6 Initialize R

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

```r
options(contrasts=c("contr.sum","contr.poly") )
load(url("http://psycserv.mcmaster.ca/bennett/psy710/datasets/faces09.Rdata") )
load(url("http://psycserv.mcmaster.ca/bennett/psy710/datasets/police09.Rdata") )
```

7 faces data

An experiment was done to measure the effects of stimulus inversion and contrast reversal on face identification. On each trial, a single face (i.e., the target) was shown for 500 ms, followed by a pair of faces presented simultaneously, side by side. The subject’s task was to indicate which face was the target by pressing one of two buttons as quickly as possible. The orientation of the faces was either upright or inverted; the contrast of the faces was either positive (i.e., normal) or negative (i.e., like a photographic negative). Face orientation and contrast was crossed factorially to create four stimulus conditions: upright-positive, upright-negative, inverted-positive, inverted-negative. The dependent variable was the mean response time (in milliseconds) on all trials in which the subject responded correctly. Forty subjects were assigned randomly to one of the four conditions, with the constraint that there were 10 subjects per condition. The data are stored in the data frame `faces`, with the variables `rt`, `contrast`, `orient`, and `condition`.

Tasks:

1. Use the data and variables in `faces` to recreate Figure 7. Use this figure to evaluate the assumption that the data within each cell are distributed normally.

   ```r
   boxplot(rt~condition,data=faces,ylab="RT",xlab="Condition",main="Faces Experiment")
   ```

2. One assumption made by factorial analysis of variance is that variance is constant across cells. Inspection of Figure 7 suggests that this assumption is valid for the `faces` data. Now do a statistical test to evaluate the constant variance assumption.

   **Answer:** We can evaluate the constant variance assumption using `bartlett.test`. However, that command works properly only when the groups – which in this case corresponds to individual cells in our two-way factorial design – are specified by a single factor. Therefore, we need to use the factor `condition`, which has a name for each of the four cells:

   ```r
   bartlett.test(rt~condition,data=faces)
   ```
Faces Experiment

<table>
<thead>
<tr>
<th>Condition</th>
<th>RT</th>
</tr>
</thead>
<tbody>
<tr>
<td>posUp</td>
<td>400</td>
</tr>
<tr>
<td>posInv</td>
<td>500</td>
</tr>
<tr>
<td>negUp</td>
<td>600</td>
</tr>
<tr>
<td>negInv</td>
<td>700</td>
</tr>
</tbody>
</table>
## Bartlett test of homogeneity of variances

### data: rt by condition

Bartlett's K-squared = 5.8979, df = 3, p-value = 0.1167

# Here is how you can make the condition variable within R:

```R
faces$cellname <- interaction(faces$contrast, faces$orient)
levels(faces$cellname) # shows levels of new factor
```

## [1] "positive.upright" "negative.upright" "positive.inverted"
## [4] "negative.inverted"

# we can shorten the level names like this:
levels(faces$cellname) <- c("posUp", "negUp", "posInv", "negInv")
levels(faces$cellname) # verify levels have new names

## [1] "posUp" "negUp" "posInv" "negInv"

3. The following code illustrates how to use the `tapply` command to construct a table that lists the number of observations in each cell in the design. Note that the design is balanced:

```R
# note the list of two factors:
with(faces, tapply(rt, list(contrast, orient), length))
```

### upright inverted
### positive 10 10
### negative 10 10

In the next example, we drop `orient` from the list, to calculate the number of observations at each level of orientation ignoring the other factor:

```R
with(faces, tapply(rt, list(contrast), length)) # same as following...
```

### positive negative
### 20 20

(a) Create tables showing the mean and standard deviation of `rt` for each cell in the design.

```R
# answer:
with(faces, tapply(rt, list(contrast, orient), mean))
```

### upright inverted
### positive 522.2708 545.7524
### negative 552.8309 660.3908

```R
with(faces, tapply(rt, list(contrast, orient), sd))
```

