

Lecture 9

Completely Randomized Designs

Reading: Oehlert 2010 Chapter 3; DAE 2017 Chapter 3

DSA 8020 Statistical Methods II

Completely
Randomized Designs

ANOVA & Multiple
Comparisons

Checking Model
Assumptions

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1 Completely Randomized Designs

2 ANOVA & Multiple Comparisons

3 Checking Model Assumptions

Motivating Example: Maze Training in Mice

Research Question

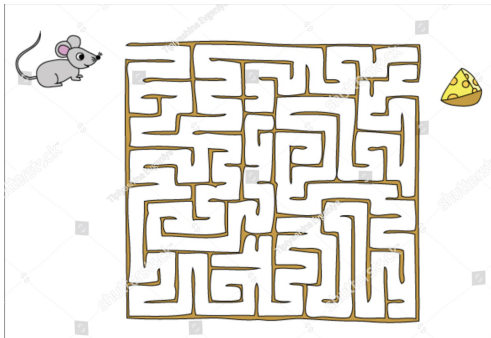
Does maze training improve navigation speed in mice?

Treatments

- 1, 2, 3, or 4 training runs

Response Variable

- Time required to complete the maze



Completely Randomized Designs (CRD)

A Completely Randomized Design (CRD) assigns treatments (say g treatments) to experimental units completely at random, where $\sum_{i=1}^g n_i = N$.

Why use a CRD?

- Simple experimental structure
- Easy to analyze
- Flexible and robust
- Often sufficient when experimental units are homogeneous

Key Idea:

Randomization helps protect against bias

In a CRD, we are usually interested in:

- 1 Determining whether treatment means differ overall

$$H_0 : \mu_1 = \mu_2 = \dots = \mu_g$$

- 2 Identifying which treatment means differ
- 3 Estimating treatment means and treatment differences

Main tools:

- ANOVA
- Multiple comparisons
- Confidence intervals

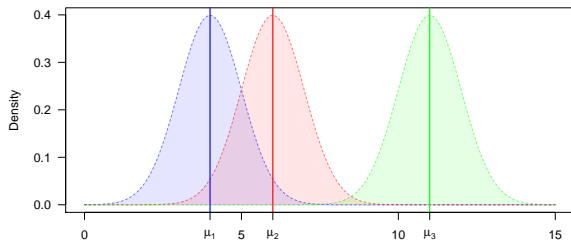
Means Model

The simplest ANOVA model assumes each treatment has its own mean:

$$y_{ij} = \mu_i + \epsilon_{ij}, \quad i = 1, \dots, g, \quad j = 1, \dots, n_i, \quad \epsilon_{ij} \sim N(0, \sigma^2),$$

where:

- μ_i = mean response for treatment i
- ϵ_{ij} = random error



Interpretation:

Each treatment group has its own population mean

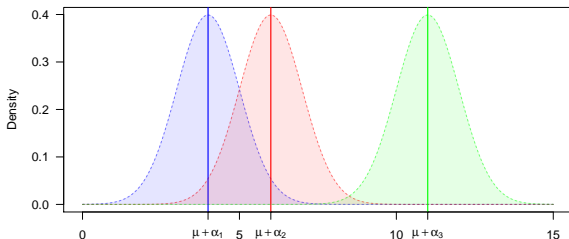
Effects Model

We can rewrite the treatment means as $\mu_i = \mu + \alpha_i$, which gives

$$y_{ij} = \mu + \alpha_i + \epsilon_{ij}, \quad i = 1, \dots, g, \quad j = 1, \dots, n_i, \quad \epsilon_{ij} \sim N(0, \sigma^2),$$

where:

- μ = baseline mean
- α_i = treatment effect



Overparameterized: a constraint is needed to define the baseline and make the parameters identifiable

Effects Model: Why Do We Need Constraints?

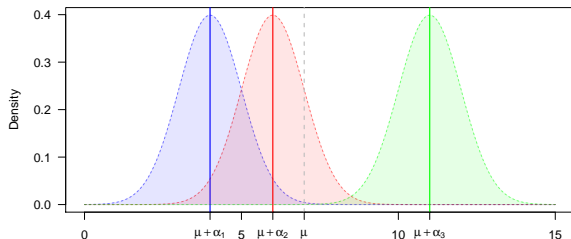
The effects model is overparameterized

Different combinations of μ and α_i can produce the same treatment means.

