

Chapter 7

Factorial Analysis of Variance

7.1 Concepts

A *factor* is just another name for a categorical explanatory variable. The term is usually used in experimental studies with more than one categorical explanatory variable, where cases (subjects, patients, experimental units) are randomly assigned to treatment conditions that represent *combinations* of the explanatory variable values. For example, consider an agricultural study in which the cases are plots of land (small fields), the response variable is crop yield in kilograms, and the explanatory variables are fertilizer type (three values) and type of irrigation (Sprinkler *versus* Drip). Table 7.1 shows the six treatment combinations, one for each *cell* of the table.

Table 7.1 is an example of a *complete* factorial design, in which data are collected for all combinations of the explanatory variable values. In an *incomplete*, or *fractional* factorial design, certain treatment combinations are deliberately omitted, leading to $n = 0$ in one or more cells. When done in an organized way¹, this practice can save quite a bit of money — say, in a crash test study where the cases are automobiles. In this course, we shall mostly confine our attention to complete factorial designs.

Naturally, a factorial study can have more than two factors. The only limitations are imposed by time and budget. And there is more than one vocabulary floating around².

¹If it is safe to assume that certain contrasts of the treatment means equal zero, it is often possible to estimate and test other contrasts of interest even with zero observations in some cells. The feasibility of substituting *assumptions* for missing data is an illustration of Data Analysis Hint 4 on page 109.

²This is typical. There are different *dialects* of Statistics, corresponding roughly to groups of users from different disciplines. These groups tend not to talk with one another, and often each one has its own

Table 7.1: A Two-Factor Design

	Fertilizer 1	Fertilizer 2	Fertilizer 3
Sprinkler Irrigation			
Drip Irrigation			

A three-factor design can also be described as a three-*way* design; there is one “way” for each dimension of the table of treatment means.

When Sir Ronald Fisher (in whose honour the F -test is named) dreamed up factorial designs, he pointed out that they enable the scientist to investigate the effects of several explanatory variables at much less expense than if a separate experiment had to be conducted to test each one. In addition, they allow one to ask systematically whether the effect of one explanatory variable depends on the value of another explanatory variable. If the effect of one explanatory variable depends on another, we will say there is an *interaction* between those variables. This kind of “it depends” conclusion is a lot easier to see when both factors are systematically varied in the same study. Otherwise, one might easily think that the results two studies carried out under somewhat different conditions were inconsistent with one another. We talk about an A “by” B or $A \times B$ interaction. Again, an interaction means “it depends.”

A common beginner’s mistake is to confuse the idea of an *interaction* between variables with the idea of a *relationship* between variables. They are different. Consider a version of Table 7.1 in which the cases are farms and the study is purely observational. A *relationship* between Irrigation Type and Fertilizer Type would mean that farms using different types of fertilizer tend to use different irrigation systems; in other words, the percentage of farms using Drip irrigation would not be the same for Fertilizer Types 1, 2 and 3. This is something that you might assess with a chi-square test of independence. But an *interaction* between Irrigation Type and Fertilizer Type would mean that the effect of Irrigation Type on average crop yield *depends* on the kind of fertilizer used. As we will see, this is equivalent to saying that certain contrasts of the treatment means are not all equal to zero.

7.1.1 Main Effects and Interactions as Contrasts

Testing for main effects by testing contrasts Table 7.2 is an expanded version of Table 7.1. In addition to population crop yield for each treatment combination (denoted by μ_1 through μ_6), it shows *marginal means* – quantities like $\frac{\mu_1 + \mu_4}{2}$, which are obtained by averaging over rows or columns. If there are differences among marginal means for a categorical explanatory variable in a two-way (or higher) layout like this, we say there is a main effect for that variable. Tests for main effects are of great interest; they can indicate whether, averaging over the values of the other categorical explanatory variables in the design, whether the explanatory variable in question is related to the response variable. Note that averaging over the values of other explanatory variables is not the same thing as controlling for them, but it can still be very informative.

Notice how any difference between marginal means corresponds to a *contrast* of the treatment means. It helps to string out all the combinations of factor levels into one long categorical explanatory variable. Let’s call this a *combination variable*. For the crop yield example of Tables 7.1 and 7.2, the combination variable has six values, corresponding to

tame experts. So the language they use, since it develops in near isolation, tends to diverge in minor ways.

Table 7.2: A Two-Factor Design with Population Means

Irrigation	Fertilizer			
	1	2	3	
Sprinkler	μ_1	μ_2	μ_3	$\frac{\mu_1 + \mu_2 + \mu_3}{3}$
Drip	μ_4	μ_5	μ_6	$\frac{\mu_4 + \mu_5 + \mu_6}{3}$
	$\frac{\mu_1 + \mu_4}{2}$	$\frac{\mu_2 + \mu_5}{2}$	$\frac{\mu_3 + \mu_6}{2}$	

the six treatment means μ_1 through μ_6 in the table. Suppose we wanted to test whether, averaging across fertilizer types, the two irrigation methods result in different average crop yield. This is another way of saying we want to test for difference between two different marginal means.

Sample Question 7.1.1

For the crop yield study of Table 7.2, suppose we wanted to know whether, averaging across different fertilizers, method of irrigation is related to average crop yield.

1. Give the null hypothesis in symbols.
2. Make a table showing the weights of the contrast or contrasts of treatment means you would test to answer the question. There should be one row for each contrast. The null hypothesis will be that all the contrasts equal zero.

Answer to Sample Question 7.1.1

1. $\frac{\mu_1 + \mu_2 + \mu_3}{3} = \frac{\mu_4 + \mu_5 + \mu_6}{3}$

2.

a_1	a_2	a_3	a_4	a_5	a_6
1	1	1	-1	-1	-1

Sample Question 7.1.2

Suppose we wanted to test for the main effect(s) of Irrigation Type.

1. Give the null hypothesis in symbols.
2. Make a table showing the weights of the contrast or contrasts of treatment means you would test to answer the question. There should be one row for each contrast. The null hypothesis will be that all the contrasts equal zero.

Answer to Sample Question 7.1.2

This is the same as Sample Question 7.1.1, and has the same answer.

Sample Question 7.1.3

Suppose we wanted to know whether, averaging across different methods of irrigation, type of fertilizer is related to average crop yield.

1. Give the null hypothesis in symbols.
2. Make a table showing the weights of the contrast or contrasts of treatment means you would test to answer the question. There should be one row for each contrast. The null hypothesis will be that all the contrasts equal zero.

Answer to Sample Question 7.1.3

1. $\frac{\mu_1 + \mu_4}{2} = \frac{\mu_2 + \mu_5}{2} = \frac{\mu_3 + \mu_6}{2}$

2.

a_1	a_2	a_3	a_4	a_5	a_6
1	-1	0	1	-1	0
0	1	-1	0	1	-1

In the answers to Sample Questions 7.1.1 and 7.1.3, notice that we are testing differences between marginal means, and the number of contrasts is equal to the number of equals signs in the null hypothesis.

Testing for interactions by testing contrasts Now we will see that tests for interactions — that is, tests for whether the effect of a factor *depends* on the level of another factor — can also be expressed as tests of contrasts. For the crop yield example, consider this question: Does the effect of Irrigation Type depend on the type of fertilizer used? For Fertilizer Type 1, the effect of Irrigation Type is represented by $\mu_1 - \mu_4$. For Fertilizer Type 2, it is represented by $\mu_2 - \mu_5$, and for Fertilizer Type 2, the effect of Irrigation Type is $\mu_3 - \mu_6$. Thus the null hypothesis of *no* interaction may be written

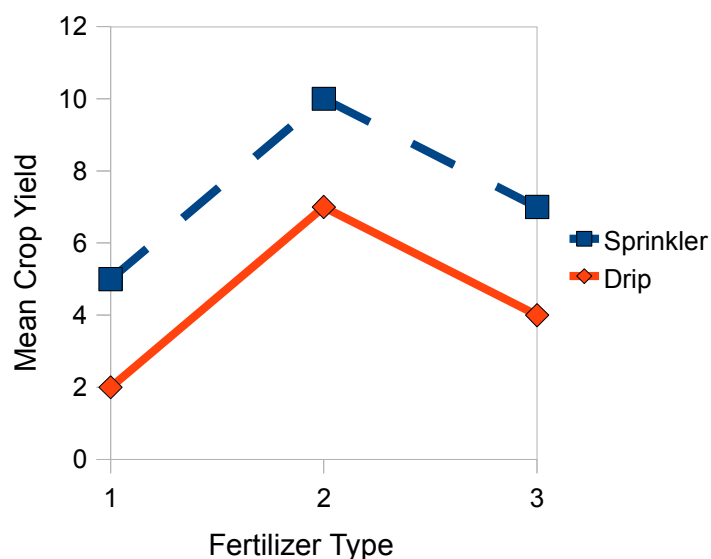
$$H_0 : \mu_1 - \mu_4 = \mu_2 - \mu_5 = \mu_3 - \mu_6. \quad (7.1)$$

Because it contains two equals signs, the null hypothesis (7.1) is equivalent to saying that two contrasts of the treatment means are equal to zero. Here are the weights of the contrasts, in tabular form.

a_1	a_2	a_3	a_4	a_5	a_6
1	-1	0	-1	1	0
0	1	-1	0	-1	1

One way of saying that there is an *interaction* between Irrigation Method and Fertilizer Type is to say that the effect of Irrigation Method depends on Fertilizer Type, and now it is clear how to set up the null hypothesis. But what if the interaction were expressed in the opposite way, by saying that the effect of Fertilizer Type depends on Irrigation Method? It turns out these two ways of expressing the concept are 100% equivalent. They imply exactly the same null hypothesis, and the significance tests will be identical.

Figure 7.1: Main Effects But No Interaction



7.1.2 Graphing Interactions

Figure 7.1 shows a hypothetical pattern of population treatment means. There are main effects for both factors, but no interaction.

For each irrigation method, the effect of fertilizer type corresponds to a *profile* – a curve showing the pattern of means for the various fertilizer types. If the profiles are parallel, then the effects of fertilizer type are the same within each irrigation method. In Figure 7.1, the profiles are parallel, meaning there is no interaction. Of course Fertilizer Type is a nominal scale variable; it consists of unordered categories. Still, even though there is nothing in between Fertilizer Types 1 and 2 or between 2 and 3, it helps visually to connect the dots.

There are two natural ways to express the parallel profiles in Figure 7.1. One way is to say that the distance between the curves is the same at every point along the Fertilizer Type axis. This directly gives the null hypothesis in Expression (7.1). The other way for the profiles to be parallel is for the line segments connecting the means for Fertilizer Types 1 and 2 to have the same slope, *and* for the line segments connecting the means for Fertilizer Types 2 and 3 to have the same slope. That is,

$$H_0 : \mu_2 - \mu_1 = \mu_5 - \mu_4 \text{ and } \mu_3 - \mu_2 = \mu_6 - \mu_5. \quad (7.2)$$

The first statement in Expression (7.2) may easily be re-arranged to yield $\mu_2 - \mu_5 = \mu_1 - \mu_4$, while the second statement may be re-arranged to yield $\mu_3 - \mu_6 = \mu_2 - \mu_5$. Thus, the null hypotheses in Expressions (7.1) and (7.2) are algebraically equivalent. They are just

different ways of writing the same null hypothesis, and it doesn't matter which one you use. Fortunately, this is a very general phenomenon.

7.1.3 Higher order designs (More than two factors)

The extension to more than two factors is straightforward. Suppose that for each combination of Irrigation Method and Fertilizer Type, a collection of plots was randomly assigned to several different types of pesticide (weed killer). Then we would have three factors: Irrigation Method, Fertilizer Type and Pesticide Type.

- For each explanatory variable, averaging over the other two variables would give marginal means – the basis for estimating and testing for main effects. That is, there are three (sets of) main effects: one for Irrigation method, one for Fertilizer type, and one for Pesticide type.
- Averaging over each of the explanatory variables in turn, we would have a two-way marginal table of means for the other two variables, and the pattern of means in that table could show a two-way interaction. That is, there are three 2-factor interactions: Irrigation by Fertilizer, Irrigation by Pesticide, and Fertilizer by Pesticide.

The full three-dimensional table of means would provide a basis for looking at a three-way, or three-factor interaction. The interpretation of a three-way interaction is that the nature of the two-way interaction depends on the value of the third variable. This principle extends to any number of factors, so we would interpret a six-way interaction to mean that the nature of the 5-way interaction depends on the value of the sixth variable. How would you graph a three-factor interaction? For each value of the third factor, make a separate two-factor plot like Figure 7.1.

Fortunately, the order in which one considers the variables does not matter. For example, we can say that the A by B interaction depends on the value of C, or that the A by C interaction depends on B, or that the B by C interaction depends on the value of A. The translations of these statements into algebra are all equivalent to one another, and lead to exactly the same test statistics and p -values for any set of data, always.

Here are the three ways of describing the three-factor interaction for the Crop Yield example.

- The nature of the Irrigation method by Fertilizer type interaction depends on the type of Pesticide.
- The nature of the Irrigation method by Pesticide type interaction depends on the type of Fertilizer.
- The nature of the Pesticide type by Fertilizer interaction depends on the Irrigation method.

Again, these statements are all equivalent. Use the one that is easiest to think about and talk about. This principle extends to any number of factors.

As you might imagine, things get increasingly complicated as the number of factors becomes large. For a four-factor design, there are

- Four (sets of) main effects
- Six two-factor interactions
- Four three-factor interactions
- One four-factor interaction; the nature of the three-factor interaction depends on the value of the 4th factor . . .
- There is an F -test for each one

Also, interpreting higher-way interactions – that is, figuring out what they mean – becomes more and more difficult for experiments with large numbers of factors. Once I knew a Psychology graduate student who obtained a significant 5-way interaction when she analyzed the data for her Ph.D. thesis. Nobody could understand it, so she disappeared for a week. When she came back, she said “I’ve got it!” But nobody could understand her explanation.

For reasons like this, sometimes the higher-order interactions are deliberately omitted from the full model in big experimental designs; they are never tested. Is this reasonable? Most of my answers are just elaborate ways to say I don’t know.

Regardless of how many factors we have, or how many levels there are in each factor, one can always form a combination variable – that is, a single categorical explanatory variable whose values represent all the combinations of explanatory variable values in the factorial design. Then, tests for main effects and interactions appear as test for collections of contrasts on the combination variable. This is helpful, for at least three reasons.

