PSYCH 710

Between-Subjects Factorial Designs
Higher-Order Interactions & Unbalanced Designs

Prof. Patrick Bennett

ANOVA example

3 x 3 factorial ANOVA

omnibus F tests

aov, aov_car, aov_ez

```
> options(contrasts=c("contr.sum","contr.poly"))
> load(url("http://pnb.mcmaster.ca/bennett/psy710/datasets/2-way-data.rda") )
> sapply(df0,class)
  subject     group      task         Y
 "factor"  "factor"  "factor" "numeric"
> xtabs(~group+task,df0)
     task
group t1 t2 t3
   g1 10 10 10
   g2 10 10 10
   g3 10 10 10
```

3 factors & 1 numeric variable

balanced factorial design

```
> summary(df0)
      subject     group     task           Y         
 s1      : 1   g1:30   t1:30   Min.   : 29.59  
 s2      : 1   g2:30   t2:30   1st Qu.: 80.68  
 s3      : 1   g3:30   t3:30   Median : 99.73  
 s4      : 1                   Mean   : 98.67  
 s5      : 1                   3rd Qu.:120.73  
 s6      : 1                   Max.   :164.22  
 (Other):84                                     
```

subject IDs

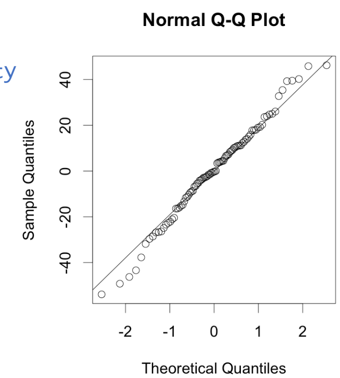
2 factors with 3 levels

```
> aov.01 <- aov(Y~group*task,df0)
> summary(aov.01)
             Df Sum Sq Mean Sq F value   Pr(>F)    
group         2  14689    7345  14.978 2.92e-06 ***
task          2   1666     833   1.698   0.1895    
group:task    4   9179    2295   4.680   0.0019 ** 
Residuals    81  39719     490                     
```

significant main effect of group & group:task interaction

check normality

```
> shapiro.test(residuals(aov.01)) # normality

Shapiro-Wilk normality test
data:  residuals(aov.01)
W = 0.9893, p-value = 0.6794

> qqnorm(residuals(aov.01))
> qqline(residuals(aov.01))
```



check constant-variance assumption

```
> df0$condition <- interaction(df0$group,df0$task)

> class(df0$condition)
[1] "factor"

> levels(df0$condition)
[1] "g1.t1" "g2.t1" "g3.t1"…
> bartlett.test(Y~condition,df0) # constant variance

Bartlett test of homogeneity of variances
data:  Y by condition
Bartlett's K-squared = 5.0176, df = 8, p-value = 0.7557
```

alternatives to lm & aov

aov_car

```
> library(afex)
> car.01 <- aov_car(Y~group*task+Error(subject),data=df0)
> summary(car.01) # this lists anova table
Anova Table (Type 3 tests)

Response: Y
           num Df den Df    MSE       F      ges    Pr(>F)    
group           2     81 490.36 14.9781 0.269982 2.917e-06 ***
task            2     81 490.36  1.6983 0.040245  0.189452    
group:task      4     81 490.36  4.6799 0.187724  0.001895 ** 

> # anova(car.01) # same as summary()
> # nice(car.01,es="pes") # anova table with partial-eta-squared (pes)
> # nice(car.01,es="ges") # anova table with generalized-eta-squared (ges)
```

alternative to lm & aov

aov_ez

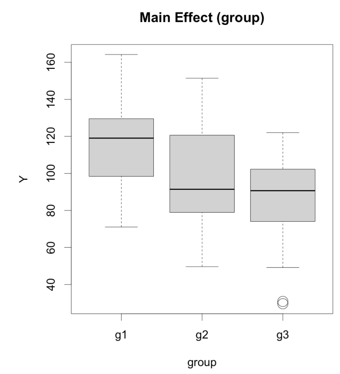
```
> library(afex)
> ez.01 <- aov_ez(id="subject",dv="Y",between=c("group","task"),data=df0)
> summary(ez.01)
Anova Table (Type 3 tests)

Response: Y
           num Df den Df    MSE       F      ges    Pr(>F)    
group           2     81 490.36 14.9781 0.269982 2.917e-06 ***
task            2     81 490.36  1.6983 0.040245  0.189452    
group:task      4     81 490.36  4.6799 0.187724  0.001895 ** 
```

decompose a main effect

(usually not wise to do this when interaction is significant)

decompose main effect of group

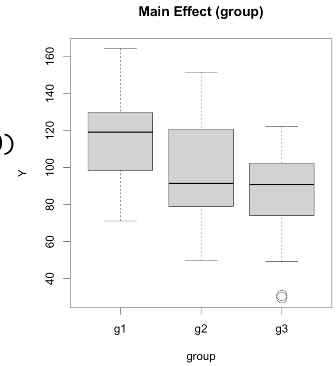
```
> aov.01 <- aov(Y~group*task,df0)
> summary(aov.01)
            Df Sum Sq Mean Sq F value   Pr(>F)
group        2  14689    7345  14.978 2.92e-06
task         2   1666     833   1.698   0.1895
group:task   4   9179    2295   4.680   0.0019
Residuals   81  39719     490
> boxplot(Y~group,df0,
+         main="Main Effect (group)")
```



decompose main effect of group

Tukey HSD

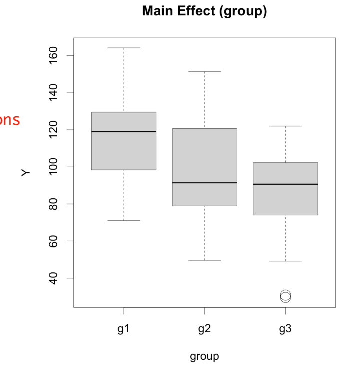
```
> TukeyHSD(aov.01,which="group")
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = Y ~ group*task,data = df0)

$group
        diff    lwr     upr    p adj
g2-g1 -21.175 -34.82  -7.524 0.0011
g3-g1 -30.541 -44.19 -16.890 0.0000
g3-g2  -9.366 -23.01   4.284 0.2356
```