To make the parameters uniquely estimable, we impose a constraint such as:

$$\sum_{i=1}^g \alpha_i = 0$$

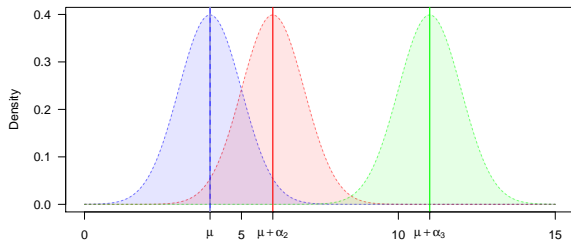
$\Rightarrow \mu$: overall mean



Effects Model Constraints Cont'd

Suppose we let $\alpha_1 = 0$

$\Rightarrow \mu$: mean of the first group (blue group in this example)



- y_{ij} : observation j from treatment i
- \bar{y}_i : sample mean for treatment i
- $\bar{y}_{..}$: overall sample mean

Example:

$$\bar{y}_{2.}$$

means:

average response for treatment group 2

ANOVA Decomposition

Decomposition of y_{ij} : $y_{ij} = \bar{y}_{..} + (\bar{y}_{i.} - \bar{y}_{..}) + (y_{ij} - \bar{y}_{i.})$

$$\Rightarrow \underbrace{\sum_{i=1}^g \sum_{j=1}^{n_i} (y_{ij} - \bar{y}_{..})^2}_{SS_T} = \underbrace{\sum_{i=1}^g n_i (\bar{y}_{i.} - \bar{y}_{..})^2}_{SS_{TRT}} + \underbrace{\sum_{i=1}^g \sum_{j=1}^{n_i} (y_{ij} - \bar{y}_{i.})^2}_{SS_E}$$

Total variability can be separated into:

Total Variation = Treatment Variation + Error Variation

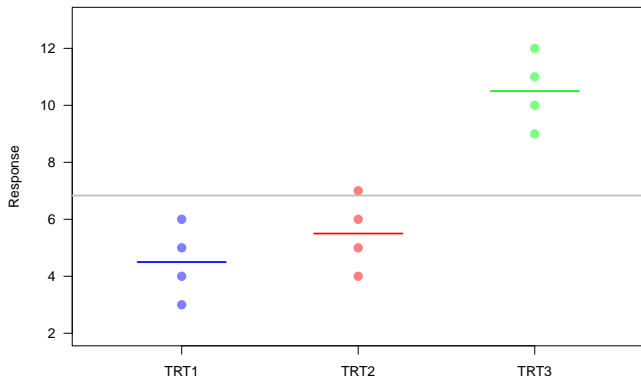
$$SS_T = SS_{TRT} + SS_E$$

Interpretation:

- Treatment variation measures differences between groups
- Error variation measures variability within groups

Graphical Illustration of ANOVA Decomposition

$$\underbrace{\text{Total Variation}}_{SS_T} = \underbrace{\text{Treatment Variation}}_{SS_{TRT}} + \underbrace{\text{Error Variation}}_{SS_E}$$



- Treatment variation measures differences between group means
- Error variation measures variability within groups

ANOVA Table

Source	df	SS	MS	F
Treatment	$g - 1$	SS_{TRT}	$MS_{TRT} = \frac{SS_{TRT}}{g-1}$	$\frac{MS_{TRT}}{MS_E}$
Error	$N - g$	SS_E	$MS_E = \frac{SS_E}{N-g}$	
Total	$N - 1$	SS_T		

Key Idea:

Large values of

$$\frac{MS_{TRT}}{MS_E}$$

suggest treatment differences

Computational details

$$SS_T = \sum_{i=1}^g \sum_{j=1}^{n_i} (y_{ij} - \bar{y}_{..})^2 = \sum_{i=1}^g \sum_{j=1}^{n_i} y_{ij}^2 - \frac{y_{..}^2}{N}$$

$$SS_{TRT} = \sum_{i=1}^g n_i (\bar{y}_{i.} - \bar{y}_{..})^2 = \sum_{i=1}^g \frac{y_{i.}^2}{n_i} - \frac{y_{..}^2}{N}$$

$$SS_E = \sum_{i=1}^g \sum_{j=1}^{n_i} (y_{ij} - \bar{y}_{i.})^2 = \sum_{i=1}^g \sum_{j=1}^{n_i} y_{ij}^2 - \sum_{i=1}^g \frac{y_{i.}^2}{n_i} = SS_T - SS_{TRT}$$

How large is large? \Rightarrow Use the *F*-test

Testing for treatment effects

$$H_0 : \alpha_i = 0 \quad \text{for all } i$$

$$H_a : \alpha_i \neq 0 \quad \text{for some } i \Rightarrow \text{at least one treatment effect differs}$$

Test statistics: $F = \frac{MS_{TRT}}{MS_E}$.