1. Thinking of an interaction as a collection of contrasts can really help you understand what it *means*. And especially for big designs, you need all the help you can get.
2. Once you have seen the tests for main effects and interactions as collections of contrasts, it is straightforward to compose a test for any collection of effects (or components of an effect) that is of interest.
3. Seeing main effects and interactions in terms of contrasts makes it easy to see how they can be modified to become Bonferroni or Scheffé follow-ups to an initial significant one-way ANOVA on the combination variable — if you choose to follow this conservative data analytic strategy.

7.1.4 Effect coding

While it is helpful to think of main effects and interactions in terms of contrasts, the details become unpleasant for designs with more than two factors. The combination variables become *long*, and thinking of interactions as collections of differences between differences of differences can give you a headache. An alternative is to use a regression

Table 7.3: Expected values in terms of regression coefficients with effect coding: Crop yield study

Fertilizer	Water	f_1	f_2	w	f_1w	f_2w	$E[Y \mathbf{X}]$
1	Sprinkler	1	0	1	1	0	$\beta_0 + \beta_1 + \beta_3 + \beta_4$
1	Drip	1	0	-1	-1	0	$\beta_0 + \beta_1 - \beta_3 - \beta_4$
2	Sprinkler	0	1	1	0	1	$\beta_0 + \beta_2 + \beta_3 + \beta_5$
2	Drip	0	1	-1	0	-1	$\beta_0 + \beta_2 - \beta_3 - \beta_5$
3	Sprinkler	-1	-1	1	-1	-1	$\beta_0 - \beta_1 - \beta_2 + \beta_3 - \beta_4 - \beta_5$
3	Drip	-1	-1	-1	1	1	$\beta_0 - \beta_1 - \beta_2 - \beta_3 + \beta_4 + \beta_5$

model with dummy variable coding. For almost any regression model with interactions between categorical explanatory variables, the easiest dummy variable coding scheme is *effect coding*.

Recall from Section 5.6.3 (see page 120) that effect coding is just like indicator dummy variable coding with an intercept, except that the last category gets a minus one instead of a zero. For a single categorical explanatory variable (factor), the regression coefficients are deviations of the treatment means from the *grand mean*, or mean of treatment means. Thus, the regression coefficients are exactly the *effects* as described in standard textbooks on the analysis of variance.

For the two-factor Crop Yield study of Table 7.1 on page 178, here is how the effect coding dummy variables would be defined for Fertilizer type and Irrigation method (Water).

Fertilizer	f_1	f_2
1	1	0
2	0	1
3	-1	-1

Water	w
Sprinkler	1
Drip	-1

As in the quantitative by quantitative case (page ??) than the quantitative by categorical case (page ??) the interaction effects are the regression coefficients corresponding to *products* of explanatory variables. For a two-factor design, the products come from multiplying each dummy variable for one factor by each dummy variable for the other factor. You *never* multiply dummy variables for the same factor with each other. Here is the regression equation for conditional expected crop yield.

$$E[Y|\mathbf{X}] = \beta_0 + \beta_1 f_1 + \beta_2 f_2 + \beta_3 w + \beta_4 f_1 w + \beta_5 f_2 w$$

The last two explanatory variables are quite literally the products of the dummy variables for Fertilizer type and Irrigation method.

To understand what we have, let's make a table showing the conditional expected value of the dependent variable for each treatment combination. That's correct but not

Table 7.4: Cell and marginal means in terms of regression coefficients with effect coding

Fert	Irrigation		
	Sprinkler	Drip	
1	$\mu_1 = \beta_0 + \beta_1 + \beta_3 + \beta_4$	$\mu_4 = \beta_0 + \beta_1 - \beta_3 - \beta_4$	$\frac{\mu_1 + \mu_4}{2} = \beta_0 + \beta_1$
2	$\mu_2 = \beta_0 + \beta_2 + \beta_3 + \beta_5$	$\mu_5 = \beta_0 + \beta_2 - \beta_3 - \beta_5$	$\frac{\mu_2 + \mu_5}{2} = \beta_0 + \beta_2$
3	$\mu_3 = \beta_0 - \beta_1 - \beta_2 + \beta_3 - \beta_4 - \beta_5$	$\mu_6 = \beta_0 - \beta_1 - \beta_2 - \beta_3 + \beta_4 + \beta_5$	$\frac{\mu_3 + \mu_6}{2} = \beta_0 - \beta_1 - \beta_2$
	$\frac{\mu_1 + \mu_2 + \mu_3}{3} = \beta_0 + \beta_3$	$\frac{\mu_4 + \mu_5 + \mu_6}{3} = \beta_0 - \beta_3$	$\frac{1}{6} \sum_{j=1}^6 \mu_j = \beta_0$

very informative, yet. In Table 7.4, the means are arranged in a row by column form like Table 7.2, except that rows and columns are transposed because it fits better on the page that way.

Immediately, it is clear what $\beta_0, \beta_1, \beta_2$ and β_3 mean.

- The intercept β_0 is the *grand mean* — the mean of (population) treatment means. It is also the mean of the marginal means, averaging over either rows or columns.
- β_1 is the difference between the marginal mean for Fertilizer Type 1 and the grand mean.
- β_2 is the difference between the marginal mean for Fertilizer Type 2 and the grand mean.
- So β_1 and β_2 are main effects for Fertilizer Type³. The marginal means for fertilizer Type are equal if and only if $\beta_1 = \beta_2 = 0$.
- β_3 is the difference between the marginal mean for Irrigation by Sprinkler and the grand mean. And, $\beta_3 = 0$ if and only if the two marginal means for Irrigation method are equal.

Furthermore, the two remaining regression coefficients — the ones corresponding to the product terms — are interaction effects. On page 181, the interaction between Irrigation method and Fertilizer type was expressed by saying that the effect of Irrigation method depended on Fertilizer type. The null hypothesis was that the effect of Irrigation method was identical for the three Fertilizer types. In other words, we had (Equation 7.1)

$$H_0 : \mu_1 - \mu_4 = \mu_2 - \mu_5 = \mu_3 - \mu_6.$$

Using Table 7.4 and substituting for the μ s in terms of β s, a little algebra shows that this null hypothesis is equivalent to

$$\beta_4 = \beta_5 = -\beta_4 - \beta_5.$$

³Technically, there is a third main effect for Fertilizer Type: $\beta_1 - \beta_2$. Any factor with k levels has k main effects that add up to zero.

This, in turn, is equivalent to saying that $\beta_4 = \beta_5 = 0$. So to test for an interaction, we just test whether the regression coefficients for the product terms equal zero.

General Rules Everything in this example generalizes nicely to an arbitrary number of factors.

- The regression model has an intercept.
- Define effect coding dummy variables for each factor. If the factor has k levels, there will be $k - 1$ dummy variables. Each dummy variable has a one for one of the factor levels, minus one for the last level, and zero for the rest.
- Form new explanatory variables that are products of the dummy variables. For any pair of factors A and B , multiply each dummy variable for A by each dummy variable for B .
- If there are more than two factors, form all three-way products, 4-way products, and so on.
- It's not hard to get all the products for a multifactor design without missing any. After you have calculated all the products for factors A and B , take the dummy variables for factor C and
 - Multiply each dummy variable for C by each dummy variable for A . These products correspond to the $A \times C$ interaction.
 - Multiply each dummy variable for C by each dummy variable for B . These products correspond to the $B \times C$ interaction.
 - Multiply each dummy variable for C by each $A \times B$ product. These three-variable products correspond to the $A \times B \times C$ interaction.
- It is straightforward to extend the process, multiplying each dummy variable for a fourth factor D by the dummy variables and products in the $A \times B \times C$ set. And so on there.
- To test main effects (differences between marginal means) for a factor, the null hypothesis is that the regression coefficients for that factor's dummy variables are all equal to zero.
- For any two-factor interaction, test the regression coefficients corresponding to the two-way products. For three-factor interactions, test the three-way products, and so on.
- Quantitative covariates may be included in the model, with or without interactions between covariates, or between covariates and factors. They work as expected. Multi-factor analysis of covariance is just a big multiple regression model.

7.2 Two-factor ANOVA with SAS: The Potato Data

This was covered in class.

7.3 Another example: The Greenhouse Study

This is an extension of the *tubes* example (see page 72) of Section 3.3. The seeds of the canola plant yield a high-quality cooking oil. Canola is one of Canada's biggest cash crops. But each year, millions of dollars are lost because of a fungus that kills canola plants. Or is it just one fungus? All this stuff looks the same. It's a nasty black rot that grows fastest under moist, warm conditions. It looks quite a bit like the fungus that grows in between shower tiles.

A team of botanists recognized that although the fungus may look the same, there are actually several different kinds that are genetically distinct. There are also quite a few strains of canola plant, so the questions arose

- Are some strains of fungus more aggressive than others? That is, do they grow faster and overwhelm the plant's defenses faster?
- Are some strains of canola plant more vulnerable to infection than others?
- Are some strains of fungus more dangerous to certain strains of plant and less dangerous to others?

These questions can be answered directly by looking at main effects and the interaction, so a factorial experiment was designed in which canola plants of three different varieties were randomly selected to be infected with one of six genetically different types of fungus. The way they did it was to scrape a little patch at the base of the plant, and wrap the wound with a moist band-aid that had some fungus on it. Then the plant was placed in a very moist dark environment for three days. After three days the bandage was removed and the plant was put in a commercial greenhouse. On each of 14 consecutive days, various measurements were made on the plant. Here, we will be concerned with lesion length, the length of the fungus patch on the plant, measured in millimeters.

The response variable will be mean lesion length; the mean is over the 14 daily lesion length measurements for each plant. The explanatory variables are Cultivar (type of canola plant) and MCG (type of fungus). Type of plant is called cultivar because the fungus grows (is "cultivated") on the plant. MCG stands for "Mycelial Compatibility Group." This strange name comes from the way that the botanists decided whether two types of fungus were genetically distinct. They would grow two samples on the same dish in a nutrient solution, and if the two fungus patches stayed separate, they were genetically different. If they grew together into a single patch of fungus (that is, they were compatible), then they were genetically identical. Apparently, this phenomenon is well established.

Here is the SAS program `green1.sas`. As usual, the entire program is listed first. Then pieces of the program are repeated, together with pieces of output and discussion.

```
/* green1.sas */
%include '/folders/myfolders/ghread.sas';
options pagesize=100;
proc freq;
    tables plant*mcg /norow nocol nopercent;
proc glm;
    class plant mcg;
    model meanlng = plant|mcg;
    means plant|mcg;
proc tabulate;
    class mcg plant;
    var meanlng ;
    table (mcg all),(plant all) * (mean*meanlng);

/* Replicate tests for main effects and interactions, using contrasts on a
combination variable. This is the hard way to do it, but if you can do
this, you understand interactions and you can test any collection of
contrasts. The definition of the variable combo could have been in
ghread.sas */

data slime;
    set mould; /* mould was created by ghread91.sas */
    if      plant=1 and mcg=1 then combo = 1;
    else if plant=1 and mcg=2 then combo = 2;
    else if plant=1 and mcg=3 then combo = 3;
    else if plant=1 and mcg=7 then combo = 4;
    else if plant=1 and mcg=8 then combo = 5;
    else if plant=1 and mcg=9 then combo = 6;
    else if plant=2 and mcg=1 then combo = 7;
    else if plant=2 and mcg=2 then combo = 8;
    else if plant=2 and mcg=3 then combo = 9;
    else if plant=2 and mcg=7 then combo = 10;
    else if plant=2 and mcg=8 then combo = 11;
    else if plant=2 and mcg=9 then combo = 12;
    else if plant=3 and mcg=1 then combo = 13;
    else if plant=3 and mcg=2 then combo = 14;
    else if plant=3 and mcg=3 then combo = 15;
    else if plant=3 and mcg=7 then combo = 16;
    else if plant=3 and mcg=8 then combo = 17;
    else if plant=3 and mcg=9 then combo = 18;
    label combo = 'Plant-MCG Combo';

/* Getting main effects and the interaction with CONTRAST statements */
proc glm;
```

```

class combo;
model meanlng = combo;
contrast 'Plant Main Effect'
  combo 1 1 1 1 1 1 -1 -1 -1 -1 -1 -1 0 0 0 0 0 0,
  combo 0 0 0 0 0 0 1 1 1 1 1 1 -1 -1 -1 -1 -1 -1;
contrast 'MCG Main Effect'
  combo 1 -1 0 0 0 0 1 -1 0 0 0 0 1 -1 0 0 0 0,
  combo 0 1 -1 0 0 0 0 1 -1 0 0 0 0 1 -1 0 0 0,
  combo 0 0 1 -1 0 0 0 0 1 -1 0 0 0 0 1 -1 0 0,
  combo 0 0 0 1 -1 0 0 0 0 1 -1 0 0 0 0 1 -1 0,
  combo 0 0 0 0 1 -1 0 0 0 0 1 -1 0 0 0 0 1 -1;
contrast 'Plant by MCG Interaction'
  combo -1 1 0 0 0 0 1 -1 0 0 0 0 0 0 0 0 0 0,
  combo 0 0 0 0 0 0 -1 1 0 0 0 0 1 -1 0 0 0 0,
  combo 0 -1 1 0 0 0 0 1 -1 0 0 0 0 0 0 0 0 0,
  combo 0 0 0 0 0 0 0 -1 1 0 0 0 0 1 -1 0 0 0,
  combo 0 0 -1 1 0 0 0 0 1 -1 0 0 0 0 0 0 0 0,
  combo 0 0 0 0 0 0 0 0 -1 1 0 0 0 0 1 -1 0 0,
  combo 0 0 0 -1 1 0 0 0 0 1 -1 0 0 0 0 0 0 0,
  combo 0 0 0 0 0 0 0 0 0 -1 1 0 0 0 0 1 -1 0,
  combo 0 0 0 0 -1 1 0 0 0 0 1 -1 0 0 0 0 0 0,
  combo 0 0 0 0 0 0 0 0 0 0 -1 1 0 0 0 0 1 -1;

/* proc reg's test statement may be easier, but first we need to
   make 16 dummy variables for cell means coding. This will illustrate
   arrays and loops, too */

data yucky;
  set slime;
  array mu{18} mu1-mu18;
  do i=1 to 18;
    if combo=. then mu{i}=.;
    else if combo=i then mu{i}=1;
    else mu{i}=0;
  end;

proc reg;
  model meanlng = mu1-mu18 / noint;
  alleq: test mu1=mu2=mu3=mu4=mu5=mu6=mu7=mu8=mu9=mu10=mu11=mu12
            = mu13=mu14=mu15=mu16=mu17=mu18;

  plant: test mu1+mu2+mu3+mu4+mu5+mu6 = mu7+mu8+mu9+mu10+mu11+mu12,
            mu7+mu8+mu9+mu10+mu11+mu12 = mu13+mu14+mu15+mu16+mu17+mu18;

