

BMEG 802 – Advanced Biomedical Experimental Design and Analysis

Repeated Measures (Within) Analysis of Variance (ANOVA)

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Recap

- Two-Way ANOVA
 - linear model approach
 - interpret main effects and interactions
 - follow up mean comparisons
- n-Way ANOVA
 - general concepts
 - limitations

Today

- 1-Way Repeated Measures (“within” subjects) Design
 - Repeated Measures ANOVA
 - Greenhouse-Geisser Corrections
 - Multivariate Approach
 - Friedman Test
- 2-Way Repeated Measures
 - Repeated Measures ANOVA
 - Greenhouse-Geisser Corrections
 - Multivariate Approach

Repeated Measures (Within) ANOVA

- each individual (or culture, etc) contributes a score for **each level of a factor**
- each individual contributes multiple scores (e.g., pre vs post tests)
 - paired differences between time points
- individuals serve as their own control
- variance between different conditions is no longer due to [effect + between-group sampling variance] multiple tests on the same individual, cell culture, etc.
- it's the same group of subjects! there is no “between- group” sampling variance
- variance only due to the effect

Examples of a Within Design

1. effects of placebo, drug A and drug B can be studied in the same subjects; each subject can serve as their own control
2. behaviour of a culture studied over time; a measurement can be taken from the same culture at multiple time points

Advantages of Repeated Measures Designs

1. more information is obtained from each subject than in a between-subjects design
 - within-subjects design: each subject contributes a scores (a is the number of conditions tested)
 - between-subjects design: each subject contributes only one score
 - # of subjects needed to reach a given level of statistical power is often much lower with within-subjects designs
2. variability in individual differences between subjects is totally removed from the error term
3. each subject serves as his/her own control
4. error term is reduced
5. statistical power increases (few participants needed)

General Linear Model (GLM)

Let's develop a full and restricted model.

Full Model: $Y_{ij} = \mu + \alpha_j + \pi_i + \epsilon_{i,j}$

Restricted Model: $Y_{ij} = \mu + \pi_i + \epsilon_{i,j}$

Effect of Factor

Effect of Subjects

- restricted model only includes effect of subjects (effect of factor is zero)
- so the difference here compared to regular “between- subjects” models is simply the inclusion of terms accounting for the effects of subjects
- remember: the more variance you can account for, the smaller the error term, the higher the F value, and the more powerful the statistical test

Defining Error and DF For the General Case

just as always, we can compute an F statistic based on Error for the full model and Error for the restricted model:

$$F = \frac{(E_{restricted} - E_{full}) / (df_{restricted} - df_{full})}{(E_{full} / df_{full})}$$

$$df_{full} = (n - 1)(a - 1)$$

$$df_{restricted} = n(a - 1)$$

$$df_{restricted} - df_{full} = (a - 1)$$

see Chapter 11 of Maxwell, Delaney, and Kelley for (the complicated) calculations of $E_{restricted}$ and E_{full}

Assumptions of Repeated Measures ANOVA

- random sampling from population
- independence of subjects
- normality
- homogeneity of treatment-difference variances
 - variance of difference scores between any two levels of a factor must be equal to variance of differences scores between all other pairs of levels of the factor
 - equivalent to showing that the population covariance matrix has a certain form, that is, it displays the property of sphericity
 - this is all very mathematical and we don't need to know the details
 - fortunately there is (1) a test to see if we have violated the assumption, and (2) a method to correct for violations

Homogeneity of Treatment-Difference Variances

- Within ANOVA very sensitive and often violates sphericity
- We will see how to perform a test of sphericity in R
- R will report a number of corrected versions of the F test assuming sphericity is violated
- “Greenhouse-Geisser” adjustment adjusts the degrees of freedom (reducing them) so that F_{crit} is larger (more conservative test)
- many people use G-G
- others like Huynh-Feldt because it's slightly less conservative

Disadvantages of Repeated Measures Designs

- Position Effect
 - When an observed response differs due to order of treatment
 - Must randomize the sequence of treatments or counterbalance
- Carry-over effect:
 - When an observed response is actually due to residual effect of a previous treatment
 - Must allow sufficient time (“washout period”) and a controlled amount of time between treatments
 - Can't always control with counterbalancing since some effects are permanent (e.g., learning, memory, etc.)
 - Some scientific questions are better suited to between-subjects designs

