STAT 8200 — Design of Experiments for Research Workers
Lab 5 – Due Friday, Sept. 27, 2013

Example:

As part of the production of a liquid medication, the producer, a large pharmaceutical company, mixes batches of medication in large vats. To determine the degree to which their product is consistent from batch to batch, the company takes a random sample of five batches from a month's production. From each batch four samples were obtained and for each sample, an important characteristic of the medication was measured, yielding the data below.

Batch				
1	2	3	4	5
3.2	2.6	3.4	4.2	1.8
3.8	2.9	3.9	4.4	2.3
3.5	2.8	3.3	4.3	1.9
3.0	2.0	3.1	4.2	2.1

The file "drug.sas" contains a SAS program for analyzing these data with a one-way random effects ANOVA model. Copy this program from the public data directory to your home directory and run the program in SAS.

- drug.sas illustrates the use of both PROC GLM and PROC MIXED to implement the one-way random effects ANOVA model. First, we use PROC GLM:

- To test $H_0 : \sigma_a^2 = 0$, the hypothesis that there is no batch-to-batch variability we use $F = MS_A/MS_E = 2.987/0.0918 = 32.53$ (p.2 of the output). Comparing this statistic to its distribution, $F(a-1, N-a) = F(4, 15)$ gives a $p-$value of less than 0.0001, so we reject the null hypothesis and conclude that there is significant batch-to-batch variability.

- To estimate the variance components: We estimate the within-batch variance (the error variance) with $\hat{\sigma}^2 = MS_E = 0.0918$ (p.2). We estimate the between batch variability with

$$\hat{\sigma}_a^2 = \frac{MS_A - MS_E}{n} = \frac{2.987 - 0.0918}{4} = 0.724$$

- To form confidence intervals: A 95% interval for σ^2 is given by

$$\left(\frac{(N-a)MS_E}{\chi^2_{.05/2}(N-a)}, \frac{(N-a)MS_E}{\chi^2_{1-.05/2}(N-a)} \right) = \left(\frac{(15)0.0918}{\chi^2_{.025}(15)}, \frac{(15)0.0918}{\chi^2_{.975}(15)} \right)$$
$$= \left(\frac{1.377}{27.488}, \frac{1.377}{6.262} \right) = (0.0501, 0.220).$$

A 95% interval for $\theta = \sigma_a^2/\sigma^2$ is given by $[L, U]$ where

$$L = \frac{1}{n}\left(\frac{MS_A}{MS_E F_{\alpha/2}(a-1, N-a)} - 1\right), \quad U = \frac{1}{n}\left(\frac{MS_A}{MS_E F_{1-\alpha/2}(a-1, N-a)} - 1\right)$$

So

$$\begin{aligned} L &= \frac{1}{4}\left(\frac{2.987}{(0.0918)F_{.05/2}(4,15)} - 1\right) = \frac{1}{4}\left(\frac{2.987}{(0.0918)3.804} - 1\right) \\ &= 1.888 \end{aligned}$$

and

$$\begin{aligned} U &= \frac{1}{4}\left(\frac{2.987}{(0.0918)F_{1-.05/2}(4,15)} - 1\right) = \frac{1}{4}\left(\frac{2.987}{(0.0918)0.116} - 1\right) \\ &= 69.875 \end{aligned}$$

So we're 95% confident that the ratio of the batch-to-batch variability to the within-batch variability is between $(1.888, 69.875)$.
A 95% interval for ρ is

$$\left(\frac{L}{1+L}, \frac{U}{1+U}\right) = \left(\frac{1.888}{1+1.888}, \frac{69.875}{1+69.875}\right) = (0.654, 0.986)$$

So we're 95% confident that the ratio of the batch-to-batch variability to the total variability is between $(0.654, 0.986)$.

- In drug.sas, PROC MIXED is also used to analyze the data. This gives the estimates of σ^2, σ_a^2 and θ that we computed above based on the PROC GLM output (see p.5 of the SAS output).

- In addition to doing the random effects analysis, the SAS program drug.sas also illustrates the modified Levene's test for homogeneity of variance (implemented with the option hovtest=bf on the means statement in PROC GLM), and shows how to produce residual plots.

- Externally studentized residuals vs. fitteds are plotted on the first page of the graphics output window. This plot shows no obvious non-constant variance. This agrees with the result of the modified Levene's test ($p = .5371$ – see p.3 of the SAS output).

- Finally, we use PROC UNIVARIATE to conduct tests of normality on the internally studentized residuals from the model and to produce a normal quantile-quantile plot of these residuals. Several normality tests are given on p.8 of the SAS output. The most commonly used normality test is the Shapiro-Wilk test which, in this case, fails to reject the hypothesis of normality.

- **Remember though, non-normality is a <u>much less</u> important problem than lack of independence among the experimental units and non-constant variance.** It is really only a major problem if (i) the sample size is very small, and/or (ii) the non-normality is extreme (e.g., highly skewed data; binary data; highly discrete data such as counts that tend to be small or polytomous data such as Likert scale data).

STAT 8200 — Lab 5

Name:_____

Exercise:

Several ovens in a metal working shop are used to heat metal specimens. All the ovens are supposed to operate at the same temperature, although it is suspected that this may not be true. Three ovens are selected at random and their temperatures on successive heats are noted. The data collected are as follows:

Oven	Temperature				
1	491.50	498.30	498.10	493.50	493.60
2	488.50	484.65	479.90	477.35	478.65
3	490.10	484.80	488.25	473.00	471.85

These data are contained in the file 'oven.dat' in the public data directory. Copy this data file to your home directory and write a SAS program do the following:

1. State and test the appropriate null hypothesis for this design. State your conclusion.

2. Estimate the component of variance due to between-oven variability and the component of variance for within-oven variability.

3. Obtain a 95% confidence interval for the ratio of between to within oven variability.

4. Plot the internally studentized residuals versus the fitted values and also conduct modified Levene's test for constant variance. What is the conclusion from modified Levene's test? Does it agree with the impression given by the plot of residuals versus fitteds?

Please hand in page 3, incuding your answers. Remember to write your name at the top. You may keep pages 1–2 for your notes.