decompose main effect of group

linear contrast

```
> levels(df0$group)
[1] "g1" "g2" “g3"
> myC <- c(1,-1/2,-1/2)
> library(emmeans)
> aov.emm <- emmeans(aov.01,specs="group")
NOTE: Results may be misleading due to involvement in interactions

> cres <- contrast(aov.emm,
+            method=list(T1vsT2_T3=myC))

> summary(cres,adjust="scheffe",scheffe.rank=2)
 contrast  estimate   SE df   t      p.value
 T1vsT2_T3     25.9 4.95 81   5.22   <.0001
Results are averaged over the levels of: task
P value adjustment: scheffe method with rank 2
```



decompose an interaction

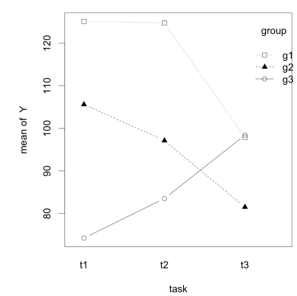
simple main effects

simple main effects

simple main effect of task at g1

```
> MS.resid <- 490 # from original ANOVA
> df.resid <- 81 # from original ANOVA
> aov.task.g1 <- aov(Y~task,
+                data=subset(df0,group=="g1"))

> summary(aov.task.g1)
            Df Sum Sq Mean Sq F value  Pr(>F)
task         2   4877    2438   8.075 0.00178
Residuals   27   8153     302

> (F.task <- 2438/MS.resid)
[1] 4.97551
> (p.task <- 1-pf(F.task,2,df.resid))
[1] 0.009160864
```

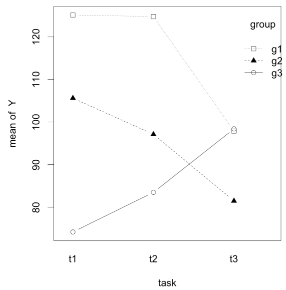
```
> with(df0, interaction.plot(task,
+          group,
+          Y,
+          type="b",
+          fixed=TRUE,
+          pch=c(0,17,1)))
```



analyze sub-effect in a simple main effect

decompose task-in-g1 with 2 contrasts

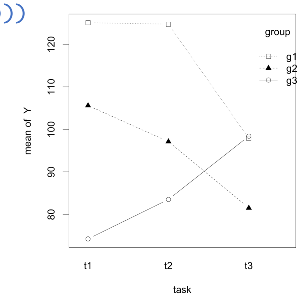
```
> levels(df0$task)
[1] "t1" "t2" "t3"
> T3vsT1T2 <- c(1/2,1/2,-1)
> T1vsT2 <- c(-1,1,0)
> # sum(T3vsT1T2*T1vsT2) # orthogonal
> contrasts(df0$task) <- cbind(T3vsT1T2,T1vsT2)
```



analyze sub-effect in simple main effect

decompose task-in-g1 simple main effect with 2 contrasts

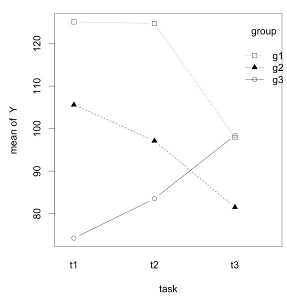
```
> aov.task.g1.02 <- aov(Y~task,data=subset(df0,group=="g1"))
> summary(aov.task.g1.02,
         split=list(task=list(T3vsT1T2=1,T1vsT2=2)))
                  Df    SS      MS      F       Pr(>F)
task               2    4877    2439    8.075   0.002
  task: T3vsT1T2   1    4876    4876   16.148  <0.001
  task: T1vsT2     1       1       1    0.002   0.964
Residuals         27    8153     302

> ( F.T3vsT1T2 <- 4876/MS.resid )
[1] 9.951
> ( p.T3vsT1T2 <- 1-pf(F.T3vsT1T2,1,df.resid) )
[1] 0.002
```



simple main effects

simple main effect of task at g2

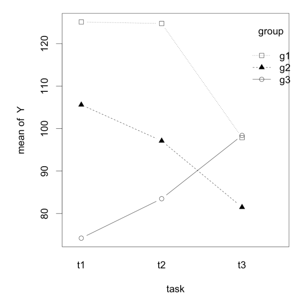
```
> MS.resid <- 490 # from original ANOVA
> df.resid <- 81 # from original ANOVA
> aov.task.g2 <- aov(Y~task,
+             data=subset(df0,group=="g2"))
> summary(aov.task.g2)
            Df Sum Sq Mean Sq F value Pr(>F)
task         2   2991  1495.7   2.301  0.119
Residuals   27  17552   650.1

> (F.task <- 1495.7/MS.resid)
[1] 3.0524
> (p.task <- 1-pf(F.task,2,df.resid))
[1] 0.0527
```



simple main effects

simple main effect of task at g3

```
> MS.resid <- 490 # from original ANOVA
> df.resid <- 81 # from original ANOVA
> aov.task.g3 <- aov(Y~task,
+             data=subset(df0,group=="g3"))
> summary(aov.task.g3)
            Df    SS      MS     F      Pr(>F)
task         2    2976    1488   2.867  0.0743
Residuals   27   14014     519

> (F.task <- 1488/MS.resid)
[1] 3.036
> (p.task <- 1-pf(F.task,2,df.resid))
[1] 0.053
```

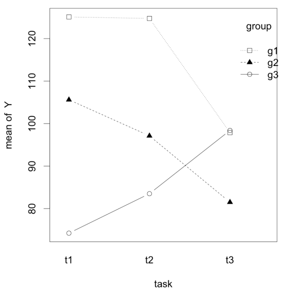


using emmeans

simple main effects

using joint_tests in emmeans

```
> library(emmeans)
> # note formula
> aov.01.emm <- emmeans(aov.01,specs=~task|group)
> joint_tests(aov.01.emm,by="group")
group = g1:
 model term df1 df2 F.ratio p.value
 task         2  81   4.973  0.0092
group = g2:
 model term df1 df2 F.ratio p.value
 task         2  81   3.050  0.0528
group = g3:
 model term df1 df2 F.ratio p.value
 task         2  81   3.035  0.0536
```