Experimental Design Considerations

Counterbalancing

- counterbalance the order in which treatments are administered
- e.g., Drug A then Drug B to half the participants. Drug B then Drug A to the other half
- Participants are randomly assigned to each group
- Known as a “crossover design”
- Counterbalance an experiment with more than two levels? (e.g. 4)
- there are actually 24 different orderings of 4 conditions
- we would need 24 subjects to represent each order only once ($4! = 4 \times 3 \times 2 \times 1$)

Experimental Design Considerations

Two alternatives:

- randomize the order for each subject; order effects will be controlled for “in the long run”
- Latin Square Designs: an arrangement of conditions so that each condition appears exactly once in each possible order

Order				
Ss	1	2	3	4
1	A	B	C	D
2	B	C	D	A
3	C	D	A	B
4	D	A	B	C

Three Group Example in R

Let's determine if there is a main effect of physical therapy treatment over time. Lower values represent pain level out of 10.

Subject	Treatment 1	Treatment 2	Treatment 3	Treatment 4
S1	8	10	7	5
S2	9	9	8	6
S3	7	5	8	4
S4	9	6	5	7
S5	8	7	7	6
S6	5	4	4	3
S7	7	6	5	4
S8	8	8	6	6
S9	9	8	6	5
S10	7	7	4	5

$$H_0 : \alpha_1 = \alpha_2 = \alpha_3 = \alpha_4$$

Restricted Model: $Y_{ij} = \mu + \pi_i + \epsilon_{i,j}$

$$H_1 : \alpha_1 \neq \alpha_2 \neq \alpha_3 \neq \alpha_4$$

Full Model: $Y_{ij} = \mu + \alpha_j + \pi_i + \epsilon_{i,j}$

Four Treatment Group Example

```
dv <- c(8,10,7,5,9,9,8,6,7,5,8,4,9,6,  
        5,7,8,7,7,6,5,4,4,3,7,6,5,4,8,  
        8,6,6,9,8,6,5,7,7,4,5)  
treatment <- factor(rep(c(1,2,3,4),10))  
subject <- factor(c(rep(1,4),rep(2,4),rep(3,4),  
                    rep(4,4),rep(5,4),rep(6,4),  
                    rep(7,4),rep(8,4),rep(9,4),rep(10,4)))  
mydata <- data.frame(dv, treatment, subject)
```

Four Treatment Group Example

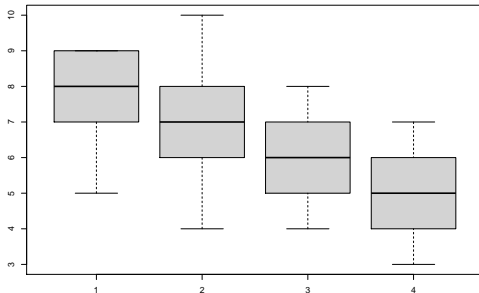
mydata

##	dv	treatment	subject
## 1	8	1	1
## 2	10	2	1
## 3	7	3	1
## 4	5	4	1
## 5	9	1	2
## 6	9	2	2
## 7	8	3	2
## 8	6	4	2
## 9	7	1	3
## 10	5	2	3
## 11	8	3	3
## 12	4	4	3
## 13	9	1	4
## 14	6	2	4
## 15	5	3	4
## 16	7	4	4
## 17	8	1	5
## 18	7	2	5
## 19	7	3	5
## 20	6	4	5
## 21	5	1	6
## 22	4	2	6
## 23	4	3	6
## 24	3	4	6
## 25	7	1	7

Visualize Data

Many ways to visualize data. Lets try out a box and whisker plot this time.

```
boxplot(split(mydata$dv,mydata$treatment))
```



