7 Initialize R

Initialize R by entering the following commands at the prompt. You must type the commands \textit{exactly} as shown.

```
options(contrasts=c("contr.sum","contr.poly") ) # set definition of contrasts
load(url("http://psycserv.mcmaster.ca/bennett/psy710/datasets/L5dat1.Rdata") )
load(url("http://psycserv.mcmaster.ca/bennett/psy710/datasets/L5dat2.Rdata") )
goats <- read.csv(file=url("http://psycserv.mcmaster.ca/bennett/psy710/datasets/goat.csv") )
closeAllConnections()
```

7.1 ab data

An experiment was done to measure the effects of treatment A and treatment B on a dependent variable, y, using a crossed-factorial design. The data are stored in the dataframe \textit{L5.dat.1}.

Tasks:

1. Conduct an ANOVA that evaluates the effects of A and B on y. Explain your results.

```
ab.aov.01 <- aov(y~A + B + A:B,data=L5.dat.1)
summary(ab.aov.01)
```

```
## Df Sum Sq Mean Sq F value Pr(>F)
## A  1  81.63  81.63 11.815 0.001744 **
## B  2 143.47  71.74 10.383 0.000374 ***
## A:B  2  54.13  27.07  3.917 0.030794 *
## Residuals 30 207.28  6.91
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

\textbf{Answer:} There was a significant main effect of A \((F(1, 30) = 11.81, p = .0017)\), so we reject the null hypothesis of no differences between the marginal means of A. There was a main effect of B \((F(2, 30) = 10.38, p = .00037)\), so the null hypothesis of no difference among the marginal means of B is rejected. Finally, the A \times B interaction was significant \((F(2, 30) = 3.92, p = .031)\), and therefore the effect of A depends on the level of B, and the effect of B depends on the level of A.

2. Interpreting interactions:

\textbf{Example:} Before computing the simple main effects, it might be helpful to graph the data. The following command created Figure 1.
Example: The following code calculates the simple main effect of A at b1:

```r
MS.resid <- 6.909  # from main anova
df.resid <- 30      # from main anova
levels(L5.dat.1$B)  # levels of B
```

```r
B.b1 <- subset(L5.dat.1,B=="b1")  # get subset of data
aov.A.at.B1 <- aov(y~A,data=B.b1);  # one-way anova of A at b1
summary(aov.A.at.B1)  # anova table
```

```
## Df Sum Sq Mean Sq F value Pr(>F)
## A    1  0.03  0.029  0.004 0.95
## Residuals 10 69.84 6.984
```

```
(F.A.b1 <- 0.029/MS.resid)  # recalculate F
```

---

**Figure 1:** Interaction plot of the AB data.
Bennett, PJ  PSYCH 710  Lab #7

Task: Calculate the simple main effect of B at each level of A.

Answer: Here is how you calculate the simple main effect of B at a1 and a2:

```r
MS.resid <- 6.909  # from main anova
df.resid <- 30  # from main anova
levels(L5.dat.1$A)

## [1] "a1" "a2"

A.a1 <- subset(L5.dat.1, A=="a1")
summary(aov(y~B, data=A.a1))

# Df  Sum Sq  Mean Sq F value  Pr(>F)
# B      2   147.27  73.63  13.52 0.000441 ***
# Residuals 15   81.72  5.45

(F.B.a1 <- 73.634/MS.resid)

## [1] 10.65769

(1-pf(F.B.a1, df1=2, df2=df.resid))

## [1] 0.0003184966

A.a2 <- subset(L5.dat.1, A=="a2")
summary(aov(y~B, data=A.a2))

# Df  Sum Sq  Mean Sq F value  Pr(>F)
# B      2    50.34  25.17  3.007 0.0798 .
# Residuals 15  125.55  8.37

(F.B.a2 <- 25.168/MS.resid)

## [1] 3.642785

(1-pf(F.B.a2, df1=2, df2=df.resid))

## [1] 0.03834485
```
The simple main effect of B at a1 is significant ($F(2, 30) = 10.65, p = .0003$), as is the simple main effect of B at a2 ($F(2, 30) = 3.64, p = .038$). Note that the second simple main effect would not have been significant if we had used the Bonferroni adjustment to maintain a familywise Type I error rate of .05.

3. Pairwise comparisons:

**Example:** The following code shows how to use TukeyHSD to do pairwise comparisons of each level on factor B. Note that the functions computes 90% adjusted confidence intervals, and the familywise $\alpha$ therefore is 0.1:

