

Notes on Maxwell & Delaney

PSY710

9 Designs with Covariates

9.1 Blocking

Consider the following hypothetical experiment. We want to measure the effect of a drug on locomotor activity in hyperactive children. Children are assigned randomly to three groups that differ in the dosage of the drug (i.e., zero, low, and high), and the dependent measure is the amount of locomotor activity during some fixed period of time after administration of the drug. Now, children in our sample are likely to vary in the amount of locomotor activity that they produce *before* the administration of the drug: some children are more active than others. Should we worry about this inter-subject variability? Probably. These individual differences are likely to increase the variability of our dependent measure, and therefore make it more difficult to detect a significant effect of the drug. Is there some way of reducing the impact of these individual differences on the sensitivity of our experiment?

One way of addressing this issue would be to screen subjects and test only those children whose activity fell within a limited range. However, using this strategy would mean that our conclusions would be restricted to children exhibiting that particular level of activity used in your experiment. Another strategy would be to divide pre-drug activity into several levels (e.g., “low”, “medium”, “high”, and “very high”), select N subjects at each level, and then randomly assign subjects to a drug condition. This scheme of creating homogeneous sets of subjects is referred to as **blocking**; in this case our blocking variable would be pre-drug, or baseline, activity. Because subjects within each block are assigned randomly to treatment groups, this type of design is referred to as a **randomized blocks** design¹. When analyzing the data, baseline activity is treated as a factor. Incorporating the blocking variable into our statistical model means that variability in the dependent variable that is related to baseline activity will be assigned to the the blocking factor instead of error. Hence, error will be reduced.

The following example illustrates a randomized blocks experiment. First, we create fake data. The variable `activity` represents baseline locomotor activity in 48 subjects.

¹Typically, randomized block designs have only a subjects per block, where a is the number of levels on the treatment variable. In other words, only one subject in each block would be assigned to each level of the treatment variable. The current design, which has 12 subjects per block assigned randomly to 3 treatments (i.e., 4 subjects per treatment) is an example of a generalized randomized block design (Kirk, 1995).

The variable `block` is a factor that divides `activity` into four groups that differ in mean activity: in other words, `block` is our blocking variable. Next, we create the effects (i.e., the alpha's) associated with each level of the drug and store them in `drug.effect`. The variable `drug` is a factor that indicates the level of drug received by the subjects. Finally, we create a fake dependent variable `y`. Notice that `y` is related linearly to `activity`, and is affected by the dosage of the drug.

```
> options(contrasts=c("contr.sum","contr.poly")) # sum-to-zero definition of factor effects
> set.seed(437);
> activity <- sort(rnorm(n=48,mean=10,sd=3));
> block <- factor(rep(c("low","med","high","very"),each=12),levels=c("low","med","high","very"),ordered=FALSE);
> drug <- factor(rep(c("zero","low","high","high","low","zero"),times=8),levels=c("zero","low","high"),ordered=FALSE)
> drug.effect<-rep(c(-1,0,1,1,0,-1),times=8)
> y <- 1 + 0.6*activity + 1.1*drug.effect + rnorm(activity,mean=0,sd=3);
> theData <- data.frame(y, block,drug,activity,drug.effect)
```

First, we want to see if our blocking variable really is capturing variability among our subjects. The next several commands list the mean baseline activity within each block of subjects and then determines if the blocks differ significantly. The blocks *do* differ, so we succeeded in creating groups in which the between-block differences are large relative to the within-block differences.

```
> with(theData, tapply(activity, block,mean));
```

```
      low      med      high      very
5.153699 8.007714 10.287328 13.818771
```

```
> summary(aov(activity ~ block, data=theData) );
```

```
              Df Sum Sq Mean Sq F value Pr(>F)
block          3  483.1  161.02   106.3 <2e-16 ***
Residuals     44   66.6    1.51
---