Repeated Measures ANOVA - Univariate Approach

```
m1 <- aov(dv ~ treatment + Error(subject/treatment), data=mydata)
summary(m1)
```

```
##
## Error: subject
##           Df Sum Sq Mean Sq F value Pr(>F)
## Residuals  9  48.4   5.378
##
## Error: subject:treatment
##           Df Sum Sq Mean Sq F value   Pr(>F)
## treatment  3   38.9  12.967   12.24 3.06e-05 ***
## Residuals 27   28.6   1.059
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Here we see a significant influence of treatment ($p < 0.001$)

note: The Error() term tells R to slice out of the model an additional error term corresponding to the variance accounted for by subjects ($MS = 5.378$).

Univariate: a single dependent variables (we have been doing this throughout the course)

Repeated Measures ANOVA - Sphericity Violations

Repeated Measures are very sensitive to Sphericity Violations

1. Greenhouse-Geisser Corrections
2. Multivariate Approach
 - less sensitive to sphericity violations
 - assumes normality
 - Can also consider one or more dependent measures (e.g., MANOVA).
 - see Maxwell, Delaney, Kelley text for details.
3. Friedman Test
 - nonparametric
 - 1-way designs only

Let's do the GG, and we'll come back to Multivariate & Friedman afterwards.

Repeated Measures ANOVA - Greenhouse Geisser

First, we must reorganize the data into a format in which each row represents a single subject, and columns represent levels of the treatment factor.

```
response <- with(mydata, cbind(dv[treatment==1], dv[treatment==2], dv[treatment==3], dv[treatment==4]))
response
```

##		[,1]	[,2]	[,3]	[,4]
##	[1,]	8	10	7	5
##	[2,]	9	9	8	6
##	[3,]	7	5	8	4
##	[4,]	9	6	5	7
##	[5,]	8	7	7	6
##	[6,]	5	4	4	3
##	[7,]	7	6	5	4
##	[8,]	8	8	6	6
##	[9,]	9	8	6	5
##	[10,]	7	7	4	5

Repeated Measures ANOVA - Greenhouse Geisser

Next, for the linear model.

```
mlm1 <- lm(response ~ 1)
mlm1

##
## Call:
## lm(formula = response ~ 1)
##
## Coefficients:
##              [,1]  [,2]  [,3]  [,4]
## (Intercept)  7.7   7.0   6.0   5.1
```

The ~1 notation simply tells R that there are no between-subjects factors here

- in other words, only fit the model using intercepts.

Repeated Measures ANOVA - Greenhouse Geisser

Now we must set up a variable that defines the design of our study, which is a single factor with four levels:

```
rfactor <- factor(c("r1", "r2", "r3", "r4"))  
design = data.frame(rfactor)
```

Repeated Measures ANOVA - Greenhouse Geisser

Now we must set up a variable that defines the design of our study, which is a single factor with four levels:

```
install.packages("car")
```

```
library(car)
```

```
## Loading required package: carData
```

```
mlm1.aov <- Anova(mlm1, idata=design,  
                  idesign = ~rfactor, type="III")
```

- `mlm1`, is our multivariate model defined above.
- `idata=design` defines the number of levels
- `idesign=~rfactor` defines repeated-measures variable.
- `type="III"`, instructs `Anova()` to calculate the "Type-III" sums of squares (there are different types of sums of squares (see Maxwell, Delaney, Kelley)

Repeated Measures ANOVA - Greenhouse Geisser

See next slide for full output

```
summary(mlm1.aov, multivariate=FALSE)
```

```
##
## Univariate Type III Repeated-Measures ANOVA Assuming Sphericity
##
##              Sum Sq num Df Error SS den Df F value    Pr(>F)
## (Intercept) 1664.1      1   48.4      9 309.440 2.808e-08 ***
## rfactor      38.9      3   28.6     27  12.241 3.060e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## Mauchly Tests for Sphericity
```


Repeated Measures ANOVA - Greenhouse Geisser