```

```

fungus:  test mu1+mu7+mu13 = mu2+mu8+mu14 = mu3+mu9+mu15
           = mu4+mu10+mu16 = mu5+mu11+mu17 = mu6+mu12+mu18;

p_by_f:  test mu2-mu1=mu8-mu7=mu14-mu13,
           mu3-mu2=mu9-mu8=mu15-mu14,
           mu4-mu3=mu10-mu9=mu16-mu15,
           mu5-mu4=mu11-mu10=mu17-mu16,
           mu6-mu5=mu12-mu11=mu18-mu17;

/* Now illustrate effect coding, with the interaction represented by a
   collection of product terms. */

data nasty;
  set yucky;
  /* Two dummy variables for plant */
  if plant=. then p1=.;
  else if plant=1 then p1=1;
  else if plant=3 then p1=-1;
  else p1=0;
  if plant=. then p2=.;
  else if plant=2 then p2=1;
  else if plant=3 then p2=-1;
  else p2=0;
  /* Five dummy variables for mcg */
  if mcg=. then f1=.;
  else if mcg=1 then f1=1;
  else if mcg=9 then f1=-1;
  else f1=0;
  if mcg=. then f2=.;
  else if mcg=2 then f2=1;
  else if mcg=9 then f2=-1;
  else f2=0;
  if mcg=. then f3=.;
  else if mcg=3 then f3=1;
  else if mcg=9 then f3=-1;
  else f3=0;
  if mcg=. then f4=.;
  else if mcg=7 then f4=1;
  else if mcg=9 then f4=-1;
  else f4=0;
  if mcg=. then f5=.;
  else if mcg=8 then f5=1;
  else if mcg=9 then f5=-1;
  else f5=0;

```

```

/* Product terms for interactions */
  p1f1 = p1*f1; p1f2=p1*f2 ; p1f3=p1*f3 ; p1f4=p1*f4; p1f5=p1*f5;
  p2f1 = p2*f1; p2f2=p2*f2 ; p2f3=p2*f3 ; p2f4=p2*f4; p2f5=p2*f5;

proc reg;
  model meanlng = p1 -- p2f5;
  plant: test p1=p2=0;
  mcg: test f1=f2=f3=f4=f5=0;
  p_by_f: test p1f1=p1f2=p1f3=p1f4=p1f5=p2f1=p2f2=p2f3=p2f4=p2f5 = 0;

```

The SAS program starts with a `%include` statement that reads `ghread.sas`. The file `ghread.sas` consists of a single big data step. We'll skip it, because all we really need are the two explanatory variables `plant` and `mcg`, and the response variable `meanlng`.

Just to see what we've got, we do a `proc freq` to show the sample sizes.

```

proc freq;
  tables plant*mcg /norow nocol nopercnt;

```

and we get

TABLE OF PLANT BY MCG

PLANT(Type of Plant)	MCG(Mycelial Compatibility Group)						Total
Frequency	1	2	3	7	8	9	
GP159	6	6	6	6	6	6	36
HANNA	6	6	6	6	6	6	36
WESTAR	6	6	6	6	6	6	36
Total	18	18	18	18	18	18	108

So it's a nice 3 by 6 factorial design, with 6 plants in each treatment combination. The `proc glm` for analyzing this is straightforward. Again, we get all main effects and interactions for the factor names separated by vertical bars.

```

proc glm;
  class plant mcg;
  model meanlng = plant|mcg;
  means plant|mcg;

```

And the output is

General Linear Models Procedure
Class Level Information

Class	Levels	Values
PLANT	3	GP159 HANNA WESTAR
MCG	6	1 2 3 7 8 9

Number of observations in data set = 108

1991 Greenhouse Study

3

General Linear Models Procedure

Dependent Variable: MEANLNG Average Lesion length

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	17	328016.87350	19295.11021	19.83	0.0001
Error	90	87585.62589	973.17362		
Corrected Total	107	415602.49939			

R-Square	C.V.	Root MSE	MEANLNG Mean
0.789256	48.31044	31.195731	64.573479

Source	DF	Type I SS	Mean Square	F Value	Pr > F
PLANT	2	221695.12747	110847.56373	113.90	0.0001
MCG	5	58740.26456	11748.05291	12.07	0.0001
PLANT*MCG	10	47581.48147	4758.14815	4.89	0.0001

Source	DF	Type III SS	Mean Square	F Value	Pr > F
PLANT	2	221695.12747	110847.56373	113.90	0.0001
MCG	5	58740.26456	11748.05291	12.07	0.0001
PLANT*MCG	10	47581.48147	4758.14815	4.89	0.0001

Notice that the Type I and Type III tests are the same. This always happens when the sample sizes are equal. Now we take a look at marginal means and cell (treatment) means. This is the output of the means statement of proc glm.

1991 Greenhouse Study

4

General Linear Models Procedure

Level of PLANT	N	Mean	SD
GP159	36	14.055159	12.1640757
HANNA	36	55.700198	30.0137912
WESTAR	36	123.965079	67.0180440

Level of MCG	N	Mean	SD
1	18	41.4500000	33.6183462
2	18	92.1333333	78.3509451
3	18	87.5857143	61.7086751
7	18	81.7603175	82.6711755
8	18	50.8579365	39.3417859
9	18	33.6535714	39.1480830

Level of PLANT	Level of MCG	N	Mean	SD
GP159	1	6	12.863095	12.8830306
GP159	2	6	21.623810	17.3001296
GP159	3	6	14.460714	7.2165396
GP159	7	6	17.686905	16.4258441
GP159	8	6	8.911905	7.3162618
GP159	9	6	8.784524	6.5970501
HANNA	1	6	45.578571	26.1430472
HANNA	2	6	67.296429	30.2424997
HANNA	3	6	94.192857	20.2877876
HANNA	7	6	53.621429	24.8563497
HANNA	8	6	47.838095	12.6419109
HANNA	9	6	25.673810	17.1723150
WESTAR	1	6	65.908333	35.6968616
WESTAR	2	6	187.479762	45.1992178

WESTAR	3	6	154.103571	26.5469183
WESTAR	7	6	173.972619	79.1793105
WESTAR	8	6	95.823810	22.3712022
WESTAR	9	6	66.502381	52.5253101

The marginal are fairly easy to look at, and we definitely can construct a plot from the 18 cell means (or copy them into a nicer-looking table. But the following `proc tabulate` does the grunt work. In general, it's usually preferable to get the computer to do clerical tasks for you, especially if it's something you might want to do more than once.

```
proc tabulate;
  class mcg plant;
  var meanlng ;
  table (mcg all),(plant all) * (mean*meanlng);
```

The syntax of `proc tabulate` is fairly elaborate, but at times it's worth the effort. Any reader who has seen the type of stub-and-banner tables favoured by professional market researchers will be impressed to hear that `proc tabulate` can come close to that. I figured out how to make the table below by looking in the manual. I then promptly forgot the overall principles, because it's not a tool I use a lot – and the syntax is rather arcane. However, this example is easy to follow if you want to produce good-looking two-way tables of means. Here's the output.

	Type of Plant			
	GP159	HANNA	WESTAR	ALL
	MEAN	MEAN	MEAN	MEAN
	Average Lesion length	Average Lesion length	Average Lesion length	Average Lesion length
Mycelial Compatibility Group				
1	12.86	45.58	65.91	41.45
2	21.62	67.30	187.48	92.13

Table 7.5: Cell Means for the Greenhouse Study

Cultivar (Type of Plant)	MCG (Type of Fungus)					
	1	2	3	7	8	9
GP159	μ_1	μ_2	μ_3	μ_4	μ_5	μ_6
Hanna	μ_7	μ_8	μ_9	μ_{10}	μ_{11}	μ_{12}
Westar	μ_{13}	μ_{14}	μ_{15}	μ_{16}	μ_{17}	μ_{18}

3		14.46	94.19	154.10	87.59
-----+	-----+	-----+	-----+	-----+	-----+
7		17.69	53.62	173.97	81.76
-----+	-----+	-----+	-----+	-----+	-----+
8		8.91	47.84	95.82	50.86
-----+	-----+	-----+	-----+	-----+	-----+
9		8.78	25.67	66.50	33.65
-----+	-----+	-----+	-----+	-----+	-----+
ALL		14.06	55.70	123.97	64.57
-----+	-----+	-----+	-----+	-----+	-----+

The proc tabulate output makes it easy to graph the means. But before we do so, let's look at the main effects and interactions as collections of contrasts. This will actually make it easier to figure out what the results mean, once we see what they are.

We have a three by six factorial design that looks like this. Population means are shown in the cells. The single-subscript notation encourages us to think of the combination of MCG and cultivar as a single categorical explanatory variable with 18 categories.

Next is the part of the SAS program that creates the combination variable. Notice that it involves a data step that comes after the proc glm. This usually doesn't happen. I did it by creating a new data set called `slime` that starts by being identical to `mould`, which was created in the file `ghread.sas`. The `set` command is used to read in the data set `mould`, and then we start from there. This is done just for teaching purposes. Ordinarily, I would not create multiple data sets that are mostly copies of each other. I'd put the whole thing in one data step. Here's the code. Because all 18 possibilities are mentioned explicitly, anything else (like a missing value) is automatically missing.

```
data slime;
  set mould; /* mould was created by ghread91.sas */
  if      plant=1 and mcg=1 then combo = 1;
  else if plant=1 and mcg=2 then combo = 2;
  else if plant=1 and mcg=3 then combo = 3;
  else if plant=1 and mcg=7 then combo = 4;
  else if plant=1 and mcg=8 then combo = 5;
```

Table 7.6: Weights of the linear combinations for testing a main effect of cultivar

a_1	a_2	a_3	a_4	a_5	a_6	a_7	a_8	a_9	a_{10}	a_{11}	a_{12}	a_{13}	a_{14}	a_{15}	a_{16}	a_{17}	a_{18}
1	1	1	1	1	1	-1	-1	-1	-1	-1	-1	0	0	0	0	0	0
0	0	0	0	0	0	1	1	1	1	1	1	-1	-1	-1	-1	-1	-1

```

else if plant=1 and mcg=9 then combo = 6;
else if plant=2 and mcg=1 then combo = 7;
else if plant=2 and mcg=2 then combo = 8;
else if plant=2 and mcg=3 then combo = 9;
else if plant=2 and mcg=7 then combo = 10;
else if plant=2 and mcg=8 then combo = 11;
else if plant=2 and mcg=9 then combo = 12;
else if plant=3 and mcg=1 then combo = 13;
else if plant=3 and mcg=2 then combo = 14;
else if plant=3 and mcg=3 then combo = 15;
else if plant=3 and mcg=7 then combo = 16;
else if plant=3 and mcg=8 then combo = 17;
else if plant=3 and mcg=9 then combo = 18;
label combo = 'Plant-MCG Combo';

```

From Table 7.5 on page 196, it is clear that the absence of a main effect for Cultivar is the same as.

$$\mu_1 + \mu_2 + \mu_3 + \mu_4 + \mu_5 + \mu_6 = \mu_7 + \mu_8 + \mu_9 + \mu_{10} + \mu_{11} + \mu_{12} = \mu_{13} + \mu_{14} + \mu_{15} + \mu_{16}. \quad (7.3)$$

There are two equalities here, and they are saying that two contrasts of the eighteen cell means are equal to zero. To see why this is true, recall that a contrast of the 18 treatment means is a linear combination of the form

$$L = a_1\mu_1 + a_2\mu_2 + \dots + a_{18}\mu_{18},$$

where the a weights add up to zero. The table below gives the weights of the contrasts defining the test for the main effect of plant, one set of weights in each row. The first row corresponds to the first equals sign in Equation 7.3. It says that

$$\mu_1 + \mu_2 + \mu_3 + \mu_4 + \mu_5 + \mu_6 - (\mu_7 + \mu_8 + \mu_9 + \mu_{10} + \mu_{11} + \mu_{12}) = 0.$$

The second row corresponds to the second equals sign in Equation 7.3. It says that

$$\mu_7 + \mu_8 + \mu_9 + \mu_{10} + \mu_{11} + \mu_{12} - (\mu_{13} + \mu_{14} + \mu_{15} + \mu_{16}) = 0.$$

Table 7.6 is the basis of the first `contrast` statement in `proc glm`. Notice how the contrasts are separated by commas. Also notice that the variable on which we're doing contrasts (`combo`) has to be repeated for each contrast.

Table 7.7: Weights of the linear combinations for testing a main effect of MCG (Fungus type)

a_1	a_2	a_3	a_4	a_5	a_6	a_7	a_8	a_9	a_{10}	a_{11}	a_{12}	a_{13}	a_{14}	a_{15}	a_{16}	a_{17}	a_{18}
1	-1	0	0	0	0	1	-1	0	0	0	0	1	-1	0	0	0	0
0	1	-1	0	0	0	0	1	-1	0	0	0	0	1	-1	0	0	0
0	0	1	-1	0	0	0	0	1	-1	0	0	0	0	1	-1	0	0
0	0	0	1	-1	0	0	0	0	1	-1	0	0	0	0	1	-1	0
0	0	0	0	1	-1	0	0	0	0	1	-1	0	0	0	0	1	-1

```

/* Getting main effects and the interaction with CONTRAST statements */
proc glm;
  class combo;
  model meanlng = combo;
  contrast 'Plant Main Effect'
    combo 1 1 1 1 1 1 -1 -1 -1 -1 -1 -1 0 0 0 0 0 0,
    combo 0 0 0 0 0 0 1 1 1 1 1 1 -1 -1 -1 -1 -1 -1;

```

If there is no main effect for MCG, we are saying

$$\mu_1 + \mu_7 + \mu_{13} = \mu_2 + \mu_8 + \mu_{14} = \mu_3 + \mu_9 + \mu_{15} = \mu_4 + \mu_{10} + \mu_{16} = \mu_5 + \mu_{11} + \mu_{17} = \mu_6 + \mu_{12} + \mu_{18}.$$

There are 5 contrasts here, one for each equals sign; there is always an equals sign for each contrast. Table 7.7 shows the weights of the contrasts.