```

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

Now we evaluate two nested linear models: The first model does not include our blocking factor, but the second one does.

```
> aov.1<-aov(y~drug,data=theData)
> aov.2<-aov(y~block+drug+block:drug,data=theData)
> summary(aov.1)
```

```
              Df Sum Sq Mean Sq F value Pr(>F)
drug          2   37.1  18.539   2.173  0.126
Residuals     45  384.0   8.532
```

```
> summary(aov.2)

              Df Sum Sq Mean Sq F value    Pr(>F)
block          3 129.84   43.28   6.964 0.000818 ***
drug           2  37.08   18.54   2.983 0.063294 .
block:drug     6  30.37    5.06   0.815 0.565798
Residuals    36 223.75    6.22

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

Notice that SS_{total} is the same for both analyses, however $SS_{residuals}$ is much smaller in the analysis that includes `block`. Why? Because $SS_{residuals}$ in `aov.1` has been partitioned into two pieces: one due to error and another due to variation among blocks. You can verify this statement by summing the sums-of-squares for residuals, `block`, and `block:drug` in `aov.2`: the total should equal $SS_{residual}$ from `aov.1`. The reduction in $SS_{residuals}$ from 383.96 to 223.748 means that F_{drug} increases from 2.1727 to 2.9828, although it still is not significant ($df = (2, 36)$, $p = 0.063$). Hence, even after accounting for the effects of `block` (i.e., baseline activity), we fail to reject the null hypothesis of no effect of `drug`. The effect of `block` is significant, but that is not surprising.

9.2 ancova

I created the fake dependent variable, `y`, so that it was linearly related to baseline activity. Our blocking variable was a qualitative factor, however, and so did not take full advantage of the structure in the data. An alternative approach would be to include the numeric values themselves, rather than the level of a blocking factor, into our model. This is the approach used in the **analysis of covariance**. In the analysis of covariance, or ANCOVA, SS_{drug} is estimated by comparing the residuals from the following models:

$$Y \sim X + A$$

$$Y \sim X$$

where X and A are the covariate and grouping variables, respectively. In other words, SS_A represents the variation in Y that is due to A after controlling for the *linear* association between Y and X . The following commands perform an analysis of covariance on the current data:

```
> lm.1<-lm(y~activity+drug,data=theData)
> lm.2<-lm(y~activity,data=theData)
> anova(lm.2,lm.1)
```

Analysis of Variance Table

```
Model 1: y ~ activity
```

```
Model 2: y ~ activity + drug
```

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	46	278.92				
2	44	239.64	2	39.286	3.6066	0.03544 *

```
---
```

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

SS_{drug} equals 39.286, which is significant ($F = 3.6066$, $p = 0.035$). The same results can be obtained by using `drop1`, which also calculates $SS_{activity}$ after controlling for the effects of `drug`.

```
> drop1(lm.1, .~., test="F")
```

Single term deletions

```
Model:
```

```
y ~ activity + drug
```

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>			239.64	85.181		
activity	1	144.324	383.96	105.808	26.4993	5.91e-06 ***
drug	2	39.286	278.92	88.467	3.6066	0.03544 *

```
---
```

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

Finally, we could simply construct an ANOVA table from the full model:

```
> anova(lm.1)
```

Analysis of Variance Table

```
Response: y
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
activity	1	142.116	142.116	26.0939	6.739e-06 ***
drug	2	39.286	19.643	3.6066	0.03544 *
Residuals	44	239.638	5.446		

```
---
```

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

R prints sequential sums of squares, so SS_{drug} is calculated after controlling for the linear association between `activity` and the dependent variable.

So, the analysis of covariance indicates that the effect of drug is significant after controlling for the linear association between the covariate and independent variable. Note that the ANCOVA is more sensitive than the blocking strategy used in the previous section. This increased sensitivity reflects the fact that the relation between the covariate and dependent variable is *linear*. If the relation was nonlinear, then the blocking design may have been more sensitive. (N.B. It is possible, however, to alter the ANCOVA model to include a nonlinear term). Note also that the covariate in the ANCOVA model uses only a single degree of freedom, whereas the blocking factor used two degrees of freedom.

9.2.1 graphical representation

Figure 1 is a graphical illustration of an ancova model fit to data from two treatment groups. The two dashed lines are the best-fitting (least-squares) lines for the two sets of data, with the constraint that the lines have the same slopes. Because we defined our effects (i.e., the α 's) using the sum-to-zero constraint, the intercepts for the two lines — i.e., the value of Y when the covariate, X , is zero — are $\mu + \alpha_1$ and $\mu + \alpha_2$. In this example there are only two groups, therefore $\alpha_2 = -\alpha_1$ and the two intercepts are $\mu + \alpha_1$ and $\mu - \alpha_1$.

