60   pint2    0    1
38              30   pint4   -1   -1
39              30   pint4   -1   -1
40              30   pint4   -1   -1
41              55   pint4   -1   -1
```

2.3.3 Interaction Contrasts

We also need contrasts for the interaction. We create the interaction contrasts by multiplying the columns for sex, alc1, and alc2. You can see how we do so in the code below.

```
gdata <- gdata %>%
  mutate(int1 = sex*alc1,
         int2 = sex*alc2)
```

Now check out the full coding off all predictors. When the regression is run, and the ANOVA results created, these are the columns that are actually analyzed.

```
gdata %>%
  select(attractiveness, sex, alc1, alc2, int1, int2) %>%
  as.data.frame()
```

```
  attractiveness sex alc1 alc2 int1 int2
1             60   1    1    0    1    0
2             60   1    1    0    1    0
3             55   1    1    0    1    0
4             60   1    1    0    1    0
5             55   1    1    0    1    0
```

6		70	1	0	1	0	1
7		65	1	0	1	0	1
8		60	1	0	1	0	1
9		70	1	0	1	0	1
10		65	1	0	1	0	1
11		60	1	0	1	0	1
12		60	1	0	1	0	1
13		50	1	0	1	0	1
14		55	1	-1	-1	-1	-1
15		65	1	-1	-1	-1	-1
16		70	1	-1	-1	-1	-1
17		55	1	-1	-1	-1	-1
18		55	1	-1	-1	-1	-1
19		60	1	-1	-1	-1	-1
20		50	1	-1	-1	-1	-1
21		50	1	-1	-1	-1	-1
22		50	-1	1	0	-1	0
23		55	-1	1	0	-1	0
24		80	-1	1	0	-1	0
25		65	-1	1	0	-1	0
26		70	-1	1	0	-1	0
27		75	-1	1	0	-1	0
28		75	-1	1	0	-1	0
29		65	-1	1	0	-1	0
30		45	-1	0	1	0	-1
31		60	-1	0	1	0	-1
32		85	-1	0	1	0	-1
33		65	-1	0	1	0	-1
34		70	-1	0	1	0	-1
35		70	-1	0	1	0	-1
36		80	-1	0	1	0	-1
37		60	-1	0	1	0	-1
38		30	-1	-1	-1	1	1
39		30	-1	-1	-1	1	1
40		30	-1	-1	-1	1	1
41		55	-1	-1	-1	1	1

2.4 Degrees of Freedom

When you look at the the columns in the above output notice the number of columns we use for each predictor corresponds the degrees of freedom for that predictor.

Predictor	df	Number of contrast columns	Contrast column names
sex	$df_a = a - 1 = 2 - 1 = 1$	1	sex
alcohol	$df_b = b - 1 = 3 - 1 = 2$	2	alc1, alch2
sex by alcohol	$df_{int} = df_a * df_b = (a-1)(b-1) = 1(2) = 2$	2	int1, int2

2.5 Regression command (i.e., lm) overview

To get ANOVA results that are consistent with what are typically used in psychology you need to 1) Specify the contr.sum() contrast 2) Calculate the Sum of Squares using the logic for Type III Sum of Squares

When you run an ANOVA using the command:

```
options(contrasts = c("contr.sum", "contr.poly"))
lm_output <- lm(attractiveness ~ gender*alcohol, data = gdata)
```

R actually runs a whole series of regressions for you and combines them into the single output table you saw above. These models fall into two categories Full and Restricted Models.

2.6 Full and Restricted Models

2.6.1 Full Model

First, the Full Model is run that includes all of the predictor columns:

```
lm_full                    <- lm(attractiveness ~ sex + alc1 + alc2 + int1 + int2, data = g
```

2.6.2 Restricted Models

Next a series of restricted models are run that excluded an effect of interest for each restricted model.

```
lm_restricted_no_sex         <- lm(attractiveness ~       alc1 + alc2 + int1 + int2, data
lm_restricted_no_alcohol     <- lm(attractiveness ~ sex +               int1 + int2, data
lm_restricted_no_interaction <- lm(attractiveness ~ sex + alc1 + alc2              , data
lm_restricted_no_intercept   <- lm(attractiveness ~ sex + alc1 + alc2 + int1 + int2 - 1, d
```

2.7 Logic: Model Comparison

The ANOVA table is created by comparing each of these restricted models to the full model. For example, to determine the main effect for gender we compare the model lm_restricted_no_sex to the model lm_full. If lm_full accounts for substantially more variance than lm_restricted_no_sex it is significant.

This is effectively identical to when we looked at comparing two regression models previous. Using that logic, we could just write the code:

```
# try this, it works!
library(apaTables)
apa.reg.table(lm_restricted_no_sex, lm_restricted_all)
```

The result would tell us if the main effect of sex is significant. The logic of calculating things this way is the Type III Sum of Squares logic. HOWEVER, we don't tend to use the output in the form provided in this type of table. Rather the output if reformatted to by consistent with the way ANOVA's are typically presented. The next few sections show you how the table below is created:

Predictor	SS	df	MS	F	p	$\eta^2_{partial}$	90% CI
(Intercept)	127477.89	1	127477.89	1490.97	<.001		
gender	67.37	1	67.37	0.79	.381	.02	[.00, .15]
alcohol	2230.76	2	1115.38	13.05	<.001	.43	[.19, .56]
gender x alcohol	1508.65	2	754.33	8.82	.001	.34	[.11, .48]
Error	2992.50	35	85.50				

2.8 Explanation 1: Comparing Models

2.8.1 Sex

```
anova(lm_restricted_no_sex, lm_full)
```

```
Analysis of Variance Table
```

```
Model 1: attractiveness ~ alc1 + alc2 + int1 + int2
Model 2: attractiveness ~ sex + alc1 + alc2 + int1 + int2
  Res.Df    RSS Df Sum of Sq      F Pr(>F)
1     36 3059.9
2     35 2992.5  1    67.368 0.7879 0.3808
```

Compare the $F-$ and p-values in the above output to those in the table below.

Predictor	SS	df	MS	F	p	$\eta^2_{partial}$	90% CI
(Intercept)	127477.89	1	127477.89	1490.97	<.001		
gender	67.37	1	67.37	0.79	.381	.02	[.00, .15]
alcohol	2230.76	2	1115.38	13.05	<.001	.43	[.19, .56]
gender x alcohol	1508.65	2	754.33	8.82	.001	.34	[.11, .48]
Error	2992.50	35	85.50				

2.8.2 Alcohol

```
anova(lm_restricted_no_alcohol, lm_full)
```

```
Analysis of Variance Table

Model 1: attractiveness ~ sex + int1 + int2
Model 2: attractiveness ~ sex + alc1 + alc2 + int1 + int2
  Res.Df    RSS Df Sum of Sq      F    Pr(>F)
1     37 5223.3
2     35 2992.5  2    2230.8 13.045 5.843e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Compare the $F-$ and p-values in the above output to those in the table below.

Predictor	SS	df	MS	F	p	$\eta^2_{partial}$	90% CI
(Intercept)	127477.89	1	127477.89	1490.97	<.001		
gender	67.37	1	67.37	0.79	.381	.02	[.00, .15]
alcohol	2230.76	2	1115.38	13.05	<.001	.43	[.19, .56]
gender x alcohol	1508.65	2	754.33	8.82	.001	.34	[.11, .48]
Error	2992.50	35	85.50				

2.8.3 Interaction

```
anova(lm_restricted_no_interaction, lm_full)
```

```
Analysis of Variance Table

Model 1: attractiveness ~ sex + alc1 + alc2
Model 2: attractiveness ~ sex + alc1 + alc2 + int1 + int2
  Res.Df    RSS Df Sum of Sq      F    Pr(>F)
1     37 4501.2
2     35 2992.5  2    1508.7 8.8225 0.0007896 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Compare the $F-$ and p-values in the above output to those in the table below.

Predictor	SS	df	MS	F	p	$\eta^2_{partial}$	90% CI
(Intercept)	127477.89	1	127477.89	1490.97	<.001		
gender	67.37	1	67.37	0.79	.381	.02	[.00, .15]
alcohol	2230.76	2	1115.38	13.05	<.001	.43	[.19, .56]
gender x alcohol	1508.65	2	754.33	8.82	.001	.34	[.11, .48]
Error	2992.50	35	85.50				

2.9 Explanation 2: Sum of Squares to ANOVA

Notice the first column of the ANOVA table above is the Sum of Squares column. How are those values calculated? Let's consider the example of alcohol as a predictor. We want to determine the Sum of Squares for alcohol.

We begin by calculating predicted scores for the Full Model (lm_full):

$$\hat{y}_{\text{full}} = b_0 + b_1 sex + b_2 alc1 + b_3 alc2 + b_4 int1 + b_5 int2$$

Next, we calculate the predicted scores for the alcohol restricted model (lm_restricted_no_alcohol)

$$\hat{y}_{\text{restricted no alcohol}} = b_0 + b_1 sex + b_2 int1 + b_3 int2$$

Then we calculated the difference between these two sets of predicted scores:

$$\hat{y}_{\text{difference}} = \hat{y}_{\text{full}} - \hat{y}_{\text{restricted no alcohol}}$$

Then we square these values and add them up.

$$SS_{alcohol} = \sum \hat{y}^2_{\text{difference}}$$

We follow this process below for each predictor (including the intercept).

2.9.1 Intercept

