**PSYCH 710**

**Between-Subjects Factorial Designs**

**Main Effects & Interactions**

Prof. Patrick Bennett

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**Crossed-factorial designs**

- at least 2 independent variables/factors (A, B, C, etc.)
- each level of one factor combined with all levels of other factors
- balanced: equal n per cell/condition
- is variation among cell means “statistically significant”?
- is variation compatible with hypothesis that variation is due to chance?
- factorial ANOVA decomposes variation into main effects & interactions
  - main effect: effect associated with one factor
  - interaction: effect associated with combination of factors

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**Linear Model**

\[ Y_{ijk} = \mu + \alpha_j + \beta_k + (\alpha\beta)_{jk} + \epsilon_{ijk} \]

- intercept
- main effects
- interaction

<table>
<thead>
<tr>
<th>Factor A</th>
<th>B1</th>
<th>B2</th>
<th>B3</th>
</tr>
</thead>
<tbody>
<tr>
<td>A1</td>
<td>A1B1</td>
<td>A1B2</td>
<td>A1B3</td>
</tr>
<tr>
<td>A2</td>
<td>A2B1</td>
<td>A2B2</td>
<td>A2B3</td>
</tr>
<tr>
<td>A3</td>
<td>A3B1</td>
<td>A3B2</td>
<td>A3B3</td>
</tr>
<tr>
<td>A4</td>
<td>A4B1</td>
<td>A4B2</td>
<td>A4B3</td>
</tr>
</tbody>
</table>

---

**Main Effect of A**

\[ \hat{\mu}_j = \bar{Y}_j. \]

\[ \alpha_j = \mu_j - \mu. \]

\[ \bar{y}_j = \text{marginal row mean [average of cell means in row j]} \]

\[ \mu = \text{grand mean [all scores]} \]

\[ \sum_{j=1}^{n} \alpha_j = 0 \quad \text{df}_a = a-1 \]

---

**Marginal Row Means**

\[ \bar{Y}_1, \bar{Y}_2, \bar{Y}_3, \bar{Y}_4 \]
Main Effect of B

\[
Y_{ijk} = \mu + \alpha_j + \beta_k + (\alpha\beta)_{jk} + \epsilon_{ijk}
\]

\[
\beta_k = \mu_k - \mu.
\]

\[
\mu = \text{marginal column mean [average of cell means in column k]}
\]

\[
\mu_k = \bar{Y}_k.
\]

\[
\sum_{k=1}^{b} \beta_k = 0 \quad \text{df}_k = b-1
\]

Interaction Effects (A x B)

\[
Y_{ijk} = \mu + \alpha_j + \beta_k + (\alpha\beta)_{jk} + \epsilon_{ijk}
\]

\[
\sum_{j=1}^{a} (\alpha\beta)_{jk} = 0 \quad \text{for each value of } k
\]

\[
\sum_{k=1}^{b} (\alpha\beta)_{jk} = 0 \quad \text{for each value of } j
\]

Least-squares Estimates of Parameters

\[
Y_{ijk} = \mu + \alpha_j + \beta_k + (\alpha\beta)_{jk} + \epsilon_{ijk}
\]

\[
\alpha_j = \bar{Y}_j - \bar{Y}_. \\
\beta_k = \bar{Y}_k - \bar{Y}_. \\
(\alpha\beta)_{jk} = \bar{Y}_{jk} - (\bar{Y}_j - \bar{Y}_.) + (\bar{Y}_k - \bar{Y}_.)
\]

\[
\hat{Y}_{jk} = \hat{\bar{Y}}_j - \hat{\alpha}_j - \hat{\beta}_k
\]

\[
\text{degrees-of-freedom:} \\
\text{df}_k = (a-1) \\
\text{df}_b = (b-1) \\
\text{df}_{a:b} = (a-1)(b-1)
\]

Interpretation of Model

\[
Y_{ijk} = \mu + \alpha_j + \beta_k + (\alpha\beta)_{jk} + \epsilon_{ijk}
\]

\[
Y_{ijk} = Y_{ij} + \epsilon_{ijk}
\]

\[
Y_{ijk} = \mu + \alpha_j + \beta_k + (\alpha\beta)_{jk}
\]

\[
Y_{ijk} = \bar{Y}_{ij}
\]

\[
Y_{ijk} = \bar{Y}_{ij} + \epsilon_{ijk}
\]

anova breaks variation among cell means into 3 independent components:
variation due to A, variation due to B, and variation due to AxB

model has 1 + (a-1) + (b-1) + (a-1)(b-1) free parameters, or one for each cell mean
Evaluating Main Effect of A