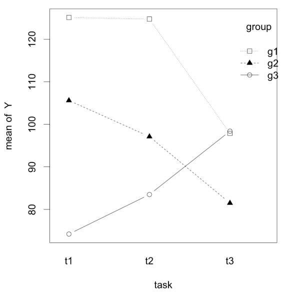


N.B. joint_tests uses error term from overall ANOVA

pairwise tests within each level

using pairs in emmeans

```
> aov.01.emm <- emmeans(aov.01,specs=~task|group)
> pairs(aov.01.emm) # tukey adjustment by default
group = g1:
 contrast estimate  SE df t.ratio p.value
 t1 - t2     0.356 9.9 81   0.036  0.9993
 t1 - t3    27.224 9.9 81   2.749  0.0199
 t2 - t3    26.868 9.9 81   2.713  0.0220
group = g2:
 contrast estimate  SE df t.ratio p.value
 t1 - t2     8.489 9.9 81   0.857  0.6687
 t1 - t3    24.111 9.9 81   2.435  0.0446
 t2 - t3    15.622 9.9 81   1.577  0.2612
group = g3:
 contrast estimate  SE df t.ratio p.value
 t1 - t2    -9.288 9.9 81  -0.938  0.6180
 t1 - t3   -24.182 9.9 81  -2.442  0.0438
 t2 - t3   -14.894 9.9 81  -1.504  0.2944
P value adjustment: tukey method for comparing a family of 3 estimates
```



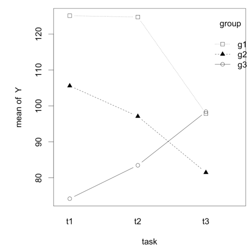
decompose an interaction

interaction contrasts

interaction contrast

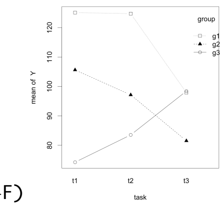
does task-contrast differ across groups?

```
> # interaction contrast
> levels(df0$task)
[1] "t1" "t2" “t3"
> T3vsT1T2 <- c(1/2,1/2,-1)
> T1vsT2 <- c(-1,1,0)

> levels(df0$group)
[1] "g1" "g2" "g3"
> G3vsG1G2 <- c(1/2,1/2,-1)
> G1vsG2 <- c(1,-1,0)

> contrasts(df0$task) <- cbind(T3vsT1T2,T1vsT2)
> contrasts(df0$group) <- cbind(G3vsG1G2,G1vsG2)
```



interaction contrast

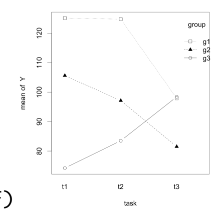
does task contrast differ across groups?



```
> aov.10 <- aov(Y~group*task,data=df0)
> summary(aov.10,
+         split=list(task=list(T3vsT1T2=1,T1vsT2=2),
+                    group=list(G3vsG1G2=1,G1vsG2=2)))
                             Df    SS    MS     F Pr(>F)
group                         2 14689  7345 14.98 <.001
  group: G3vsG1G2             1  7964  7964 16.24 <.001
  group: G1vsG2               1  6726  6726 13.72 <.001
task                          2  1666   833  1.69 0.189
  task: T3vsT1T2              1  1665  1665  3.39 0.069
  task: T1vsT2                1     0     0  0.00 0.979
group:task                    4  9179  2295  4.68 0.001
  group:task: G3vsG1G2.T3vsT1T2 1  8216  8216 16.75 <.001
  group:task: G1vsG2.T3vsT1T2 1   172   172  0.35 0.555
  group:task: G3vsG1G2.T1vsT2 1   627   627  1.28 0.261
  group:task: G1vsG2.T1vsT2   1   165   165  0.34 0.563
Residuals                    81 39719   490
```

interaction contrast

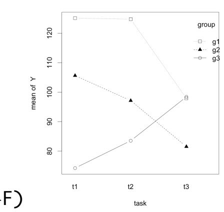
does task contrast differ across groups?



```
> aov.10 <- aov(Y~group*task,data=df0)
> summary(aov.10,
+         split=list(task=list(T3vsT1T2=1,T1vsT2=2),
+                    group=list(G3vsG1G2=1,G1vsG2=2)))
                             Df    SS    MS     F Pr(>F)
group                         2 14689  7345 14.98 <.001
  group: G3vsG1G2             1  7964  7964 16.24 <.001
  group: G1vsG2               1  6726  6726 13.72 <.001
task                          2  1666   833  1.69 0.189
  task: T3vsT1T2              1  1665  1665  3.39 0.069
  task: T1vsT2                1     0     0  0.00 0.979
group:task                    4  9179  2295  4.68 0.001
  group:task: G3vsG1G2.T3vsT1T2 1  8216  8216 16.75 <.001
  group:task: G1vsG2.T3vsT1T2 1   172   172  0.35 0.555
  group:task: G3vsG1G2.T1vsT2 1   627   627  1.28 0.261
  group:task: G1vsG2.T1vsT2   1   165   165  0.34 0.563
Residuals                    81 39719   490
```

interaction contrast

does task contrast differ across groups?

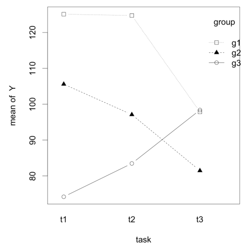


```
> aov.10 <- aov(Y~group*task,data=df0)
> summary(aov.10,
+         split=list(task=list(T3vsT1T2=1,T1vsT2=2),
+                    group=list(G3vsG1G2=1,G1vsG2=2)))
                             Df    SS    MS     F Pr(>F)
group                         2 14689  7345 14.98 <.001
  group: G3vsG1G2             1  7964  7964 16.24 <.001
  group: G1vsG2               1  6726  6726 13.72 <.001
task                          2  1666   833  1.69 0.189
  task: T3vsT1T2              1  1665  1665  3.39 0.069
  task: T1vsT2                1     0     0  0.00 0.979
group:task                    4  9179  2295  4.68 0.001
  group:task: G3vsG1G2.T3vsT1T2 1  8216  8216 16.75 <.001
  group:task: G1vsG2.T3vsT1T2 1   172   172  0.35 0.555
  group:task: G3vsG1G2.T1vsT2 1   627   627  1.28 0.261
  group:task: G1vsG2.T1vsT2   1   165   165  0.34 0.563
Residuals                    81 39719   490
```

interaction contrast

does task contrast differ across groups?

```
group:task                         4   9179    2295    4.68 0.001
  group:task: G3vsG1G2.T3vsT1T2    1   8216    8216   16.75 <.001
  group:task: G1vsG2.T3vsT1T2      1    172     172    0.35 0.555
Residuals                         81  39719     490
```



- T3vsT1T2 compares Task 3 to average of Tasks 1 & 2
  - compute value of this contrast (PSI) for each group
- 1st interaction contrast compares value of T3vsT1T2 in Group 3 to the average of the values in Groups 1 & 2: it is significant
- 2nd interaction contrast compares the value of the T3vsT1T2 contrast in Group 1 to the value in Group 2: it is NOT significant

interaction contrast

contrast (psi) = weighted sum of cell means

contrast weights

		Task		
		1/2	1/2	-1
g1	1/2	1/4	1/4	-1/2
g2	1/2	1/4	1/4	-1/2
g3	-1	-1/2	-1/2	1

cell means

		Task		
		1/2	1/2	-1
g1	1/2	125.1	124.7	97.9
g2	1/2	105.6	97.1	81.5
g3	-1	74.2	83.5	93.4