Under H_0 , the test statistic follows an $F_{g-1, N-g}$ distribution

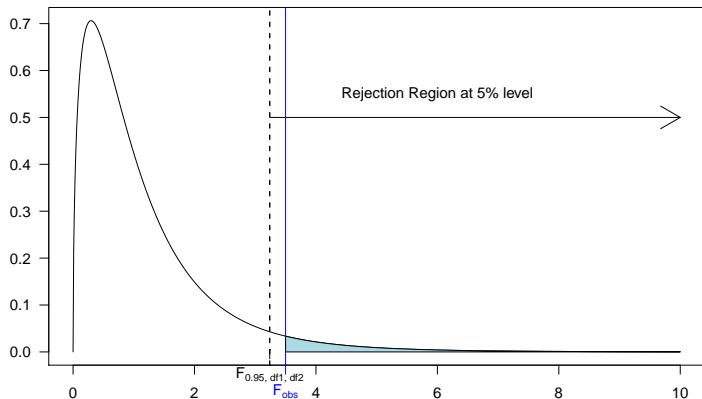
Reject H_0 if

$$F_{obs} > F_{g-1, N-g; \alpha}$$

for an α -level test, $F_{g-1, N-g; \alpha}$ is the upper $100(1 - \alpha)\%$ percentile of the $F_{g-1, N-g}$ distribution

p -value = $P(F > F_{obs})$; reject H_0 if p -value $< \alpha \Rightarrow$ Large F provide evidence against H_0

F Distribution and the F-Test

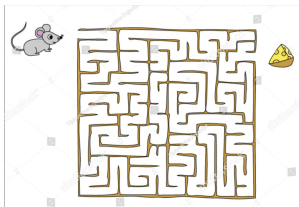


Interpretation:

The shaded region represents values leading to rejection of H_0

Mice Example Revisited

An experiment was conducted to determine if experience has an effect on the time it takes for mice to run a maze. Four treatment groups, consisting of mice having been trained on the maze one, two, three and four times were run through the maze and their times recorded.



Source: <https://www.shutterstock.com/image-vector/find-your-way-cheese-mouse-maze-232569073>

Training runs	1	2	3	4
n_i	5	5	5	5
\bar{y}_i	9.14	7.24	6.76	5.18
s_i^2	0.308	0.418	0.313	0.262

Example Cont'd

Training runs	1	2	3	4
n_i	5	5	5	5
$\bar{y}_{i\cdot}$	9.14	7.24	6.76	5.18
s_i^2	0.308	0.418	0.313	0.262

- Write down the model.
- Fill out the ANOVA table and test whether the time to run the maze is affected by training. Use a significant level of .05.

All models are wrong, but some are useful—G.E.P Box

Model:

$$y_{ij} = \mu + \alpha_i + \epsilon_{ij}, \quad i = 1, \dots, g, \quad j = 1, \dots, n_i.$$

We make the following **assumptions**:

- Errors normally distributed
- Errors have constant variance
- Errors are independent

$$\Rightarrow \epsilon_{ij} \stackrel{i.i.d.}{\sim} N(0, \sigma^2)$$

What If Assumptions are Violated?

If the assumptions are not true, our statistical inferences might not be valid, for example,

- A confidence interval might not cover with the stated coverage rate
- A test with nominal type I error could actually have a larger or smaller type I error rate

We need good strategy for checking model assumptions,
i.e., $\epsilon_{ij} \stackrel{i.i.d.}{\sim} N(0, \sigma^2)$.