```
## Univariate Type III Repeated-Measures ANOVA Assuming Sphericity
##
##               Sum Sq num Df Error SS den Df F value    Pr(>F)
## (Intercept) 1664.1      1   48.4     9 309.440 2.808e-08 ***
## rfactor      38.9      3   28.6    27 12.241 3.060e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
## Mauchly Tests for Sphericity
##
##           Test statistic p-value
## rfactor      0.34613 0.14884
##
##
## Greenhouse-Geisser and Huynh-Feldt Corrections
## for Departure from Sphericity
##
##           GG eps Pr(>F[GG])
## rfactor 0.7426  0.0002388 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##           HF eps  Pr(>F[HF])
## rfactor 0.9981017 3.106252e-05
```

- Mauchly Test for Sphericity not violated ($p = 0.149$) [i.e., $p > 0.05$]
- Typical to report the GG corrected values (df, F-statistics, p-values).

Repeated Measures ANOVA - Greenhouse Geisser

Kind of silly, but R reports the GG epsilon correction factor.

- Just multiply the associated degrees of freedom (df)
- input these corrected values to calculate the adjusted F-statistic

```
pval = 0.0002388
GGeps = 0.7426
df1_adj = 3 * GGeps # adjusted df
df2_adj = 27 * GGeps
Fscore = qf(1 - pval, df1=df1_adj, df2=df2_adj) # chi-square function
df1_adj
```

```
## [1] 2.2278
```

```
df2_adj
```

```
## [1] 20.0502
```

```
Fscore
```

```
## [1] 12.24109
```

- GG corrected values $[F(2.2, 20.1) = 12.2, p = 0.0002]$.

Organize Data by Treatment

Let's quickly split our data into each treatment

```
treat1 = response[1:10]  
treat2 = response[11:20]  
treat3 = response[21:30]  
treat4 = response[31:40]
```

Testing normality

Performed on the PAIRED differences

```
shapiro.test(treat2-treat1)$p.value #
```

```
## [1] 0.4208624
```

```
shapiro.test(treat3-treat1)$p.value #
```

```
## [1] 0.5195284
```

```
shapiro.test(treat4-treat1)$p.value #
```

```
## [1] 0.008488973
```

```
shapiro.test(treat3-treat2)$p.value #
```

```
## [1] 0.1526917
```

```
shapiro.test(treat4-treat2)$p.value #
```

```
## [1] 0.6088367
```

```
shapiro.test(treat4-treat3)$p.value #
```

```
## [1] 0.6420479
```

normality violated—consider using Friedman Test, Wilcoxon signed-rank, CLES

Follow up Mean Comparisons

```
p1v2 = t.test(treat1, treat2, paired = TRUE, alternative = "two.sided")$p.value #
p1v3 = t.test(treat1, treat3, paired = TRUE, alternative = "two.sided")$p.value #
p1v4 = t.test(treat1, treat4, paired = TRUE, alternative = "two.sided")$p.value #
p2v3 = t.test(treat2, treat3, paired = TRUE, alternative = "two.sided")$p.value #
p2v4 = t.test(treat2, treat4, paired = TRUE, alternative = "two.sided")$p.value #
p3v4 = t.test(treat3, treat4, paired = TRUE, alternative = "two.sided")$p.value #
pvals = c(p1v2, p1v3, p1v4, p2v3, p2v4, p3v4)
pvals_holm = p.adjust(pvals, method = "holm", n = length(pvals))
sprintf("%.5f", pvals_holm) #outputs in decimal (not scientific notation)
```

```
## [1] "0.31977" "0.02139" "0.00001" "0.31977" "0.02139" "0.31977"
```

There is a reduction in pain between treatments 1 and 3 ($p = 0.021$), treatments 1 and 4 ($p < 0.001$), and treatment 2 and 4 ($p = 0.021$)

Paired Sample Effect Sizes

```
install.packages("effsize")  
library(effsize)  
cohen.d(treat1, treat2, paired = TRUE)$estimate #
```

```
## [1] 0.4182333
```

```
cohen.d(treat1, treat3, paired = TRUE)$estimate #
```

```
## [1] 1.226729
```

```
cohen.d(treat1, treat4, paired = TRUE)$estimate #
```

```
## [1] 2.117492
```

```
cohen.d(treat2, treat3, paired = TRUE)$estimate #
```

```
## [1] 0.5951196
```

```
cohen.d(treat2, treat4, paired = TRUE)$estimate #
```

```
## [1] 1.181162
```

```
cohen.d(treat3, treat4, paired = TRUE)$estimate #
```

```
## [1] 0.6631177
```

ANOVA Effect Size in R

Bakeman, R. (2005). Recommended effect size statistics for repeated measures designs. Behavior research methods, 37(3), 379-384.