```r
ab.aov.01 <- aov(y~A + B + A:B, data=L5.dat.1) # the anova
TukeyHSD(ab.aov.01,which="B",conf.level=0.90)
```

```r
## Tukey multiple comparisons of means
## 90% family-wise confidence level
##
## Fit: aov(formula = y ~ A + B + A:B, data = L5.dat.1)
##
## $B
##  diff lwr upr p adj
## b2-b1 -1.904411 -4.1938774  0.3850549  0.1952390
## b3-b1  2.948288  0.6588215  5.2377538  0.0264344
## b3-b2  4.852699  2.5632327  7.1421650  0.0002573
```

**Task:** Use TukeyHSD to evaluate all pairwise comparisons of cell means while maintaining a familywise $\alpha = 0.10$. Are all of these comparisons equally interesting?

```r
# answer:
TukeyHSD(ab.aov.01,which="A:B",conf.level=0.90)
```

```r
## Tukey multiple comparisons of means
## 90% family-wise confidence level
##
## Fit: aov(formula = y ~ A + B + A:B, data = L5.dat.1)
##
## $`A:B`
##  diff lwr upr p adj
## a2:b1-a1:b1  0.09809082 -4.0344212  4.2306029  0.9999998
## a1:b2-a1:b1 -0.23713304 -4.3696451  3.8953790  0.9999855
## a2:b2-a1:b1 -3.47359855 -7.6061106  0.6589135  0.2298522
## a1:b3-a1:b1  5.94563800  1.8131259 10.0781501  0.0057991
## a2:b3-a1:b1  0.04902811 -4.0834840  4.1815402  1.0000000
## a1:b2-a2:b1 -0.33522386 -4.4677359  3.8322882  0.9999196
## a2:b2-a2:b1 -3.57168938 -7.7042014  0.5608227  0.2050023
## a1:b3-a2:b1  5.84754717  1.7150351 10.9800592  0.0068602
## a2:b3-a2:b1 -0.04906272 -4.1815748  4.0925414  1.0000000
## a2:b2-a1:b2 -3.23646552 -7.3689776  0.8960465  0.2984798
## a1:b3-a1:b2  6.18277103  2.0502590 10.3152831  0.0038465
## a2:b3-a1:b2  0.28616114 -3.8463509  4.4186732  0.9999632
## a1:b3-a2:b2  9.41923655  5.2867245 13.5517486  0.0000109
```
Answer: Comparisons of cells within a single row or column are more interesting than comparisons in different rows and columns because cells in the latter kinds of comparisons differ on two factors and therefore are difficult to interpret.

4. Calculate Cohen’s $f$ for the $A \times B$ interaction. (For more information about calculation Cohen’s $f$ in a factorial design, see Section 7.8 in the notes.)

```r
# answer:
F.AxB <- 3.9174 # AxB F taken from anova
df.AxB <- 2; # from anova
N <- sum( with(L5.dat.1, tapply(y, B, length)) )
(omega.AxB <- (df.AxB * (F.AxB - 1))/(df.AxB * (F.AxB - 1) + N))

## [1] 0.1394724

(cohens.f <- sqrt(omega.AxB / (1-omega.AxB)))

## [1] 0.4025888
```

Answer: The association strength and effect size are large.

### 7.2 cd data

This section, in which we analyze data from an **unbalanced** design, draws on material in Sections 7.12.3-7.12.12 in the course notes.

An experiment was done to measure the effects of treatment $C$ and treatment $D$ on a dependent variable, $y$, using a crossed-factorial design. Six subjects were assigned randomly to each condition, however the data from two subjects in one of the conditions were lost. The data are stored in the dataframe `L5.dat.2`.

1. Verify that the CD data are unbalanced.

```r
with(L5.dat.2,tapply(y,list(C,D),length))
```

```
##       b1 b2 b3
## a1     6  6  6
## a2     6  6  4
```

2. Verify that the results of the two-way ANOVA depend on the order of the terms in the full linear model.

