

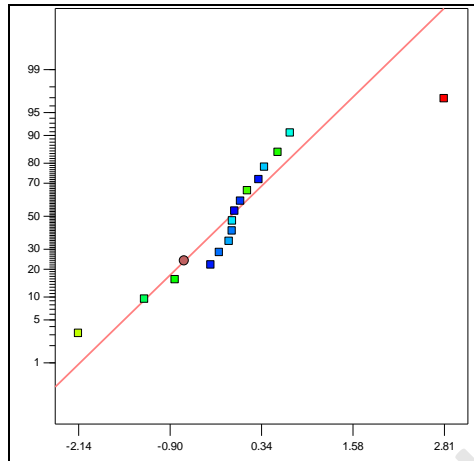
Residual Analysis and Diagnostic Plots Guide (p1/5)

Residual analysis is necessary to confirm that the assumptions for the ANOVA are met. Other diagnostic plots may provide interesting information in some situations. ALWAYS review these plots!

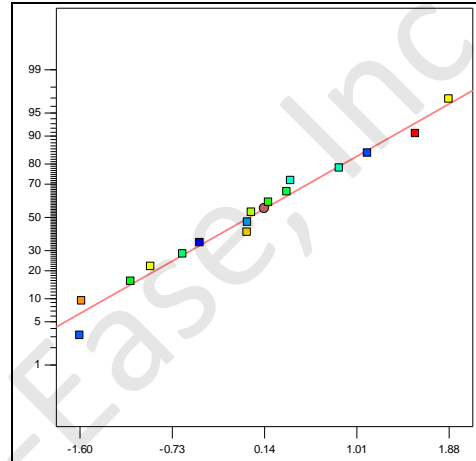
A. Diagnostic plots

1. Plot the (internally) studentized residuals:

a) **Normal plot** - should be straight line.

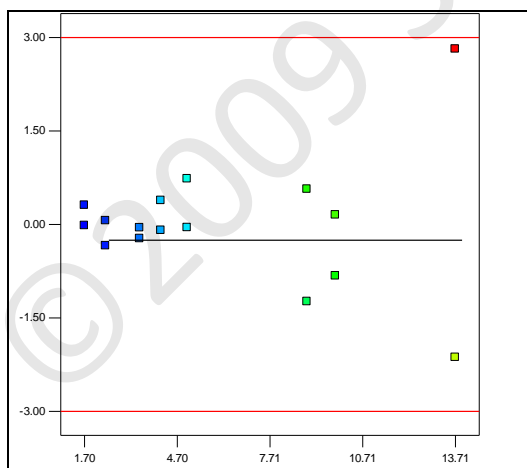


BAD: S shape

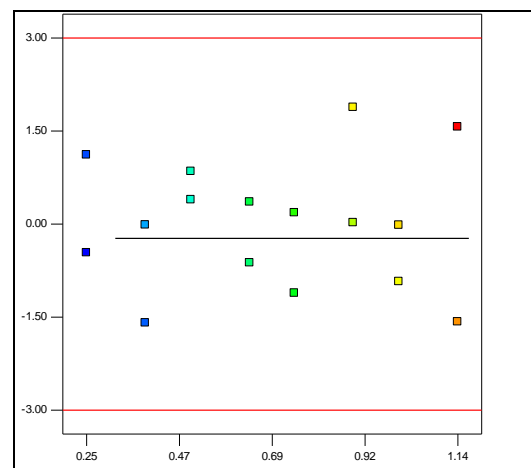


GOOD: Linear or Normal

b) **Residuals (e_i) vs predicted** value - should be random scatter.