9.2.2 adjusted means

The **adjusted means** for the two groups correspond to the height at which the regression lines intersect the vertical dotted line located at the overall mean of the covariate, \bar{X} (see Figure 1). In other words, the adjusted means represent the means that we would expect if all of the groups were equivalent on the covariate. The adjusted means can be calculated for each group from the coefficients of the ancova model:

$$\bar{Y}'_j = \mu + \beta\bar{X} + \alpha_j$$

where β is the coefficient for the covariate (i.e., the slope of the lines in Figure 1), μ is the model's intercept, and α_j is the effect for group j . The coefficients for the model fit to the current data are

```
> dummy.coef(lm.1);
```

Full coefficients are

```
(Intercept):      1.28519
activity:         0.5124572
drug:              zero          low          high
                  -0.8216185 -0.4386966  1.2603150
```

The mean of the covariate is

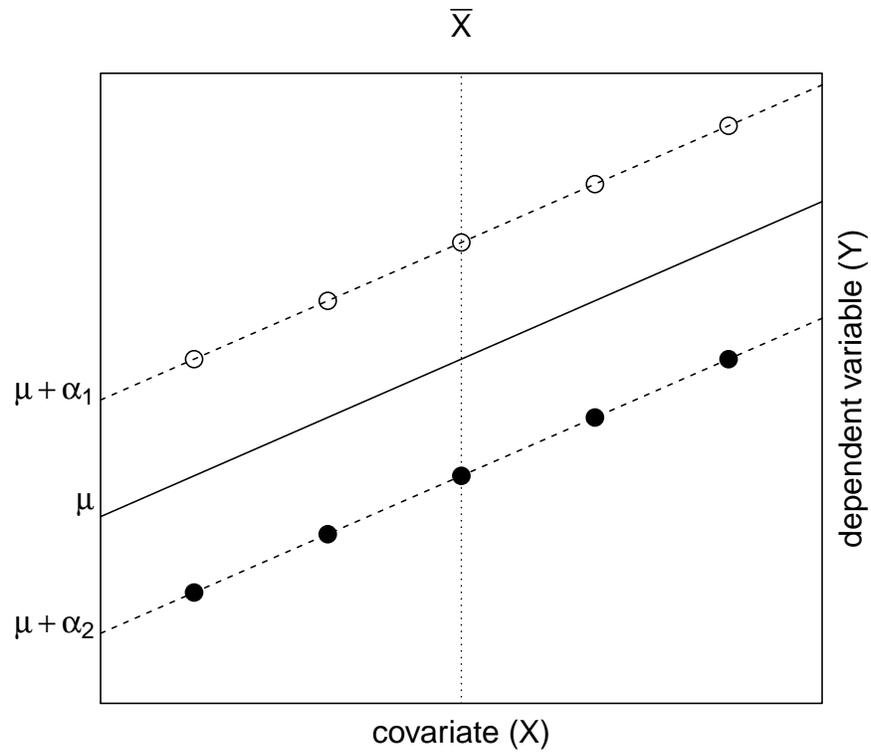


Figure 1: Graphical illustration of ancova model.

```
> mean(theData$activity)
```

```
[1] 9.316878
```

so the adjusted means for the three treatment groups are

```
> 1.28519 + 0.5124*9.3168-0.8216
```

```
[1] 5.237518
```

```
> 1.28519 + 0.5124*9.3168-0.4386
```

```
[1] 5.620518
```

```
> 1.28519 + 0.5124*9.3168+1.2603
```

```
[1] 7.319418
```

There are some advantages to using a centered covariate — a covariate that is centered on zero. A centered variable is obtained simply by subtracting the mean value from the original variable. The next few commands create a centered covariate `activity.c` and then refit the ancova model using the new covariate.

```
> theData$activity.c <- theData$activity - mean(theData$activity)
```

```
> lm.3 <- lm(y~activity.c + drug,data=theData)
```

```
> drop1(lm.3,~,test="F")
```

Single term deletions

Model:

```
y ~ activity.c + drug
```

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>			239.64	85.181		
activity.c	1	144.324	383.96	105.808	26.4993	5.91e-06 ***
drug	2	39.286	278.92	88.467	3.6066	0.03544 *