And here is the corresponding test statement in `proc glm`.

```

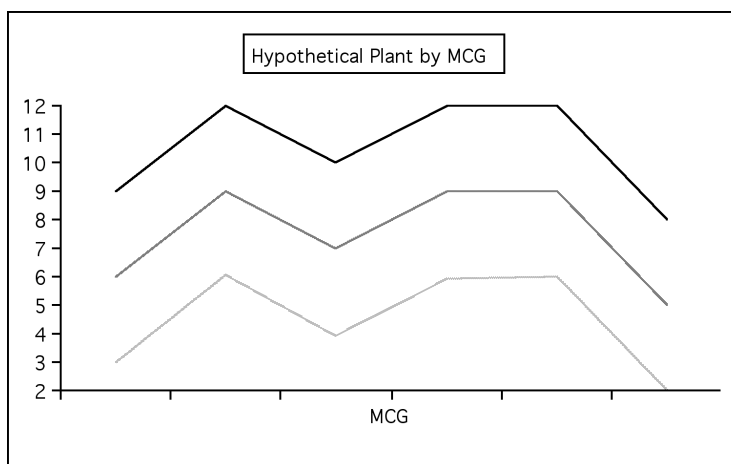
contrast 'MCG Main Effect'
  combo 1 -1 0 0 0 0 1 -1 0 0 0 0 1 -1 0 0 0 0,
  combo 0 1 -1 0 0 0 0 1 -1 0 0 0 0 1 -1 0 0 0,
  combo 0 0 1 -1 0 0 0 0 1 -1 0 0 0 0 1 -1 0 0,
  combo 0 0 0 1 -1 0 0 0 0 1 -1 0 0 0 0 1 -1 0,
  combo 0 0 0 0 1 -1 0 0 0 0 1 -1 0 0 0 0 1 -1;

```

To compose the Plant by MCG interaction, consider the hypothetical graph in Figure 7.2. You can think of the “effect” of MCG as a profile, representing a pattern of differences among means. If the three profiles are the same shape for each type of plant – that is, if they are parallel, the effect of MCG does not depend on the type of plant, and there is no interaction.

For the profiles to be parallel, each set of corresponding line segments must be parallel. To start with the three line segments on the left, the rise represented by $\mu_2 - \mu_1$ must

Figure 7.2: No Interaction



equal the rise $\mu_8 - \mu_7$, and $\mu_8 - \mu_7$ must equal $\mu_{14} - \mu_{13}$. This is two contrasts that equal zero under the null hypothesis

$$\mu_2 - \mu_1 - \mu_8 + \mu_7 = 0 \text{ and } \mu_8 - \mu_7 - \mu_{14} + \mu_{13} = 0$$

There are two contrasts for each of the four remaining sets of three line segments, for a total of ten contrasts. They appear directly in the `contrast` statement of `proc glm`. Notice how each row adds to zero; these are *contrasts*, not just linear combinations.

```
contrast 'Plant by MCG Interaction'
  combo -1  1  0  0  0  0  1 -1  0  0  0  0  0  0  0  0  0,
  combo  0  0  0  0  0  0 -1  1  0  0  0  0  1 -1  0  0  0,
  combo  0 -1  1  0  0  0  0  1 -1  0  0  0  0  0  0  0  0,
  combo  0  0  0  0  0  0  0 -1  1  0  0  0  0  1 -1  0  0,
  combo  0  0 -1  1  0  0  0  0  1 -1  0  0  0  0  0  0  0,
  combo  0  0  0  0  0  0  0  0 -1  1  0  0  0  0  1 -1  0  0,
  combo  0  0  0 -1  1  0  0  0  0  1 -1  0  0  0  0  0  0  0,
  combo  0  0  0  0  0  0  0  0  0 -1  1  0  0  0  0  1 -1  0,
  combo  0  0  0  0 -1  1  0  0  0  0  1 -1  0  0  0  0  0  0,
  combo  0  0  0  0  0  0  0  0  0  0 -1  1  0  0  0  0  1 -1;
```

Now we can compare the tests we get from these contrast statements with what we got from a two-way ANOVA. For easy reference, here is part of the two-way output.

Source	DF	Type III SS	Mean Square	F Value	Pr > F
PLANT	2	221695.12747	110847.56373	113.90	0.0001
MCG	5	58740.26456	11748.05291	12.07	0.0001
PLANT*MCG	10	47581.48147	4758.14815	4.89	0.0001

And here is the output from the contrast statements.

Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
Plant Main Effect	2	221695.12747	110847.56373	113.90	0.0001
MCG Main Effect	5	58740.26456	11748.05291	12.07	0.0001
Plant by MCG Interac	10	47581.48147	4758.14815	4.89	0.0001

So it worked. Here are some comments.

- Of course this is not the way you'd want to test for main effects and interactions. On the contrary, it makes you appreciate all the work that `glm` does for you when you say `model meanlng = plant|mcg;`
- These contrasts are supposed to be an aid to understanding — understanding what main effects and interactions really are, and understanding how you can test nearly any hypothesis you can think of in a multi-factor design. Almost without exception, what you want to do is test whether some collection of contrasts are equal to zero. Now you can do it, whether the collection you're interested in happens to be standard, or not.
- On the other hand, this was brutal. The size of the design made specifying those contrasts an unpleasant experience. There is an easier way.

Cell means coding Because the `test` statement of `proc reg` has a more flexible syntax than the `contrast` statement of `proc glm`, it's a lot easier if you use cell means dummy variable coding, fit a model with no intercept in `proc reg`, and use `test` statements. In the following example, the indicator dummy variables are named μ_1 to μ_{18} . This choice makes it possible to directly transcribe statements about the population cell means into `test` statements⁴. I highly recommend it. Of course if you really hate Greek letters, you could always name them m_1 to m_{18} or something.

⁴Here's why it works. In `test` statements, `proc reg` uses the name of the explanatory variable to stand for the regression coefficient for that explanatory variable. And with cell means coding, the regression coefficients (β values) are identical to the cell means (μ values). So if the name of each cell means coding indicator is the same as the μ for that cell in the first place, you can just directly state the null hypothesis in the `test` statement.

First, we need to define 18 dummy variables. In general, it's a bit more tedious to define dummy variables than to make a combination variable. Here, I use the combination variable `combo` (which has already been created) to make the task a bit easier – and also to illustrate the use of arrays and loops in the data step. The data set `yucky` below is the same as `slime`, except that it also has the eighteen indicators for the 18 combinations of `plant` and `mcg`. It's pretty self-explanatory, except that the name of the array does not need to be the same as the names of the variables. All you need is a valid SAS name for the array, and a list of variables. There can be more than one `array` statement, so you can have more than one array.

```

/* proc reg's test statement may be easier, but first we need to
   make 16 dummy variables for cell means coding. This will illustrate
   arrays and loops, too */

data yucky;
  set slime;
  array mu{18} mu1-mu18;
  do i=1 to 18;
    if combo=. then mu{i}=.;
    else if combo=i then mu{i}=1;
    else mu{i}=0;
  end;

proc reg;
  model meanlmg = mu1-mu18 / noint;
  alleq:  test mu1=mu2=mu3=mu4=mu5=mu6=mu7=mu8=mu9=mu10=mu11=mu12
            = mu13=mu14=mu15=mu16=mu17=mu18;

  plant:  test mu1+mu2+mu3+mu4+mu5+mu6      = mu7+mu8+mu9+mu10+mu11+mu12,
            mu7+mu8+mu9+mu10+mu11+mu12 = mu13+mu14+mu15+mu16+mu17+mu18;

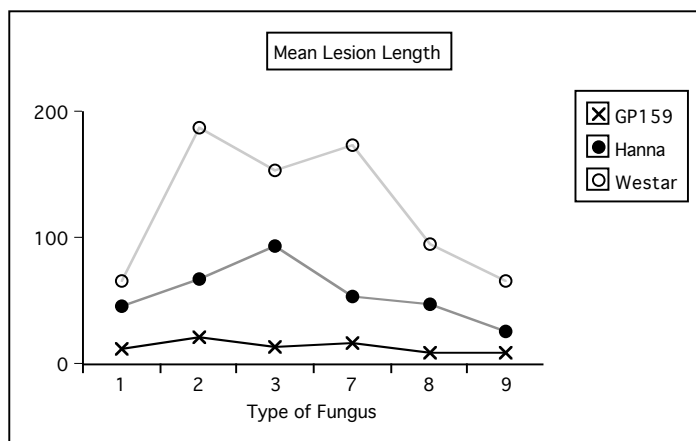
  fungus: test mu1+mu7+mu13 = mu2+mu8+mu14 = mu3+mu9+mu15
            = mu4+mu10+mu16 = mu5+mu11+mu17 = mu6+mu12+mu18;

  p_by_f: test mu2-mu1=mu8-mu7=mu14-mu13,
            mu3-mu2=mu9-mu8=mu15-mu14,
            mu4-mu3=mu10-mu9=mu16-mu15,
            mu5-mu4=mu11-mu10=mu17-mu16,
            mu6-mu5=mu12-mu11=mu18-mu17;

```

Looking again at the table of means (Table 7.5 on page 196), it's easy to see how natural the syntax is. And again, the tests are correct. First, repeat the output from the `contrast` statements of `proc glm` (which matched the `proc glm` two-way ANOVA output).

Figure 7.3: Plant by MCG: Mean Lesion Length



Contrast	DF	Contrast SS	Mean Square	F Value	Pr > F
Plant Main Effect	2	221695.12747	110847.56373	113.90	0.0001
MCG Main Effect	5	58740.26456	11748.05291	12.07	0.0001
Plant by MCG Interac	10	47581.48147	4758.14815	4.89	0.0001

Then, compare output from the test statements of proc reg.

Dependent Variable: MEANLNG

Test: ALLEQ Numerator: 19295.1102 DF: 17 F value: 19.8270
 Denominator: 973.1736 DF: 90 Prob>F: 0.0001

Dependent Variable: MEANLNG

Test: PLANT Numerator: 110847.5637 DF: 2 F value: 113.9032
 Denominator: 973.1736 DF: 90 Prob>F: 0.0001

Dependent Variable: MEANLNG

Test: FUNGUS Numerator: 11748.0529 DF: 5 F value: 12.0719
 Denominator: 973.1736 DF: 90 Prob>F: 0.0001

Dependent Variable: MEANLNG

Test: P_BY_F Numerator: 4758.1481 DF: 10 F value: 4.8893
 Denominator: 973.1736 DF: 90 Prob>F: 0.0001

Okay, now we know how to do anything. Finally, it is time to graph the interaction, and find out what these results mean!

First, we see a sizable and clear main effect for Plant. In fact, going back to the analysis of variance summary tables and dividing the Sum of Squares explained by Plant by the Total Sum of Squares, we observe that Plant explains around 53 percent of the variation in mean lesion length. That's huge. We will definitely want to look at pairwise comparisons of marginal means, too; we'll get back to this later.

Looking at the pattern of means, it's clear that while the main effect of fungus type is statistically significant, this is not something that should be interpreted, because which one is best (worst) depends on the type of plant. That is, we need to look at the interaction.

Before proceeding I should mention that many text advise us to *never* interpret main effects if the interaction is statistically significant. I disagree, and Figure 7.3 is a good example of why. It is clear that while the magnitudes of the differences depend on type of fungus, the lesion lengths are generally largest on Westar and smallest on GP159. So averaging over fungus types is a reasonable thing to do.

This does not mean the interaction should be ignored; the three profiles really look different. In particular, GP159 not only has a smaller average lesion length, but it seems to exhibit less responsiveness to different strains of fungus. A test for the equality of μ_1 through μ_6 would be valuable. Pairwise comparisons of the 6 means for Hanna and the 6 means for Westar look promising, too.

A Brief Consideration of Multiple Comparisons The mention of pairwise comparisons brings up the issue of formal multiple comparison follow-up tests for this problem. The way people often do follow-up tests for factorial designs is to make a combination variable and then do all pairwise comparisons. It seems like they do this because they think it's the only thing the software will let them do. Certainly it's better than nothing. Here are some comments:

- With SAS, pairwise comparisons of cell means are not the only thing you can do. `Proc glm` will do all pairwise comparisons of marginal means quite easily. This means it's easy to follow up a significant and meaningful main effect.
- For the present problem, there are 120 possible pairwise comparisons of the 16 cell means. If we do all these as one-at-a-time tests, the chances of false significance are certainly mounting. There is a strong case here for protecting the tests at a single joint significance level.
- Since the sample sizes are equal, Tukey tests are most powerful for all pairwise comparisons. But it's not so simple. Pairwise comparisons within plants (for example, comparing the 6 means for Westar) are interesting, and pairwise comparisons within fungus types (for example, comparison of Hanna, Westar and GP159 for fungus Type 1) are interesting, but the remaining 57 pairwise comparisons are a lot less so.
- Also, pairwise comparisons of cell means are not all we want to do. We've already mentioned the need for pairwise comparisons of the marginal means for plants, and

we'll soon see that other, less standard comparisons are of interest.

Everything we need to do will involve testing collections of contrasts. The approach we'll take is to do everything as a one-at-a-time custom test initially, and then figure out how we should correct for the fact that we've done a lot of tests.

It's good to be guided by the data. Here we go. The analyses will be done in the SAS program `green2.sas`. As usual, the entire program is given first. But you should be aware that the program was written one piece at a time and executed many times, with later analyses being suggested by the earlier ones.