Null Hypothesis
\[ a_1 = a_2 = \cdots = a_u = 0 \]
\[ \bar{Y}_1 = \bar{Y}_2 = \cdots = \bar{Y}_u \]

Nested Models
\[ Y_{ijk} = \mu + a_j + b_k + (a\beta)_{jk} + \epsilon_{ijk} \]
\[ Y_{ijk} = \mu + b_k + (a\beta)_{jk} + \epsilon_{ijk} \]
\[ Y_{ijk} = \mu + \epsilon_{ijk} \]

full model
reduced model
reduced model

Marginality
- lower-order effects are marginal to higher-order effects
  - main effects are marginal to 2-way their interactions
  - 2-way interactions are marginal to their 3-way interactions
  - linear interactions (x) are marginal to quadratic & cubic predictors (e.g., \( x^2, x^3 \))
- principle of marginality: linear models that include higher-order effects/predeators should not exclude the effects that are marginal to them
  - if a model includes A x B it should also include A and B
  - if a model includes \( x^2 \) it should also include \( x \)
- why? Because, in general, models that violate marginality are not invariant to changes in measurement units
  - http://pnb.mcmaster.ca/bennett/psy710/notes/mw7-marginality-example.html

Calculating Sum-of-Squares A (\( SS_A \))

Nested Models
\[ Y_{ijk} = \mu + a_j + (a\beta)_{jk} + \epsilon_{ijk} \]
\[ Y_{ijk} = \mu + (a\beta)_{jk} + \epsilon_{ijk} \]
\[ Y_{ijk} = \mu + \epsilon_{ijk} \]

full model
reduced model
[violates principle of marginality. Bad!]

SS\( _A \) is change in \( SS_{model} \) that occurs when all alphas are set to zero.
For balanced designs, SS\( _A \) is the same in all cases.

Marginality
http://pnb.mcmaster.ca/bennett/psy710/notes/mw7-marginality-example.html

ANOVARs are identical

http://pnb.mcmaster.ca/bennett/psy710/notes/mw7-marginality-example.html

both marginals obey marginality principle
Marginality

省内要与

ANOVA are NOT identical

\[ a < 4 + 0.5x \]

\[ b \times 2 \times 1 \]

both marginals violate marginality principle

Calculating Sum-of-Squares B (SSB)

### Nested Models

\[
Y_{ijk} = \mu + \alpha_j + (\alpha\beta)_{jk} + \epsilon_{ijk}
\]

**full model**

\[
Y_{ijk} = \mu + \alpha_j + \beta_k + \epsilon_{ijk}
\]

**reduced model**  [violates principle of marginality. Bad!]

\[
Y_{ijk} = \mu + \epsilon_{ijk}
\]

**reduced model**

\[
Y_{ijk} = \mu + \beta_k + \epsilon_{ijk}
\]

**full model (ignores A and AxB)**

\[
Y_{ijk} = \mu + \alpha_j + \epsilon_{ijk}
\]

**reduced model**

\[
Y_{ijk} = \mu + \alpha_j + \beta_k + \epsilon_{ijk}
\]

**full model (ignores AxB)**

SSB is change in SSResidual, that occurs when all betas are set to zero.
For balanced designs, SSB is the same in all cases.

Evaluating Main Effect of A

\[
\alpha_1 = \alpha_2 = \cdots = \alpha_a = 0
\]

\[
\bar{Y}_1 = \bar{Y}_2 = \cdots = \bar{Y}_a
\]

[null hypothesis]

\[
SS_A = E_F - E_E = \sum_{j=1}^{a} \sum_{i=1}^{n} \alpha_i^2
\]

\[
SS_{Residual} = E_F = \sum_{j=1}^{a} \sum_{k=1}^{b} \sum_{i=1}^{n} (Y_{ijk} - \bar{Y}_j)^2
\]