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

```
> dummy.coef(lm.3)
```

Full coefficients are

```
(Intercept):      6.059691
activity.c:       0.5124572
drug:
  zero      low      high
-0.8216185 -0.4386966  1.2603150
```

The main results are the same, however the intercept now corresponds to the point at which the average regression line (i.e., the solid line in Figure 1) intersects with the vertical dotted line (i.e., $X = \bar{X}$). Therefore, the adjusted means can be computed by simply adding the intercept and alpha's:

```
> 6.0596-0.8216
```

```
[1] 5.238
```

```
> 6.0596-0.4386
```

```
[1] 5.621
```

```
> 6.0596+1.2603
```

```
[1] 7.3199
```

The values are the same (to within rounding error) of those obtained previously.

The `effects` package can be used to calculate the adjusted means. If you have not yet installed the package on your computer, do so now using the following command:

```
> install.packages("effects")
```

Next, you must load the package into memory with the command `library(effects)` command. Note that you only need to use this command once per R session. The adjusted means are calculated thusly:

```
> library(effects)
> effect(term="drug",lm.1)
```

```
drug effect
drug
  zero    low    high
5.238072 5.620994 7.320006
```

```
> effect(term="drug",lm.3)
```

```
drug effect
drug
  zero    low    high
5.238072 5.620994 7.320006
```

9.2.3 homogeneity of slopes assumption

The ancova model fits regression lines to each group with the constraint that the slopes of the lines are equal. This constraint is equivalent to assuming that there is no interaction between the covariate and the treatment variable. If the assumption is valid, then the differences between groups — the vertical distances between the regression lines — are constant for all values of the covariate. However, if there is an interaction, then the differences between groups will depend on the value of the covariate. In this situation, it may not make sense to talk about the main effect of the treatment variable. Therefore, it is important to test the validity of the homogeneity of slopes assumption by comparing the goodness of fit obtained by models that do and do not have an interaction term:

```
> lm.4 <- lm(y~activity.c + drug + activity.c:drug,data=theData)
> anova(lm.3,lm.4)
```

Analysis of Variance Table

Model 1: y ~ activity.c + drug

Model 2: y ~ activity.c + drug + activity.c:drug

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	44	239.64				
2	42	225.34	2	14.298	1.3324	0.2748

Alternatively, we can simply list the anova table for the full model:

```
> anova(lm.4)
```

Analysis of Variance Table

Response: y

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
activity.c	1	142.116	142.116	26.4881	6.604e-06 ***
drug	2	39.286	19.643	3.6611	0.03422 *
activity.c:drug	2	14.298	7.149	1.3324	0.27476
Residuals	42	225.340	5.365		

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

$SS_{interaction} = 14.298$, which is not significant ($F = 1.332$, $df = (2, 42)$, $p = 0.274$). Therefore, the assumption appears to be valid for these data.

9.3 strength of association

The strength of association between the treatment variable and the dependent variable — omega squared — can be estimated with the following equation:

$$\omega^2 = \frac{df_{effect}(MS_{effect} - MS_{residuals})}{SS_{total} + MS_{residuals}}$$

I'll illustrate this calculation using the data presented in Table 9.7 of your textbook.

```
> mw97<-read.table("chapter_9_table_7.dat")
> mw97[1:4,]

  V1 V2 V3
1  1 18 12
2  1 16  0
3  1 16 10
4  1 15  9

> names(mw97)<-c("group", "pre", "post")
> mw97$treatment<-factor(mw97$group, labels=c("ssri", "placebo", "waitList"), ordered=FALSE)
> mw97[1:4,]
```

```
  group pre post treatment
1     1  18  12     ssri
2     1  16   0     ssri
3     1  16  10     ssri
4     1  15   9     ssri
```

```
> mw97.lm.1<-lm(post~pre+treatment, data=mw97)
> drop1(mw97.lm.1, .~., test="F")
```

Single term deletions

Model:

post ~ pre + treatment

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>			756.33	104.82		
pre	1	313.37	1069.70	113.22	10.7723	0.002937 **
treatment	2	217.15	973.48	108.39	3.7324	0.037584 *

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

```
> anova(mw97.lm.1)
```