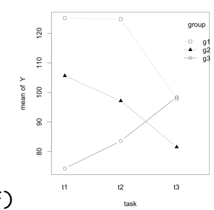
$$\Psi = 42.99 = \frac{1}{4}(125.1) + \frac{1}{4}(124.7) - \frac{1}{2}(97.9) + \frac{1}{4}(105.6) + \frac{1}{4}(97.1) - \frac{1}{2}(81.5) - \frac{1}{2}(74.2) - \frac{1}{2}(83.49) + 1(98.4)$$

```
> n <- 10
> ( SS.contrast <- n*(psi^2) / (sum(t.x.g^2)) )
[1] 8216
> ( F.contrast <- SS.contrast/MS.resid )
[1] 16.76
```

$$SS_{contrast} = \frac{n\Psi^2}{\sum_i^a w_i^2}$$

interaction contrast

does task contrast differ across groups?




```
> aov.10 <- aov(Y~group*task,data=df0)
> summary(aov.10,
+         split=list(task=list(T3vsT1T2=1,T1vsT2=2),
+                    group=list(G3vsG1G2=1,G1vsG2=2)))
                             Df  SS      MS    F     Pr(>F)
group                         2  14689   7345  14.98 <.001
  group: G3vsG1G2             1   7964   7964  16.24 <.001
  group: G1vsG2               1   6726   6726  13.72 <.001
task                          2   1666    833   1.69 0.189
  task: T3vsT1T2              1   1665   1665   3.39 0.069
  task: T1vsT2                1      0      0   0.00 0.979
group:task                    4   9179   2295   4.68 0.001
  group:task: G3vsG1G2.T3vsT1T2 1 8216   8216  16.75 <.001
  group:task: G1vsG2.T3vsT1T2 1    172    172   0.35 0.555
  group:task: G3vsG1G2.T1vsT2 1    627    627   1.28 0.261
  group:task: G1vsG2.T1vsT2   1    165    165   0.34 0.563
Residuals                    81  39719    490
```

3-way ANOVAs

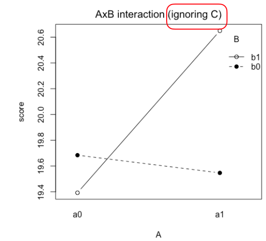
analyzing 2- and 3-way interactions in three-way factorial designs

2-way interactions

A x B interaction in an A x B x C factorial design

2 x 2 x 2 ANOVA example

```
> load(url("http://pnb.mcmaster.ca/bennett/psy710/datasets/aov-3way-data.rda"))
> aov.01 <- aov(score~A*B*C,data=myDf09)
> anova(aov.01)

Analysis of Variance Table
Response: score
           Df     SS     MS      F  Pr(>F)
A           1  9.395  9.395  9.329 0.0028
B           1  4.935  4.935  4.900 0.0288
C           1  0.261  0.261  0.259 0.6115
A:B         1 14.578 14.578 14.475 0.0002
A:C         1  0.014  0.014  0.014 0.9053
B:C         1  0.733  0.733  0.728 0.3953
A:B:C       1  0.000  0.000  0.000 0.9877
Residuals 112 112.79  1.007
```



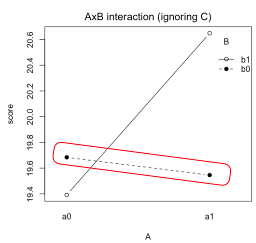

```
> with(myDf,interaction.plot(x.factor=A,
+     trace.factor=B,
+     response=score,
+     type="b",
+     ylab="score",
+     pch=c(19,21)))
> mtext(side=3,
+      text="AxB interaction (ignoring C)",
+      line=0.5,
+      cex=1.25)
```

2 x 2 x 2 ANOVA example

simple effects of A at B0 (ignoring C)

```
> # simple main effect of A at B0 (ignoring C)
> curDf <- subset(myDf,B=="b0")
> a.b0 <- aov(score~A,data=curDf)
> summary(a.b0)
           Df    SS    MS     F  Pr(>F)
A           1  0.28 0.283 0.258 0.61
Residuals  58 63.61 1.097
```

A is the simple main effect at B_0



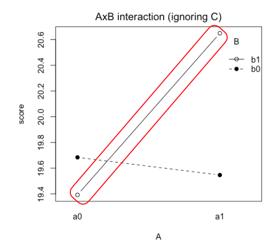
N.B. We could recalculate F & p values using MS-resid and df-resid from full model

2 x 2 x 2 ANOVA example

simple effects of A at B1 (ignoring C)

```
> # simple main effect of A at B1 (ignoring C)
> curDf <- subset(myDf,B=="b1")
> a.b1 <- aov(score~A,data=curDf)
> summary(a.b1)
           Df    SS     MS     F  Pr(>F)
A           1 23.69 23.690 27.38 <.001
Residuals  58 50.19  0.865
```

A is the simple main effect at B_1

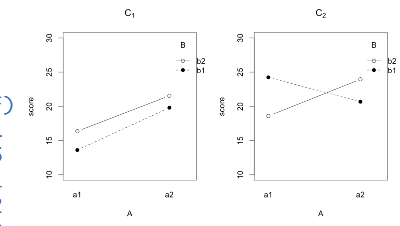


N.B. We could recalculate F & p values using MS-resid and df-resid from full model

Analyzing a 3-way interaction

decomposing a 3-way interaction

```
> load(url("http://pnb.mcmaster.ca/bennett/psy710/datasets/aov-3way-data.rda") )
> myDf10 <- data.frame(score,A,B,C,groupID)
> aov.100 <- aov(score~A*B*C,data=myDf10)
> anova(aov.100)
Analysis of Variance Table
Response: score
             Df   SS      MS      F      Pr(>F)
A             1  326.32  326.32 12.961 <.001
B             1    8.36    8.36  0.332 0.565
C             1  488.06  488.06 19.385 <.001
A:B           1  118.26  118.26  4.697 0.032
A:C           1  171.49  171.49  6.811 0.010
B:C           1   88.57   88.57  3.518 0.063
A:B:C         1  185.38  185.38  7.363 0.008
Residuals   112 2819.84   25.18
```



