## Lec 3: Model Adequacy Checking

Ying Li

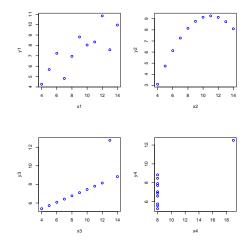
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Ying Li Lec 3: Model Adequacy Checking

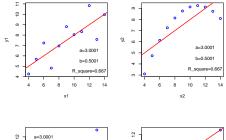
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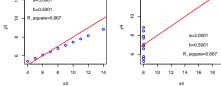
- Model validation is a very important step in the model building procedure. (one of the most overlooked)
- A high  $R^2$  value does not guarantee that the model fits the data well.
- Use of a model that does not fit the data well can not provide good answers to the underlying scientific questions.

### An interesting example: Ascombe dataset



Ying Li Lec 3: Model Adequacy Checking





- Different types of plots of residuals (histgram, Plot of residuals in time sequence, plot of residuals versus fitted values) provide information on the adequacy of different aspects of the model.
- Graphical methods have an advantage over numerical methods in model validation
  - graphical methods: a broad range of complex aspects
  - numerical methods: narrowly focused on a particular aspect(a number)

If the model fit to the data were correct, the residuals would approximate the random errors.

- If the residuals appear to behave as the assumptions of the error it suggests the model fit the data well.
- Otherwise the model fits the data poorly.(non-normality, dependency, heteroscedasticity).

### Two concepts

- Homogeneity (Homoscedasticity) : In statistics, a sequence or a vector of random variables is homoscedastic if all random variables in the sequence or vector have the same finite variance. This is also known as homogeneity of variance.
- Heteroscedasticity: a collection of random variables is heteroscedastic, or heteroscedastic, if there are sub-populations that have different variabilities than others

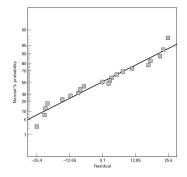
$$y_{ij} = \mu + \tau_i + \epsilon_{ij}$$

Assumptions of the errors:

- $\epsilon_{ij}$  are normally distributed
- $\epsilon_{ij}$  are independent
- $\epsilon_{ij}$  has mean zero and constant variance  $\sigma^2$ .

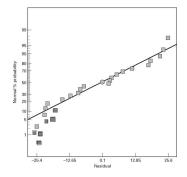
### Check the normality

Normal probability plot.

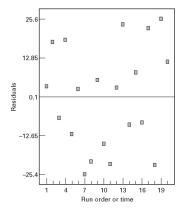


### Check the normality

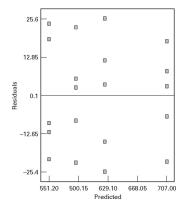
Normal probability plot.



Detect the correlation between the residuals.



### Plot of residuals versus fitted values



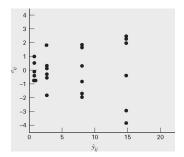
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Detect the nonconstant variance.



$$H_0: \sigma_1^2 = \sigma_2^2 = \cdots = \sigma_a^2$$
  
 $H_1:$  above not true for at least one $\sigma_i^2$ 

- Bartlett's test
- Modified Levene test

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### Bartlett's test

The test statistic is

$$\chi_0^2 = 2.3026 \frac{q}{c}$$

where

$$q = (N - a) log_{10} S_p^2 - \sum_{i=1}^{a} (n_i - 1) log_{10} S_i^2$$

$$c = 1 + rac{1}{3(a-1)} (\sum_{i=1}^{a} (n_i - 1)^{-1} - (N-a)^{-1})$$
  
 $S_p^2 = rac{\sum_{i=1}^{a} (n_i - 1) S_i^2}{N-a}$ 

and  $S_i^2$  is the sample variance of the *i*th population.

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The modified Levene test uses the absolute deviation of the observations  $y_{ij}$  in each treatment from the treatment **median**  $\tilde{y}_i$ . Denote these deviations by

$$d_{ij}=|y_{ij}-\widetilde{y}_i|.$$

The modified Levene test then evaluates whether or not the means of these deviations are equal for all treatment.

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The modified Levene test then evaluates whether or not the means of these deviations are equal for all treatment. Apply the ANOVA F test.

- Bartlett's test, good accuracy, but very sensitive to normality assumption
- Modified Levene test, robust to departures from normality.

