Lecture 16: Two-Way ANOVA

Reading Assignment:

- Muller and Fetterman, Chapter 14: "Complete, Two-Way Factorial ANOVA" (Required)

In two-way analysis of variance (ANOVA), we wish to evaluate the importance of all combinations of two categorical variables in predicting a Gaussian response.

First, we define several terms commonly used to describe studies well-suited to ANOVA:

Cell: group of observational units, all receiving same treatment.

Balanced: all cells (present) have the same number of observational units.

Complete: all cells have at least one observation.

Balanced, complete designs are the simplest and lead to unambiguous tests. We use this situation as our prototype. Other designs require careful treatment and thoughtful consideration, though they can be handled in the general linear model framework.

Model Concepts

Factorial Design

A **factorial** design includes all combinations of the levels of two or more treatments.

If factor A has a levels and factor B has b levels, then a two-way factorial contains $a \cdot b$ combinations (cells).

For example, let factor A represent drug dose ($a = 2$) and let factor B represent drug formulations ($b = 3$) for a new cholesterol-reducing compound.

Two-Way Factorial Design

N Replicates

	$DRUG_1$	$DRUG_2$	$DRUG_3$
$DOSE_1$			
$DOSE_2$			

Treatments in a factorial are completely crossed (with each other). This means that each drug is tested at each dose, and *vice versa*.

One observation per cell ($a \cdot b = 6$) gives one replicate. For a balanced design, let N equal the $\#$ of observations in each cell so that $n = Nab$. So for the balanced two-way factorial design in the previous table, each dose-drug combination is tested in N patients for a total of $6N$ patients in the study.

We generally like to see 5-10 replicates for any analysis (this allows estimation of interaction terms), though further assumptions may be made in order to make inferences for smaller studies.

Cell and Marginal Means

Define a row marginal mean for balanced data as $\mu_{i\cdot} = \sum_{j=1}^{b} \mu_{ij}/b$, which is a row average in the table, where μ_{ij} is the mean in the cell in row i and column j of the table.

Define a column marginal mean for balanced data as $\mu_{\cdot j} = \sum_{i=1}^{a} \mu_{ij}/a$, which is a column average across the rows.

Note that the first subscript indicates the row (first factor) and the second subscript indicates the column (second factor).

The marginal means of factor A, $\{\mu_{1\cdot}, \mu_{2\cdot}\}$, have been averaged across factor B, and the marginal means of factor B, $\{\mu_{\cdot 1}, \mu_{\cdot 2}, \mu_{\cdot 3}\}$, have been averaged across factor A.

Consider the following marginal means for the cholesterol drug example.

Two-Way Factorial Design

	$DRUG_1$	$DRUG_2$	$DRUG_3$	
$DOSE_1$	μ_{11}	μ_{12}	μ_{13}	$\mu_{1\cdot}$
$DOSE_2$	μ_{21}	μ_{22}	μ_{23}	$\mu_{2\cdot}$
	$\mu_{\cdot 1}$	$\mu_{\cdot 2}$	$\mu_{\cdot 3}$	$\mu_{\cdot\cdot}$

1. μ_{12} is the population mean cholesterol for the N subjects taking dose 1 of drug 2,
2. $\mu_{1\cdot}$ is the population mean cholesterol for the $3N$ patients taking dose 1, averaged over all three drugs,
3. $\mu_{\cdot 2}$ is the population mean cholesterol for the $2N$ patients taking drug 2, averaged over the two doses, and
4. $\mu_{\cdot\cdot}$ is the population mean cholesterol over all $n = 6N$ subjects in the study.

Primary Hypotheses

In a model without *interaction*, main effects describe marginal means. To test equality of marginal means, we have the hypotheses:

$$H_0 : \mu_{1\cdot} = \mu_{2\cdot} = \ldots = \mu_{a\cdot}$$

and

$$H_0 : \mu_{\cdot 1} = \mu_{\cdot 2} = \ldots = \mu_{\cdot b},$$

which correspond to testing if the factor A means are the same and if the factor B means are the same, respectively. These are called the tests of the *main effects* of factors A and B.