```r
cd.aov.01 <- aov(y~C+D+C:D, data=L5.dat.2)
cd.aov.02 <- aov(y~D+C+D:C, data=L5.dat.2)
summary(cd.aov.01)
```
3. Your book defines Type I sums of squares as the sums of squares associated with one main effect when all other variables are ignored. According to this definition, what are the Type I sums of squares for C and D? What null hypotheses about the main effects are being evaluated with these Type I sums of squares?

C.t1.ss <- 65.338
D.t1.ss <- 205.121

4. What are the Type II sums of squares for C and D? Use Type II sums of squares to evaluate the main effects of C and D.

C.t2.ss <- 47.276
D.t2.ss <- 187.059

**Answer:** Using Type II sums-of-squares, the main effect of D (after controlling for C but ignoring the interaction) is significant ($F(2, 28) = 16.323$, $p < .0001$). Alternatively, we could use a model that sets the interaction to zero:
The SS value is the same, but the F and p values are different because the error term is estimated with a model that assumes that the interaction effects are all zero. Is this a good assumption in this case? No, because the F value suggests that there may be a small interaction effect (i.e., the CxD effect size is small, but non-zero). The following table shows that the Type II SS for C, after controlling for D but ignoring the interaction, is significant ($F(1, 28) = 8.25, p = .0076$):

```r
summary(cd.aov.02)
```

## Response: y
## Sum Sq Df F value Pr(>F)
## C 47.276 1 8.2512 0.007681 **
## D 187.059 2 16.3237 1.999e-05 ***
## C:D 30.226 2 2.6377 0.089226 .
## Residuals 160.431 28
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 1

Anova package provides a simpler way of doing Type II tests. First, if the car package has not been installed previously, install it with the command `install.packages("car")`, and then load it with the command `library(car)`. Then use car’s `Anova` command to do the Type II tests. Note the capital A in the `Anova` command:

```r
Anova(cd.aov.01,type="II")
```

## Anova Table (Type II tests)
## Sum Sq Df F value Pr(>F)
## C 47.276 1 8.251 0.007681 **
## D 187.059 2 16.324 1.999e-05 ***
## C:D 30.226 2 2.638 0.089226 .
## Residuals 160.431 28
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 1

```r
Anova(cd.aov.02,type="II")
```

## Anova Table (Type II tests)
## Sum Sq Df F value Pr(>F)
## C 47.276 1 8.251 0.007681 **
## D 187.059 2 16.324 1.999e-05 ***
## C:D 30.226 2 2.638 0.089226 .
## Residuals 160.431 28
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 1
5. Use \texttt{drop1} to compute the Type III sums of squares for C and D. Verify that these sums of squares do not depend on the order of terms in the model. What null hypotheses about the main effects are being evaluated with these Type III sums of squares? (See Section 7.12.7 in the course notes for an example of how to use \texttt{drop1}.)

\textbf{Answer:} The following code shows that the Type III sums of squares, as computed using \texttt{drop1}, are independent of the order of terms in the model:

\begin{verbatim}
drop1(cd.aov.01,.~.,test="F")
## Single term deletions
##
## Model:
## y ~ C + D + C:D
##
## Df Sum of Sq RSS AIC F value Pr(>F)
##  <none> 160.43 64.751
## C 1 52.182 212.61 72.326 9.1074 0.005374 **
## D 2 170.580 331.01 85.377 14.8857 3.947e-05 ***
## C:D 2 30.226 190.66 66.620 2.6377 0.089226 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

drop1(cd.aov.02,.~.,test="F")
## Single term deletions
##
## Model:
## y ~ D + C + D:C
##
## Df Sum of Sq RSS AIC F value Pr(>F)
##  <none> 160.43 64.751
## D 2 170.580 331.01 85.377 14.8857 3.947e-05 ***
## C 1 52.182 212.61 72.326 9.1074 0.005374 **
## D:C 2 30.226 190.66 66.620 2.6377 0.089226 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

C.t3.ss <- 52.18
D.t3.ss <- 170.58
\end{verbatim}
When effects are defined using the sum-to-zero constraint, Type III sums of squares can be used to test the null hypothesis of no difference among unweighted marginal means. One last thing: the following code shows how to compute Type III SSs with `Anova`:

```r
Anova(cd.aov.01,type="III")
```

## Anova Table (Type III tests)
##
## # Response: y
## #
## # (Intercept) 4831.5 1 843.2456 < 2.2e-16 ***
## # C 52.2 1 9.1074 0.006374 **
## # D 170.6 2 14.8857 3.947e-05 ***
## # C:D 30.2 2 2.6377 0.089226 .
## # Residuals 160.4 28
## --
## # Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```r
Anova(cd.aov.02,type="III")
```

## Anova Table (Type III tests)
##
## # Response: y
## #
## # (Intercept) 4831.5 1 843.2456 < 2.2e-16 ***
## # D 170.6 2 14.8857 3.947e-05 ***
## # C 52.2 1 9.1074 0.005374 **
## # D:C 30.2 2 2.6377 0.089226 .
## # Residuals 160.4 28
## --
## # Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

7.3 goats

The following text was taken from material posted at [www.statlab.uni-heidelberg.de/data/ancova/goats.story.html](http://www.statlab.uni-heidelberg.de/data/ancova/goats.story.html).