The program starts by reading in the file `ghbread.sas`, which is just `ghread.sas` with the additional variables defined (especially `combo` and `mu1` through `mu18`) that were defined in `green1.sas`.

```

/* green2.sas: */
%include '/folders/myfolders/ghbread.sas';
options pagesize=100;

proc glm;
  title 'Repeating initial Plant by MCG ANOVA, full design';
  class plant mcg;
  model meanlng = plant|mcg;
  means plant|mcg;

/* A. Pairwise comparisons of marginal means for plant, full design
   B. Test all GP159 means equal, full design
   C. Test profiles for Hanna & Westar parallel, full design      */

proc reg;
  model meanlng = mu1-mu18 / noint;
  A_GvsH: test mu1+mu2+mu3+mu4+mu5+mu6 = mu7+mu8+mu9+mu10+mu11+mu12;
  A_GvsW: test mu1+mu2+mu3+mu4+mu5+mu6 = mu13+mu14+mu15+mu16+mu17+mu18;
  A_HvsW: test mu7+mu8+mu9+mu10+mu11+mu12 = mu13+mu14+mu15+mu16+mu17+mu18;
  B_G159eq: test mu1=mu2=mu3=mu4=mu5=mu6;
  C_HWpar: test mu8-mu7=mu14-mu13, mu9-mu8=mu15-mu14,
               mu10-mu9=mu16-mu15, mu11-mu10=mu17-mu16,
               mu12-mu11=mu18-mu17;

/* D. Oneway on mcg, GP158 subset */

data just159; /* This data set will have just GP159 */
  set mould;
  if plant=1;

```

```

proc glm data=just159;
  title 'D. Oneway on mcg, GP158 subset';
  class mcg;
  model meanlng = mcg;

/* E. Plant by MCG, Hanna-Westar subset */

data hanstar; /* This data set will have just Hanna and Westar */
  set mould;
  if plant ne 1;

proc glm data=hanstar;
  title 'E. Plant by MCG, Hanna-Westar subset';
  class plant mcg;
  model meanlng = plant|mcg;

/* F. Plant by MCG followup, Hanna-Westar subset
      Interaction: Follow with all pairwise differences of
      Westar minus Hanna differences
  G. Differences within Hanna?
  H. Differences within Westar? */

proc reg;
  model meanlng = mu7-mu18 / noint;
  F_inter: test mu13-mu7=mu14-mu8=mu15-mu9
              = mu16-mu10=mu17-mu11=mu18-mu12;
  F_1vs2: test mu13-mu7=mu14-mu8;
  F_1vs3: test mu13-mu7=mu15-mu9;
  F_1vs7: test mu13-mu7=mu16-mu10;
  F_1vs8: test mu13-mu7=mu17-mu11;
  F_1vs9: test mu13-mu7=mu18-mu12;
  F_2vs3: test mu14-mu8=mu15-mu9;
  F_2vs7: test mu14-mu8=mu16-mu10;
  F_2vs8: test mu14-mu8=mu17-mu11;
  F_2vs9: test mu14-mu8=mu18-mu12;
  F_3vs7: test mu15-mu9=mu16-mu10;
  F_3vs8: test mu15-mu9=mu17-mu11;
  F_3vs9: test mu15-mu9=mu18-mu12;
  F_7vs8: test mu16-mu10=mu17-mu11;
  F_7vs9: test mu16-mu10=mu18-mu12;
  F_8vs9: test mu17-mu11=mu18-mu12;
  G_Hanaeq: test mu7=mu8=mu9=mu10=mu11=mu12;
  H_Westeq: test mu13=mu14=mu15=mu16=mu17=mu18;

```

```

proc glm data=hanstar;
  class combo;
  model meanlng = combo;
  lsmeans combo / pdiff adjust=scheffe;

proc iml;
title 'Table of Scheffe critical values for COLLECTIONS of contrasts';
title2 'Start with interaction';
  numdf = 5; /* Numerator degrees of freedom for initial test */
  dendf = 60; /* Denominator degrees of freedom for initial test */
  alpha = 0.05;
  critval = finv(1-alpha,numdf,dendf);
  zero = {0 0}; S_table = repeat(zero,numdf,1); /* Make empty matrix */
  /* Label the columns */
  namz = {"Number of Contrasts in followup test"
         "   Scheffe Critical Value"};
  mattrib S_table colname=namz;
  do i = 1 to numdf;
    s_table(|i,1|) = i;
    s_table(|i,2|) = numdf/i * critval;
  end;
  reset noname; /* Makes output look nicer in this case */
  print "Initial test has" numdf " and " dendf "degrees of freedom."
        "Using significance level alpha = " alpha;
  print s_table;

proc iml;
title 'Table of Scheffe critical values for COLLECTIONS of contrasts';
title2 'Start with all means equal';
  numdf = 11; /* Numerator degrees of freedom for initial test */
  dendf = 60; /* Denominator degrees of freedom for initial test */
  alpha = 0.05;
  critval = finv(1-alpha,numdf,dendf);
  zero = {0 0}; S_table = repeat(zero,numdf,1); /* Make empty matrix */
  /* Label the columns */
  namz = {"Number of Contrasts in followup test"
         "   Scheffe Critical Value"};
  mattrib S_table colname=namz;
  do i = 1 to numdf;
    s_table(|i,1|) = i;
    s_table(|i,2|) = numdf/i * critval;
  end;
  reset noname; /* Makes output look nicer in this case */
  print "Initial test has" numdf " and " dendf "degrees of freedom."

```

```

        "Using significance level alpha = " alpha;
    print s_table;

proc reg data=hanstar;
    title 'One more try at following up the interaction';
    model meanlng = mu7-mu18 / noint;
    onemore: test mu8-mu7 = mu14-mu13;

```

After reading and defining the data with a `%include` statement, the program repeats the initial three by six ANOVA from `green1.sas`. This is just for completeness. Then the SAS program performs tasks labelled **A** through **H**.

Task A `proc reg` is used to fit a cell means model, and then test for all three pairwise differences among Plant means. They are all significantly different from each other, confirming what appears visually in the interaction plot.

```

proc reg;
    model meanlng = mu1-mu18 / noint;
    A_GvsH: test mu1+mu2+mu3+mu4+mu5+mu6 = mu7+mu8+mu9+mu10+mu11+mu12;
    A_GvsW: test mu1+mu2+mu3+mu4+mu5+mu6 = mu13+mu14+mu15+mu16+mu17+mu18;
    A_HvsW: test mu7+mu8+mu9+mu10+mu11+mu12 = mu13+mu14+mu15+mu16+mu17+mu18;

```

Dependent Variable: MEANLNG

Test: A_GVSH	Numerator:	31217.5679	DF:	1	F value:	32.0781
	Denominator:	973.1736	DF:	90	Prob>F:	0.0001

Dependent Variable: MEANLNG

Test: A_GVSW	Numerator:	217443.4318	DF:	1	F value:	223.4374
	Denominator:	973.1736	DF:	90	Prob>F:	0.0001

Dependent Variable: MEANLNG

Test: A_HVSW	Numerator:	83881.6915	DF:	1	F value:	86.1940
	Denominator:	973.1736	DF:	90	Prob>F:	0.0001

As mentioned earlier, GP159 not only has a smaller average lesion length, but it seems to exhibit less variation in its vulnerability to different strains of fungus. Part of the significant interaction must come from this, and part from differences in the profiles of Hanna and Westar. Two questions arise:

1. Are μ_1 through μ_6 (the means for GP159) actually different from each other?

2. Are the profiles for Hanna and Westar different?

There are two natural ways to address these questions. The naive way is to subset the data — that is, do a one-way ANOVA to compare the 6 means for GP159, and a two-way (2 by 6) on the Hanna-Westar subset. In the latter analysis, the interaction of Plant by MCG would indicate whether the two profiles were different.

A more sophisticated approach is not to subset the data, but to recognize that both questions can be answered by testing collections of contrasts of the entire set of 18 means; it's easy to do with the test statement of `proc reg`.

The advantage of the sophisticated approach is this. Remember that the model specifies a conditional normal distribution of the response variable for each combination of explanatory variable values (in this case there are 18 combinations of explanatory variable values), and that each conditional distribution has the *same variance*. The test for, say, the equality of μ_1 through μ_6 would use only \bar{Y}_1 through \bar{Y}_6 (that is, just GP159 data) to estimate the 5 contrasts involved, but it would use *all* the data to estimate the common error variance. From both a commonsense viewpoint and the deepest possible theoretical viewpoint, it's better not to throw information away. This is why the sophisticated approach should be better.

However, this argument is convincing only if it's really true that the response variable has the same variance for every combination of explanatory variable values. Repeating some output from the means command of the very first `proc glm`,

Level of PLANT	Level of MCG	N	-----MEANLNG-----	
			Mean	SD
GP159	1	6	12.863095	12.8830306
GP159	2	6	21.623810	17.3001296
GP159	3	6	14.460714	7.2165396
GP159	7	6	17.686905	16.4258441
GP159	8	6	8.911905	7.3162618
GP159	9	6	8.784524	6.5970501
HANNA	1	6	45.578571	26.1430472
HANNA	2	6	67.296429	30.2424997
HANNA	3	6	94.192857	20.2877876
HANNA	7	6	53.621429	24.8563497
HANNA	8	6	47.838095	12.6419109
HANNA	9	6	25.673810	17.1723150
WESTAR	1	6	65.908333	35.6968616
WESTAR	2	6	187.479762	45.1992178
WESTAR	3	6	154.103571	26.5469183
WESTAR	7	6	173.972619	79.1793105
WESTAR	8	6	95.823810	22.3712022
WESTAR	9	6	66.502381	52.5253101

We see that the sample standard deviations for GP159 look quite a bit smaller on average. Without bothering to do a formal test, we have some reason to doubt the equal variances assumption. It's easy to see why GP159 would have less plant-to-plant variation in lesion length. It's so resistant to the fungus that there's just not that much fungal growth, period. So there's less *opportunity* for variation.

Note that the equal variances assumption is essentially just a mathematical convenience. Here, it's clearly unrealistic. But what's the consequence of violating it? It's well known that the equal variance assumption can be safely violated if the cell sample sizes are equal and large. Well, here they're equal, but $n = 6$ is not large. So this is not reassuring.

It's not easy to say in general *how* the tests will be affected when the equal variance assumption is violated, but for the two particular cases we're interested in here (are the GP159 means equal and are the Hanna and Westar profiles parallel), we can figure it out. Formula 5.4 for the F -test (see page 125) says

$$F = \frac{(SSR_F - SSR_R)/r}{MSE_F}.$$

The denominator (Mean Squared Error from the full model) is the estimated population error variance. That's the variance that's supposed to be the same for each conditional distribution. Since

$$MSE = \frac{\sum_{i=1}^n (Y_i - \hat{Y}_i)^2}{n - p}$$

and the predicted value \hat{Y}_i is always the cell mean, we can draw the following conclusions. Assume that the true variance is smaller for GP159.

1. When we test for equality of the GP159 means, using the Hanna-Westar data to help compute MSE will make the denominator of F bigger than it should be. So F will be smaller, and the test is too conservative. That is, it is less likely to detect differences that are really present.
2. When we test whether the Hanna and Westar profiles are parallel, use of the GP159 data to help compute MSE will make the denominator of F *smaller* than it should be – so F will be bigger, and the test will not be conservative enough. That is, the chance of significance if the effect is absent will be greater than 0.05. And a Type I error rate above 0.05 is always to be avoided if possible.

This makes me inclined to favour the "naive" subsetting approach. Because the GP159 means *look* so equal, and I want them to be equal, I'd like to give the test for difference among them the best possible chance. And because it looks like the profiles for Hanna and Westar are not parallel (and I want them to be non-parallel, because it's more interesting if the effect of Fungus type depends on type of Plant), I want a more conservative test.

Another argument in favour of subsetting is based on botany rather than statistics. Hanna and Westar are commercial canola crop varieties, but while GP159 is definitely in

the canola family, it is more like a hardy weed than a food plant. It's just a different kind of entity, and so analyzing its data separately makes a lot of sense.

You may wonder, if it's so different, why was it included in the design in the first place? Well, taxonomically it's quite similar to Hanna and Westar; really no one knew it would be such a vigorous monster in terms of resisting fungus. That's why people do research – to find out things they didn't already know.

Anyway, we'll do the analysis both ways – both the seemingly naive way which is probably better once you think about it, and the sophisticated way that uses the complete set of data for all analyses.

Tasks B and C These represent the “sophisticated” approach that does not subset the data.

B: Test all GP159 means equal, full design

C: Test profiles for Hanna and Westar parallel, full design

```
proc reg;
  model meanlng = mu1-mu18 / noint;
  A_GvsH: test mu1+mu2+mu3+mu4+mu5+mu6 = mu7+mu8+mu9+mu10+mu11+mu12;
  A_GvsW: test mu1+mu2+mu3+mu4+mu5+mu6 = mu13+mu14+mu15+mu16+mu17+mu18;
  A_HvsW: test mu7+mu8+mu9+mu10+mu11+mu12 = mu13+mu14+mu15+mu16+mu17+mu18;
  B_G159eq: test mu1=mu2=mu3=mu4=mu5=mu6;
  C_HWpar: test mu8-mu7=mu14-mu13, mu9-mu8=mu15-mu14,
               mu10-mu9=mu16-mu15, mu11-mu10=mu17-mu16,
               mu12-mu11=mu18-mu17;
```

Dependent Variable: MEANLNG

Test: B_G159EQ	Numerator:	151.5506	DF:	5	F value:	0.1557
	Denominator:	973.1736	DF:	90	Prob>F:	0.9778

Dependent Variable: MEANLNG

Test: C_HWP	Numerator:	5364.0437	DF:	5	F value:	5.5119
	Denominator:	973.1736	DF:	90	Prob>F:	0.0002

This confirms the visual impression of no differences among means for GP159, and non-parallel profiles for Hanna and Westar.

Task D Now compare the subsetting approach. We will carry out a oneway ANOVA on MCG, using just the GP159 subset. Notice the creation of SAS data sets with subsets of the data.

```

data just159; /* This data set will have just GP159 */
  set mould;
  if plant=1;

proc glm data=just159;
  title 'D. Oneway on mcg, GP158 subset';
  class mcg;
  model meanlng = mcg;

```

D. Oneway on mcg, GP158 subset						2
General Linear Models Procedure						
Dependent Variable: MEANLNG		Average Lesion length				
Source	DF	Sum of Squares	Mean Square	F Value	Pr > F	
Model	5	757.75319161	151.55063832	1.03	0.4189	
Error	30	4421.01258503	147.36708617			
Corrected Total	35	5178.76577664				
	R-Square	C.V.	Root MSE	MEANLNG Mean		
	0.146319	86.37031	12.139485	14.055159		
Source	DF	Type I SS	Mean Square	F Value	Pr > F	
MCG	5	757.75319161	151.55063832	1.03	0.4189	
Source	DF	Type III SS	Mean Square	F Value	Pr > F	
MCG	5	757.75319161	151.55063832	1.03	0.4189	

This analysis is consistent with what we got without subsetting the data. That is, it does not provide evidence that the means for GP159 are different. But when we didn't subset the data, we had $p = 0.9778$. This happened exactly because including Hanna and Westar data made MSE larger, F smaller, and hence p bigger.