```
install.packages("effectsize")
```

```
library(effectsize)
```

```
omega_squared(mlm1.aov)
```

```
## Parameter | Omega2 (partial) |          90% CI
## -----
## rfactor   |                0.92 | [0.75, 0.96]
```

Summary of One-Way Repeated Measures ANOVA

We found a significant main effect of Treatment [$F(2.2, 20.1) = 12.2$, $p = 0.0002$, $\omega^2 = 0.92$]. There was a reduction in pain between treatments 1 and 3 ($p = 0.021$, $d = 1.23$), treatments 1 and 4 ($p < 0.001$, $d = 2.12$), and treatment 2 and 4 ($p = 0.021$, $d = 1.18$).

Power Analysis on ANOVA

```
install.packages("WebPower")
```

```
library(WebPower)
```

```
## Loading required package: MASS
```

```
## Loading required package: lme4
```

```
## Loading required package: Matrix
```

```
## Registered S3 methods overwritten by 'lme4':
```

```
##      method                                from
```

```
##      cooks.distance.influence.merMod car
```

```
##      influence.merMod                    car
```

```
##      dfbeta.influence.merMod            car
```

```
##      dfbetas.influence.merMod           car
```

```
## Loading required package: lavaan
```

```
## This is lavaan 0.6-7
```

Power Analysis on ANOVA

```
install.packages("WebPower")
```

```
library(WebPower)
```

```
# n=sub, ng=#ofgroups, nm=#ofmeasurements, nscor=sphericity(1=perfect)  
#type "0" between-effect; "1" within-effect; and "2" interaction effect
```

```
wp.rmanova(n = NULL, ng = 1, nm = 4, f = .4, nscor = 1,  
           alpha = 0.05, power = 0.8, type = 1)
```

```
## Repeated-measures ANOVA analysis
```

```
##
```

```
##           n    f  ng nm nscor alpha power
```

```
##      69.45101 0.4  1  4      1  0.05   0.8
```

```
##
```

```
## NOTE: Power analysis for within-effect test
```

```
## URL: http://psychstat.org/rmanova
```

We need 70 participants per group for a sufficiently powered.

Repeated Measures ANOVA - Multivariate Approach

Multivariate approach does not require the assumption of sphericity

- Good news, we can use the same linear model and set Multivariate = TRUE
- See next slide for multivariate output

```
summary(mlm1.aov, multivariate=TRUE)
```

```
##  
## Type III Repeated Measures MANOVA Tests:  
##  
## -----  
##  
## Term: (Intercept)  
##  
## Response transformation matrix:  
## (Intercept)
```

Repeated Measures ANOVA - Multivariate Approach

Term: rfactor

Response transformation matrix:

	rfactor1	rfactor2	rfactor3
[1,]	1	0	0
[2,]	0	1	0
[3,]	0	0	1
[4,]	-1	-1	-1

Sum of squares and products for the hypothesis:

	rfactor1	rfactor2	rfactor3
rfactor1	67.6	49.4	23.4
rfactor2	49.4	36.1	17.1
rfactor3	23.4	17.1	8.1

Multivariate Tests: rfactor

	Df	test stat	approx F	num Df	den Df	Pr(>F)
Pillai	1	0.95080	45.09192	3	7	6.0316e-05 ***
Wilks	1	0.04920	45.09192	3	7	6.0316e-05 ***
Hotelling-Lawley	1	19.32511	45.09192	3	7	6.0316e-05 ***
Roy	1	19.32511	45.09192	3	7	6.0316e-05 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

There is a significant main effect of group ($p < 0.001$).

I suggest using Pillai's Trace because it is the most robust. Can use the same mean comparisons and effect size estimates we did with univariate approach.

Friedman Test

Nonparametric omnibus test for a 1-way repeated measures design. Let's perform this test on the previous example