Experiments were carried out on six commercial goat farms to determine whether the standard worm drenching program was adequate. Forty goats were used in each experiment. Twenty of these, chosen completely at random, were drenched according to the standard program, while the remaining twenty were drenched more frequently. The goats were individually tagged, and weighed at the start and end of the year-long study. For the first farm in the study the resulting liveweight gains are given along with the initial liveweights. In each experiment the main interest was in the comparison of the liveweight gains between the two treatments.

The data from one of these experiments was taken from [www.statlab.uni-heidelberg.de/data/ancova/goats.data](http://www.statlab.uni-heidelberg.de/data/ancova/goats.data) and is stored in the data frame `goats`. Values of baseline (i.e., pre-treatment) weight and weight gain are stored in the variables `wt` and `gain`, respectively. Type of worm drenching – standard and intensive – is stored in the variable `treatment`. 
### 7.3.1 linear regression

The following code uses linear regression to evaluate the linear relation between `gain` and `wt`:

```r
goats.lm.01 <- lm(gain~wt, data=goats)
summary(goats.lm.01)
```

The `summary` function prints a regression table, which the regression coefficient, or $\beta$, for `wt` as -0.35, which differs significantly from zero ($t(38) = -4.47, p < .0001$). This regression coefficient means that for every increase of 1 in `wt`, the value of `gain` decreases (on average) by 0.35. The intercept is 14.39, and the `t` test shows that it differs significantly from zero. Together, the intercept and regression coefficient define a straight line

$$\text{gain} = \text{intercept} - 0.354 \times \text{wt}$$ (1)

The overall fit of the regression model, as indexed by $R^2 = 0.34$, also is significant, $F(1, 38) = 20.05, p < .0001$. $R^2$ is evaluated by noting the change in the goodness-of-fit that occurs when all of the parameters except the intercept are set to zero. In this case, there is only one parameter – the regression coefficient for `wt` – and so you would think that the overall $F$ test should be related to the $t$ test for `wt`'s $\beta$ value... and you would be correct. In the case of a regression model that has only one regression coefficient, the overall $F$ equals $t^2$: $F = t^2 = -4.478^2 = 20.05$.

The following code uses `plot` to create a scatter plot of `gain` vs. `wt` and then uses the function `abline` to add the regression line defined by Equation 1. The resulting graph is shown in Figure 2.

```r
with(goats,plot(wt,gain,"p",xlab="wt",ylab="gain"))
abline(goats.lm.01)
```

### 7.3.2 ANOVA & ANCOVA

In this section we will use ANOVA and ANCOVA to evaluate the effect of `treatment`.

1. Conduct an ANOVA to evaluate the effect of `treatment` on `gain`. Calculate the strength of association between `treatment` and `gain`.

```r
with(goats,tapply(gain,treatment,mean)) # group means
```

## intensive standard
## 6.85 5.55

with (goats, plot (wt, gain, "p", xlab = "wt", ylab = "gain"))
abline (goats.lm.01)
Figure 2: Plot of weight gain as a function of pre-treatment weight. The solid line shows the regression line.
## Analysis of Variance Table

## Response: gain

<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>treatment</td>
<td>1</td>
<td>16.9000</td>
<td>16.9000</td>
<td>4.1299</td>
</tr>
<tr>
<td>Residuals</td>
<td>38</td>
<td>155.5000</td>
<td>4.0921</td>
<td></td>
</tr>
</tbody>
</table>

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

adj.r.squared <- summary(goats.lm.02)$adj.r.squared # short-cut
(omega.squared <- adj.r.squared) # approximation for 1-way design

## [1] 0.07429173

**Answer:** The effect of treatment was significant ($F(1,38) = 4.13, p = 0.049$), so weight gain differed between the two groups.