In the absence of interaction, we test main effects using contrasts like those in one-way ANOVA.

The *interaction* describes the difference among differences (is the dose effect the same for all three drugs?). If the interaction is significant, then the effect of factor B depends on the level of factor A or *vice versa*. Consider the hypothesis that the dose effect of drug A is the same as the dose effect of drug B:

$$H_0 : \qquad \mu_{11} - \mu_{21} = \mu_{12} - \mu_{22}$$

$$\iff$$

$$H_0 : \qquad (\mu_{11} - \mu_{21}) - (\mu_{12} - \mu_{22}) = 0.$$

If the null hypothesis is true, then the change in cholesterol going from dose 1 to dose 2 on drug A is the same as the change in cholesterol going from dose 1 to dose 2 on drug B. If the null hypothesis is false, then the dose effect is larger for one drug than for the other.

Coding and Computation

How *do* we code an interaction model? If we use classical ANOVA coding (like SAS), we have the model

$$E(y_{ijk}) = \mu + \alpha_i + \beta_j + \gamma_{ij},$$

$i = 1, 2$, $j = 1, 2, 3$, $k = 1, \ldots, N$. In this case, we have $2 \times 3 = 6$ dose-drug combinations but $1 + 2 + 3 + 6 = 12$ parameters! This model is grossly overparameterized, since we can fit only 6 cell means (thus 6 primary parameters are not estimable).

We could use cell means and fit the model

$$E(y_{ijk}) = \gamma_{ij},$$

in which each γ represents a cell mean for a given dose-drug combination. A more popular approach is to use reference cell coding, which sets one level of each drug and dose to be the reference. For the above example, if we set the highest level of each variable to be the

reference, we have the model

$$E(y_{ijk}) = \mu + \alpha_i + \beta_j + \gamma_{ij},$$

$i = 1$, $j = 1, 2$, $k = 1, \ldots, N$. With only these six parameters in the model, everything is now estimable.

Reference Cell (Regression) Coding

Consider reference cell coding for our cholesterol drug example. Suppose that we have two replicates and that our reference dose is dose 2 and our reference drug is drug 3. There is one column of 1's for the reference cell mean, $a - 1$ columns for the main effect of factor A, $b - 1$ columns for the main effect of factor B, and $(a - 1)(b - 1)$ columns for the interaction.

$$\begin{bmatrix} y_{111} \\ y_{112} \\ y_{121} \\ y_{122} \\ y_{131} \\ y_{132} \\ y_{211} \\ y_{212} \\ y_{221} \\ y_{222} \\ y_{231} \\ y_{232} \end{bmatrix} = \left[\begin{array}{c:c:cc:c:cc} 1 & 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 1 & 0 & 1 \\ 1 & 1 & 0 & 1 & 0 & 1 \\ 1 & 1 & 0 & 0 & 0 & 0 \\ 1 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \end{array}\right] \begin{bmatrix} \mu \\ \alpha_1 \\ \beta_1 \\ \beta_2 \\ \gamma_{11} \\ \gamma_{12} \end{bmatrix} + \boldsymbol{\varepsilon}$$

The interpretations of the parameters may be obtained by considering $E(y_{ij})$ for subjects on various doses (indexed by i) of various drugs (indexed by j). This means, for example, that we no longer have one parameter in our model that describes the dose effect – instead, we have 3 parameters that describe the dose effect; one for each drug.

In this example, μ represents the average cholesterol for subjects at dose 2 of drug 3. α_1 is the difference in cholesterol for subjects on dose 1 of drug 3 compared to subjects on dose 2 of drug 3. β_1 is the difference in cholesterol for subjects on dose 2 of drug 1 compared to subjects on dose 2 of drug 3. β_2 is the difference in cholesterol for subjects on dose 2 of drug 2 compared to subjects on dose 2 of drug 3.

The difference in dose effects for drug 1 versus drug 3 is given by γ_{11}, and the difference in dose effects for drug 2 versus drug 3 is given by γ_{12}.