### upright inverted
### positive 47.57741 84.97116
### negative 92.04335 49.77230
(b) Calculate the marginal means of \( r_t \) for each level of contrast and orient.

```r
# answer:
with(faces, tapply(rt, contrast, length))
## positive negative
##      20       20

with(faces, tapply(rt, contrast, mean))
## positive negative
## 534.0116 606.6108

with(faces, tapply(rt, orient, length))
## upright inverted
##      20       20

with(faces, tapply(rt, orient, mean))
## upright inverted
## 537.5509 603.0716
```

4. The following code shows how to use `aov` and `lm` to conduct an ANOVA that evaluates the main effects of factors A and B and the \( A \times B \) interaction. In this example, the dependent variable is \( y \) and the data are stored in the data frame `myData`:

```r
my.aov.01 <- aov(y ~ A + B + A:B, data=myData)
anova(my.aov.01)  # make anova table, or...
summary(my.aov.01)  # make anova table
my.lm.01 <- lm(y ~ A + B + A:B, data=myData)
anova(my.lm.01)
```

(a) Use the data in `faces` to do an ANOVA that evaluates the main effects of contrast and orientation, and the contrast \( \times \) orientation interaction, on the dependent variable \( r_t \). Explain what each line in the ANOVA table means.

**Answer:** The following table shows **SEQUENTIAL (TYPE 1) SUMS-OF-SQUARES**. Each line shows SS for a variable after controlling for all effects on previous lines. The first line shows SS contrast (i.e., change in goodness-of-fit) produced by going from the intercept-only model to one that includes an intercept and the effects of contrast. The second line shows change in goodness-of-fit when you add the effects of orientation to a model that has includes an intercept and contrast. The third line shows the change in goodness-of-fit when you add the contrast:orient interaction effects to a model that has intercept, orientation, and contrast. In each case, the change in goodness-of-fit is evaluated by comparing the Mean Square value to the Mean Square Residuals from the full model.

```r
faces.aov.01 <- aov(rt ~ contrast + orient + contrast:orient, data=faces)
summary(faces.aov.01, intercept=TRUE)
```

<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>13010196</td>
<td>13010196</td>
<td>2546.903 &lt; 2e-16 ***</td>
<td></td>
</tr>
<tr>
<td>contrast</td>
<td>1</td>
<td>52706</td>
<td>52706</td>
<td>10.318 0.00277 **</td>
<td></td>
</tr>
<tr>
<td>orient</td>
<td>1</td>
<td>42930</td>
<td>42930</td>
<td>8.404 0.00634 **</td>
<td></td>
</tr>
<tr>
<td>contrast:orient</td>
<td>1</td>
<td>17673</td>
<td>17673</td>
<td>3.460 0.07107 .</td>
<td></td>
</tr>
</tbody>
</table>
Answer: The sum-of-squares for each effect represents the variation in the dependent variable that is associated with that effect. Another way of thinking about each sum-of-squares is that it represents the change in SS-residuals that occurs when the coefficients for that effect (i.e., α's, β's, or (αβ)'s) are added, one after the other, to an initial model that includes only the intercept. The mean-squares are the sums-of-squares per degree of freedom. In this experimental design, if the null hypothesis is true and all of the effects are zero, then each mean square has the same expected value: \( \sigma^2_e \), population error variance. Therefore, therefore each \( F \) should be \( \approx 1 \) when the null hypothesis (for that effect) is true. When the null hypothesis is false, then each mean square will be the sum of the estimated population error variance plus a component that is related to the magnitude of the effects (i.e., the α’s, β’s, or (αβ)’s), and therefore the value of \( F \) should be greater than 1. Each \( p \) value represents the probability of getting an \( F \) that is at least as large as the observed \( F \) when the null hypothesis is true. The null hypothesis for each main effect is that the marginal means are all equal. The null hypothesis for the interaction is that the mean for each cell does not differ from the sum of three terms: a constant (intercept), one main effect (i.e., \( \alpha_j \)), and another main effect (i.e., \( \beta_k \)). The last line in the table shows the sum of squared residuals for the full model: you can verify this statement by calculating the sum of squared residuals yourself using the command

```r
sum(residuals(faces.aov.01)^2)
```

The degrees of freedom equals the number of observations minus the number of parameters in the model, which in this case is 40-4 or 36. The mean square value in the last row is an estimate of population error variance.