Task E Now we will do a Plant by MCG analysis, using just the Hanna-Westar subset of the data.

```

data hanstar; /* This data set will have just Hanna and Westar */

```

```

set mould;
if plant ne 1;

proc glm data=hanstar;
  title 'E. Plant by MCG, Hanna-Westar subset';
  class plant mcg;
  model meanlng = plant|mcg;

```

E. Plant by MCG, Hanna-Westar subset 3

General Linear Models Procedure
Class Level Information

Class	Levels	Values
PLANT	2	HANNA WESTAR
MCG	6	1 2 3 7 8 9

Number of observations in data set = 72

E. Plant by MCG, Hanna-Westar subset 4

General Linear Models Procedure

Dependent Variable: MEANLNG		Average Lesion length			
Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	11	189445.68433	17222.33494	12.43	0.0001
Error	60	83164.61331	1386.07689		
Corrected Total	71	272610.29764			
	R-Square	C.V.	Root MSE	MEANLNG Mean	
	0.694932	41.44379	37.230054	89.832639	

Source	DF	Type I SS	Mean Square	F Value	Pr > F
PLANT	1	83881.691486	83881.691486	60.52	0.0001
MCG	5	78743.774570	15748.754914	11.36	0.0001
PLANT*MCG	5	26820.218272	5364.043654	3.87	0.0042

Source	DF	Type III SS	Mean Square	F Value	Pr > F
PLANT	1	83881.691486	83881.691486	60.52	0.0001
MCG	5	78743.774570	15748.754914	11.36	0.0001
PLANT*MCG	5	26820.218272	5364.043654	3.87	0.0042

The significant interaction indicates that the profiles for Hanna and Westar are non-parallel, confirming the visual impression we got from the interaction plot. But the p-value is larger this time. When all the data were used to calculate the error term, we had $p = 0.0002$; but now it rises to $p = 0.0042$. This is definitely due to the low variation in GP159. Further analyses will be limited to the Hanna-Westar subset.

Now think of the interaction in a different way. Overall, Hanna is more vulnerable than Westar, but the interaction says that the degree of that greater vulnerability depends on the type of fungus. For each of the 6 types of fungus, there is a *difference* between Hanna and Westar. Let's look at pairwise differences of these differences. We might be able to say, then, something like this: "The difference in vulnerability between Hanna and Westar is greater for Fungus Type 2 than Fungus Type 1."

Task F: Plant by MCG followup, Hanna-Westar subset. First, verify that the interaction can be expressed as a collection of differences between differences. Of course it can.

```
proc reg;
  model meanlmg = mu7-mu18 / noint;
  F_inter: test  mu13-mu7=mu14-mu8=mu15-mu9
                = mu16-mu10=mu17-mu11=mu18-mu12;
  F_1vs2: test  mu13-mu7=mu14-mu8;
  F_1vs3: test  mu13-mu7=mu15-mu9;
  F_1vs7: test  mu13-mu7=mu16-mu10;
  F_1vs8: test  mu13-mu7=mu17-mu11;
  F_1vs9: test  mu13-mu7=mu18-mu12;
  F_2vs3: test  mu14-mu8=mu15-mu9;
  F_2vs7: test  mu14-mu8=mu16-mu10;
  F_2vs8: test  mu14-mu8=mu17-mu11;
  F_2vs9: test  mu14-mu8=mu18-mu12;
  F_3vs7: test  mu15-mu9=mu16-mu10;
  F_3vs8: test  mu15-mu9=mu17-mu11;
```

F_3vs9: test $\mu_{15}-\mu_9=\mu_{18}-\mu_{12}$;
 F_7vs8: test $\mu_{16}-\mu_{10}=\mu_{17}-\mu_{11}$;
 F_7vs9: test $\mu_{16}-\mu_{10}=\mu_{18}-\mu_{12}$;
 F_8vs9: test $\mu_{17}-\mu_{11}=\mu_{18}-\mu_{12}$;

Dependent Variable: MEANLNG

Test: F_INTER Numerator: 5364.0437 DF: 5 F value: 3.8699
 Denominator: 1386.077 DF: 60 Prob>F: 0.0042

Dependent Variable: MEANLNG

Test: F_1VS2 Numerator: 14956.1036 DF: 1 F value: 10.7902
 Denominator: 1386.077 DF: 60 Prob>F: 0.0017

Dependent Variable: MEANLNG

Test: F_1VS3 Numerator: 2349.9777 DF: 1 F value: 1.6954
 Denominator: 1386.077 DF: 60 Prob>F: 0.1979

Dependent Variable: MEANLNG

Test: F_1VS7 Numerator: 15006.4293 DF: 1 F value: 10.8265
 Denominator: 1386.077 DF: 60 Prob>F: 0.0017

Dependent Variable: MEANLNG

Test: F_1VS8 Numerator: 1147.2776 DF: 1 F value: 0.8277
 Denominator: 1386.077 DF: 60 Prob>F: 0.3666

Dependent Variable: MEANLNG

Test: F_1VS9 Numerator: 630.3018 DF: 1 F value: 0.4547
 Denominator: 1386.077 DF: 60 Prob>F: 0.5027

Dependent Variable: MEANLNG

Test: F_2VS3 Numerator: 5449.1829 DF: 1 F value: 3.9314
 Denominator: 1386.077 DF: 60 Prob>F: 0.0520

Dependent Variable: MEANLNG

Test: F_2VS7 Numerator: 0.0423 DF: 1 F value: 0.0000
 Denominator: 1386.077 DF: 60 Prob>F: 0.9956

Dependent Variable: MEANLNG

Test: F_2VS8 Numerator: 7818.7443 DF: 1 F value: 5.6409
 Denominator: 1386.077 DF: 60 Prob>F: 0.0208

Dependent Variable: MEANLNG

Test: F_2VS9 Numerator: 9445.7674 DF: 1 F value: 6.8147
 Denominator: 1386.077 DF: 60 Prob>F: 0.0114

Dependent Variable: MEANLNG

Test: F_3VS7 Numerator: 5479.5767 DF: 1 F value: 3.9533
 Denominator: 1386.077 DF: 60 Prob>F: 0.0513

Dependent Variable: MEANLNG

Test: F_3VS8 Numerator: 213.3084 DF: 1 F value: 0.1539
 Denominator: 1386.077 DF: 60 Prob>F: 0.6962

Dependent Variable: MEANLNG

Test: F_3VS9 Numerator: 546.1923 DF: 1 F value: 0.3941
 Denominator: 1386.077 DF: 60 Prob>F: 0.5326

Dependent Variable: MEANLNG

Test: F_7VS8 Numerator: 7855.1432 DF: 1 F value: 5.6672
 Denominator: 1386.077 DF: 60 Prob>F: 0.0205

Dependent Variable: MEANLNG

Test: F_7VS9 Numerator: 9485.7704 DF: 1 F value: 6.8436
 Denominator: 1386.077 DF: 60 Prob>F: 0.0112

Dependent Variable: MEANLNG

Test: F_8VS9 Numerator: 76.8370 DF: 1 F value: 0.0554
 Denominator: 1386.077 DF: 60 Prob>F: 0.8147

Tasks G and H Finally we test separately for MCG differences within Hanna and within Westar.

G_Hanaeq: test $\mu_7=\mu_8=\mu_9=\mu_{10}=\mu_{11}=\mu_{12}$;
 H_Westeq: test $\mu_{13}=\mu_{14}=\mu_{15}=\mu_{16}=\mu_{17}=\mu_{18}$;

 E. Plant by MCG, Hanna-Westar subset
 The REG Procedure

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Test G_Hanaeq Results for Dependent Variable meanlng

Source	DF	Mean Square	F Value	Pr > F
--------	----	----------------	---------	--------

Numerator	5	3223.58717	2.33	0.0536
Denominator	60	1386.07689		

Test H_Westeq Results for Dependent Variable meanlg

Source	DF	Mean Square	F Value	Pr > F
Numerator	5	17889	12.91	<.0001
Denominator	60	1386.07689		

There is evidence of differences in mean lesion length within Westar, but not Hanna. It makes sense to follow up with pairwise comparisons of the MCG means for just Westar, but first let's review what we've done so far, limiting the discussion to just the Hanna-Westar subset of the data. We've tested

- Overall difference among the 12 means
- Main effect for PLANT
- Main effect for MCG
- PLANT*MCG interaction
- 15 pairwise comparisons of the Hanna-Westar difference, following up the interaction
- One comparison of the 6 means for Hanna
- One comparison of the 6 means for Westar

That's 21 tests in all, and we really should do at least 15 more, testing for pairwise differences among the Westar means. Somehow, we should make this into a set of proper post-hoc tests, and correct for the fact that we've done a lot of them. But how? Tukey tests are only good for pairwise comparisons, and a Bonferroni correction is very ill-advised, since these tests were not all planned before seeing the data. This pretty much leaves us with Scheffé or nothing.

Scheffé Tests Because some of the tests we've done are for more than one contrast at a time, the discussion of Scheffé tests for *collections* of contrasts in Section 3.4.5 (page 89) is relevant. But Section 3.4.5 is focused on the case where we are following up a significant difference among *all* the treatment means. Here, the initial test may or may not be a test for equality of all the means. We might start somewhere else, like with a test for an interaction or main effect. It's a special case of Scheffé tests for regression (Section 5.10, page 143).

Assume a multifactor design. Create a combination explanatory variable whose values are all combinations of factor levels. All the tests we do will be tests for collections consisting of one or more contrasts of the cell means. Start with a statistically significant initial test, an F -test for r contrasts. A Scheffé follow-up test will be a test for s contrasts, not necessarily a subset of the contrasts of the initial test. The follow-up test must obey these rules:

- $s < r$
- If all r contrasts of the initial test are zero in the population, then all s contrasts of the follow-up test must be zero in the population. In other words, the null hypothesis of the follow-up test must be implied by the null hypothesis of the initial test. (The follow-up tests are *proper* follow-ups; see Section 3.4.6, page 91).

Next, compute the ordinary one-at-a-time F statistic for the follow-up test (it will have s and $n - p$ degrees of freedom). Then, use the Scheffé critical value of Equation 5.8 on page 143, which is repeated here for convenience:

$$f_{Sch} = \frac{r}{s} f_{crit},$$

where f_{crit} is the usual critical value for the initial test. Then, considered as a Scheffé follow-up, the test is significant at the *joint* 0.05 level if the computed value of F for the collection of contrasts is greater than f_{Sch} .

Actually, the formula given above is more general. It applies to testing linear combinations of regression coefficients in a multiple regression setting (see Section 5.10, page 143). The initial test is a test of r linear constraints on the regression coefficients, and the follow-up test is a test of s linear constraints, where $s < r$ and the linear constraints of the initial test imply the linear constraints of the follow-up test. This is very nice because it allows, for example, Scheffé follow-ups to a significant analysis of covariance.

Before applying Scheffé adjustments to the tests we have done on the greenhouse data, a few comments are in order.

- The term “linear constraints” may sound imposing, but a linear constraint is just a statement that some linear combination equals a constant. Almost always, the constant is zero. So for example, saying that a contrast of cell means is equal to zero is the same as specifying a linear constraint on the betas of a multiple regression model (for example, with cell means coding).
- If you’re testing 6 explanatory variables controlling for some other set of explanatory variables, the null hypothesis says that 6 regression coefficients are equal to zero. That’s six linear constraints on the regression coefficients.
- In the initial one-way ANOVA setting (Section 3.4.3, page 84) where we were testing single contrasts of p cell means, the Scheffé adjusted critical value was defined by $f_{Sch} = (p - 1)f_{crit}$. This was a special case of $f_{Sch} = \frac{r}{s}f_{crit}$. The initial test for equality of p means involved $p - 1$ contrasts, so $r = p - 1$. The followup tests were all for single contrasts, so $s = 1$.

- As in the case of testing single contrasts in a one-way design, it is impossible for a follow-up to be significant if the initial test is not. And if the initial test is significant, there is always something to find in the family of Scheffé follow-ups.
- Suppose we have a follow-up test for s linear constraints, and it's not significant. Then every Scheffé follow-up test whose null hypothesis is implied by those constraints will also be non-significant. To use the metaphor of data fishing, once you've looked for fish in a particular region of the lake and determined that there's nothing there, further detailed exploration in that region is a waste of time.

The formula $f_{Sch} = \frac{r}{s} f_{crit}$ is very simple to apply. There are only two potential complications, and they are related to one another.

- First, you have to know what significance test you are following up. For example, if your initial test is the test for equality of all cell means, then the test for a given main effect could be carried out as a Scheffé follow-up, and a pairwise comparison of marginal means would be another follow-up to the same initial test. Or, you could start with the test for the main effect. Then, the pairwise comparison of marginal means would be a follow-up to the one-at-a-time test for the main effect. You could do it either way, and the conclusions might differ. Where you start is a matter of data-analytic philosophy. But starting with the standard tests for main effects and interactions is more traditional.
- The second potential complication is that you really have to be sure that the null hypothesis of the initial test implies the null hypothesis of the follow-up test. In terms of `proc reg` syntax, it means that the `test` statement of the initial test implies the `test` statements of all the follow-up tests. Sometimes this is easy to check, and sometimes it is tricky. To a large extent, how easy it is to check depends on what the initial test is.
 - If the initial test is a test for all cell means being equal (a one-way ANOVA on the combination variable), then it's easy, because if all the cell means are equal, then any possible contrast of the cell means equals zero. The proof is one line of High School algebra.
 - Similarly, suppose we are using a regression model with an intercept, and the initial test is for all the regression coefficients except β_0 simultaneously. This means that the null hypothesis of the initial test is $H_0 : \beta_1 = \dots = \beta_{p-1} = 0$, and therefore any linear combination of those quantities is zero. This means that you can test any subset of explanatory variables controlling for all the others as a proper Scheffé follow-up to the first test SAS prints.
 - If you're following up tests for main effects, then the standard test for any contrast of marginal means is a proper follow-up to the test for the main effect.