Analysis of Variance Table

Response: post

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
pre	1	336.68	336.68	11.5739	0.002174 **
treatment	2	217.15	108.57	3.7324	0.037584 *
Residuals	26	756.33	29.09		

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

```
> df.effect <- 2;
> SS.total <- 336.68+217.15+756.33;
> (omega.2 <- df.effect*(108.57-29.09) / (SS.total+29.09) )
```

```
[1] 0.1186933
```

The value of ω^2 is 0.118, so the treatment accounts for approximately 12% of the total variance in post-test scores in the population. Note that this definition of association strength treats the covariate as an intrinsic factor. In other words, the value of ω^2 is the proportion of variance in the dependent measure that is explained by the treatment while *ignoring* the effects of the covariate. An alternative measure of association strength, partial omega squared, is the the proportion of variance that is accounted for after *controlling* for the effects of the covariate.

$$\omega_{\text{partial}(group)}^2 = \frac{df_{\text{group}}(F_{\text{group}} - 1)}{df_{\text{group}}(F_{\text{group}} - 1) + N}$$

where N is the number of subjects in the experiment (Keppel and Wickens, 2004). For the data in Table 9.7, partial omega squared is 0.154.

9.4 comparisons among group means

Tests of specific contrasts are done on *adjusted* means. The value of a linear contrast is obtained in the usual way:

$$\hat{\psi} = \sum_{j=1}^a c_j \bar{Y}_j'$$

However, calculation of the variance of the contrast differs from before:

$$s_{\hat{\psi}}^2 = MS_{\text{residuals}} \left[\sum_{j=1}^a \frac{c_j^2}{n_j} + \frac{\left(\sum_{j=1}^a c_j \bar{X}_j \right)^2}{\sum_{j=1}^a \sum_{i=1}^n (X_{ij} - \bar{X}_j)^2} \right]$$

where $MS_{\text{residuals}}$ is taken from the full model (e.g., `lm.1`). The test statistic is

$$F = \frac{\hat{\psi}^2}{s_{\hat{\psi}}^2}$$

which is distributed as an F variable with 1 and $N - a - 1$ degrees of freedom. If the comparisons are post-hoc, you should use the Scheffe method to control Type I error rate. The critical value of F for a study that had a levels on the treatment variable would be $(a - 1)F_{\alpha}(df_1 = (a - 1), df_2 = N - a - 1)$, where α is the desired Type I error rate.

These calculations are tedious, so I have written a function for R that do them for you.

```

> psi.adj<-function(y.adj,x,group,c.weights,ms.error){
+   groups <- levels(group);
+   ng <- length(groups); # number of group levels
+   x.means <- tapply(x,group,mean); # group means on X
+   n<-tapply(x,group,length); # group n
+   psi <- sum(c.weights*y.adj); # value of comparison
+   # calculate variance of comparison
+   term.1 <- sum( c.weights*c.weights/n);
+   term.2 <- (sum(c.weights*x.means))^2;
+   x.bar.j <-tmp<-rep(x=x.means,times=n);
+   ss.x <- sum( (x-x.bar.j)^2 );
+   psi.var <- ms.error * (term.1 + (term.2 / ss.x) );
+   F.psi <- (psi*psi)/psi.var; # F value
+   p <- 1-pf(F.psi,df1=1,df2=(length(x)-ng-1)); # p value
+   the.results <- list(psi=psi,psi.var=psi.var,F=F.psi,p.value=p)
+   the.results # show results
+ }

```

The `psi.adj` function can be loaded into R from the course website with the following command:

```
> source("http://psycserv.mcmaster.ca/bennett/psy710/Rscripts/psi_adj.R")
```

Alternatively, you can type the `psi.adj` commands into a word processor, save the commands as an ascii text file placed in your working directory, and then read it into R using the command `source("filename.txt")` command. The following commands show how to use it evaluate all pairwise comparisons between groups in the activity example:

```
> anova(lm.1)
```

Analysis of Variance Table

Response: y

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
activity	1	142.116	142.116	26.0939	6.739e-06	***
drug	2	39.286	19.643	3.6066	0.03544	*
Residuals	44	239.638	5.446			