Generating Cell Means

$\boldsymbol{C}$ =Es($\boldsymbol{X}$) gives the cell means, $\boldsymbol{C\beta}$ =Es($\boldsymbol{X}$)$\boldsymbol{\beta} = \boldsymbol{\theta} = \{\mu_{jk}\}$, for complete designs, whether balanced or not.

For the cholesterol example, the cell means are provided below.

$$\mathbf{C} = \begin{bmatrix} 1 & 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 0 & 1 & 0 & 1 \\ 1 & 1 & 0 & 0 & 0 & 0 \\ 1 & 0 & 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 & 0 & 0 \end{bmatrix} \quad \begin{bmatrix} \mu \\ \alpha_1 \\ \beta_1 \\ \beta_2 \\ \gamma_{11} \\ \gamma_{12} \end{bmatrix},$$

so that we have the following cell means.

Dose	*Drug*	*Mean*
1	1	$\mu + \alpha_1 + \beta_1 + \gamma_{11}$
1	2	$\mu + \alpha_1 + \beta_2 + \gamma_{12}$
1	3	$\mu + \alpha_1$
2	1	$\mu + \beta_1$
2	2	$\mu + \beta_2$
2	3	μ

Computing Estimates and Tests

Balanced, Complete Designs with Equal Cell Size

We can use simple formulae for hand computation in balanced designs, leading to simple interpretations.

Source	df	SS
A	$a-1$	$bN\sum_{i=1}^{a}(\overline{y}_{i..}-\overline{y}_{...})^2$
B	$b-1$	$aN\sum_{j=1}^{b}(\overline{y}_{.j.}-\overline{y}_{...})^2$
AB	$(a-1)(b-1)$	$N\sum_{i=1}^{a}\sum_{j=1}^{b}(\overline{y}_{ij.}-\overline{y}_{i..}-\overline{y}_{.j.}+\overline{y}_{...})^2$
Error	$ab(N-1)$	$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{N}(y_{ijk}-\overline{y}_{ij.})^2$
Total	$abN-1$	$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{N}(y_{ijk}-\overline{y}_{...})^2$

The SS formulae presented here are correct only with complete, balanced data, unless explicitly stated otherwise.

Unbalanced, Complete Data

With unbalanced, complete data, we revert to the general linear model framework and fit $\boldsymbol{y} = \boldsymbol{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon}$. By specifying the appropriate contrast matrices, we are able to carry out the appropriate tests.

One must fit multiple models in order to generate added-in-order tests.

Contrast Matrices for Marginal Means

Mean Estimation with Reference Cell Coding

Start with the matrix which computes cell means that correspond to the interaction in our cholesterol example: $\boldsymbol{C}_{\mathsf{A}\times\mathsf{B}} = \mathsf{Es}(\boldsymbol{X})$

$$\boldsymbol{C}_{\mathsf{A}\times\mathsf{B}}\boldsymbol{\beta} = \mathsf{Es}(\boldsymbol{X})\,\boldsymbol{\beta} = \{\mu_{jk}\}$$

$$\boldsymbol{\theta}_{\mathsf{A}\times\mathsf{B}} = \{\mu_{jk}\} = \begin{bmatrix} \mu_{11} \\ \mu_{12} \\ \vdots \\ \mu_{23} \end{bmatrix}.$$

To estimate the marginal means of factor A (dose) for our example, we use

$$\boldsymbol{C}_{\text{A ref}} = \begin{bmatrix} 1 & \vdots & 1 & \vdots & \frac{1}{3} & \frac{1}{3} & \vdots & \frac{1}{3} & \frac{1}{3} \\ & & & & & & & & \\ 1 & \vdots & 0 & \vdots & \frac{1}{3} & \frac{1}{3} & \vdots & 0 & 0 \end{bmatrix}$$

to obtain $\boldsymbol{\theta}_A = \begin{bmatrix} \mu_{1\cdot} \\ \mu_{2\cdot} \end{bmatrix}$.

This becomes clear if we think about averaging the expected values by dose.