[calculated using full model]

\[
F_A = \frac{SS_A / (a - 1)}{SS_{Residual} / (ab(n - 1))}
\]

df = \{(a-1), ab(n-1)\}

Evaluating Main Effect of B

\[
\beta_1 = \beta_2 = \cdots = \beta_b = 0
\]

\[
\bar{Y}_1 = \bar{Y}_2 = \cdots = \bar{Y}_b
\]

[null hypothesis]

\[
SS_B = \sum_{k=1}^{b} \sum_{i=1}^{n} \beta_j^2
\]

\[
SS_{Residual} = E_F = \sum_{j=1}^{a} \sum_{k=1}^{b} \sum_{i=1}^{n} (Y_{ijk} - \bar{Y}_j)^2
\]

[calculated using full model]

\[
F_B = \frac{SS_B / (b - 1)}{SS_{Residual} / (ab(n - 1))}
\]

F_B = MSB / MSResidual

df = \{(b-1), ab(n-1)\}
Calculating Sum-of-Squares AxB (SS\textsubscript{AxB})

Nested Models

<table>
<thead>
<tr>
<th>Model</th>
<th>Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>Full model</td>
<td>$Y_{ijk} = \mu + \alpha_j + \beta_k + (\alpha\beta)<em>{jk} + \epsilon</em>{ijk}$</td>
</tr>
<tr>
<td>Reduced model</td>
<td>$Y_{ijk} = \mu + \alpha_j + \beta_k + \epsilon_{ijk}$</td>
</tr>
</tbody>
</table>

**SS\textsubscript{AxB}** is change in SS\textsubscript{residuals} that occurs when all interaction effects are set to zero.

Evaluating AxB Interaction

The null hypothesis for the main effect of

$$H_0: (\alpha\beta)_{12} = \cdots = (\alpha\beta)_{ab} = 0$$

is represented as

$$F = \frac{SS_{AB} / \text{(a-1)\text{(b-1)}}}{SS_{\text{Residuals}} / \text{(ab(n-1))}}$$

where

$$SS_{AB} = \sum_{j=1}^{a} \sum_{k=1}^{b} (\alpha\beta)_{jk}$$

and

$$SS_{\text{Residuals}} = \sum_{j=1}^{a} \sum_{k=1}^{b} \sum_{i=1}^{n} (Y_{ijk} - \bar{Y}_{jk})^2$$

ANOVA table

<table>
<thead>
<tr>
<th>Source</th>
<th>SS</th>
<th>df</th>
<th>MS</th>
<th>F</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>SS\textsubscript{A}</td>
<td>df\textsubscript{A} = a-1</td>
<td>MS\textsubscript{A} = SS\textsubscript{A}/df\textsubscript{A}</td>
<td>MS\textsubscript{A}/MS\textsubscript{W}</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>SS\textsubscript{B}</td>
<td>df\textsubscript{B} = b-1</td>
<td>MS\textsubscript{B} = SS\textsubscript{B}/df\textsubscript{B}</td>
<td>MS\textsubscript{B}/MS\textsubscript{W}</td>
<td></td>
</tr>
<tr>
<td>A x B</td>
<td>SS\textsubscript{AxB}</td>
<td>df\textsubscript{AxB} = (a-1)(b-1)</td>
<td>MS\textsubscript{AxB} = SS\textsubscript{AxB}/df\textsubscript{AxB}</td>
<td>MS\textsubscript{AxB}/MS\textsubscript{W}</td>
<td></td>
</tr>
<tr>
<td>Within Cell (residuals)</td>
<td>SS\textsubscript{W}</td>
<td>df\textsubscript{W} = ab(n-1)</td>
<td>MS\textsubscript{W} = SS\textsubscript{W}/df\textsubscript{W}</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Interpreting Interactions
**Interpreting AxB Interaction**

- Interaction effect is the difference between cell mean and the sum of the intercept & main effects:
  \[(\alpha \beta)_{ij} = \bar{Y}_{ij} - \mu - \alpha_j - \beta_k\]

- If interaction effects are zero, then differences among cell means are due to differences between alpha's and/or beta's (row & column effects).
- If interactions are not zero then effect of A depends on level of B (and effect of B depends on level of A).

