CHECKING MODEL ASSUMPTIONS (CHAPTER 5)

The experimenter should carefully choose a model before collecting data. However, information may be limited, so it is also important to use the data, once it has been collected, to check the model. This is typically done by *residual plots*. The *residuals* are

$$\hat{e}_{it} = y_{it} - (\hat{\mu} + \hat{\tau}_i) = y_{it} - \overline{y}_{i\cdot}$$

Plots of residuals will typically show trends more readily than plots of the response values.

Note:
- Minitab will store residuals when doing an Analysis of Variance if you check the appropriate box in the dialogue window.
- The residuals sum to zero. This follows readily from the first step in deriving the normal equations.
- Thus the sample mean of the residuals is zero.

- Recall from the handout Estimating Parameters and Variance that ssE $= \displaystyle\sum_{i=1}^{t}\sum_{t=0}^{r_i}\hat{e}_{it}^{\,2}$.

- The sample variance of the residuals is thus $\displaystyle\sum_{i=1}^{t}\sum_{t=0}^{r_i}\hat{e}_{it}^{\,2}/(n-1) = $ ssE/(n-1).

Recall from the model assumptions that the errors ε_{it} are independent random variables with distributions $N(0, \sigma^2)$. Since the $\hat{e}_{it}$'s are estimates of the ε_{it}'s, they should also be approximately independent, with approximate $N(0, \sigma^2)$ distributions.

Note: Since the residuals sum to zero, they are *not* independent. But other evidence of lack of independence may be taken as lending doubt to the assumption that the errors ε_{it} are independent.

Many people prefer to use *standardized residuals* -- residuals divided by their standard deviation:

$$z_{it} = \frac{\hat{e}_{it}}{\sqrt{ssE/(n-1)}}$$

(Since the sample mean of the residuals is zero, this fits the usual idea of standardizing: Subtract the sample mean and divide by the sample standard deviation.) Plots of standardized residuals make it a little easier to identify outliers than do plain residual plots. As above, if the model assumptions are correct, the standardized residuals should be approximately independent (except for the fact that they sum to zero) and have approximately a $N(0,1)$ distribution.

Note: Standardized residuals can be formed from residuals in Minitab by using the Calculate menu.

Suggested Order for Checking Model Assumptions:

      1. Check the form of the model.
      2. Check for outliers
      3. Check for independence.
      4. Check for constant variance.
      5. Check for normality.

1. *Check the form of the model*. Plot residuals against :
- Each independent variable (treatment factor, block factor, or covariate) included in the model.
- Levels of factors not included in the model.

Any non-random pattern suggests lack of fit of the model.

Example: Battery experiment -- Plot residuals against type, order

2. *Check for outliers*. Plot (standardized) residuals against levels of treatment factor.
- If normality assumption is true, standardized residuals beyond ± 3 are likely outliers.
- Outliers should be investigated for possible recording errors. (See Battery example p. 108)
- Outliers or unusual numbers of standardized residuals beyond ±2 may indicate non-normality.
- Outliers should not automatically be discarded.

3. *Check for independence of error terms*.
- Needs to precede checks for constant variance and normality.
- Plot residuals against time or spatial variables, or anything else likely to cause lack of independence.
- If you detect lack of independence, do not use ANOVA.
- Data showing time or other dependence might be salvaged by analysis of covariance. (We will probably not cover this in this class.)

Example: Battery against order.

4. *Check for equal variance*

- Plot residuals against fitted values. A pattern of increasing variance as mean increases is the most common (but not the only possible) sign of unequal variances.
- Also compare sample variances of residuals for each treatment:

$$s_i^2 = \frac{1}{r_i - 1} \sum_{t=1}^{r_i} \hat{e}_{it}^2$$ is an unbiased estimator of the error variance σ_i^2 of the ith treatment group.

Rule of thumb (from simulation studies): If the ratio s^2_{max}/ s^2_{min} of the largest treatment variance to the smallest does not exceed 3 (some people say 4), then the inference procedures for the equal variance model are still valid. (However, a larger ratio might also occur by chance even when model assumptions are correct.)

- With unequal sample sizes, departures from equal variance can have different effects depending on the relationship between sample size and treatment variance. (See p. 111 for more detail.)

- With unequal sample sizes and/or unequal variance, looking at the p-value (effectively setting a smaller alpha) may give additional information in deciding whether to reject the null hypotheses.

Methods for dealing with unequal variance:

a. Transform the response variable: Replace Y with h(Y), so that the model becomes
   - $h(Y_{it}) = \mu^* + \tau_i^* + \varepsilon_{it}^*$
   - The ε_{it}^*'s are independent random variables.
   - For each i and t, $\varepsilon_{it}^* \sim N(0, \sigma^2)$
(More on this later)

b. Use a method such as Satterthwaite's (pp. 116 - 117)
   - It's only approximate and less powerful than an equal - variance model.
   - It may be useful if there is no suitable transformation available or if it is important to keep the original units.

c. There are also "Weighted ANOVA" methods, analogous to weighted least squares regression.

d. Use a non-parametric test such as the Kruskal-Wallis test for medians. (Not covered in this course.)

e. In some circumstances, graphical techniques may be sufficient. (e.g., if the purpose is to see if the groups are really the same in the variable of interest, and there is enough data to be confident from graphical methods that one group has a distribution vastly different from that of the others.)

f. Resampling, quantile regression, or Bayesian methods might be helpful.

5. *Check for normality*
- Form a *normal probability plot* of residuals (Details shortly.)
- Approximate normality is usually good enough for inferences concerning treatment means and contrasts to be reasonably good.
- Heavy tails can be a problem -- non-parametric methods may be better in this case.
- Transformations can sometimes achieve normality -- but care is needed to get equal variance as well.

Probability Plots

Many tests or other procedures in statistics assume a certain (e.g., normal) distribution. Some procedures are *robust* (i.e., still work pretty well) to some departures from assumptions, but often not to dramatic ones.

This raises the question: How to judge whether data come from a given distribution?

Histograms don't serve this purpose well -- e.g., bin sizes, samples sizes, and their interaction cause problems.

Probability plots (also known as *Q-Q plots* or *quantile plots*) are not perfect, but somewhat better. The idea:

- Order the data: $y_1 \leq y_2 \leq \ldots \leq y_n$.
- Plot vs $q_1 \leq q_2 \leq \ldots \leq q_n$, where

    q_k = the expected value (as approximated by computer) of the kth smallest member of a simple random sample of size n from the distribution of interest.

If the data come from this distribution, we expect $y_k \approx q_k$, so the graph will lie approximately along the line y = x.

Variation often used to test for normality:

Take the q_k's from the *standard normal* distribution. So if the y_k's are sampled from an $N(\mu,\sigma)$ distribution, then the transformed data $\dfrac{y_k - \mu}{\sigma}$ come from a standard normal distribution, so we expect $\dfrac{y_k - \mu}{\sigma} \approx q_k$

In other words, if the y_k's are sampled from an $N(\mu,\sigma)$ distribution, then

$$y_k \approx \sigma q_k + \mu,$$

so the graph should lie approximately on a straight line with slope and intercept σ and μ, respectively.