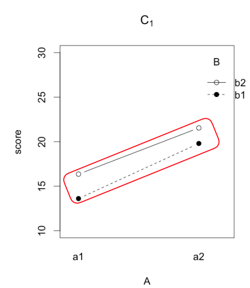
A x B interaction at C_1 A x B interaction at C_2

decomposing a 3-way interaction

evaluate simple AxB interaction at C_1

```
> # simple AxB interaction at c1:
> aov.101.c1 <- aov(score~A*B,data=subset(myDf10,C=="c1"))
> anova(aov.101.c1)
Analysis of Variance Table
Response: score
           Df  SS      MS      F       Pr(>F)
A           1  485.46  485.46 17.3717 0.0001
B           1   75.68   75.68  2.7083 0.1054
A:B         1    3.76    3.76  0.1344 0.7152
Residuals  56 1564.95   27.95
```

In this ANOVA table, A is the simple main effect of A at C_1



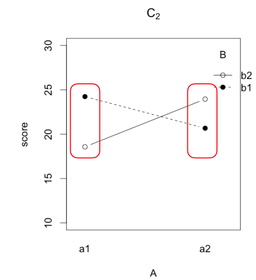
N.B. We could recalculate F & p values using MS-resid and df-resid from full model

decomposing a 3-way interaction

simple AxB interaction at C_2

```
> # simple AxB interaction at c2:
> aov.101.c2 <- aov(score~A*B,data=subset(myDf10,C=="c2"))
> anova(aov.101.c2)
Analysis of Variance Table
Response: score
           Df   SS      MS      F     Pr(>F)
A           1   12.35   12.35  0.551 0.461
B           1   21.25   21.25  0.948 0.334
A:B         1  299.89  299.89 13.382 <.001
Residuals  56 1254.89   22.41
```

A:B is the simple AxB interaction at C_2



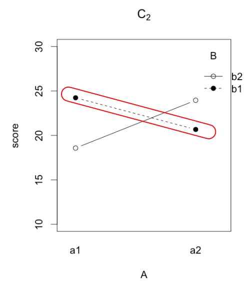
N.B. We could recalculate F & p values using MS-resid and df-resid from full model

decomposing a 3-way interaction

analyze AxB interaction at C_2: simple simple main effect of A at B_1 & C_2

```
> # evaluate simple simple main effect of A at B1 & C2:
> aov.101.c2.b1 <- aov(score~A,
+             data=subset(myDf10,B=="b1"&C=="c2"))
> anova(aov.101.c2.b1)
Analysis of Variance Table
Response: score
          Df  SS     MS     F    Pr(>F)
A          1  95.27  95.3  3.69 0.065
Residuals 28 721.91  25.8
```

simple simple main effect of A at B_1 & C_2



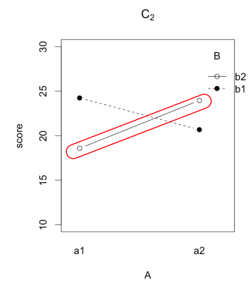
N.B. We could recalculate F & p values using MS-resid and df-resid from full model

decomposing a 3-way interaction

analyze AxB interaction at C_2: simple simple main effect of A at B_2 & C_2

```
> # evaluate simple simple main effect of A at B2 & C2:
> aov.101.c2.b2 <- aov(score~A,
+             data=subset(myDf10,B=="b2"&C=="c2"))
> anova(aov.101.c2.b2)
Analysis of Variance Table
Response: score
          Df SS   MS   F     Pr(>F)
A          1 217  217  11.39 0.002
Residuals 28 533   19
```

simple simple main effect of A at B_2 & C_2



N.B. We could recalculate F & p values using MS-resid and df-resid from full model

effect size

Measures of Association Strength

partial omega-squared

$$\omega^2_{A,partial} = \frac{\sum_{j=1}^{a}(\alpha_j^2/a)}{\sigma_e^2 + \sum_{j=1}^{a}(\alpha_j^2/a)}$$

$$\omega^2_{B,partial} = \frac{\sum_{k=1}^{b}(\beta_k^2/b)}{\sigma_e^2 + \sum_{k=1}^{b}(\beta_k^2/b)}$$

$$\omega^2_{AB,partial} = \frac{\sum_{j=1}^{a}\sum_{k=1}^{b}\left[(\alpha\beta)^2_{jk}/(ab)\right]}{\sigma_e^2 + \sum_{j=1}^{a}\sum_{k=1}^{b}\left[(\alpha\beta)^2_{jk}/(ab)\right]}$$

variance of treatment effects relative to sum of treatment effect variance + error variance calculated from full model

each partial omega-squared ignores variation in dependent variable that is due to other effects in the model

Measures of Association Strength

partial omega-squared

$$\omega^2_{A,partial} = \frac{df_A(F_A-1)}{df_A(F_A-1)+N} \qquad \omega^2_{A,partial} = \frac{SS_A - df_A MS_{Residuals}}{SS_A + (N-df_A)MS_{Residuals}}$$

$$\omega^2_{B,partial} = \frac{df_B(F_B-1)}{df_B(F_B-1)+N} \qquad \omega^2_{B,partial} = \frac{SS_B - df_B MS_{Residuals}}{SS_B + (N-df_B)MS_{Residuals}}$$

$$\omega^2_{AB,partial} = \frac{df_{AB}(F_{AB}-1)}{df_{AB}(F_{AB}-1)+N} \qquad \omega^2_{AB,partial} = \frac{SS_{AB} - df_{AB} MS_{Residuals}}{SS_{AB} + (N-df_{AB})MS_{Residuals}}$$

Cohen 1988:

$$\begin{aligned}\omega^2_{partial} &= 0.010 \text{ is a small association}\\ \omega^2_{partial} &= 0.059 \text{ is a medium association}\\ \omega^2_{partial} &\geq 0.138 \text{ is a large association}\end{aligned}$$

Measures of Association Strength

$$\eta^2_{A,partial} = \frac{SS_A}{SS_{Residuals} + SS_A}$$

- partial eta-squared (pes)
  - similar to partial omega squared
  - slightly biased estimate of population value
- generalized eta-squared (ges)
  - Olegnik & Algina (2003) Psychological Methods, 8(4): 434-447
  - analogous to partial omega squared
  - distinguishes between manipulated & observed variables
    - partial omega squared ignores variation in DV due to all other effects in model
    - ges does not remove variation due to observed variables (e.g., age, gender, etc.)
  - ges may be more invariant across different experimental designs

Measures of Effect Size

Cohen's f

$$f_{treatment} = \sqrt{\frac{\omega^2_{partial}}{1-\omega^2_{partial}}}$$

Cohen 1988:

0.01 = small effect
0.25 = medium effect
0.40 = large effect

N.B. cohens_f in effectsize package uses partial eta-squared

Cohen's f is a generalization of Cohen's d, and for balanced designs is approximately equal to the mean standardized difference between group/marginal means and the grand mean

Association Strength & Effect Size (effectsize)

```
library(effectsize)
cohens_f(lm.full.model) # uses eta-squared, not omega-squared

## # Effect Size for ANOVA (Type I)
##
## Parameter | Cohen's f (partial) |       90% CI
## ---------------------------------------------
## A         |                2.06 | [1.39, 2.69]
## B         |                1.02 | [0.56, 1.46]
## A:B       |                0.46 | [0.00, 0.84]
```

```
omega_squared(lm.full.model)

## # Effect Size for ANOVA (Type I)
##
## Parameter | Omega2 (partial) |       90% CI
## ------------------------------------------
## A         |             0.78 | [0.61, 0.86]
## B         |             0.45 | [0.18, 0.64]
## A:B       |             0.12 | [0.00, 0.35]
```

power

Power for F test

df in numerator & denominator

Cohen's f^2
(N.B. f=.1 is a small effect)

```
> library(pwr)
> pwr.f2.test(u=3-1,v=30,f2=(0.1^2),sig.level=.05)

     Multiple regression power calculation

              u = 2
              v = 30
             f2 = 0.01
      sig.level = 0.05
          power = 0.07319046
```

Power for F test

```
> pwr.f2.test(u=3-1,f2=(0.1^2),sig.level=.05,power=.8)

     Multiple regression power calculation

              u = 2
              v = 963.4709
             f2 = 0.01
      sig.level = 0.05
          power = 0.8
```

need df=963 in denominator for power=0.8

- total N = 963+1 = 964
- if you using a (3x2) factorial design => 6 condition
- 964/6 = 162 Ss per condition

Unbalanced Data

unequal N per cell

	no alcohol	alcohol	Row Means
Michigan	13 15 14 16 12 $\bar{Y}_{11} = 14$	18 20 22 19 21 23 17 18 22 20 $\bar{Y}_{12} = 20$	$\bar{Y}_{1.} = 18$
Arizona	13 15 18 14 10 12 16 17 15 10 14 $\bar{Y}_{21} = 14$	24 25 17 16 18 $\bar{Y}_{22} = 20$	$\bar{Y}_{2.} = 15.9$
Column Means	$\bar{Y}_{.1} = 14$	$\bar{Y}_{.2} = 20$	

Sequential SS for unbalanced designs

$$score \sim 1 + state + alcohol + state : alcohol$$
$$score \sim 1 + alcohol + state + alcohol : state$$

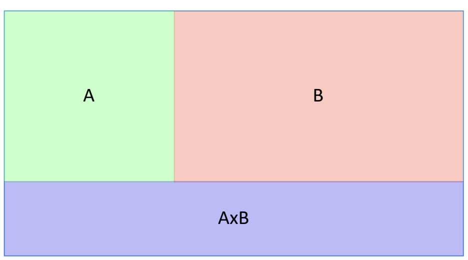
- 2 models differ only in the order of terms
- yet SS assigned to main effects differs between models
- this order dependence is a sign that design is unbalanced
- the main effects are not orthogonal

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
state	1	34.96	34.96	5.13	0.0318
alcohol	1	243.75	243.75	35.77	0.0000
state:alcohol	1	0.00	0.00	0.00	1.0000
Residuals	27	184.00	6.81		

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
alcohol	1	278.71	278.71	40.90	0.0000
state	1	0.00	0.00	0.00	1.0000
alcohol:state	1	0.00	0.00	0.00	1.0000
Residuals	27	184.00	6.81		

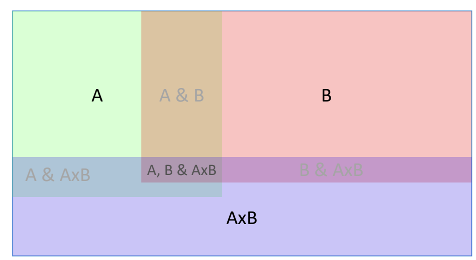
Table 3: ANOVA tables for Model 1 (top) and Model 2 (bottom).

Assigning portions of SS_{total} to A, B, and AxB



ANOVA assigns variation in dependent variable to A, B, and AxB
Balanced designs: A, B, & AxB account for separate components of SS_{total}

Assigning portions of SS_{total} to A, B, and AxB



ANOVA assigns variation in dependent variable to A, B, and AxB
Unbalanced designs: A, B, & AxB account for overlapping components of SS_{total}
No unique way of partitioning SS_{total}

Rules of assigning Sums of Squares

- Type I (Sequential): SS calculated sequentially/hierarchically.
  - SS for an effect adjusted only for preceding terms in model
- Type II: SS for an effect adjusted for all other terms that that do not include the effect in question
- Type III: SS for an effect adjusted for all other terms in the model
- For balanced designs: Type 1 = Type 2 = Type 3
- For highest-order interaction: Type 1 = Type 2 = Type 3

Type I (Sequential) Sum of Squares

SS depends on the order of terms listed in the model

Type I Sums of Squares

[order determined by model formula (R uses this rule)]

SS state ignoring all other factors

1.1) $score \sim 1$
1.2) $score \sim 1 + state$
1.3) $score \sim 1 + state + alcohol$
1.4) $score \sim 1 + state + alcohol + state : alcohol$

Type I SSs

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
state	1	34.96	34.96	5.13	0.0318
alcohol	1	243.75	243.75	35.77	0.0000
state:alcohol	1	0.00	0.00	0.00	1.0000
Residuals	27	184.00	6.81		

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
alcohol	1	278.71	278.71	40.90	0.0000
state	1	0.00	0.00	0.00	1.0000
alcohol:state	1	0.00	0.00	0.00	1.0000
Residuals	27	184.00	6.81		

Table 3: ANOVA tables for Model 1 (top) and Model 2 (bottom).