**Graphical Depiction of AxB Interaction**

AxB interaction implies that the effect of A depends on the level of B, and the effect of B depends on the level of A.

\[ (A_1B_1 - A_1B_2) \neq (A_2B_1 - A_2B_2) \]
\[ (A_1B_1 - A_2B_1) \neq (A_1B_2 - A_2B_2) \]

**Interactions**

- 2-way (A x B) interactions assess whether the effect of one factor depends on the level of the other factor.
  - Does the effect of A depend on the level of B?
  - Does the effect of B depend on the level of A?

- 3-way (A x B x C) interactions assess whether the interaction between 2 factors depends on the level of the 3rd factor.
  - Does the AxB interaction depend on the level of C?
  - Does the AxC interaction depend on the level of B?
  - Does the BxC interaction depend on the level of A?

**Graphical representation of 2-way interactions**

Significant AxB interaction implies:
- Difference between a1 & a2 depends on level of B.
- Difference between b1 & b2 depends on level of A.

Significant 2-way interactions imply a significant deviation from parallelism.
Graphical representation of 3-way interactions

- Significant AxB interaction
- Non-significant AxBxC interaction

Significant 3-way interactions imply that the deviation from parallelism in a 2-way interaction depends on the level of the 3rd factor.

- Significant AxB interaction
- AxB interaction depends on level of C
- Significant AxB interaction in c2 but not c1

Incorrect Interpretations of Interactions

- Interaction determines if difference between 2 differences is significant
  - Is \((b_2 - b_1)\) at \(a_1\) minus \((b_2 - b_1)\) at \(a_2\) significantly different from zero?
- Not the same as doing separate tests of \((b_2 - b_1)\) at \(a_1\) and \((b_2 - b_1)\) at \(a_2\)
- Example: if t-test 1 is not significant but t-test 2 is significant, will AxB interaction be significant?
  - not necessarily...

Incorrect Interpretations of Interactions

- it often is interesting to find interactions
- But often they are "discovered" with faulty statistical methods

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Incorrect Interpretations of Interactions

• Suppose both tests are significant... does that mean that the effect of B does not depend on A?
  - i.e., that the AxB interaction is not significant?
  - not necessarily

both t-tests are significant and AxB interaction is not significant

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Incorrect Interpretations of Interactions

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  - i.e., that the AxB interaction is not significant?
  - not necessarily

both t-tests are not significant and AxB interaction is not significant

both t-tests are not significant and AxB interaction is significant

A x B ≠ Pairwise tests of differences

Knowing if AxB Interaction is significant does not inform us about pairwise tests.

Knowing if pairwise tests are significant does not inform us about AxB interaction.
Incorrect Interpretations of Interactions

Nieuwenhuis, Forstmann, & Wagenmakers, Nature Neurosci., 2011, 14, 1105-1107

- To determine if the effect of one variable depends on another...
  - e.g., if the effect of one variable differs between groups or ages or genders
- ...you need to assess the interaction between the 2 variables
- do not rely on significance tests performed separately on the different groups

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**R example**

### 7.6 an example

In this section I will illustrate how to analyze data collected in an experiment that used a balanced factorial design. There are two factors, A and B, and each factor has two levels. The dependent variable is denoted by \( y \). Finally, there are 6 scores per cell. Here is how I initialized R and created the fake data:

```r
> options(contrasts=c("contr.sum","contr.poly"))
> a<-rep(c(-1,-1,1,1),each=6)
> b<-rep(c(-1,-1,1,1),each=6)
> ab<-rep(c(-1,1,1,-1),each=6)
> y<-10+2*a+1*b+0.5*ab
> set.seed(123456);
> nz<-rnorm(y)
> y<-y+nz;
> af<-factor(a,labels=c("a1","a2"),ordered=F)
> bf<-factor(b,labels=c("b1","b2"),ordered=F)
> myData <- data.frame(y,af,bf)
> names(myData) <- c("y","A","B")
> myData

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>B</th>
</tr>
</thead>
<tbody>
<tr>
<td>a1</td>
<td>-1</td>
<td>-1</td>
</tr>
<tr>
<td>b1</td>
<td>-1</td>
<td>-1</td>
</tr>
<tr>
<td>a2</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>b2</td>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

---

**Sequential Sums of Squares**