(b) Verify that the results of the ANOVA do not depend on the order of contrast and orientation in the linear model.

```r
faces.aov.02 <- aov(rt~orient+contrast+contrast:orient,data=faces)
summary(faces.aov.02)
```

Answer: Compare the two ANOVA tables: they are the same. The fact that the results do not depend on the order of terms in the model implies that the various factors are mutually orthogonal and account for non-overlapping parts of variation in the dependent variable. Note what happens when I delete a few cases to create an unbalanced data set:

```r
tmp.faces <- faces[ ,]
with(tmp.faces,tapply(rt,list(contrast,orient),length) )
```
5. The following code constructs two nested linear models and then evaluates the difference in the goodness of fit:

```r
faces.aov.05 <- aov(rt~1+orient,data=faces) # reduced model
faced.aov.06 <- aov(rt~1+orient+contrast,data=faces) # full
anova(faces.aov.05,faces.aov.06) # comparison
```

## Analysis of Variance Table
## Model 1: rt ~ 1 + orient
## Model 2: rt ~ 1 + orient + contrast
## Res.Df RSS Df Sum of Sq F Pr(>F)
## 1 38 254276
## 2 37 201570 1 52706 9.6748 0.003588 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(a) What does the **Sum-of-Sq** value in the last row of the output represent?

**Answer:** The sum-of-squares (i.e., change in the sum-of-squared residuals) for **contrast** while controlling for the effect of orientation but **ignoring** the interaction. Although the sum-of-squares is the same as the value obtained with the full ANOVA, the *F* and *p* values differ from the ones in the ANOVA. Why? Because the error term (i.e., denominator for *F*) in this test is not the same as **MS-residuals** in the full ANOVA. Note the difference, for example, in the residuals (i.e., the denominator) degrees of freedom. In the original model the denominator df was 36, but here it is 37: Why does our error term have 1 more degree of freedom...?

(b) Compare two nested models that estimate the sum-of-squares associated with **contrast** while **ignoring** both the main effect of **orientation** and the **contrast × orientation** interaction. How does this value compare to the ones calculated previously?
faces.aov.03 <- aov(rt~1,data=faces)
faces.aov.04 <- aov(rt~1+contrast,data=faces)
anova(faces.aov.03,faces.aov.04)

## Analysis of Variance Table
##
## Model 1: rt ~ 1
## Model 2: rt ~ 1 + contrast
## Res.Df RSS Df Sum of Sq F Pr(>F)
## 1 39 297206
## 2 38 244499 1 52706 8.1916 0.006809 **
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

**Answer:** Although the sum-of-squares is the same as the value obtained with the full ANOVA, the $F$ and $p$ values differ from the ones in the ANOVA. Why? Because the error term (i.e., denominator for $F$) in this test is not the same as MS-residuals in the full ANOVA. Note the difference, for example, in the residuals (i.e., the denominator) degrees of freedom. In the original model the denominator df was 36, but here it is 38: Why does our error term have 2 more degrees of freedom...

6. The factorial ANOVA assumes that the observations are independent, that the variance is constant across cells, and that the data within each cell are distributed normally. Evaluate the normality assumption for the faces data.

**Answer:** We can evaluate the normality assumption by examining the distribution of the residuals from the full model. The following command uses a Shapiro test to evaluate the null hypothesis that the residuals are distributed normally:

```
faces.aov.01 <- aov(rt~contrast+orient+contrast:orient,data=faces)
shapiro.test(residuals(faces.aov.01))
```

```
## Shapiro-Wilk normality test
##
data:  residuals(faces.aov.01)
W = 0.97527, p-value = 0.5191
```

The Shapiro test is not significant ($W = 0.975, p = 0.52$), and so we do not reject the assumption of normality.