Similarly, for marginal means of factor B (drug), we have

$$\boldsymbol{C}_{\text{B ref}} = \left[\begin{array}{c|c|c|c|c|c|c|c} 1 & \frac{1}{2} & 1 & 0 & \frac{1}{2} & 0 \\ 1 & \frac{1}{2} & 0 & 1 & 0 & \frac{1}{2} \\ 1 & \frac{1}{2} & 0 & 0 & 0 & 0 \end{array}\right], \text{ leading to}$$

$$\boldsymbol{\theta}_{\text{B}} = \begin{bmatrix} \mu_{\cdot 1} \\ \mu_{\cdot 2} \\ \mu_{\cdot 3} \end{bmatrix}.$$

The grand mean can be thought of as the average of all cell means or as the average of either set of marginal means:

$$\boldsymbol{C}_{\text{grand mean ref}} = \begin{bmatrix} 1 & \frac{1}{2} & \frac{1}{3} & \frac{1}{3} & \frac{1}{6} & \frac{1}{6} \end{bmatrix}.$$

Testing with Reference Cell Coding

One must take care when testing the main effects of factor A or factor B in the presence of their interaction. Specifically, testing that the α's are equal to zero (or that the β's are equal to zero) is not testing marginal means. In fact, this would be a test of simple main effects *at the reference level* of the other factor.

For factor A, we really wish to test the hypothesis

$$H_0 : \mu_{1\cdot} = \mu_{2\cdot}$$

Thus we wish to test the hypothesis

$$H_0 : \begin{bmatrix} 1 & -1 \end{bmatrix} \begin{bmatrix} \mu_{1\cdot} \\ \mu_{2\cdot} \end{bmatrix} = 0.$$

Thus we may define the appropriate contrast matrix $\mathbf{C}$ for factor A as

$$\begin{aligned}
\mathbf{C} &= \begin{bmatrix} 1 & -1 \end{bmatrix} \begin{bmatrix} 1 & \vdots & 1 & \vdots & \frac{1}{3} & \frac{1}{3} & \vdots & \frac{1}{3} & \frac{1}{3} \\ & & & & & & & & \\ 1 & \vdots & 0 & \vdots & \frac{1}{3} & \frac{1}{3} & \vdots & 0 & 0 \end{bmatrix} \\
&= \begin{bmatrix} 0 & \vdots & 1 & \vdots & 0 & 0 & \vdots & \frac{1}{3} & \frac{1}{3} \end{bmatrix}.
\end{aligned}$$

Similarly, for testing marginal means of factor B, we have the contrast matrix

$$\begin{aligned}
\mathbf{C} &= \begin{bmatrix} 1 & 0 & -1 \\ 0 & 1 & -1 \end{bmatrix} \left[\begin{array}{c:c:cc:c:cc} 1 & \frac{1}{2} & 1 & 0 & \frac{1}{2} & 0 \\ 1 & \frac{1}{2} & 0 & 1 & 0 & \frac{1}{2} \\ 1 & \frac{1}{2} & 0 & 0 & 0 & 0 \end{array}\right] \\
&= \left[\begin{array}{c:c:c:cc:c:c} 0 & 0 & 1 & 0 & \frac{1}{2} & 0 \\ 0 & 0 & 0 & 1 & 0 & \frac{1}{2} \end{array}\right].
\end{aligned}$$

The test of interaction is simply a test that the interaction terms $\boldsymbol{\gamma}$ are equal to zero.

Choosing and Interpreting Tests

Model Comparisons

All GLH tests correspond to comparing two models. Note that marginal means tests in reference cell coding do not correspond to column deletions.

Testing Strategies

All testing strategies are special cases of those in Chapters 5 and 11. The recommended strategy is a backwards group-wise approach. The first group contains the main effect of A variables, the second group contains the main effect of B variables, and the third group contains the interaction variables. Start by testing the interaction. If significant, stop, and fit the full model. If not significant, drop the interaction. If the interaction is dropped, proceed with testing of the main effects.