```r
> lm.full.model <- lm(y ~ 1 + A + B + A:B, data=myData)
> anova(lm.full.model)
```

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>1</td>
<td>94.25</td>
<td>94.25</td>
<td>84.59</td>
<td>0.0000</td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td>23.21</td>
<td>23.21</td>
<td>20.83</td>
<td>0.0002</td>
</tr>
<tr>
<td>A:B</td>
<td>1</td>
<td>4.63</td>
<td>4.63</td>
<td>4.15</td>
<td>0.0550</td>
</tr>
<tr>
<td>Residuals</td>
<td>20</td>
<td>22.28</td>
<td>1.11</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Table 1: ANOVA table for full model.

\[
Y_{ijk} = \mu + \epsilon_{ijk}
\]

\[
Y_{ij} = \mu + \alpha_j + \epsilon_{ijk}
\]

\[
Y_{ij} = \mu + \alpha_j + \beta_k + \epsilon_{ijk}
\]

\[
Y_{ijk} = \mu + \alpha_j + \beta_k + (\alpha\beta)_{jk} + \epsilon_{ijk}
\]
Analysis of Variance Table

Model 1: y ~ 1
Model 2: y ~ 1 + A

<table>
<thead>
<tr>
<th>Res.Df</th>
<th>RSS</th>
<th>Df</th>
<th>Sum Sq</th>
<th>F</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>23</td>
<td>22</td>
<td>50.124</td>
<td>94.246</td>
<td>41.366</td>
</tr>
</tbody>
</table>

4.63 4.63 4.15 0.0550

---

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

Note that SS_A is the same value as the one listed in full ANOVA table.
F differs because the estimate of population error variance (the F's denominator) differs.

Analysis of Variance Table

Model 1: y ~ 1 + B
Model 2: y ~ 1 + A + B

<table>
<thead>
<tr>
<th>Res.Df</th>
<th>RSS</th>
<th>Df</th>
<th>Sum Sq</th>
<th>F</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>22</td>
<td>21</td>
<td>26.91</td>
<td>94.246</td>
<td>73.549</td>
</tr>
</tbody>
</table>

2.654e-08 ***

---

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

Note that SS_A is the same value as the one listed previously.
Again, F differs because the estimate of population error variance differs across comparisons.

---

SS_A obtained with a different comparison

Analysis of Variance Table

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>1</td>
<td>94.25</td>
<td>94.25</td>
<td>84.59</td>
<td>0.0000</td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td>23.21</td>
<td>23.21</td>
<td>20.63</td>
<td>0.0092</td>
</tr>
<tr>
<td>A:B</td>
<td>1</td>
<td>4.63</td>
<td>4.63</td>
<td>4.15</td>
<td>0.0550</td>
</tr>
<tr>
<td>Resid</td>
<td>20</td>
<td>22.28</td>
<td>1.11</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

A=94.25 B=23.21 A:B=4.63

Residuals 20 22.28

1

A=94.25 B=23.21 A:B=4.63

Residuals 20 22.28

1

SS_A computed with 4th comparison of nested models

- in theory, we could drop A from full model
  - full: y ~ 1 + A + B + A:B
  - reduced: y ~ 1 + B + A:B
  - SS_A = SS_resid
- However, this comparison does not work (easily)

R and Marginality

Analysis of Variance Table

Model 1: y ~ 1 + B + A:B
Model 2: y ~ 1 + A + B + A:B

<table>
<thead>
<tr>
<th>Res.Df</th>
<th>RSS</th>
<th>Df</th>
<th>Sum Sq</th>
<th>F</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>20</td>
<td>22</td>
<td>22.284</td>
<td>3.5527e-15</td>
<td></td>
</tr>
</tbody>
</table>