```
install.packages("rstatix")
```

```
library(rstatix)
```

```
##
```

```
## Attaching package: 'rstatix'
```

```
## The following object is masked from 'package:MASS':
```

```
##
```

```
##      select
```

```
## The following objects are masked from 'package:effectsize':
```

```
##
```

```
##      cohens d, eta squared
```

Friedman Test

```
library(rstatix)
friedman_test(dv ~ treatment | subject, data=mydata)
```

```
## # A tibble: 1 x 6
##   .y.      n statistic    df      p method
## * <chr> <int>    <dbl> <dbl>    <dbl> <chr>
## 1 dv      10      19.5     3 0.000219 Friedman test
```

There is a significant main effect of group ($p < 0.001$). Can follow up with tests for Wilcoxon signed-rank and common language effect size.

2-Way Repeated Measures

General Linear Model (GLM)

Full Model: $Y_{ij} = \mu + \alpha_j + \beta_k + \pi_i + (\alpha\beta)_{jk} + (\alpha\pi)_{ji} + (\beta\pi)_{ki} + (\alpha\beta\pi)_{jki} + \epsilon_{ijk}$

For the various restricted models, we just drop terms the associated terms

- similar to what we did of the 2-way between level ANOVA
- see Maxwell, Delaney, Kelley for details (restricted, error, df)

2-Way Repeated Measures

Factor A	A1			A2		
Factor B	B1	B2	B3	B1	B2	B3
Subject 1	420	420	480	480	600	780
Subject 2	480	480	540	660	780	780
Subject 3	540	660	540	480	660	720
Subject 4	480	480	600	360	720	840
Subject 5	540	600	540	540	720	780

e.g., Is there an Influence of Sound Volume (Factor A) and Light Luminance (Factor B) cues on Reaction Time

2-Way - Univariate Approach

```
dv1 <- c(420,420,480,480,600,780,480,480,540,660,780,780,540,660,  
        540,480,660,720,480,480,600,360,720,840,540,600,540,540,720,  
        780)  
factorA <- factor(rep(c(rep(1,3),rep(2,3)),5))  
factorB <- factor(rep(c(1,2,3),10))  
subject1 <- factor(c(rep(1,6),rep(2,6),rep(3,6),  
                    rep(4,6),rep(5,6)))  
mydata1 <- data.frame(dv1, factorA, factorB, subject1)
```

2-Way - Univariate Approach

see next slide for full output

```
m1 <- aov(dv1 ~ factorA*factorB + Error(subject1/(factorA*factorB)),  
          data=mydata1)  
summary(m1)
```

```
##  
## Error: subject1  
##           Df Sum Sq Mean Sq F value Pr(>F)  
## Residuals  4  33600     8400  
##  
## Error: subject1:factorA  
##           Df Sum Sq Mean Sq F value Pr(>F)  
## factorA    1 147000  147000    17.5 0.0139 *  
## Residuals  4  33600     8400
```

2-Way - Univariate Approach

```
Error: subject1
      Df Sum Sq Mean Sq F value Pr(>F)
Residuals  4 33600      8400

Error: subject1:factorA
      Df Sum Sq Mean Sq F value Pr(>F)
factorA  1 147000  147000   17.5 0.0139 *
Residuals  4 33600      8400
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Error: subject1:factorB
      Df Sum Sq Mean Sq F value Pr(>F)
factorB  2 138480   69240   14.16 0.00235 **
Residuals  8 39120    4890
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Error: subject1:factorA:factorB
      Df Sum Sq Mean Sq F value Pr(>F)
factorA:factorB  2  67920    33960   11.67 0.00425 **
Residuals      8  23280     2910
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Significant Interaction between A and B ($p = 0.004$)

- Since there is a significant interaction, don't look at main effects (SAME RULES AS A 2-way between ANOVA!)

2-Way - Greenhouse Geisser Corrections

Reorganizing data

```
DV1 <- with(mydata1, cbind(dv1[(factorA==1 & factorB == 1)],  
                           dv1[(factorA==1 & factorB == 2)],  
                           dv1[(factorA==1 & factorB == 3)],  
                           dv1[(factorA==2 & factorB == 1)],  
                           dv1[(factorA==2 & factorB == 2)],  
                           dv1[(factorA==2 & factorB == 3)]))
```

DV1

##		[,1]	[,2]	[,3]	[,4]	[,5]	[,6]
##	[1,]	420	420	480	480	600	780
##	[2,]	480	480	540	660	780	780
##	[3,]	540	660	540	480	660	720
##	[4,]	480	480	600	360	720	840
##	[5,]	540	600	540	540	720	780