Step-Down Tests

Simple Main Effect Tests

A simple main effect equals a difference in cell means within a column $(\mu_{jk} - \mu_{j'k})$ or within a row $(\mu_{jk} - \mu_{jk'})$. These tests are of interest if the interaction terms are significant. The simple main effect (SME) test evaluates one effect while holding the other constant. There exist b SME tests for factor A and a SME tests for factor B. In our example, we may wish to use a simple main effect test to determine, for example, if there is a dose effect for drug A.

Second Level Step-Down Tests

If a SME with two or more numerator degrees of freedom is significant, additional tests are required to determine where the difference lies.

Missing Data

The pattern of cell sizes may have profound effects on computation and interpretation of test statistics in ANOVA. The complete, balanced case involves no missing data. The complete, unbalanced case involves at least some missing data, meaning that additional observations would be needed to make the design balanced. Careful specification of $\boldsymbol{C}$ for marginal means tests "automatically" provides valid solutions with complete unbalanced data. The model corresponds to simply deleting some rows in $\boldsymbol{X}$ and $\boldsymbol{y}$ when missing data is simply due to some lack of balance. In this case, we have a model like

$$\boldsymbol{y} = \begin{bmatrix} \boldsymbol{J}_{n_1} & & \\ & \boldsymbol{J}_{n_2} & \\ & & \boldsymbol{J}_{n_3} \end{bmatrix} \begin{bmatrix} \mu_1 \\ \mu_2 \\ \mu_3 \end{bmatrix} + \boldsymbol{\varepsilon}$$

with $n = n_1 + n_2 + n_3$. For this model $\widehat{\boldsymbol{\beta}} = \begin{bmatrix} \widehat{\mu}_1 & \widehat{\mu}_2 & \widehat{\mu}_3 \end{bmatrix}'$.

Strongly unbalanced data create additional difficulties.

With unbalanced data avoid automatic coding schemes provided by computer programs (such as the CLASS statement in PROC GLM).

More About Missing Data

The above comments apply when data is unbalanced *by design*. Suppose we originally planned to treat 50 patients on dose 1 and 40 patients on dose 2. Alternatively, suppose that originally 50 patients were taking each dose, but 10 patients taking dose 2 dropped out of the study due to toxic side effects at that dose. In the second case, a *complete case analysis*, or an analysis that deletes some rows in $\mathbf{X}$ and $\mathbf{y}$, may lead to biased parameter estimates.

The validity of any analysis with incomplete data depends on the reasons for which data (response or covariates) are missing.

A *complete case analysis* is valid only when data are *missing completely at random (MCAR)*, which means that the completely observed subjects are a completely random sample of all the subjects in the study. Complete case analysis is the default analysis in SAS PROC REG and SAS PROC GLM when data (responses or covariates) are missing, regardless of its validity for the data in question.

Other types of missingness include *missing at random (MAR)*, which means that missingness does not depend on the values of the variables that are missing but may depend on observed quantities. Examples of MAR mechanisms

- A subject may be removed from a trial if his/her condition is not controlled sufficiently well (according to pre-defined criteria on the

response).

- Two measurements of the same variable are made at the same time. If they differ by more than a given amount a third is taken. This third measurement is missing for those that do not differ by the given amount.

Nonignorable missingness, which means that the missingness may depend on the values of the variables that are missing.

In the latter two cases, the *complete case analysis* is not valid in general and may lead to considerable bias and faulty results. If a *complete case analysis* is carried out, deleted observations must be reported, and the investigator must seriously consider the validity of the analysis.

Even in the "ideal" MCAR situation, replacing missing data with simple imputed values (such as the average for all subjects) biases the

estimate of error variance downward and therefore inflates the type I error rate. Despite this relatively well-known fact, many investigators substitute means for missing values by default. "Making up" data in this manner can have extremely severe consequences and should be avoided.

Recently, SAS has implemented PROC MI and PROC MIANALYZE, which carry out multiple imputation, a more sophisticated method for handling missing observations. However, these procedures are still in the development stages and are not yet available for a wide class of problems (currently, PROC MI requires all variables to follow Gaussian distributions for general missing data patterns).