2. Conduct an analysis of covariance (ANCOVA) that evaluates the effect of treatment after controlling for the linear association between weight and gain.

```
options(contrasts=c("contr.sum","contr.poly")) # make sure to use sum-to-zero effects
goats.lm.03 <- lm(gain~wt+treatment,data=goats) # ancova model
anova(goats.lm.03) # anova table
```

## Analysis of Variance Table

## Response: gain

<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>wt</td>
<td>1</td>
<td>59.548</td>
<td>59.548</td>
<td>22.7478</td>
</tr>
<tr>
<td>treatment</td>
<td>1</td>
<td>15.995</td>
<td>15.995</td>
<td>6.1104</td>
</tr>
<tr>
<td>Residuals</td>
<td>37</td>
<td>96.857</td>
<td>2.618</td>
<td></td>
</tr>
</tbody>
</table>

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

**Answer:** An analysis of covariance revealed a significant effect of treatment ($F(1,37) = 6.11, p = 0.018$) after controlling for the linear association between weight gain and the covariate, $wt$ ($F(1,37) = 22.7, p < 0.0001$).

3. Use the function `coef` to examine the coefficients, or parameters, of the ANCOVA model. What are the values of the parameters (i.e., the $\alpha$'s) for the two levels of treatment? Explain what the coefficients for the ANCOVA model mean.

```
levels(goats$treatment)
```

## [1] "intensive" "standard"

```
coef(goats.lm.03)
```

## (Intercept)   wt treatment1
## 14.3341789   -0.3513684   0.6324316

**Answer:** The ANCOVA model coefficients for the two levels of treatment are interpreted as follows:

- **(Intercept)**: This represents the average gain for the intensive treatment condition, adjusted for the covariate $wt$. It is the baseline from which the treatment effects are measured.

- **wt**: This coefficient represents the slope of the linear association between weight and gain. A negative coefficient suggests that as weight increases, gain decreases, and vice versa.

- **treatment1**: This coefficient represents the difference in gain between the intensive and standard treatments, adjusted for weight. A positive coefficient indicates that the intensive treatment results in a higher gain compared to the standard treatment, after controlling for weight.
Answer: The parameters define two straight lines, fit separately to the data from the intensive and standard treatment groups, that relate weight gain to pre-treatment weight. The two lines have the same slope, \( m = -0.351 \), which means that a 1 pound increase in pre-treatment weight was associated with a decrease of 0.35 pounds in the expected value of weight gain. The intercepts of the lines – i.e., the values where the lines intercept the y-axis – are 14.33 + 0.632 for the intensive group and 14.33 – 0.632 for the standard. To illustrate these points graphically, the following code uses the ANCOVA parameters to draw the lines fit to the standard and intensive groups. For comparison, the figure includes the regression line fit to all of the data.

```r
alpha.intensive <- 0.632;
alpha.standard <- 0 - 0.632;

# Fit straight lines to intensive and standard group data
x.range <- range(goats$wt)  # [min, max] for x-axis
y.range <- range(goats$gain)  # [min, max] for y-axis

# Subset data for intensive and standard groups
goats.intensive <- subset(goats, treatment == "intensive")
goats.standard <- subset(goats, treatment == "standard")

# Plot data and lines
with(goats.intensive, plot(wt, gain, "p", pch=21, cex=2, xlim=x.range, ylim=y.range, xlab="wt", ylab="gain"))
with(goats.standard, points(wt, gain, pch=19))  # add points for standard group
abline(a=14.33 + alpha.intensive, b=-0.351, lty=2)  # line for intensive group
abline(a=14.33 + alpha.standard, b=-0.351, lty=2)  # line for standard group
abline(goats.lm.01)  # overall regression line

# Label lines:
text(x=28.5, y=5, "intensive")
text(x=27, y=4, "standard")
text(x=28, y=4.5, "all points")

# Legend
legend(x=26, y=10.5, legend=c("intensive", "standard"), pch=c(21, 19))
```