Notice that df hasn’t changed although we dropped A from model.
R and Marginality

> anova(lm.04)

Analysis of Variance Table

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1</td>
<td>10.467</td>
<td>10.467</td>
<td></td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td>22.083</td>
<td>22.083</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A:B</td>
<td>2</td>
<td>98.872</td>
<td>49.436</td>
<td>4.43e-08</td>
<td>***</td>
</tr>
<tr>
<td>Residuals</td>
<td>20</td>
<td>1.114</td>
<td>0.0555</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

R and Marginality

- R intentionally makes it difficult (though not impossible) to violate marginality
- later we will use drop1 command to evaluate models that violate marginality

alternatives to lm & aov

library(aftx)
N <- dim(myData)[1] # number of rows/subjects
myData$subj <- factor(x=1:N, labels = "s")
car.model.01 <- aov_car(y~1+A+B+A:B*Error(subject), data=myData)
ez.model.01 <- ez_model.01 <- ez_model(car.model.01) # this command gives same anova table as next line...

> dummy.coef(lm.full.model)

Full coefficients are
(Intercept): 10.46698
A: a1 a2
   b1     b2
  0.4390275 0.4900275 0.490275 -0.490275
B: b1 b2
   0.9834858 0.9834858
A:B: a1:b1 a2:b1 a1:b2 a2:b2
  -2.420677 -1.542622 2.420677 1.542622

> dummy.coef(lm.04)

Full coefficients are
(Intercept): 10.46698
A: b1 b2
   b1
  -0.9834858
B: b1 b2
   0.9834858
A:B: a1:b1 a2:b1 a1:b2 a2:b2
  -2.420677 -1.542622 2.420677 1.542622

R and Marginality

> anova(lm.04, lm.full.model)

LM.04 <- lm(y~1+B+A:B, data=myData)

> anova(LM.04)

Analysis of Variance Table

<table>
<thead>
<tr>
<th></th>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>(Intercept)</td>
<td>1</td>
<td>10.467</td>
<td>10.467</td>
<td></td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td>22.083</td>
<td>22.083</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A:B</td>
<td>2</td>
<td>98.872</td>
<td>49.436</td>
<td>4.43e-08</td>
<td>***</td>
</tr>
<tr>
<td>Residuals</td>
<td>20</td>
<td>1.114</td>
<td>0.0555</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

SS A,partial = 22.083
SS B,partial = 10.467
SS AB,partial = 98.872

F values:

<table>
<thead>
<tr>
<th>Effect</th>
<th>df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>1</td>
<td>22.083</td>
<td>22.083</td>
<td></td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td>10.467</td>
<td>10.467</td>
<td></td>
<td></td>
</tr>
<tr>
<td>A:B</td>
<td>2</td>
<td>98.872</td>
<td>49.436</td>
<td>4.43e-08</td>
<td>***</td>
</tr>
</tbody>
</table>

partial omega squared

<table>
<thead>
<tr>
<th>Effect</th>
<th>df</th>
<th>SS</th>
<th>Omega sq</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>1</td>
<td>22.083</td>
<td>0.1</td>
</tr>
<tr>
<td>B</td>
<td>1</td>
<td>10.467</td>
<td>0.05</td>
</tr>
<tr>
<td>A:B</td>
<td>2</td>
<td>98.872</td>
<td>0.7</td>
</tr>
</tbody>
</table>

The bottom line is that R intentionally makes it difficult for you to construct and compare models that violate the marginality principle.
Analyzing a Significant Main Effect

### Tukey HSD [all pairs of marginal means]