Beyond these principles, the logical connection between initial and follow-up tests really needs to be checked on a case-by-case basis. Often, the initial test can be expressed

more than one way in the test statement of `proc reg`, and one of those statements will make things clear enough so you don't need to do any algebra. This is what I did with the significant Plant by Fungus interaction for the Hanna-Westar subset. When the interaction was written as

```
F_inter: test  mu13-mu7=mu14-mu8=mu15-mu9
              = mu16-mu10=mu17-mu11=mu18-mu12;
```

it was clear that all the pairwise comparisons of Westar-Hanna differences were implied.

```
F_1vs2: test  mu13-mu7=mu14-mu8;
F_1vs3: test  mu13-mu7=mu15-mu9;
F_1vs7: test  mu13-mu7=mu16-mu10;
F_1vs8: test  mu13-mu7=mu17-mu11;
F_1vs9: test  mu13-mu7=mu18-mu12;
F_2vs3: test  mu14-mu8=mu15-mu9;
F_2vs7: test  mu14-mu8=mu16-mu10;
F_2vs8: test  mu14-mu8=mu17-mu11;
F_2vs9: test  mu14-mu8=mu18-mu12;
F_3vs7: test  mu15-mu9=mu16-mu10;
F_3vs8: test  mu15-mu9=mu17-mu11;
F_3vs9: test  mu15-mu9=mu18-mu12;
F_7vs8: test  mu16-mu10=mu17-mu11;
F_7vs9: test  mu16-mu10=mu18-mu12;
F_8vs9: test  mu17-mu11=mu18-mu12;
```

Sometimes it is easy to get this wrong. Just note that SAS will do all pairwise comparisons of marginal means (in the `means` statement of `proc glm`) as Scheffé follow-ups, but don't trust it unless the sample sizes are equal. Do it yourself. This warning applies up to SAS version 6.10. Is it a real error, or was it done deliberately to minimize calls to technical support? It's impossible to tell.

Now let's proceed, limiting the analysis to the Hanna-Westar subset. Just for fun, we'll start in two places. Our initial test will be either the test for equality of all 12 cell means, or the test for the Plant by Fungus interaction. Thus, we need two tables of critical values.

```
proc iml;
title 'Table of Scheffe critical values for COLLECTIONS of contrasts';
title2 'Start with all means equal';
  numdf = 11; /* Numerator degrees of freedom for initial test */
  dendf = 60; /* Denominator degrees of freedom for initial test */
  alpha = 0.05;
  critval = finv(1-alpha,numdf,dendf);
  zero = {0 0}; S_table = repeat(zero,numdf,1); /* Make empty matrix */
  /* Label the columns */
```

```

namz = {"Number of Contrasts in followup test"
        "    Scheffe Critical Value"};
mattrib S_table colname=namz;
do i = 1 to numdf;
    s_table(|i,1|) = i;
    s_table(|i,2|) = numdf/i * critval;
end;
reset noname; /* Makes output look nicer in this case */
print "Initial test has" numdf " and " dendf "degrees of freedom."
      "Using significance level alpha = " alpha;
print s_table;

```

Table of Scheffe critical values for COLLECTIONS of contrasts
Start with all means equal

37

Initial test has 11 and 60 degrees of freedom.
Using significance level alpha = 0.05

Number of Contrasts in followup test	Scheffe Critical Value
1	21.474331
2	10.737166
3	7.1581104
4	5.3685828
5	4.2948663
6	3.5790552
7	3.0677616
8	2.6842914
9	2.3860368
10	2.1474331
11	1.9522119

Let's start by treating the tests for main effects and the interaction as follow-ups to the significant ANOVA on the combination variable ($F = 12.43$; $df = 11, 71$; $p < .0001$). The table below collects numbers displayed earlier.

The interesting Plant by MCG interaction is no longer significant as a Scheffe test. This means that all the pairwise comparisons among Westar-Hanna differences will also be non-significant, as Scheffé follow-ups to the oneway ANOVA on the combination variable. There are no fish in that part of the lake. Just to check, the biggest Westar-Hanna difference was 120.35 for MCG 7, and the smallest was 20.33 for MCG 1. Comparing these two differences yielded a one-at-a-time F of 10.83. But $s = 1$ here, and the first

Table 7.8: Scheffé follow-ups to the test for differences among 12 means (Just Hanna and Westar)

Effect	s	F	Scheffé Critical Value	Significant?
Plant	1	60.52	21.47	Yes
MCG	5	11.36	4.29	Yes
Plant \times MCG	5	3.87	4.29	No
All Hanna Equal?	5	2.33	4.29	No
All Westar Equal?	5	12.91	4.29	Yes

row of Table 7.8 has the Scheffé critical value of $f_{Sch} = 21.47$, which may also be found in the `proc iml` output further above. So $F = 10.83$ falls short of the value required for significance, and as expected, none of the proper Scheffé follow-ups to a non-significant Scheffé follow-up are significant.

The last row of Table 7.8 shows that the MCG differences for just Westar are significant as a Scheffé follow-up, and so pairwise comparisons of the Westar means are of interest. The easiest way to do this is with Scheffé tests on pairwise differences using `proc glm`.

```
proc glm data=hanstar;
  class combo;
  model meanlng = combo;
  lsmeans combo / pdiff adjust=scheffe;
```

Adjustment for Multiple Comparisons: Scheffe

combo	meanlng LSMEAN	LSMEAN Number
7	45.578571	1
8	67.296429	2
9	94.192857	3
10	53.621429	4
11	47.838095	5
12	25.673810	6
13	65.908333	7
14	187.479762	8
15	154.103571	9
16	173.972619	10
17	95.823810	11
18	66.502381	12

Least Squares Means for effect combo
Pr > |t| for H0: LSMean(i)=LSMean(j)

Dependent Variable: meanlg

i/j	1	2	3	4	5	6
1		0.9999	0.9175	1.0000	1.0000	1.0000
2	0.9999		0.9994	1.0000	1.0000	0.9726
3	0.9175	0.9994		0.9775	0.9401	0.5241
4	1.0000	1.0000	0.9775		1.0000	0.9991
5	1.0000	1.0000	0.9401	1.0000		0.9999
6	1.0000	0.9726	0.5241	0.9991	0.9999	
7	1.0000	1.0000	0.9990	1.0000	1.0000	0.9789
8	0.0002	0.0047	0.0923	0.0008	0.0003	<.0001
9	0.0191	0.1620	0.7277	0.0457	0.0246	0.0016
10	0.0016	0.0235	0.2742	0.0046	0.0022	<.0001
11	0.8979	0.9989	1.0000	0.9696	0.9243	0.4845
12	0.9999	1.0000	0.9992	1.0000	1.0000	0.9764

Least Squares Means for effect combo
Pr > |t| for H0: LSMean(i)=LSMean(j)

Dependent Variable: meanlg

i/j	7	8	9	10	11	12
1	1.0000	0.0002	0.0191	0.0016	0.8979	0.9999
2	1.0000	0.0047	0.1620	0.0235	0.9989	1.0000
3	0.9990	0.0923	0.7277	0.2742	1.0000	0.9992
4	1.0000	0.0008	0.0457	0.0046	0.9696	1.0000
5	1.0000	0.0003	0.0246	0.0022	0.9243	1.0000
6	0.9789	<.0001	0.0016	<.0001	0.4845	0.9764
7		0.0039	0.1445	0.0201	0.9983	1.0000
8	0.0039		0.9955	1.0000	0.1071	0.0042
9	0.1445	0.9955		1.0000	0.7623	0.1518
10	0.0201	1.0000	1.0000		0.3058	0.0215
11	0.9983	0.1071	0.7623	0.3058		0.9986
12	1.0000	0.0042	0.1518	0.0215	0.9986	

It's actually just the last 6 means that we want to compare. Editing the output above by

hand and re-labelling the means with the MCG codes (1,2,3,7,8,9), we have

```

Least Squares Means for effect combo
Pr > |t| for H0: LSMean(i)=LSMean(j)

Dependent Variable: meanlng

i/j      1      2      3      7      8      9
1          0.0039  0.1445  0.0201  0.9983  1.0000
2    0.0039          0.9955  1.0000  0.1071  0.0042
3    0.1445    0.9955          1.0000  0.7623  0.1518
7    0.0201    1.0000    1.0000          0.3058  0.0215
8    0.9983    0.1071    0.7623    0.3058          0.9986
9    1.0000    0.0042    0.1518    0.0215    0.9986

```

In the following display (also edited by hand, but similar to what SAS produces with `means combo / scheffe;`) means with the same letter are not significantly different by a Scheffé test.

MCG	meanlng LSMEAN		
1	65.908333	A	
9	66.502381	A	
8	95.823810	A	B
3	154.103571	A	B
7	173.972619		B
2	187.479762		B

On Westar, fungus types 2 and 7 grow faster than types 1 and 9; types 8 and 3 occupy a middle ground, and their growth rates are not significantly different from either extreme group.

Comparing marginal MCG Means I still need to do this. Put it in `green2.sas`.

Starting with the Interaction Logically, a test for interaction can be a follow-up test, but almost no one ever does this in practice. It's much more traditional to start with a one-at-a-time test for interaction and then, if you're very sophisticated, do multiple comparison follow-ups to that initial test. Now we'll do this with Scheffé follow-ups In the present case $r = 5$, and the critical values are obtained from `proc iml` as before:

```

proc iml;
title 'Table of Scheffe critical values for COLLECTIONS of contrasts';
title2 'Start with interaction';
  numdf = 5; /* Numerator degrees of freedom for initial test */
  dendf = 60; /* Denominator degrees of freedom for initial test */
  alpha = 0.05;
  critval = finv(1-alpha,numdf,dendf);
  zero = {0 0}; S_table = repeat(zero,numdf,1); /* Make empty matrix */
  /* Label the columns */
  namz = {"Number of Contrasts in followup test"
         "      Scheffe Critical Value"};
  mattrib S_table colname=namz;
  do i = 1 to numdf;
    s_table(|i,1|) = i;
    s_table(|i,2|) = numdf/i * critval;
  end;
  reset noname; /* Makes output look nicer in this case */
  print "Initial test has" numdf " and " dendf "degrees of freedom."
        "Using significance level alpha = " alpha;
  print s_table;

```

Table of Scheffe critical values for COLLECTIONS of contrasts
Start with interaction

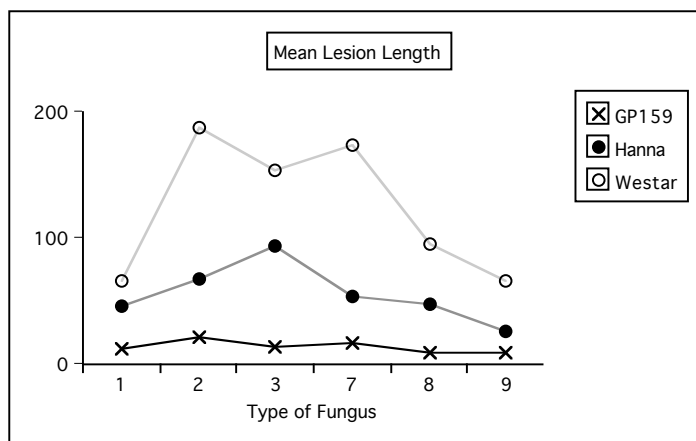
36

Initial test has 5 and 60 degrees of freedom.
 Using significance level alpha = 0.05

Number of Contrasts in followup test	Scheffe Critical Value
1	11.841351
2	5.9206756
3	3.9471171
4	2.9603378
5	2.3682702

So the Scheffé critical value for any single contrast is $f_{Sch} = 11.84$, and *none* none of the pairwise comparisons of Westar-Hanna differences reaches statistical significance as a Scheffé follow-up – even though they look very promising. As a mathematical certainty, there *is* a single-contrast Scheffé follow-up to the interaction that is significant, but it's

not one of these. Let's give it one more try. Look again at Figure 7.3 from page 202.



The profile for Westar goes up sharply between MCG 1 and 2, while it goes up less steeply for Hanna. This is the biggest absolute difference in line segment slopes.

```
proc reg data=hanstar;
  title 'One more try at following up the interaction';
  model meanlng = mu7-mu18 / noint;
  onemore: test mu8-mu7 = mu14-mu13;
```

One more try at following up the interaction

39

The REG Procedure

Model: MODEL1

Test onemore Results for Dependent Variable meanlng

Source	DF	Mean Square	F Value	Pr > F
Numerator	1	14956	10.79	0.0017
Denominator	60	1386.07689		

The F statistic does not reach the Scheffé critical value of 11.84, so this promising component of the interaction is also non-significant. Again, while we know that there *is* a contrast of the cell means that is significantly different from zero as a Scheffé follow-up, that does not mean it is easy to find.

7.4 Nested and random effects

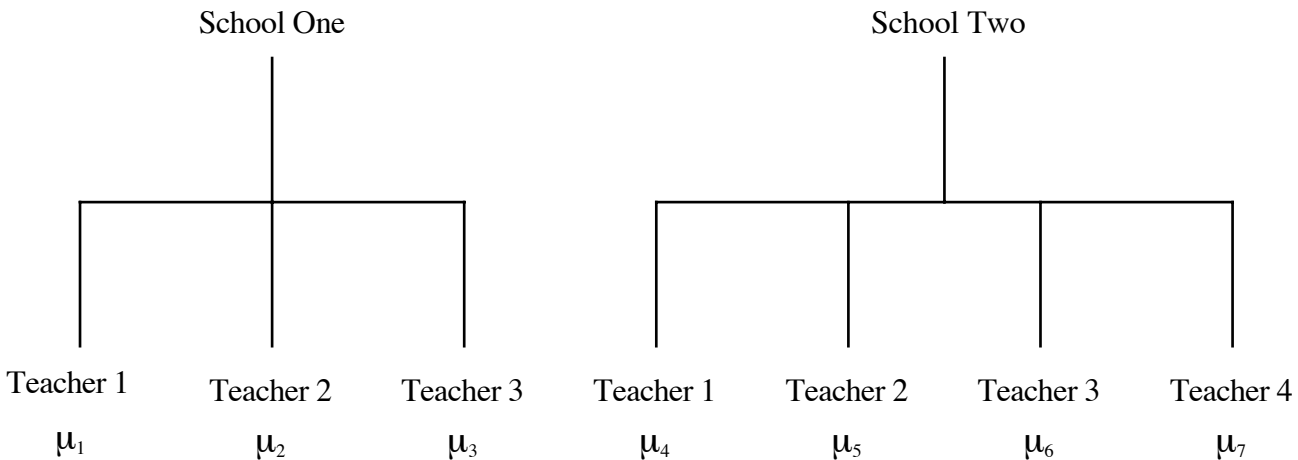
Rough draft begins on the following page. Of course it's not really Chapter 4.