2-Way - Greenhouse Geisser Corrections

Defining the Design

```
FACTOR_A <- factor(c(rep(1,3),rep(2,3)))  
FACTOR_B <- factor(rep(c(1,2,3),2))  
design1 <- data.frame(FACTOR_A, FACTOR_B)  
design1
```

##	FACTOR_A	FACTOR_B
## 1	1	1
## 2	1	2
## 3	1	3
## 4	2	1
## 5	2	2
## 6	2	3

2-Way - Greenhouse Geisser Corrections

Multivariate, linear model.

```
mlm2 <- lm(DV1 ~ 1)
```

```
mlm2
```

```
##
```

```
## Call:
```

```
## lm(formula = DV1 ~ 1)
```

```
##
```

```
## Coefficients:
```

```
##           [,1]  [,2]  [,3]  [,4]  [,5]  [,6]
```

```
## (Intercept) 492   528   540   504   696   780
```

2-Way - Greenhouse Geisser Corrections

```
install.packages("car")
```

```
library(car)
```

```
mlm2.aov <- Anova(mlm2, idata=design1,  
                  idesign = ~FACTOR_A*FACTOR_B, type="III")
```


2-Way - Greenhouse Geisser Corrections

See next slide for full output

```
summary(mlm2.aov, multivariate=FALSE, univariate=TRUE)
```

```
## Warning in summary.Anova.mlm(mlm2.aov, multivariate = FALSE, univariate
```

```
## HF eps > 1 treated as 1
```

##

Univariate Type III Repeated-Measures ANOVA Assuming Sphericity

##

```
##          Sum Sq num Df Error SS den Df  F value    Pr(>F)
```

## (Intercept)	10443000	1	33600	4	1243.214	3.861e-06	**
----------------	----------	---	-------	---	----------	-----------	----

##	FACTOR_A	147000	1	33600	4	17.500	0.013881	*
----	----------	--------	---	-------	---	--------	----------	---

##	FACTOR_B	138480	2	39120	8	14.159	0.002354	**
----	----------	--------	---	-------	---	--------	----------	----

##	FACTOR_A:FACTOR_B						
67920	2	23280	8	11.670	0.004246	49*	



2-Way - Greenhouse Geisser Corrections

Univariate Type III Repeated-Measures ANOVA Assuming Sphericity

	Sum Sq	num Df	Error SS	den Df	F value	Pr(>F)
(Intercept)	10443000	1	33600	4	1243.214	3.861e-06 ***
FACTOR_A	147000	1	33600	4	17.500	0.013881 *
FACTOR_B	138480	2	39120	8	14.159	0.002354 **
FACTOR_A:FACTOR_B	67920	2	23280	8	11.670	0.004246 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Mauchly Tests for Sphericity

	Test statistic	p-value
FACTOR_B	0.76047	0.66317
FACTOR_A:FACTOR_B	0.96131	0.94254

Greenhouse-Geisser and Huynh-Feldt Corrections
for Departure from Sphericity

	GG eps	Pr(>F[GG])
FACTOR_B	0.80676	0.005291 **
FACTOR_A:FACTOR_B	0.96275	0.004857 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

	HF eps	Pr(>F[HF])
FACTOR_B	1.271242	0.002354093
FACTOR_A:FACTOR_B	1.838414	0.004245732

Sphericity not violated (Mauchly Test, $p > 0.05$). GG-corrected interaction significant ($p = 0.004857$)

2-Way - Multivariate Approach

See Partial Output on next page

```
summary(mlm2.aov, multivariate=TRUE, univariate=FALSE)
```

```
##  
## Type III Repeated Measures MANOVA Tests:  
##  
## -----  
##  
## Term: (Intercept)  
##  
## Response transformation matrix:  
##      (Intercept)  
## [1,]          1  
## [2,]          1
```