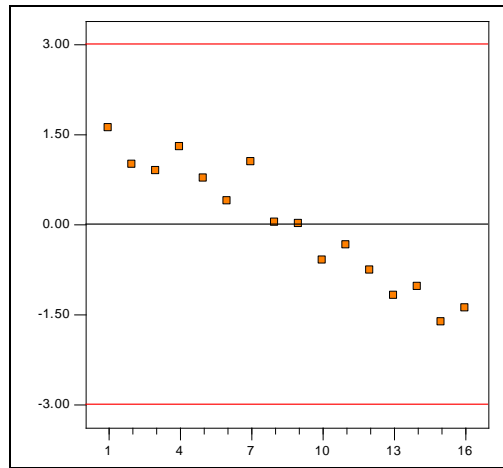
BAD: Megaphone shape



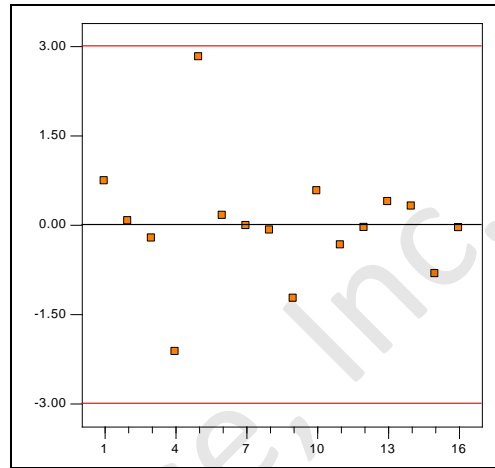
GOOD: Random scatter

Residual Analysis and Diagnostic Plots Guide (p2/5)

- c) **Residuals (e_i) vs run** - should be random scatter, no trends.

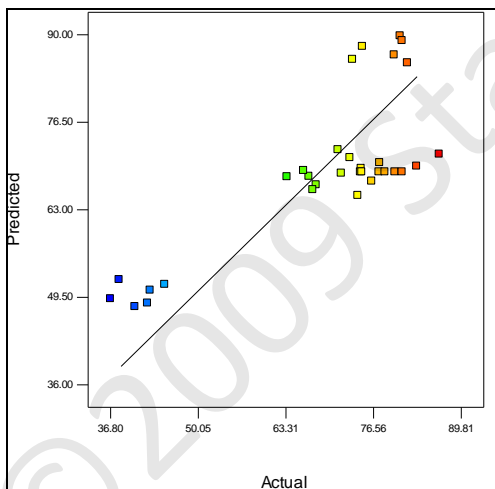


BAD: Trend

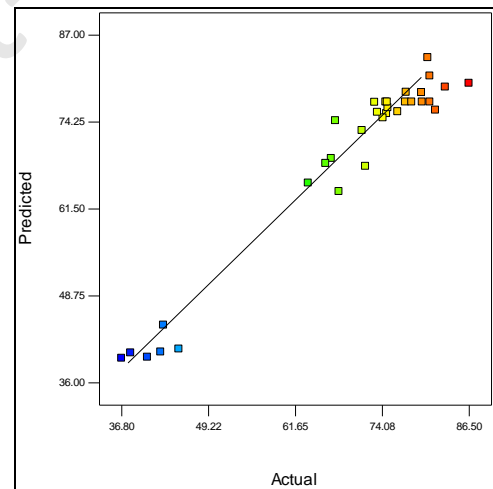


GOOD: No pattern

2. Look at the **predicted vs actual** lot. The points should be randomly scattered along the 45 deg line. Groups of points above or below the line indicate areas of over or under prediction.



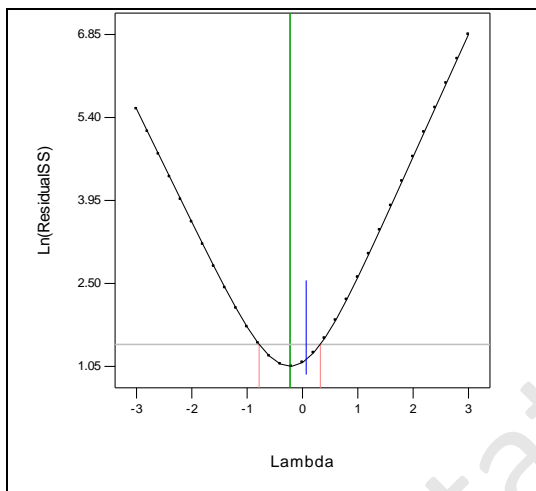
Poor Prediction



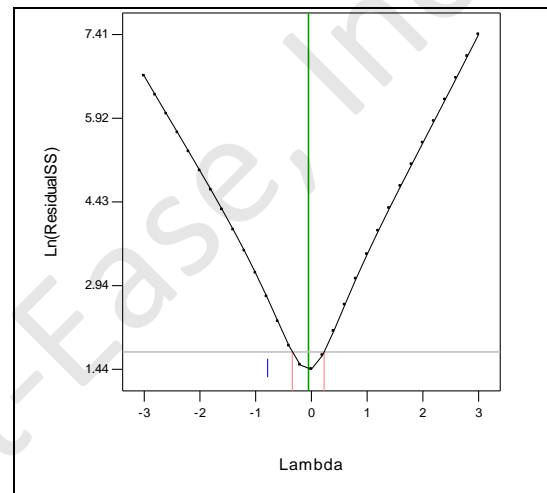
Better Prediction

Residual Analysis and Diagnostic Plots Guide (p3/5)