Chapter Four: Nested and Random Effects Models

Nested Designs

Suppose a chain of commercial business colleges is teaching a software certification course. After 6 weeks of instruction, students take a certification exam and receive a score ranging from zero to 100. The owners of the business school chain want to see whether performance is related to which school students attend, or which instructor they have -- or both. They compare two schools; one of the schools has three instructors teaching the course, and the other school has 4 instructors teaching the course. A teacher only works in one school.

There are two independent variables, school and teacher. But it's not a factorial design, because "Teacher 1" does not mean the same thing in School 1 and School 2; it's a different person. This is called a **nested** design. By the way, it's also **unbalanced**, because there are different numbers of teachers within each school. We say that *teacher is nested within school*. The diagram below shows what is going on, and give a clue about how to conduct the analysis.



To compare schools, we want to test $\frac{1}{3} (\mu_1 + \mu_2 + \mu_3) = \frac{1}{4} (\mu_4 + \mu_5 + \mu_6 + \mu_7)$.

To compare instructors within schools, we want to test $\mu_1 = \mu_2 = \mu_3$ and $\mu_4 = \mu_5 = \mu_6 = \mu_7$ simultaneously.

The first test involves one contrast of μ_1 through μ_7 ; the second test involves five contrasts. There really is nothing to it.

You can specify the contrasts yourself, or you can take advantage of `proc glm`'s syntax for nested models.

```
proc glm;
  class school teacher;
  model score = school teacher(school);
```

The notation `teacher(school)` should be read "teacher within school."

- It's easy to extend this to more than one level of nesting. You could have climate zones, lakes within climate zones, fishing boats within lakes, ...
- There is no problem with combining nested and factorial structures. You just have to keep track of what's nested within what. Factors that are not nested are sometimes called "crossed."

Random Effect Models The preceding discussion (and indeed, the entire course to this point) has been limited to "fixed effects" models. In a **random effects** model, *the values of the categorical independent variables represent a random sample from some population of values*. For example, suppose the business school had 200 branches, and just selected 2 of them at random for the investigation. Also, maybe each school has a lot of teachers, and we randomly sampled teachers within schools. Then, teachers within schools would be a random effects factor too.

It's quite possible to have random effect factors and fixed effect factors in the same design; such designs are called "mixed." SAS `proc mixed` is built around this, but it does a lot of other things too.

Nested models are often viewed as random effects models, but there is no necessary connection between the two concepts. It depends on how the study was conducted. Were the two schools randomly selected from some population of schools, or did someone just pick those two (maybe because there are just two schools)?

Random effects, like fixed effects, can either be nested or not; it depends on the logic of the design. An interesting case of nested and purely random effects is provided by **sub-sampling**. For example, we take a random sample of towns, from each town we select a random sample of households, and from each household we select a random sample of individuals to test, or measure, or question.

In such cases the population variance of the DV can truly be partitioned into pieces -- the variance due to towns, the variance due to households within towns, and the variance due to individuals within households. These components of variance can be estimated, and they are, by a program called `proc nested`, a specialized tool for just exactly this design. All effects are random, and each is nested within the preceding one.

Another example: Suppose we are studying waste water treatment, specifically the porosity of "flocks," nasty little pieces of something floating in the tanks. We randomly select a sample of flocks, and then cut each one up into very thin slices. We then randomly select a sample of slices (called "sections") from each flock, look at it under a microscope, and assign a number representing how porous it is (how much empty space there is in a designated region of the section). The independent variables are flock and section. The research question is whether section is explaining a significant amount of the variance in porosity -- because if not, we can use just one section per flock, and save considerable time & expense.

The SAS syntax for this would be

```
proc sort; by flock section; /* Data must be sorted */
proc nested;
  class flock section;
  var por;
```

The F tests on the output are easy to locate. The last column of output ("Percent of total") is estimated percent of total variance due to the effect. It's fairly close to R^2 , but not the same. To include a covariate (say "window"), just use `var window por;` instead of `var por;`. You'll get an analysis of `por` with `window` as the covariate (which is what you want) and an analysis of `window` with `por` as the covariate (which you should ignore).

Of course lots of the time, nothing is randomly selected -- but people use random effects models anyway. Why pretend? Well, sometimes they are thinking that in a better world, lakes *would* have been randomly selected. Or sometimes, the scientists are thinking that they really would like to generalize to the entire population of lakes, and

therefore should use statistical tools that support such generalization -- even if there was no random sampling. (By the way, no statistical method can compensate for a biased sample.) Or sometimes it's just a tradition in certain sub-areas of research, and everybody expects to see random effects models.

In the traditional analysis of models with random or mixed effects and a normal assumption, F-tests are often possible, but they don't always use Mean Squared Error in the denominator of the F statistic. Often, it's the Mean Square for some interaction term or other. The choice of what error term to use is relatively mechanical for balanced models with equal sample sizes (and SAS will do it for you), but even then, sometimes (especially when it's a mixed model) a valid F-test for an effect of interest just doesn't exist.

The following shows how one can obtain classical F tests for random effects and mixed models using `proc glm`. Some things to bear in mind are:

- The interaction of any random factor with another factor (whether fixed or random) is random. But you have to tell `proc glm` this explicitly.
- You have to tell `proc glm` that you want significance tests, using `/ test`.
- Regardless of what you specify in the random statement, the output from `proc glm` starts with tests that assume all effects are fixed. If you believe that one or more effects are random, then these tests are meaningless, and should be ignored.
- The tests for random and mixed effects are preceded by expected mean squares, in a notation one can get used to. This part of the output can be a blessing, especially in courses that go into nitty-gritty detail about the classical tests. We will ignore it.

Here is the program `mixed3.sas`, which has no content but shows the syntax.

```

/***** mixed3.sas *****/
Three levels of factor A, four levels of B
  Pretend both fixed
  Pretend both random
  Pretend A fixed, B random
*****/

options linesize=79 noovp formdlim=' ';

data mixedup;
  infile 'ch19pr14.data';
  input Y A garbage B;

/* By default, both are considered fixed */
proc glm;
  title 'Both effects Fixed';
  class A B ;
  model y = a | b;

/* Now both random */
proc glm;
  title 'Both effects random';
  class A B ;
  model y = a | b;
  random a b a*b / test; /* Have to specify interaction random too! */

/* Now A fixed, B random */
proc glm;
  title 'A fixed, B random';
  class A B ;
  model y = a | b;
  random b a*b / test;

/* Now B fixed, A random */
proc glm;
  title 'B fixed, A random';
  class A B ;
  model y = a | b;
  random a a*b / test;

```

Here is the output in mixed.lst:

Both effects Fixed

1

The GLM Procedure

Class Level Information

Class	Levels	Values
A	3	1 2 3
B	4	1 2 3 4

Number of Observations Read 36
 Number of Observations Used 36

Both effects Fixed

2

The GLM Procedure

Dependent Variable: Y

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	11	220.2833333	20.0257576	3.11	0.0097
Error	24	154.4466667	6.4352778		
Corrected Total	35	374.7300000			

R-Square 0.587845
 Coeff Var 35.31487
 Root MSE 2.536785
 Y Mean 7.183333

Source	DF	Type I SS	Mean Square	F Value	Pr > F
A	2	220.0200000	110.0100000	17.09	<.0001
B	3	0.0722222	0.0240741	0.00	0.9997
A*B	6	0.1911111	0.0318519	0.00	1.0000

Source	DF	Type III SS	Mean Square	F Value	Pr > F
A	2	220.0200000	110.0100000	17.09	<.0001
B	3	0.0722222	0.0240741	0.00	0.9997
A*B	6	0.1911111	0.0318519	0.00	1.0000

Both effects random

3

The GLM Procedure

Class Level Information

Class	Levels	Values
A	3	1 2 3
B	4	1 2 3 4

Number of Observations Read 36
 Number of Observations Used 36

Both effects random

4

The GLM Procedure

Dependent Variable: Y

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	11	220.2833333	20.0257576	3.11	0.0097
Error	24	154.4466667	6.4352778		
Corrected Total	35	374.7300000			

R-Square 0.587845
 Coeff Var 35.31487
 Root MSE 2.536785
 Y Mean 7.183333

Source	DF	Type I SS	Mean Square	F Value	Pr > F
A	2	220.0200000	110.0100000	17.09	<.0001
B	3	0.0722222	0.0240741	0.00	0.9997
A*B	6	0.1911111	0.0318519	0.00	1.0000

Source	DF	Type III SS	Mean Square	F Value	Pr > F
A	2	220.0200000	110.0100000	17.09	<.0001
B	3	0.0722222	0.0240741	0.00	0.9997
A*B	6	0.1911111	0.0318519	0.00	1.0000

Both effects random

5

The GLM Procedure

Source	Type III Expected Mean Square
A	$\text{Var}(\text{Error}) + 3 \text{Var}(A*B) + 12 \text{Var}(A)$
B	$\text{Var}(\text{Error}) + 3 \text{Var}(A*B) + 9 \text{Var}(B)$
A*B	$\text{Var}(\text{Error}) + 3 \text{Var}(A*B)$

Both effects random

6

The GLM Procedure

Tests of Hypotheses for Random Model Analysis of Variance

Dependent Variable: Y

Source	DF	Type III SS	Mean Square	F Value	Pr > F
A	2	220.020000	110.010000	3453.80	<.0001
B	3	0.072222	0.024074	0.76	0.5582
Error: MS(A*B)	6	0.191111	0.031852		

Source	DF	Type III SS	Mean Square	F Value	Pr > F
A*B	6	0.191111	0.031852	0.00	1.0000
Error: MS(Error)	24	154.446667	6.435278		

A fixed, B random

7

The GLM Procedure

Class Level Information

Class	Levels	Values
A	3	1 2 3
B	4	1 2 3 4

Number of Observations Read 36
 Number of Observations Used 36

A fixed, B random

8

The GLM Procedure

Dependent Variable: Y

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	11	220.2833333	20.0257576	3.11	0.0097
Error	24	154.4466667	6.4352778		
Corrected Total	35	374.7300000			

R-Square 0.587845
 Coeff Var 35.31487
 Root MSE 2.536785
 Y Mean 7.183333

Source	DF	Type I SS	Mean Square	F Value	Pr > F
A	2	220.0200000	110.0100000	17.09	<.0001
B	3	0.0722222	0.0240741	0.00	0.9997
A*B	6	0.1911111	0.0318519	0.00	1.0000

Source	DF	Type III SS	Mean Square	F Value	Pr > F
A	2	220.0200000	110.0100000	17.09	<.0001
B	3	0.0722222	0.0240741	0.00	0.9997
A*B	6	0.1911111	0.0318519	0.00	1.0000

A fixed, B random

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The GLM Procedure

Source	Type III Expected Mean Square
A	$\text{Var}(\text{Error}) + 3 \text{Var}(A*B) + Q(A)$
B	$\text{Var}(\text{Error}) + 3 \text{Var}(A*B) + 9 \text{Var}(B)$
A*B	$\text{Var}(\text{Error}) + 3 \text{Var}(A*B)$

A fixed, B random

10

The GLM Procedure

Tests of Hypotheses for Mixed Model Analysis of Variance

Dependent Variable: Y

Source	DF	Type III SS	Mean Square	F Value	Pr > F
A	2	220.020000	110.010000	3453.80	<.0001
B	3	0.072222	0.024074	0.76	0.5582
Error: MS(A*B)	6	0.191111	0.031852		

Source	DF	Type III SS	Mean Square	F Value	Pr > F
A*B	6	0.191111	0.031852	0.00	1.0000
Error: MS(Error)	24	154.446667	6.435278		

B fixed, A random

11

The GLM Procedure

Class Level Information

Class	Levels	Values
A	3	1 2 3
B	4	1 2 3 4

Number of Observations Read 36
 Number of Observations Used 36

B fixed, A random

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The GLM Procedure

Dependent Variable: Y

Source	DF	Sum of Squares	Mean Square	F Value	Pr > F
Model	11	220.2833333	20.0257576	3.11	0.0097
Error	24	154.4466667	6.4352778		
Corrected Total	35	374.7300000			

R-Square 0.587845
 Coeff Var 35.31487
 Root MSE 2.536785
 Y Mean 7.183333

Source	DF	Type I SS	Mean Square	F Value	Pr > F
A	2	220.0200000	110.0100000	17.09	<.0001
B	3	0.0722222	0.0240741	0.00	0.9997
A*B	6	0.1911111	0.0318519	0.00	1.0000

Source	DF	Type III SS	Mean Square	F Value	Pr > F
A	2	220.0200000	110.0100000	17.09	<.0001
B	3	0.0722222	0.0240741	0.00	0.9997
A*B	6	0.1911111	0.0318519	0.00	1.0000

B fixed, A random

13

The GLM Procedure

Source	Type III Expected Mean Square
A	$\text{Var}(\text{Error}) + 3 \text{Var}(A*B) + 12 \text{Var}(A)$
B	$\text{Var}(\text{Error}) + 3 \text{Var}(A*B) + Q(B)$
A*B	$\text{Var}(\text{Error}) + 3 \text{Var}(A*B)$

B fixed, A random

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The GLM Procedure

Tests of Hypotheses for Mixed Model Analysis of Variance

Dependent Variable: Y

Source	DF	Type III SS	Mean Square	F Value	Pr > F
A	2	220.020000	110.010000	3453.80	<.0001
B	3	0.072222	0.024074	0.76	0.5582
Error: MS(A*B)	6	0.191111	0.031852		

Source	DF	Type III SS	Mean Square	F Value	Pr > F
A*B	6	0.191111	0.031852	0.00	1.0000
Error: MS(Error)	24	154.446667	6.435278		

When the design is unbalanced or has unequal sample sizes, the classical approach based on expected mean squares fails, and a valid F-test rarely exists. It's a real pain. Sometimes, you can find an error term that produces a valid F-test *assuming* that some interaction (or maybe more than one interaction) is absent. Usually, you can't test for that interaction either. But people do it anyway and hope for the best.

SAS proc mixed goes a long way toward solving these problems. It's a great piece of software, based on recent, state-of-the-art research as well as more venerable stuff. Examples will be given in lecture.