4. Evaluate the ANCOVA’s homogeneity of slopes assumption.

```r
# Fit linear model with treatment and interaction terms
goats.lm.04 <- lm(gain ~ wt + treatment + wt:treatment, data=goats)
anova(goats.lm.04)

## Analysis of Variance Table
## Response: gain
## Df    Sum Sq Mean Sq F value    Pr(>F)
## wt     1 59.548 59.548 22.2115 3.6e-05 ***
## treatment 1 15.995 15.995  5.9663 0.01962 *
## wt:treatment 1  0.342  0.342  0.1277 0.72296
## Residuals 36  96.514  2.681
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Coefficient summary
coef(goats.lm.04)

## (Intercept)    wt treatment1 wt:treatment1
## 14.36249702 -0.35253363  0.01038434  0.02686777

beta <- -0.3525;
```
Figure 3: Plot of weight gain as a function of pre-treatment weight for two treatment groups. The solid line shows the regression line fit to all of the data. The two dotted lines are the lines fit by the analysis of covariance; they are constrained to have the same slope.
Answer: Like the ANCOVA model, the model that includes an interaction term fits two lines separately to each treatment group. Unlike the ANCOVA model, however, this more complex model allows the intercept and slope to vary across groups. Denote the coefficient for \( \text{wt} \) as \( \beta = -0.3525 \), and the interaction effects for the first and second treatment groups as \( (\alpha \beta)_{\text{intensive}} = 0.02686 \) and \( (\alpha \beta)_{\text{standard}} = -0.02686 \), respectively. Then the slopes of the lines fit to the first and second treatment groups are \( \beta + (\alpha \beta)_{\text{intensive}} = -0.379 \) and \( \beta + (\alpha \beta)_{\text{standard}} = -0.325 \). When the interaction effects are zero, the slopes for the two lines will be equal and the vertical separation between the two lines – i.e., the effect of treatment – will not depend on the level of the covariate. When the slopes differ, however, then the effects of treatment vary with the level of the covariate, and it may not be meaningful to talk about the effect of treatment. Fortunately, in the current case the \( \text{wt} \times \text{treatment} \) interaction was not significant \( (F(1,37) = 0.127, p = 0.722) \), means that we have insufficient evidence to reject the null hypothesis that all of the interactions are zero. In addition to not being significant, the effect size for the interaction is small: when \( F < 1 \), it is common to set the association strength and effect size to zero. Therefore, we have good reason to accept the homogeneity assumption as being valid, and to examine effects of the treatment knowing that it does not depend strongly on the level of the covariate.

5. Calculate the adjusted means for the two treatment conditions.

```r
#install.packages(effects) # only need this if effects package isn't on your computer
library(effects)
effect(term="treatment",goats.lm.03)
```

##
## treatment effect
## intensive standard
## 6.832432 5.567568

6. Use `TukeyHSD` to evaluate each pairwise difference between adjusted means. (N.B. There are only two groups, so a Tukey test obviously is unnecessary in this case. Our purpose here is to show that the command works with an ANCOVA model.)

```r
goats.aov.03 <- aov(gain~wt+treatment,data=goats) # ancova model
tukeyHSD(goats.aov.03,which="treatment")
```

## Warning in replications(paste("~", xx), data = mf): non-factors ignored: wt
7. Calculate the strength of association between treatment and gain using omega-squared and partial omega-squared. (See Section 9.3 of the course notes.)

```
with(goats,tapply(gain,treatment,length))
##   intensive standard
##       20       20

N <- 20 + 20; with(goats.lm.03) # anova table

## Analysis of Variance Table
## # Response: gain
##    Df Sum Sq Mean Sq  F value Pr(>F)
## wt  1 59.548 59.5483 22.7478  2.87e-05 ***
## treatment 1 15.995 15.9952  6.1104  0.01816    *
## Residuals 37 96.857  2.6182
## ---
## Signif. codes:  0 '***'  0.001 '**'  0.01 '*'  0.05 '.'  0.1 ' ' 1

df.treat <- 1;
F.treat <- 6.11;
MS.treat <- 15.995;
MS.resids <- 2.618;
SS.total <- 59.548 + 15.995 + 96.857;
omega.squared <- (df.treat * (MS.treat - MS.resids)) / (SS.total+MS.resids)
partial.omega.squared <- (df.treat* (F.treat-1)) / (df.treat*(F.treat-1)+N)
omega.squared

# [1] 0.07643214

partial.omega.squared

# [1] 0.1132787
```

(a) What is the difference between these two measures of association strength?

**Answer:** Omega-squared treats variation in the dependent variable that is associated with the covariate as part of error variance, whereas partial omega-squared removes variation associated with the covariate from error variance. **Question:** Do you see why partial omega-squared cannot be smaller than omega squared?

(b) How do these association strengths compare to the association strength estimated from the ANOVA in question 1?
**Answer:** Because omega-squared treats variation in the dependent variable that is associated with the covariate as part of error variance, it is identical to omega-squared estimated from the one-way ANOVA (which did not include a covariate term in the model). Partial omega-squared expresses association strength after controlling for variation associated with the covariate, and therefore is larger than omega-squared estimated from the one-way ANOVA.