Example: Automobile Pollution Filter Noise

Associated Octel Company developed an automobile silencing filter, the Octel filter, that Texaco, Inc. stated (before the Air and Water Pollution Subcommittee of the Senate Public Works Committee) was just as effective as the standard silencing filter. The president of Texaco at the time presented data that we now analyze to back up his claim that the new filter (TYPE1=1 for standard, TYPE1=0 for Octel) was no more noisy than the standard filter. The dependent variable, NOISE, is noise level in decibels, with factor A as the vehicle size (small, medium, or large, with large as the reference level) and factor B as filter type (standard or Octel, with Octel as the reference level).

Our goal is to evaluate the noise levels of the three car sizes at the two filter types.

First, we define the following variables for the reference cell coding scheme.

- SIZE1, which takes the value 1 for small cars and 0 otherwise
- SIZE2, which takes the value 1 for medium cars and 0 otherwise
- S1TYPE1, which takes the value 1 for small cars with the standard filter and zero otherwise
- S2TYPE1, which takes the value 1 for medium cars with the standard filter and zero otherwise

Next, let's take a look at the mean noise levels for each car size and filter type.

Size	Silencer/Filter Type	Average Noise Level
Small	Standard	825.83
Small	Octel	822.50
Medium	Standard	845.83
Medium	Octel	821.67
Large	Standard	775.00
Large	Octel	770.00

What is your impression based on these cell means?

Next, we fit the model

$$\begin{aligned} NOISE &= \beta_0 + \beta_1 SIZE1 + \beta_2 SIZE2 + \beta_3 TYPE1 + \\ &\quad \beta_4 S1TYPE1 + \beta_5 S2TYPE1 + \varepsilon. \end{aligned}$$

The SAS code is below.

```
proc glm;
model noise=size1 size2 type1 s1type1 s2type1/solution;
estimate Grand Mean
        intercept 6 size1 2 size2 2 type1 3 s1type1 1 s2type1 1/divisor=6;
estimate Marg Mean: Small
        intercept 2 size1 2 size2 0 type1 1 s1type1 1 s2type1 0/divisor=2;
estimate Marg Mean: Medium
        intercept 2 size1 0 size2 2 type1 1 s1type1 0 s2type1 1/divisor=2;
estimate Marg Mean: Large
        intercept 2 size1 0 size2 0 type1 1 s1type1 0 s2type1 0/divisor=2;
estimate Marg Mean: Standard
        intercept 3 size1 1 size2 1 type1 3 s1type1 1 s2type1 1/divisor=3;
estimate Marg Mean: Octel
        intercept 3 size1 1 size2 1 type1 0 s1type1 0 s2type1 0/divisor=3;

contrast Interaction Silencer by Size
        intercept 0 size1 0 size2 0 type1 0 s1type1 1 s2type1 0,
        intercept 0 size1 0 size2 0 type1 0 s1type1 0 s2type1 1;
```

```
contrast Main Effect Vehicle Size
        intercept 0 size1 2 size2 0 type1 0 s1type1 1 s2type1 0,
        intercept 0 size1 0 size2 2 type1 0 s1type1 0 s2type1 1;

contrast Main Effect Silencer
        intercept 0 size1 0 size2 0 type1 3 s1type1 1 s2type1 1;
run;
```

```
/* ALTERNATIVELY, you can use the code below */
/* DANGER DANGER -- this code uses the class statement */
proc glm;
class size type;
model noise=size type size*type;
run;
```

The output is provided below.

```
                          The GLM Procedure

Dependent Variable: noise

                                   Sum of
Source                     DF       Squares    Mean Square   F Value
Model                       5   27911.80556     5582.36111     85.34
Error                      30    1962.50000       65.41667

Corrected Total            35   29874.30556

                    Source                 Pr > F
                    Model                  <.0001
                    Error

                    Corrected Total
```

R-Square	Coeff Var	Root MSE	noise Mean
0.934308	0.998354	8.088057	810.1389

Source	DF	Type I SS	Mean Square	F Value
size1	1	3542.01389	3542.01389	54.15
size2	1	22509.37500	22509.37500	344.09
type1	1	1056.25000	1056.25000	16.15
s1type1	1	253.12500	253.12500	3.87
s2type1	1	551.04167	551.04167	8.42

