

Residuals Are Not Independent

Residuals are variation unexplained by the fitted model

Assumption 3 (all residuals are independent of each other) is never true for a sample

Residuals depend on the fitted regression function, which depends on the same data that the residuals come from

With p fitting parameters, n residuals only have n - p degrees of freedom

For n sufficiently large compared to p, we can ignore this dependence

Residuals in Sequence

Other factors can prevent residual independence

Model error (usually a missing predictor variable)

Time dependence: sample aging, measurement drift

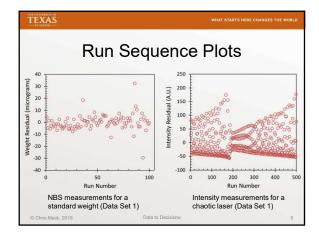
Spatial dependence: where the measurement was taken

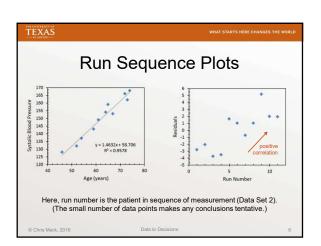
A run sequence plot shows the residuals in time sequence or other natural order to look for systematic variation

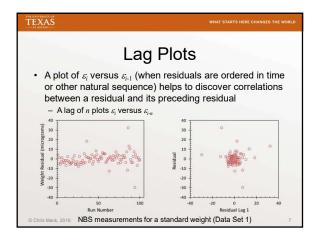
If time order corresponds to changing predictor values, the drift/aging may be hidden in the functional relationship

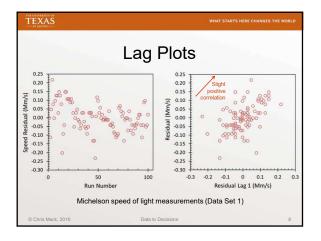
Randomization in experimental design prevents this

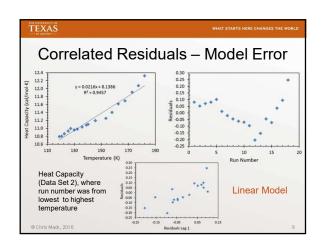
A lag plot can make systematic variation more visible

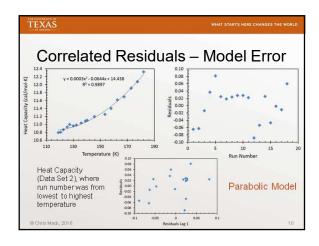












For about thirty or more residuals, we can perform the following test (usually one-tailed to test for positive correlation): -R = number of runs in the data $-\bar{R} = \frac{2n_+n_-}{n} + 1, \quad n = n_+ + n_ -s_R^2 = \frac{2n_+n_-(2n_+n_-n)}{n^2(n-1)} \qquad \text{Note: } \bar{R} \sim \frac{n}{2}, s_R \sim \frac{\sqrt{n}}{2}$ $-Z_R = \frac{R-\bar{R}}{s_R} \text{ is about normally distributed}$

Lecture 37: What have we learned? What can cause correlated (non-independent) residuals? Be able to generate and interpret a lag plot if the data sequence (order) is known Why is randomization of data order important in experimental design? What is a runs test and how is it performed?