# A dilemma

- Assume that we test for homogeneity and whether the residuals are normally distributed or not.
- The more observations, the easier it is to show that the requirement are not fulfilled.
- Conclusion: The validity of the ANOVA is reduced with the number of observation.

- ANOVA is robust against minor heteroscedasticity and minor deviations form the normal distribution.
- Do not use tests, but study the residual plot.

Suppose that the standard deviation of y is proportional to a power of the mean of y such that

$$\sigma_y \propto \mu^{lpha}$$

We want to transform the data to yield a constant variance. Usually we use

$$y^{\star} = y^{\lambda}$$

Then it can be shown that

$$\sigma_{y^\star} \propto \mu^{\lambda + \alpha - 1}$$

If we set  $\lambda = 1 - \alpha$ , the variance of the transformed data  $y^*$  is constant.

Estimate  $\alpha$  empirically from the data. Consider  $\sigma_{y_i} = \theta \mu_i^{\alpha}$ . We make the logs

$$\log \sigma_{y_i} = \log \theta + \alpha \log \mu_i.$$

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#### TABLE 3.9

#### Variance-Stabilizing Transformations

Relationship Between <b>σ</b> <sub>y</sub> and <b>μ</b>	$\alpha$ $\lambda = 1 - \alpha$		Transformation	Comment		
$\sigma_y \propto \text{constant}$	0	1	No transformation			
$\sigma_{ m y} \propto \mu^{1/2}$	1/2	1/2	Square root	Poisson (count) data		
$\sigma_y \propto \mu$	1	0	Log			
$\sigma_{y} \propto \mu^{3/2}$	3/2	-1/2	Reciprocal square root			
$\sigma_{\rm y} \propto \mu^2$	2	-1	Reciprocal			

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A civil engineer is interested in determining whether four different methods of estimating flood flow frequency produce equivalent estimates of peak discharge when applied to the same watershed.

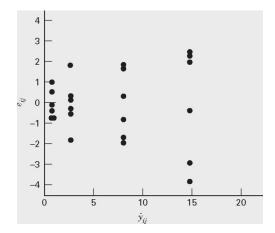
Estimation Method	Observations						$\overline{y}_{i.}$	ŷ,	Si
1	0.34	0.12	1.23	0.70	1.75	0.12	0.71	0.520	0.66
2	0.91	2.94	2.14	2.36	2.86	4.55	2.63	2.610	1.09
3	6.31	8.37	9.75	6.09	9.82	7.24	7.93	7.805	1.66
4	17.15	11.82	10.95	17.20	14.35	16.82	14.72	15.59	2.77

#### TABLE 3.8

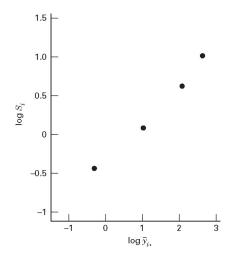
#### Analysis of Variance for Peak Discharge Data

Source of Variation	Sum of Squares	Degrees of Freedom	Mean Square	$F_0$	P-Value	
Methods	708.3471	3	236.1157	76.07	< 0.001	
Error	62.0811	20	3.1041			
Total	770.4282	23				

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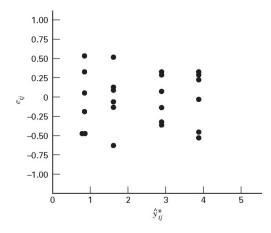
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After square-root transformation



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In the Box-Cox transformation model it is assumed that there is such that a transformation of the observed data y according to:

$$y_{\lambda} = \{ \begin{array}{c} \frac{y^{\lambda} - 1}{\lambda}, \lambda \neq 0\\ logy, \lambda = 0 \end{array}$$

- **1** Rank the observation *y*<sub>ij</sub> in ascending order.
- 2 Replace each observation it its rank  $R_{ij}$ .
- O The test statistic is

$$H = \frac{1}{S^2} \left[ \sum_{i=1}^{a} \frac{R_{i.}^2}{n_i} - \frac{N(N+1)^2}{4} \right],$$

where

$$S^2 = rac{1}{N-1} [\sum_{i=1}^{a} \sum_{j=1}^{n_i} R_{ij}^2 - rac{N(N+1)^2}{4}].$$

If n<sub>i</sub> ≥ 5, and H<sub>0</sub> is ture, H approximately~ χ<sub>a-1</sub>.
 If H > χ<sub>α,a-1</sub>, then the null hypothesis is rejected.