Statistical Methods

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Topics

Objectives

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- Carry out Tukey's multiple comparison procedure after a two-factor ANOVA with $K > 1$, and interpret the results.
- Interpret residuals and fitted values.
- Use residuals to check normality and constant standard deviation assumptions.

Multiple Comparisons for Two-Factor ANOVA ($K > 1$) when the Interaction Effect *Isn't* Significant

- When the no-interaction hypothesis H_{0AB} **is not** rejected and at least one of the two main effect hypotheses H_{0A} and H_{0B} **is** rejected, we can use **Tukey's procedure** to decide **which** levels of a factor differ.

Tukey's Multiple Comparison Procedure: If the two-factor ANOVA F test fails to reject H_{0AB}, but rejects H_{0A} or H_{0B}:

1. Choose an **overall familywise confidence level** $100(1-\alpha)\%$ (usually $\alpha = 0.05$ for a 95% confidence level).

2. For **Factor A comparisons**, compute the $I(I-1)/2$ **confidence intervals**:

$$\bar{X}_{i\cdot\cdot} - \bar{X}_{i'\cdot\cdot} \;\pm\; Q_{\alpha,I,IJ(K-1)}\sqrt{\frac{MSE}{JK}}\,.$$

   For **Factor B comparisons**, compute the $J(J-1)/2$ **confidence intervals**:

$$\bar{X}_{\cdot j\cdot} - \bar{X}_{\cdot j'\cdot} \;\pm\; Q_{\alpha,J,IJ(K-1))}\sqrt{\frac{MSE}{IK}}\,.$$

3. For any interval that **doesn't contain zero**, deem those levels of the given factor to be **different**.

Multiple Comparisons for Two-Factor ANOVA ($K > 1$) when the Interaction Effect *Is* Significant

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- When the no-interaction hypothesis H_{0AB} **is** rejected, we can use **Tukey's procedure** to decide **which *group* means** differ.

  This can be done by carrying out a ***one-factor*** **ANOVA** on the IJ ***groups*** following by the (*one-factor*) **Tukey procedure.**

Estimating Parameters (when $K > 1$)

- Recall (Slides 15) that the *full* **two-factor ANOVA model** is:

$$X_{ijk} \;=\; \mu + \alpha_i + \beta_j + \gamma_{ij} + \epsilon_{ijk} \,.$$

Model Parameter Estimators: We estimate the unknown model parameters μ, α_i, β_j, and σ using the **estimators** $\hat{\mu}$**,** $\hat{\alpha}_i$**,** $\hat{\beta}_j$, and $\hat{\sigma}$ defined as:

Model Parameter	Estimator
μ	$\hat{\mu} = \bar{X}_{...}$
$\alpha_i = \mu_{i.} - \mu$	$\hat{\alpha}_i = \bar{X}_{i..} - \bar{X}_{...}$
$\beta_j = \mu_{.j} - \mu$	$\hat{\alpha}_i = \bar{X}_{.j.} - \bar{X}_{...}$
$\gamma_{ij} = \mu_{ij} - (\mu + \alpha_i + \beta_j)$	$\hat{\gamma}_{ij} = \bar{X}_{ij.} - (\hat{\mu} + \hat{\alpha}_i + \hat{\beta}_j)$
	$= \bar{X}_{ij.} - \bar{X}_{i..} - \bar{X}_{.j.} + \bar{X}_{...}$
σ	$\hat{\sigma} = \sqrt{\text{MSE}}$

Fitted Values and Residuals

- The ***fitted value*** (or ***predicted value***) for the kth individual in the i, jth cell, $\hat{X}_{ijk}$, is

$$\begin{aligned}\hat{X}_{ij} &= \hat{\mu} + \hat{\alpha}_i + \hat{\beta}_j + \hat{\gamma}_{ij} \\ &= \bar{X}_{...} + (\bar{X}_{i..} - \bar{X}_{...}) + (\bar{X}_{.j.} - \bar{X}_{...}) \\ &\quad + (\bar{X}_{ij.} - \bar{X}_{i..} - \bar{X}_{.j.} + \bar{X}_{...}) \\ &= \bar{X}_{ij.}\,.\end{aligned}$$

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  $\hat{X}_{ijk}$ is the value we'd predict, based on the data, for the response of the kth individual in the i, jth cell.

  It's just the **i, jth group mean $\bar{X}_{ij.}$** (which is also the estimate of the true group mean μ_{ij}).

- The ***residual*** for the kth observation in the i, jth cell, e_{ijk}, is defined as

$$\begin{aligned} e_{ijk} &= X_{ijk} - \hat{X}_{ijk} \\ &= X_{ijk} - (\hat{\mu} + \hat{\alpha}_i + \hat{\beta}_j + \hat{\gamma}_{ij}) \\ &= X_{ijk} - \bar{X}_{ij.} \end{aligned}$$

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Note that a **residual** is just the **deviation** of an observed response X_{ijk} **away from** the **group mean** $\bar{X}_{ij.}$.

- **Comment**: The **error sum of squares** (Slides 15) is the **sum of squared residuals**, i.e.

$$\text{SSE} = \sum_i \sum_j \sum_k e_{ijk}^2 .$$

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- **Checking the Constant σ Assumption**: Plot the **residuals** versus the **fitted values**.

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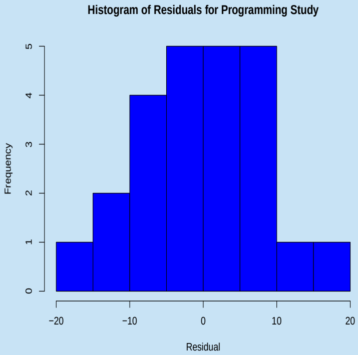
- **Checking the Normality Assumption**: Use a **histogram** or **normal probability plot** of the **residuals**.

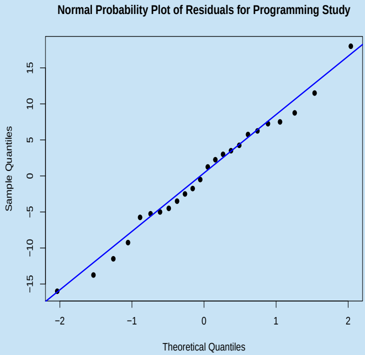
- **Checking the Constant σ Assumption**: Plot the **residuals** versus the **fitted values**.

  Usually, when σ *isn't* constant, it increases with the group mean.

Example

For the study of factors affecting programmers' errors in predicting project completion times, a **histogram** and **normal probability plot** of the **residuals** are below.





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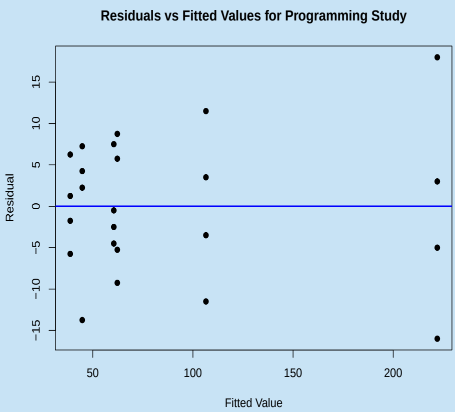
A plot of the **residuals** versus **fitted values** is on the next slide.


Residuals vs Fitted Values for Programming Study
Residual
Fitted Value
15
10
5
0
−5
−10
−15
50
100
150
200

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Thus the **ANOVA F test** results are valid.