3. Use the **Box Cox plot** to determine if a power law transformation might be appropriate for your data. The blue line indicates the current transformation (at Lambda = 1 for none) and the green line indicates the best lambda value. Red lines indicate a 95% confidence interval associated with the best lambda value. Stat-Ease software recommends the standard transformation, such as log, closest to the best lambda value unless the confidence interval includes 1, in which case the recommendation will be "None."

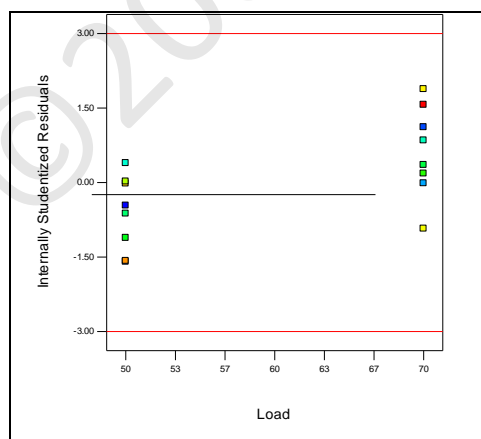


Before Transformation

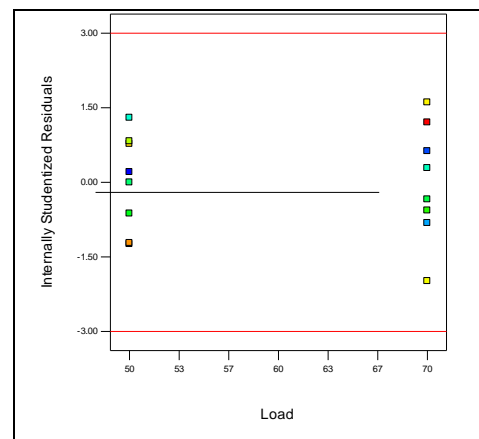


After Transformation

4. **Residuals (e_i) vs factor** - should be split by the zero-line at either end of the range – no obvious main effect (up or down). If you see an effect, go back, add it to the predictive model and assess its statistical significance.



BAD: One end higher



GOOD: Random scatter both ends

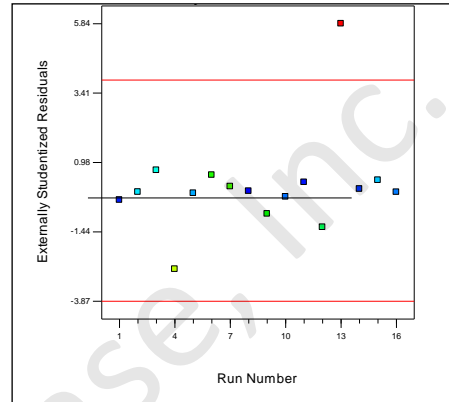
Residual Analysis and Diagnostic Plots Guide (p4/5)

Influence plots

1. Deletion diagnostics – statistics calculated by taking each run out, one after the other, and seeing how this affects the model fit.

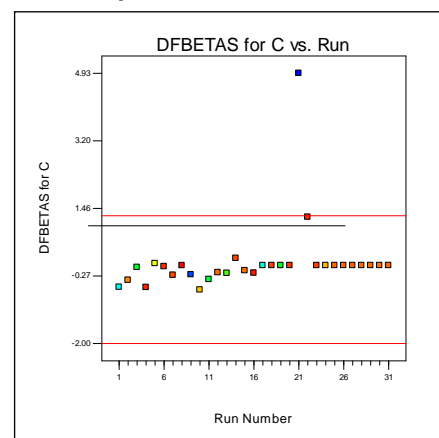
a) Look for **externally studentized residuals** (outlier t-values) outside 95 % confidence limits (roughly ± 3.5). These runs are not fit the same as the others. A high value may indicate:

- ◆ a problem with the model,
- ◆ the need for a transformation, or
- ◆ a special cause associated with that particular observation. Investigate special causes and try ignoring runs if appropriate.



b) **DFFITs** (difference in fits) is another statistic helpful for detecting influential runs. Watch for values outside of ± 2 . *Caution: For small designs this rule-of-thumb may be overly sensitive, so do not become alarmed at seeing a number of points out of limits.*

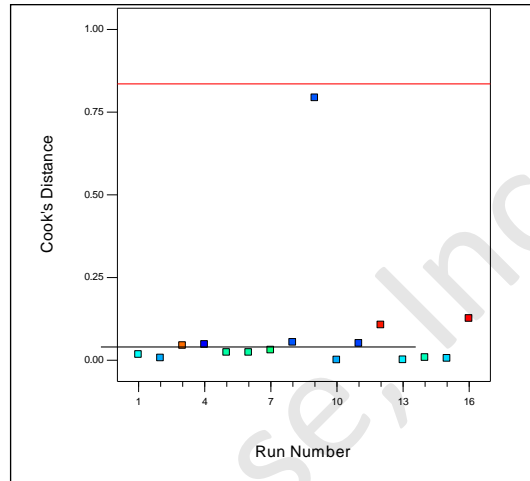
c) **DFBETAS** (difference in beta coefficients) breaks down the impact of any given run on a particular model term. If you see an excessive value for a particular factor, consider whether it falls beyond a reasonable range (for example, it may be an axial [star point] in a CCD projects outside of the feasible operating region) and, if so, try ignoring this particular run.



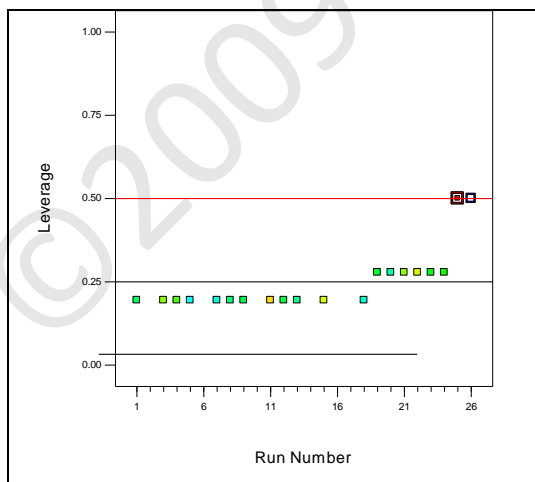
Residual Analysis and Diagnostic Plots Guide (p5/5)

2. Other measures of influence

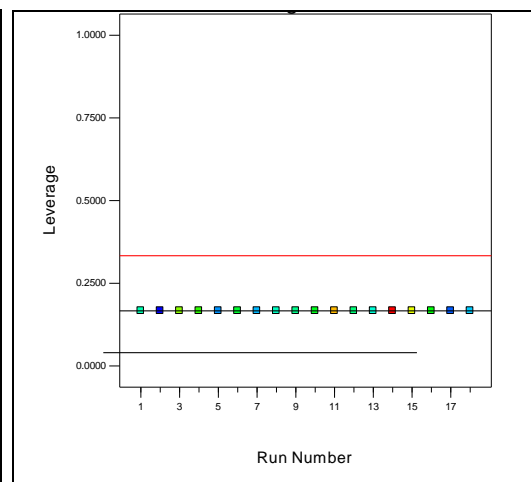
- a) **Cook's Distance** helps if you see more than one outlier in other diagnostic plots. Investigate the run with the largest Cook's Distance first. Often, if this run is ignored due to a special cause, other apparent outliers can be explained by the model.



- b) Watch for **leverage vs run** values at or beyond twice the average leverage. These runs will unduly influence at least one model parameter. If identified prior to running the experiment, it can be replicated to reduce leverage. Otherwise all you can do is check the actual responses to be sure they are as expected for the factor settings. Be especially careful of any leverages at one (1.0). These runs will be fitted exactly with no residual!



BAD: Some at twice the average



GOOD: All the same