2.1) $score \sim 1$
2.2) $score \sim 1 + alcohol$
2.3) $score \sim 1 + alcohol + state$
2.4) $score \sim 1 + alcohol + state + alcohol : state$

SS state controlling for alcohol

Type I Sums of Squares

[order automatically determined by magnitude of SS… largest SS first]

1.1) $score \sim 1$
1.2) $score \sim 1 + state$
1.3) $score \sim 1 + state + alcohol$
1.4) $score \sim 1 + state + alcohol + state : alcohol$

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
state	1	34.96	34.96	5.13	0.0318
alcohol	1	243.75	243.75	35.77	0.0000
state:alcohol	1	0.00	0.00	0.00	1.0000
Residuals	27	184.00	6.81		

Some stats programs pre-determine order of Type I SS (e.g., largest SS is first)

Type I SSs

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
alcohol	1	278.71	278.71	40.90	0.0000
state	1	0.00	0.00	0.00	1.0000
alcohol:state	1	0.00	0.00	0.00	1.0000
Residuals	27	184.00	6.81		

Table 3: ANOVA tables for Model 1 (top) and Model 2 (bottom).

2.1) $score \sim 1$
2.2) $score \sim 1 + alcohol$
2.3) $score \sim 1 + alcohol + state$
2.4) $score \sim 1 + alcohol + state + alcohol : state$

Type II Sums of Squares

control for other main effect but ignore AxB interaction

$$\begin{aligned} score &\sim 1 + state \\ score &\sim 1 + state + alcohol \end{aligned}$$

Type II SSs

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
state	1	34.96	34.96	5.13	0.0318
alcohol	1	243.75	243.75	35.77	0.0000
state:alcohol	1	0.00	0.00	0.00	1.0000
Residuals	27	184.00	6.81		

$$\begin{aligned} score &\sim 1 + alcohol \\ score &\sim 1 + alcohol + state \end{aligned}$$

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
alcohol	1	278.71	278.71	40.90	0.0000
state	1	0.00	0.00	0.00	1.0000
alcohol:state	1	0.00	0.00	0.00	1.0000
Residuals	27	184.00	6.81		

Table 3: ANOVA tables for Model 1 (top) and Model 2 (bottom).

Type III Sums of Squares

control for all other effects & identify variation that is uniquely associated with each effect

$SS_{alcohol}$

$$score \sim 1 + state + state : alcohol$$
$$score \sim 1 + state + alcohol + state : alcohol$$

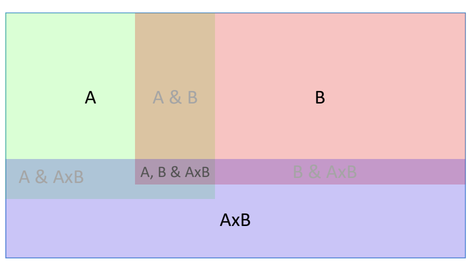
SS_{state}

$$score \sim 1 + alcohol + state : alcohol$$
$$score \sim 1 + state + alcohol + state : alcohol$$

$SS_{state\ x\ alcohol}$

$$score \sim 1 + state + alcohol$$
$$score \sim 1 + state + alcohol + state : alcohol$$

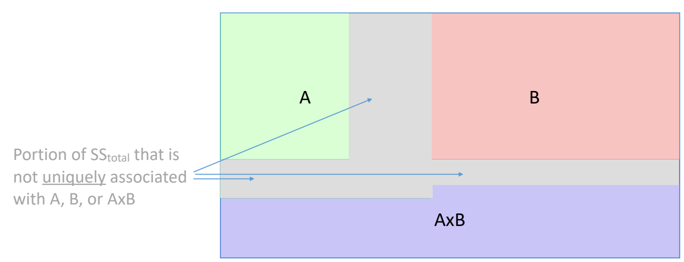
Assigning portions of SS_{total} to A, B, and AxB



ANOVA assigns variation in dependent variable to A, B, and AxB
Unbalanced designs: A, B, & AxB account for overlapping components of SS_{total}
No unique way of partitioning SS_{total}

Assigning portions of SS_{total} to A, B, and AxB

Type III SS can be uniquely associated with 1 effect



Type III SS: A, B, & AxB account for non-overlapping components of SS_{total}
Type III SS will **not** include all variation: $SS_{total} > (SS_A + SS_B + SS_{AxB} + SS_{residuals})$

calculating Type III SS with drop1

```
> load(url("http://pnb.mcmaster.ca/bennett/psy710/datasets/howell-alcohol.rda") )
> summary(howell)
      state      alcohol        score            id
 arizona :16   drink:15   Min.   :10.0   s1      : 1
 michigan:15   none :16   1st Qu.:14.0   s2      : 1
                          Median :17.0   s3      : 1
                          Mean   :16.9   s4      : 1
                          3rd Qu.:19.5   s5      : 1
                          Max.   :25.0   s6      : 1
                                         (Other):25

> xtabs(~state+alcohol,data=howell)
          alcohol
state      drink none
  arizona      5   11
  michigan    10    5
```

calculating Type III SS with drop1

Type I SS are order dependent

```
> options(contrasts=c("contr.sum","contr.poly"))
> howell.aov.01 <- aov(score ~ alcohol*state,data=howell)
> summary(howell.aov.01)
              Df Sum Sq Mean Sq F value   Pr(>F)
alcohol        1  278.7  278.71    40.9 7.52e-07 ***
state          1    0.0    0.00     0.0        1
alcohol:state  1    0.0    0.00     0.0        1
Residuals     27  184.0    6.81


> howell.aov.02 <- aov(score ~ state*alcohol,data=howell)
> summary(howell.aov.02)
              Df Sum Sq Mean Sq F value   Pr(>F)
state          1  34.96   34.96    5.13   0.0318 *
alcohol        1 243.75  243.75   35.77 2.23e-06 ***
state:alcohol  1   0.00    0.00    0.00   1.0000
Residuals     27 184.00    6.81
```

calculating Type III SS with drop1

Type III SS are order independent

```
> drop1(howell.aov.01,.~.,test="F")
Model: score ~ alcohol * state
              Df Sum of Sq    RSS    AIC F value    Pr(>F)
<none>                     184.00 63.209
alcohol        1    243.69 427.69 87.357  35.759 2.231e-06 ***
state          1      0.00 184.00 61.209   0.000         1
alcohol:state  1      0.00 184.00 61.209   0.000         1


> drop1(howell.aov.02,.~.,test="F")
Model: score ~ state * alcohol
              Df Sum of Sq    RSS    AIC F value    Pr(>F)
<none>                     184.00 63.209
state          1      0.00 184.00 61.209   0.000         1
alcohol        1    243.69 427.69 87.357  35.759 2.231e-06 ***
state:alcohol  1      0.00 184.00 61.209   0.000         1
```

genotype data

Type III & II SS with unbalanced factorial design

genotype data

```
> library(MASS)
> data(genotype)
> sapply(genotype,class)
   Litter    Mother        Wt 
 "factor"  "factor" "numeric" 

> xtabs(~Litter+Mother,
  data=genotype)
      Mother
Litter A B I J
     A 5 3 4 5
     B 4 5 4 2
     I 3 3 5 3
     J 4 3 3 5
```

```
> round(with(genotype,
   (tapply(Wt,list(Litter,Mother),mean))),
    digits=2)
      A     B     I     J
A 63.68 52.40 54.12 48.96
B 52.33 60.64 53.92 45.90
I 47.10 64.37 51.60 49.43
J 54.35 56.10 54.53 49.06

> round(with(genotype,
  (tapply(Wt,list(Litter,Mother),sd))),
   digits=2)
      A    B    I    J
A  3.27 9.37 5.32 8.76
B  5.53 5.65 5.11 7.64
I 18.10 7.12 8.62 5.37
J  5.33 3.35 8.38 5.34
```