```
## Sum of squares intercept
sum( ( predict(lm_full) - predict(lm_restricted_no_intercept) )^2 )
```

```
[1] 127477.9
```

Compare the Sum of Squares values in the above output to the one in the table below.

Predictor	SS	df	MS	F	p	$\eta^2_{partial}$	90% CI
(Intercept)	127477.89	1	127477.89	1490.97	<.001		
gender	67.37	1	67.37	0.79	.381	.02	[.00, .15]
alcohol	2230.76	2	1115.38	13.05	<.001	.43	[.19, .56]
gender x alcohol	1508.65	2	754.33	8.82	.001	.34	[.11, .48]
Error	2992.50	35	85.50				

2.9.2 Sex

```
## Sum of squares sex
sum( ( predict(lm_full) - predict(lm_restricted_no_sex) )^2 )
```

```
[1] 67.36842
```

Compare the Sum of Squares values in the above output to the one in the table below.

Predictor	SS	df	MS	F	p	$\eta^2_{partial}$	90% CI
(Intercept)	127477.89	1	127477.89	1490.97	<.001		
gender	67.37	1	67.37	0.79	.381	.02	[.00, .15]
alcohol	2230.76	2	1115.38	13.05	<.001	.43	[.19, .56]
gender x alcohol	1508.65	2	754.33	8.82	.001	.34	[.11, .48]
Error	2992.50	35	85.50				

2.9.3 Alcohol

```
## Sum of squares alcohol
sum( ( predict(lm_full) - predict(lm_restricted_no_alcohol) )^2 )
```

```
[1] 2230.757
```

Compare the Sum of Squares values in the above output to the one in the table below.

Predictor	SS	df	MS	F	p	$\eta^2_{partial}$	90% CI
(Intercept)	127477.89	1	127477.89	1490.97	<.001		
gender	67.37	1	67.37	0.79	.381	.02	[.00, .15]
alcohol	2230.76	2	1115.38	13.05	<.001	.43	[.19, .56]
gender x alcohol	1508.65	2	754.33	8.82	.001	.34	[.11, .48]
Error	2992.50	35	85.50				

2.9.4 Interaction

```
## Sum of squares interaction
sum( ( predict(lm_full) - predict(lm_restricted_no_interaction) )^2 )
```

```
[1] 1508.651
```

Compare the Sum of Squares values in the above output to the one in the table below.

Predictor	SS	df	MS	F	p	$\eta^2_{partial}$	90% CI
(Intercept)	127477.89	1	127477.89	1490.97	<.001		
gender	67.37	1	67.37	0.79	.381	.02	[.00, .15]
alcohol	2230.76	2	1115.38	13.05	<.001	.43	[.19, .56]
gender x alcohol	1508.65	2	754.33	8.82	.001	.34	[.11, .48]
Error	2992.50	35	85.50				

2.9.5 Error

```
## Sum of squares error
sum( lm_full$residuals^2 )
```

```
[1] 2992.5
```

Compare the Sum of Squares values in the above output to the one in the table below.

Predictor	SS	df	MS	F	p	$\eta^2_{partial}$	90% CI
(Intercept)	127477.89	1	127477.89	1490.97	<.001		
gender	67.37	1	67.37	0.79	.381	.02	[.00, .15]
alcohol	2230.76	2	1115.38	13.05	<.001	.43	[.19, .56]
gender x alcohol	1508.65	2	754.33	8.82	.001	.34	[.11, .48]
Error	2992.50	35	85.50				

2.9.6 SS to ANOVA

Based on the above analyses we know the Sum of Squares and the degrees of freedom for everything. We can put that information in the table below.

Predictor	SS	df	MS= $\frac{SS}{df}$	F= $\frac{MS}{MS_{error}}$	p
(Intercept)	127477.89	1			
sex	67.37	1			
alcohol	2230.76	2			
sex by alcohol	1508.65	2			
Error	2992.5	35			

A few hand calculations, and an F to p-value look-up table, provides us with the rest of the information we need:

Predictor	SS	df	MS= $\frac{SS}{df}$	F= $\frac{MS}{MS_{error}}$	p
(Intercept)	127477.89	1	$\frac{127477.89}{1} = 127477.89$	$\frac{127477.89}{85.5} = 1490.97$	<.001
sex	67.37	1	$\frac{67.37}{1} = 67.37$	$\frac{67.37}{85.5} = 0.79$	.381
alcohol	2230.76	2	$\frac{2230.76}{2} = 1115.38$	$\frac{1115.38}{85.5} = 13.05$	<.001
sex by alcohol	1508.65	2	$\frac{1508.65}{2} = 754.325$	$\frac{754.325}{85.5} = 8.82$	.001
Error	2992.5	35	$\frac{2992.5}{35} = 85.5$		

References