8 **analysis of police data**

The data.frame police contains data from a hypothetical 3x3 between-subjects, factorial experiment. A police department conducted an experiment to evaluate its humans relations course for new officers. The independent variables were the type of beat to which officers were assigned during the course (factor `beat`) and the length of the course (factor `course`). Each subject was assigned randomly to a single combination of `beat` and `course`. The factor `beat` has three levels: innercity, middleclass, and upperclass. The (unordered) factor `course` also has three levels: short, medium, and long. The dependent variable is attitude toward minority groups...
following the course. The data frame also contains a variable, id, which is an id number assigned to each subject, and the factor group.1D, which contains a unique name for each cell in the experimental design.

Tasks:

1. Calculate the mean, standard deviation, and \( n \) for each cell.

```r
names(police)

## [1] "id"   "beat"  "course" "attitude" "group.1D"

with(police,tapply(attitude,list(beat,course),mean) )

##       short medium long
## innercity  20    40    52
## middleclass 30    31    36
## upperclass  33    35    38

with(police,tapply(attitude,list(beat,course),sd) )

##       short medium long
## innercity  7.516648  6.204837  7.968689
## middleclass 6.964194  6.964194  9.513149
## upperclass  6.964194  8.803408  9.513149

with(police,tapply(attitude,list(beat,course),length) )

##       short medium long
## innercity    5     5     5
## middleclass   5     5     5
## upperclass    5     5     5
```

2. Calculate the marginal means for each level of beat and course.

```r
with(police,tapply(attitude,course,mean) )

##       short medium long
## 27.66667  35.33333  42.00000

with(police,tapply(attitude,beat,mean) )

##       innercity middleclass upperclass
## 37.33333  32.33333  35.33333
```

3. Evaluate the analysis of variance's constant-variance assumption.

```r
bartlett.test(attitude~group.1D,data=police)
```
## Bartlett test of homogeneity of variances

```r
## data: attitude by group.1D
## Bartlett's K-squared = 1.3725, df = 8, p-value = 0.9946
```

**Answer:** The Bartlett test was not significant, $K^2 = 1.37$, df=8, $p = 0.99$, and therefore the null hypothesis of constant variance is not rejected.

4. Use ANOVA to evaluate the effects of beat and course on attitude. Explain your results.

```r
police.aov.01 <- aov(attitude~beat+course+beat:course,data=police)
summary(police.aov.01)
```

```
## Df Sum Sq Mean Sq F value Pr(>F)
## beat 2 190 95.0 1.520 0.23242
## course 2 1543 771.7 12.347 8.26e-05 ***
## beat:course 4 1237 309.2 4.947 0.00278 **
## Residuals 36 2250 62.5
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

**Answer:** The main effect of beat was not significant ($F(2, 36) = 1.52, p = 0.23$), but the main effect of course ($F(2, 36) = 12.34, p < .0001$) and the beat × course interaction ($F(4, 36) = 4.94, p = 0.0027$) were significant. The lack of a significant main effect means that there is insufficient evidence to reject the null hypothesis that the marginal means of the different levels of beat are the same. The significant main effect indicates that we can reject the null hypothesis that the marginal means of the various levels of course are equal. Finally, the significant interaction implies that the effect of one variable (e.g., beat) depends on the level of the other factor (e.g., course), and therefore it might not make sense to focus on main effects.

5. Inspect the group means and take a guess about what the beat × course interaction means. You might want to try R’s `interaction.plot` command, which is described on page 21 in the notes for Chapter 7.

**Answer:** Inspection of the means gives a clue:

```r
with(police,tapply(attitude,list(beat,course),mean))
```

```
## short medium long
## innercity  20  40  52
## middleclass 30  31  36
## upperclass  33  35  38
```

**Answer:** We can get a better idea by looking at the data graphically. The following code generates Figure 1 using the `interaction.plot` function (see Section 7.11 in the notes on Chapter 7). It looks like the effect of course is larger for police assigned to an inner-city beat than it is for police assigned to the other two types of beat.
with(police, interaction.plot(course, beat, attitude))

Figure 1: Interaction plot of police data.