2-Way - Multivariate Approach

```
Multivariate Tests: FACTOR_A
      Df test stat approx F num Df den Df  Pr(>F)
Pillai      1  0.813953    17.5      1      4 0.013881 *
Wilks       1  0.186047    17.5      1      4 0.013881 *
Hotelling-Lawley 1  4.375000    17.5      1      4 0.013881 *
Roy         1  4.375000    17.5      1      4 0.013881 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Multivariate Tests: FACTOR_B
      Df test stat approx F num Df den Df  Pr(>F)
Pillai      1  0.868521  9.908686      2      3 0.047674 *
Wilks       1  0.131479  9.908686      2      3 0.047674 *
Hotelling-Lawley 1  6.605791  9.908686      2      3 0.047674 *
Roy         1  6.605791  9.908686      2      3 0.047674 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
Multivariate Tests: FACTOR_A:FACTOR_B
      Df test stat approx F num Df den Df  Pr(>F)
Pillai      1  0.849438  8.462687      2      3 0.058421 .
Wilks       1  0.150562  8.462687      2      3 0.058421 .
Hotelling-Lawley 1  5.641791  8.462687      2      3 0.058421 .
Roy         1  5.641791  8.462687      2      3 0.058421 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The multivariate approach suggests that there are only main effects of A ($p = 0.013$) and B ($p = 0.048$) on our dependent measure [Interaction ($p = 0.058$)]

2-Way - Multivariate Approach

Notes on Main Effect of A.

- We see sphericity tests for the main effect of factorB, and the factorA:factorB interaction effect.
- We don't see a test of the main effect of factorA
 - Because in this case, factorA has only two levels
 - and so there is no variances of differences-between-groups.
 - since there are only two levels, there is only a single variance of differences (between the two levels)

Different Results, What do you do?

The 2-way RM ANOVA (with and without GG corrections) suggested there was a significant interaction between factor A and B (as well as main effects), but the multivariate approach suggests there were ONLY main effects.

- Can justify that GG corrections were made and look at interactions
- Alternatively, go with the more conservative test and look at main effects (recommended)
 - replication crisis
- Ultimately you will have to justify your decisions in your paper and to reviewers.

Let's say we went with the conservative approach. Let's look at the mean comparisons for the main effects of A (sound) and B (light) on the DV (reaction time).

Main Effects of A (Sound)

Group all data sound 1 or sound 2 (ignore effect of light)

```
# sound1 vs sound2 --- group all data sound 1 or sound 2 (ignore effect of light)
sound1 = c(dv1[1:3],dv1[7:9],dv1[13:15], dv1[19:21], dv1[25:27])
sound2 = c(dv1[4:6],dv1[10:12],dv1[16:18], dv1[22:24], dv1[28:30])
t.test(sound1, sound2, paired = TRUE, alternative = "two.sided")$p.value
```

```
## [1] 0.001168222
```

There is a significant difference in reaction time between sound 1 and 2

Main Effects of B (Light)

Group all data light 1, 2, or 3 (ignore effect of sound)

```
# light1 vs light2 --- group all data light 1 or light 2 (ignore effect of sound)
light1 = c(dv1[1],dv1[4],dv1[7], dv1[10], dv1[13], dv1[16], dv1[19], dv1[22], dv1[25],dv1[28])
light2 = c(dv1[2],dv1[5],dv1[8], dv1[11], dv1[14], dv1[17], dv1[20], dv1[23], dv1[26],dv1[29])
light3 = c(dv1[3],dv1[6],dv1[9], dv1[12], dv1[15], dv1[18], dv1[21], dv1[24], dv1[27],dv1[30])
pval_l1v12 = t.test(light1, light2, paired = TRUE, alternative = "two.sided")$p.value
pval_l1v13 = t.test(light1, light3, paired = TRUE, alternative = "two.sided")$p.value
pval_l2v13 = t.test(light2, light3, paired = TRUE, alternative = "two.sided")$p.value
pvals = c(pval_l1v12, pval_l1v13, pval_l2v13)
p.adjust(pvals, method = "holm", n = length(pvals))
```

```
## [1] 0.03034858 0.06358186 0.66374348
```

There is a significant difference in reaction time between light 1 and 2

Note: You would also have to find effect sizes, test assumption, etc., as in the univariate example, but we'll stop here for today lecture.

Next Week

- Factorial (Between and Within) ANOVA