Data from a foster feeding experiment with rat mothers and litters of four different genotypes: A, B, I and J. Rat litters were separated from their natural mothers at birth and given to foster mothers to rear.

genotype data (Type III SS)

```
> options(contrasts=c("contr.sum","contr.poly"))
> rat.aov.01 <- aov(Wt~Litter*Mother,data=genotype)

> anova(rat.aov.01) # sequential SS
Analysis of Variance Table
Response: Wt
              Df Sum Sq Mean Sq F value Pr(>F)
Litter         3     60    20.1    0.37 0.7752
Mother         3    775   258.4    4.76 0.0057
Litter:Mother  9    824    91.6    1.69 0.1201
Residuals     45   2441    54.2
```

Type I (Litter)
Type II (Mother)

$SS_L + SS_M + SS_{L:M} = 1659$

```
> drop1(rat.aov.01,.~.,test="F") # Type III SS
Model: Wt ~ Litter * Mother
              Df Sum of Sq  RSS AIC F value Pr(>F)
<none>                     2441 257
Litter         3        28 2468 252    0.17  0.916
Mother         3       672 3113 266    4.13  0.011
Litter:Mother  9       824 3265 257    1.69  0.120
```

$SS_L + SS_M + SS_{L:M} = 1524$

Using Anova to compute Type II SS

```
> library(car) # contains Anova command
> rat.aov.01 <- aov(Wt~Litter*Mother,data=genotype)


> Anova(rat.aov.01,type="2")
Anova Table (Type II tests)

Response: Wt
              Sum Sq Df F value Pr(>F)
Litter            64  3    0.39 0.7600
Mother           775  3    4.76 0.0057
Litter:Mother    824  9    1.69 0.1201
Residuals       2441 45
```

Type II (Litter)
Type II (Mother)

Using Anova to compute Type III SS

```
> library(car) # contains Anova command
> rat.aov.01 <- aov(Wt~Litter*Mother,data=genotype)


> Anova(rat.aov.01,type="3")
Anova Table (Type III tests)

Response: Wt
              Sum Sq Df F value Pr(>F)
Litter            28  3    0.17  0.916
Mother           672  3    4.13  0.011
Litter:Mother    824  9    1.69  0.120
Residuals       2441 45
```

Type III (Litter)
Type III (Mother)

Using aov_ez in afex package

```
> require(afex)
> N <- dim(genotype)[1] # number of rows/subjects
> genotype$id <- factor(x=seq(1,N),labels="s")
> options(contrasts=c("contr.sum","contr.poly"))
> rat.ez.T2 <- aov_ez(id="id",dv="Wt",between=c("Litter","Mother"),
                      data=genotype,type="2")

> rat.ez.T3 <- aov_ez(id="id",dv="Wt",between=c("Litter","Mother"),
                      data=genotype,type="3")


> summary(rat.ez.T3) # type 3 SS
Anova Table (Type 3 tests)

Response: Wt
              num Df den Df  MSE    F    ges Pr(>F)
Litter             3     45 54.2 0.17 0.0112  0.916
Mother             3     45 54.2 4.13 0.2158  0.011 *
Litter:Mother      9     45 54.2 1.69 0.2524  0.120
```

Using aov_car in afex package

```
> require(afex)
> N <- dim(genotype)[1] # number of rows/subjects
> genotype$id <- factor(x=seq(1,N),labels="s")
> options(contrasts=c("contr.sum","contr.poly"))
> rat.car.T2 <- aov_car(Wt~Litter*Mother+Error(id),
                        data=genotype,type="2")

> rat.car.T3 <- aov_car(Wt~Litter*Mother+Error(id),
                        data=genotype,type="3")

> summary(rat.car.T3) # type 3 SS
Anova Table (Type 3 tests)

Response: Wt
              num Df den Df  MSE    F    ges Pr(>F)
Litter             3     45 54.2 0.17 0.0112  0.916
Mother             3     45 54.2 4.13 0.2158  0.011
Litter:Mother      9     45 54.2 1.69 0.2524  0.120
```

Linking SSs to hypotheses about group means

A x B interaction term

- for 2-way design, A x B is highest-order interaction in the model
  - SS_{AxB} computed by comparing full model to model without interaction term
- Type I, II, & III SS for highest-order interaction are <u>identical</u> numerically & conceptually
- SS_{AxB} evaluates null hypothesis that interaction effects are zero
  - "the main effect of A is the same at each level of B"
  - "the main effect of B is the same at each level of A"

Type I SS: weighted marginal means

- weighted marginal means take into account different cell *n*
  - mean of all scores within row or column
- unweighted marginal means do not take into account different cell *n*
  - simply the mean of cell means (does not depend on cell *n*)
- Type I SS evaluate null hypothesis that weighted marginal means are equal
  - (refers to SS in 1st line of Type I SS anova table)
  - differences in n across conditions affect results
  - interesting hypothesis?

Type II Sums of Squares

$$\Sigma_{k=1}^{b}\left(n_{jk} - (n_{jk}^2/n_{.k}\right)\mu_{jk} = \Sigma_{j\neq j'}\Sigma\left(n_{jk}n_{j'k}/n_{.k}\right)\mu_{j'k}$$

- difficult to state hypothesis about group means evaluated with Type II SS
  - much easier to think about comparison of nested models
    - is main effect of A significant after accounting for main effect of B (but ignoring A x B interaction)?
- when SS-interaction is very small, Type II & III SS test same hypothesis…

Type III SS: unweighted marginal means

- unweighted marginal mean is mean of cell means
- **when effects are defined using sum-to-zero constraint**
  - Type III SS evaluate null hypothesis that unweighted marginal means are equal
- when SS-interaction is very small
  - values of Type II & III SS are similar
  - and Type II SS evaluate null hypothesis re unweighted marginal means