Source	Pr > F
size1	<.0001
size2	<.0001
type1	0.0004
s1type1	0.0585
s2type1	0.0069

Source	DF	Type III SS	Mean Square	F Value
size1	1	8268.750000	8268.750000	126.40
size2	1	8008.333333	8008.333333	122.42
type1	1	75.000000	75.000000	1.15

Source	Pr > F
size1	<.0001
size2	<.0001
type1	0.2928

Source	DF	Type III SS	Mean Square	F Value
s1type1	1	4.166667	4.166667	0.06
s2type1	1	551.041667	551.041667	8.42

Source	Pr > F
s1type1	0.8025
s2type1	0.0069

Contrast	DF	Contrast SS
Interaction Silencer by Size	2	804.16667
Main Effect Vehicle Size	2	26051.38889
Main Effect Silencer	1	1056.25000

Contrast	Mean Square	F Value
Interaction Silencer by Size	402.08333	6.15
Main Effect Vehicle Size	13025.69444	199.12
Main Effect Silencer	1056.25000	16.15

Contrast	Pr > F
Interaction Silencer by Size	0.0058
Main Effect Vehicle Size	<.0001
Main Effect Silencer	0.0004

Parameter	Estimate	Standard Error	t Value	Pr > |t|
Grand Mean	810.138889	1.34800951	600.99	<.0001
Marg Mean: Small	824.166667	2.33482095	352.99	<.0001
Marg Mean: Medium	833.750000	2.33482095	357.09	<.0001
Marg Mean: Large	772.500000	2.33482095	330.86	<.0001
Marg Mean: Standard	815.555556	1.90637333	427.80	<.0001

```
Marg Mean: Octel        804.722222    1.90637333   422.12    <.0001
```

Parameter	Estimate	Standard Error	t Value	Pr > |t|
Intercept	770.0000000	3.30193546	233.20	<.0001
size1	52.5000000	4.66964191	11.24	<.0001
size2	51.6666667	4.66964191	11.06	<.0001
type1	5.0000000	4.66964191	1.07	0.2928
s1type1	-1.6666667	6.60387092	-0.25	0.8025
s2type1	19.1666667	6.60387092	2.90	0.0069

Using the SAS output, we can construct the ANOVA table as follows.

Source	df	SS	MS	F	p
Size					
Silencer					
Size*Silencer					
Error					
Total					

What further tests, if any, should we consider?

Because the interaction is significant, a logical next step is to conduct simple main effect tests of the filter effect within each car size. The SAS code below may be used to conduct these SME tests.

```
proc glm;
model noise=size1 size2 type1 s1type1 s2type1/solution;
contrast SME Silencer at Size Small
        intercept 0 size1 0 size2 0 type1 1 s1type1 1 s2type1 0;
contrast SME Silencer at Size Medium
        intercept 0 size1 0 size2 0 type1 1 s1type1 0 s2type1 1;
contrast SME Silencer at Size Large
        intercept 0 size1 0 size2 0 type1 1 s1type1 0 s2type1 0;
run;
```

The additional output is provided below.

Contrast	DF	Contrast SS
SME Silencer at Size Small	1	33.33333
SME Silencer at Size Medium	1	1752.08333
SME Silencer at Size Large	1	75.00000

Contrast	Mean Square	F Value

SME Silencer at Size Small	33.33333	0.51
SME Silencer at Size Medium	1752.08333	26.78
SME Silencer at Size Large	75.00000	1.15

Contrast	Pr > F
SME Silencer at Size Small	0.4808
SME Silencer at Size Medium	<.0001
SME Silencer at Size Large	0.2928

What do you conclude?