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

```
> MS.resid <- 5.446
```

```
> df.resid <- 44
```

```
> effect(term="drug",mod=lm.1)
```

drug effect

drug

```
      zero      low      high
5.238072 5.620994 7.320006

> y.adj<-c(5.234,5.62,7.32)
> X <- theData$activity
> G <- theData$drug
> psi.adj(y.adj,x=X,group=G,c.weights=c(-1,1,0),MS.resid)

$psi
[1] 0.386
$psi.var
[1] 0.6807519

$F
[1] 0.2188698

$p.value
[1] 0.6422115

> psi.adj(y.adj,x=X,group=G,c.weights=c(-1,0,1),MS.resid)

$psi
[1] 2.086
$psi.var
[1] 0.6808749

$F
[1] 6.390889

$p.value
[1] 0.01513523

> psi.adj(y.adj,x=X,group=G,c.weights=c(0,-1,1),MS.resid)

$psi
[1] 1.7
$psi.var
[1] 0.680846

$F
[1] 4.244719
```

```
$p.value
[1] 0.04531639
```

The p-values are not adjusted for multiple comparisons. To use Tukey's HSD, you need to compare the observed F 's to Tukey's critical value of F that is derived from the formula in your textbook's Table 5.16 (page 236):

```
> alpha.fw <- .05
> F.tukey.critical <- ( qtuikey(1-alpha.fw, nmeans=3, df=df.resid)^2 ) / 2
> F.tukey.critical

[1] 5.882963
```

Only the second comparison, between the `zero` and `high` groups, is significant ($p < .05$).

9.5 Generalization of the ANCOVA model

9.5.1 nonlinear relations

The basic ANCOVA model assumes that the relation between the dependent variable and covariate is linear. However, this is not a necessary restriction, and the model can be generalized to include nonlinear relations. For example, comparing the following models would estimate SS_{group} after controlling for the linear and quadratic effects of the covariate, X :

$$\begin{aligned} Y_{ij} &= \mu + \alpha_j + \beta_1 X_{ij} + \beta_2 X_{ij}^2 + \epsilon_{ij} \\ Y_{ij} &= \mu + \beta_1 X_{ij} + \beta_2 X_{ij}^2 + \epsilon_{ij} \end{aligned}$$

Adjusted means are calculated by computing Y when $X = \bar{X}$. The model assumes that both the linear and quadratic components of X do not interact with the treatment variable.

9.5.2 multiple factors

It is also possible to include more than one factor.

$$Y_{ij} = \mu + \alpha_j + \gamma_k + \beta X_{ij} + (\alpha\gamma)_{jk} + \epsilon_{ij}$$

Once again, the model assumes that the main effects for each factor, and the interaction, do not interact with the covariate.

When analyzing designs that include two or more factors, we often will want to do comparisons among adjusted row and column marginal means, as well as adjusted cell means. Again, computational details can be found in Kirk (1995).

9.6 An alternative to ANCOVA

You might have wondered why an ANCOVA was necessary for the data presented here. Why not just conduct an ANOVA on the difference scores computed subtracting pre- and post-treatment activity levels? I conduct that analysis here:

```
> theData$diff <- theData$y - theData$activity;
> diff.lm.1 <- lm(diff~drug,data=theData)
> anova(diff.lm.1);
```

Analysis of Variance Table

Response: diff

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
drug	2	41.46	20.7318	2.5196	0.09179
Residuals	45	370.27	8.2282		

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

The effect of group is not significant. Obviously, this analysis was less sensitive than the ANCOVA. Why? The reason is that the difference score approach is based on a more restrictive model than the one used in ANCOVA. The model is

$$Y_{ij} - X_{ij} = \mu + \alpha_j + \epsilon_{ij}$$

which can be re-written as

$$Y_{ij} = \mu + \alpha_j + X_{ij} + \epsilon_{ij}$$

This model is similar to the one used in ANCOVA, except that the slope of the linear relation between Y and X is assumed to be one. When the linear relation *does* have a slope of one (i.e., $\beta = 1$), then an ANOVA on difference scores will yield the same results as an ANCOVA. When $\beta \neq 1$, ANCOVA will have greater sensitivity.

References

- Keppel, G. and Wickens, T. (2004). *Design and analysis: A researcher's handbook*. Pearson Education, Inc., 4th edition.
- Kirk, R. E. (1995). *Experimental design: Procedures for the behavioral sciences*. Brooks/Cole, 3rd edition.