```r
TukeyHSD(mw.aov.02,which="drug")
```

<table>
<thead>
<tr>
<th>Tukey mult comparisons of means</th>
</tr>
</thead>
<tbody>
<tr>
<td>95% family-wise confidence level</td>
</tr>
<tr>
<td>Fit: aov(formula = score ~ drug * biofeedback, data = mw75)</td>
</tr>
<tr>
<td>$drug$ diff lwr upr p adj</td>
</tr>
<tr>
<td>drugf-drugx 18.1 3.09063 33.11 0.0150</td>
</tr>
<tr>
<td>drug2-drugx 16.1 0.90063 30.11 0.0484</td>
</tr>
<tr>
<td>drugf-drugy -3.0 -18.00987 12.01 0.8724</td>
</tr>
</tbody>
</table>

### Analyzing a Significant Main Effect

#### Tukey HSD [all pairs of marginal means]

```r
TukeyHSD(mw.aov.02,which="drug")
```

- fungible-drugx 18.1 3.09063 33.11 0.0150
- fungible-drugy -3.0 -18.00987 12.01 0.8724

#### Analyzing a Significant Main Effect

```
> mw.aov.01 <- aov(score~drug*biofeedback,data=mw75)
> summary(mw.aov.01)
```

<table>
<thead>
<tr>
<th>Df</th>
<th>Sum Sq</th>
<th>Mean Sq</th>
<th>F value</th>
<th>Pr(&gt;F)</th>
</tr>
</thead>
<tbody>
<tr>
<td>drug</td>
<td>2.00</td>
<td>1882.07</td>
<td>941.03</td>
<td>5.21</td>
</tr>
<tr>
<td>biofeedback</td>
<td>1.00</td>
<td>1904.03</td>
<td>1904.03</td>
<td>10.54</td>
</tr>
<tr>
<td>drug*biofeedback</td>
<td>2.00</td>
<td>1248.07</td>
<td>624.03</td>
<td>3.46</td>
</tr>
<tr>
<td>Residuals</td>
<td>24.00</td>
<td>4334.80</td>
<td>180.62</td>
<td></td>
</tr>
</tbody>
</table>

Table 3: ANOVA for biofeedback experiment.
Example (section 7.11 in course notes)

```r
> mw11.lm.01 <- lm(score ~ 1 + gf + tf + gf:tf, data = mw11)
> anova(mw11.lm.01)
```

```
Analysis of Variance Table

Response: score

  Df Sum Sq Mean Sq  F value    Pr(>F)
gf    1 1638.0 1638.0 0.00600 0.9394
tf    1 244.0  244.0 1.386e+01 0.2102
gf:tf 1  7.0   7.0 7.081e-02 0.3907
Residuals 36 5680.0 157.78

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```r
> MS.u <- 157.8
> df.u <- 36
```

```
R^2_{partial} = SS(gf) / SS(Drug) = 1638/11882 = 0.87
R^2_{effect size} = SS(gf) / SS(Total) = 1638/9369 = 0.17
```

```
summary(mw.aov.02,split=list(drug=list(1,2)))
```

```
##         Df Sum Sq Mean Sq  F value    Pr(>F)
## drug     2  1882.6  941.3 5.211e-01
## drug:C1  1  1638.0 1638.0 0.00600 0.9394
## biofeedback  1  190.4 190.4 1.056e-02
## drug:biofeedback  2  1248.0 624.0 3.448e-01
## drug:biofeedback:C1  1  1110.0 1110.0 6.155e-02
## drug:biofeedback:C2  1   38.0  38.0 7.780e-02
## Residuals 36 5680.0 157.78

Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
R^2_{partial} = SS(gf) / SS(Drug x Bio) = 1110/1248 = 0.89
R^2_{effect size} = SS(gf) / SS(Total) = 1110/9369 = 0.12
```

```
deckomposing an interaction
```

```
simple main effects
```

Example Table 7.11 in Textbook

```
interaction.plot(x.factor=mw11$gf, trace.factor=mw11$tf, response=mw11$score, trace.label="task")
```

```
illustration of group x task interaction
```

```
analyze simple main effect of task in each group
```

```
decomposing an interaction
```

```
simple main effects
```
Simple Main Effect of Task

1) Analyze task within each group:

> lm.task.hunt <- lm(score ~ 1 + tf, data = subset(mw11, gf == "huntingtons"))
> lm.task.amnestic <- lm(score ~ 1 + tf, data = subset(mw11, gf == "amnestic"))
> lm.task.control <- lm(score ~ 1 + tf, data = subset(mw11, gf == "control"))

2) Print ANOVA table:

> anova(lm.task.hunt)
Analysis of Variance Table
Response: score
                      Df Sum Sq Mean Sq  F value    Pr(>F)
tf                        2    9250   4625.0 29.3650 2.385e-05 ***
Residuals                12   1890   157.5
Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

3) Recalculate F & P values:

> (F.task.hunt <- 4625/MS.w)
[1] 29.30925
> (p.task.hunt <- 1 - pf(F.task.hunt, df1 = 2, df2 = df.w))
[1] 2.791744e-08

Finally, we print the anova table for each model, extract the appropriate columns, and compute Tukey HSD between the three group means.

```r
library(emmeans)
mw11.em <- emmeans(mw11.lm.01, specs = "tf|g") # note the formula
joint_tests(mw11.em, by="g") # simple main effect of task for each group
```

Tukey HSD applied to Simple Main Effect (emmeans)

```r
library(emmeans)
mw11.em <- emmeans(mw11.lm.01, specs = "tf|g") # note the formula
pairs(mw11.em) # tukey adjustment used by default
```

Decomposing an interaction

First, we decompose the interaction contrasts:

```r
# df = amnestic:
## contrast estimate SE df t.ratio p.value
## grammar-classification -10 7.94 36 -1.259 0.2473
## grammar-recognition -9 7.94 36 -0.929 0.3605
## classification-recognition 3 7.94 36 0.329 0.7430
#
# df = huntingtons:
## contrast estimate SE df t.ratio p.value
## grammar-classification -7 7.94 36 -0.829 0.4124
## grammar-recognition -6 7.94 36 -0.993 <.0001
## classification-recognition -3 7.94 36 -0.359 0.7246
#
# df = control:
## contrast estimate SE df t.ratio p.value
## grammar-classification 0 7.94 36 0.000 1.0000
## grammar-recognition -15 7.94 36 -1.988 0.1667
## classification-recognition -15 7.94 36 -1.988 0.1667
#
# P value adjustment: tukey method for comparing a family of 3 estimates
```

Decomposing an interaction
evaluating specific interactions

- often an experimenter expects an interaction
  - a particular sub-effect on one factor to vary across levels of other factor
  - Example: predictions for task x group interaction
    - Task sub-effect: difference between implicit & explicit memory tasks
    - task contrast = (0.5*grammar + 0.5*classification) - (1*recognition) ≠ 0
    - prediction: task contrast differs between Amnesic & Huntington's patients
    - Amnesic patients have deficits on explicit, not implicit, memory tasks
    - Huntington's patients have deficits on implicit, not explicit, memory tasks
    - Task Contrast\textsubscript{Amnesic} - Task Contrast\textsubscript{Huntington's} ≠ 0

creating interaction contrast weights

derive weights to determine if implicit/explicit contrast differs between Amnesic & Huntington's groups

<table>
<thead>
<tr>
<th>weights for task contrast</th>
</tr>
</thead>
<tbody>
<tr>
<td>Grammar</td>
</tr>
<tr>
<td>0.5</td>
</tr>
</tbody>
</table>

weights for group contrast

<table>
<thead>
<tr>
<th>weights for group contrast</th>
</tr>
</thead>
<tbody>
<tr>
<td>Amnesic</td>
</tr>
<tr>
<td>1</td>
</tr>
</tbody>
</table>

creating interaction contrast weights

derive weights to determine if implicit/explicit contrast differs between Amnesic & Huntington's groups

<table>
<thead>
<tr>
<th>Grammar</th>
<th>Classification</th>
<th>Recognition</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.5</td>
<td>0.5</td>
<td>-1</td>
</tr>
</tbody>
</table>

interaction contrast

cell weight = row x column

$R^2_{\text{effect}} = \frac{SS_{\text{contrast}}}{SS_{\text{total}}} = \frac{4594}{(5250+5250+5000+5680)} = 0.217$

$R^2_{\text{alerting}} = \frac{SS_{\text{contrast}}}{SS_{\text{interaction}}} = \frac{4594}{(5000)} = 0.919$

almost all of the interaction is accounted for by our contrast
alternative method

apply contrast to 1-way layout of our 2x3 design

creating interaction contrast weights
derive weights to determine if implicit/explicit contrast differs between Amnesic & Huntington's groups

<table>
<thead>
<tr>
<th>Cell</th>
<th>task</th>
<th>group</th>
<th>task x group</th>
</tr>
</thead>
<tbody>
<tr>
<td>Amnesic-Grammar</td>
<td>0.5</td>
<td>1</td>
<td>0.5</td>
</tr>
<tr>
<td>Amnesic-Classification</td>
<td>0.5</td>
<td>1</td>
<td>0.5</td>
</tr>
<tr>
<td>Amnesic-Recog</td>
<td>-1</td>
<td>1</td>
<td>-1</td>
</tr>
<tr>
<td>Huntington's - Grammar</td>
<td>0.5</td>
<td>-1</td>
<td>-0.5</td>
</tr>
<tr>
<td>Huntington's - Classification</td>
<td>0.5</td>
<td>-1</td>
<td>-0.5</td>
</tr>
<tr>
<td>Huntington's - Recog</td>
<td>-1</td>
<td>-1</td>
<td>1</td>
</tr>
<tr>
<td>Control - Grammar</td>
<td>0.5</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Control - Classification</td>
<td>0.5</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Control - Recog</td>
<td>-1</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

interaction contrast
(convert 2-way factorial to 1-way design)

interaction contrast with emmeans

$$R^2_{effect} = \frac{SS_{contrast}}{SS_{total}} = \frac{4594}{(15500+5680)} = 0.217$$