Alternatively (less logically?), you could have tested the SME of car size for each filter type. The SAS code and additional output are provided below.

```
proc glm;
model noise=size1 size2 type1 s1type1 s2type1/solution;
contrast SME Size at Standard Silencer
        intercept 0 size1 1 size2 -1 type1 0 s1type1 1 s2type1 -1,
        intercept 0 size1 1 size2 0 type1 0 s1type1 1 s2type1 0;
contrast SME Size at Octel Silencer
        intercept 0 size1 1 size2 -1 type1 0 s1type1 0 s2type1 0,
        intercept 0 size1 1 size2 0 type1 0 s1type1 0 s2type1 0;
run;
```

```
************************************************************

 Contrast                                          DF     Contrast SS

 SME Size at Standard Silencer                      2     16002.77778
 SME Size at Octel Silencer                         2     10852.77778

Contrast                                    Mean Square    F Value
```

SME Size at Standard Silencer	8001.38889	122.31
SME Size at Octel Silencer	5426.38889	82.95

Contrast	Pr > F
SME Size at Standard Silencer	<.0001
SME Size at Octel Silencer	<.0001

What do you conclude?

Because the SME tests for size were significant for both filter types, we can now carry out step-down tests to determine specifically which car type means differ for each filter type.

```
proc glm;
model noise=size1 size2 type1 s1type1 s2type1/solution;
contrast Step-Down of SME at Std: Small vs. Med
        intercept 0 size1 1 size2 -1 type1 0 s1type1 1 s2type1 -1;
contrast Step-Down of SME at Std: Small vs. Large
        intercept 0 size1 1 size2 0 type1 0 s1type1 0 s2type1 0;
contrast Step-Down of SME at Std: Med vs. Large
        intercept 0 size1 0 size2 1 type1 0 s1type1 0 s2type1 1;
contrast Step-Down of SME at Octel: Small vs. Med
        intercept 0 size1 1 size2 -1 type1 0 s1type1 0 s2type1 0;
contrast Step-Down of SME at Octel: Small vs. Large
        intercept 0 size1 1 size2 0 type1 0 s1type1 0 s2type1 0;
contrast Step-Down of SME at Octel: Med vs. Large
        intercept 0 size1 0 size2 1 type1 0 s1type1 0 s2type1 0;
run;
```

****

Contrast	DF	Contrast SS
Step-Down of SME at Std: Small vs. Med	1	1200.00000
Step-Down of SME at Std: Small vs. Large	1	8268.75000
Step-Down of SME at Std: Med vs. Large	1	15052.08333

Contrast	Mean Square	F Value
Step-Down of SME at Std: Small vs. Med	1200.00000	18.34
Step-Down of SME at Std: Small vs. Large	8268.75000	126.40
Step-Down of SME at Std: Med vs. Large	15052.08333	230.10

Contrast	Pr > F
Step-Down of SME at Std: Small vs. Med	0.0002
Step-Down of SME at Std: Small vs. Large	<.0001
Step-Down of SME at Std: Med vs. Large	<.0001

Contrast	DF	Contrast SS
Step-Down of SME at Octel: Small vs. Med	1	2.08333
Step-Down of SME at Octel: Small vs. Large	1	8268.75000
Step-Down of SME at Octel: Med vs. Large	1	8008.33333

Contrast	Mean Square	F Value
Step-Down of SME at Octel: Small vs. Med	2.08333	0.03
Step-Down of SME at Octel: Small vs. Large	8268.75000	126.40
Step-Down of SME at Octel: Med vs. Large	8008.33333	122.42

Contrast	Pr > F
Step-Down of SME at Octel: Small vs. Med	0.8596
Step-Down of SME at Octel: Small vs. Large	<.0001
Step-Down of SME at Octel: Med vs. Large	<.0001

What do you conclude?

For this analysis, we considered engine size as a *factor* instead of as a continuous or ordinal variable. Suppose instead we use one variable,

$$SIZE = \begin{cases} 1 & \text{small} \\ 2 & \text{medium} \\ 3 & \text{large} \end{cases}$$

to describe engine size. What are the implications for our analysis?

Next: Logistic Regression

Reading Assignment:

- Weisberg Chapter 12 and KKMN, Chapter 23: "Logistic Regression Analysis"