Checking Model Assumptions

We need to check if these assumptions reasonably met

Model:

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

Data:

$$\begin{array}{rclcl} y_{ij} & = & (\bar{y}_{..} + (\bar{y}_{i.} - \bar{y}_{..})) & + & (y_{ij} - \bar{y}_{i.}) \\ y_{ij} & = & \hat{y}_{ij} & + & \hat{\epsilon}_{ij} (r_{ij}) \\ \text{observed} & = & \text{predicted} & + & \text{residual} \end{array}$$

Residuals are our “estimates” of unobservable errors ϵ'_{ij} s

We will conduct model diagnostics using **residual** and **predicted** values.

We will use residuals to assess the model assumptions.

- Raw residual:

$$r_{ij} = y_{ij} - \hat{y}_{ij}, \text{ where } \hat{y}_{ij} = \hat{\mu} + \hat{\alpha}_i = \bar{y}_i.$$

- Standardized residual (internally Studentized residual)
adjusts r_{ij} for its estimated standard deviation

$$s_{ij} = \frac{r_{ij}}{\sqrt{MS_E(1 - \frac{1}{n_i})}}$$

- Studentized residual (externally Studentized residual)

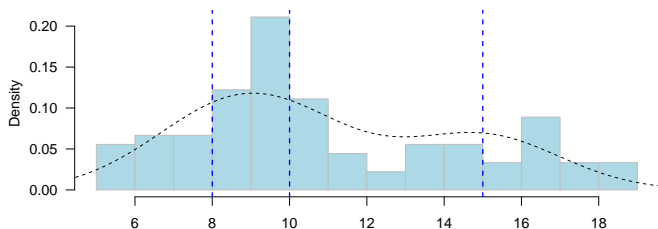
$$t_{ij} = s_{ij} \sqrt{\frac{N - g - 1}{N - g - s_{ij}^2}}$$

$t_{ij} \sim t_{df=N-g-1}$ if the model is correct \Rightarrow can be used to identify **outliers**

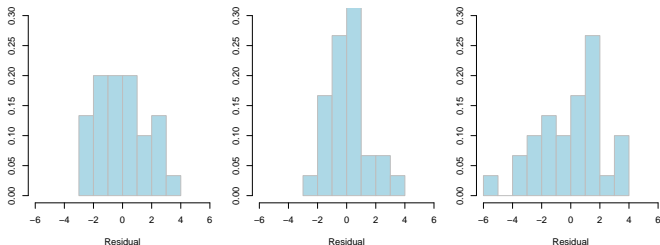
Assessing Normality

We DO NOT assume all y'_{ij} s come from the same normal distribution, instead we assume ϵ'_{ij} s come from the same normal distribution \Rightarrow Not informative to plot a histogram for all the data—treatment effects lead to non-normality

Example: Suppose $g = 3$, $(\mu_1, \mu_2, \mu_3) = (8, 10, 15)$ and $\epsilon'_{ij}s \sim N(0, 2^2)$



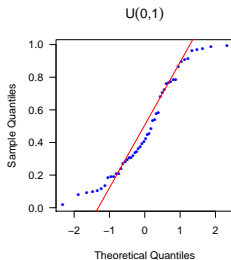
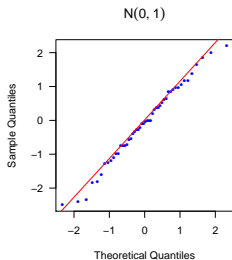
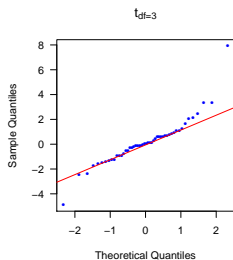
- If sample sizes are large, histograms of **residuals** can be constructed from each treatment separately



- Also, if sample sizes are large, QQ-plots or normal quantile plots can be generated for each treatment

Normal Quantile Plots

Plots $r_{(k)}$ versus $\Phi^{-1}\left(\frac{k}{n+1}\right)$, $k = 1, \dots, n$, where $r_{(k)}$ is the k^{th} ordered residual and $\Phi^{-1}\left(\frac{k}{n+1}\right)$ is its corresponding (standard) normal score.



Interpretation

- Points near a straight line support normality
- Strong curvature suggests non-normality
- Extreme deviations may indicate outliers

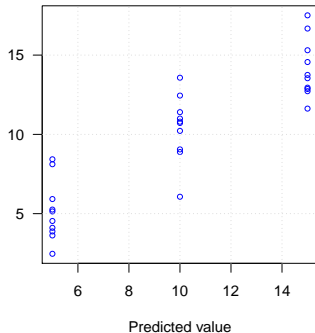
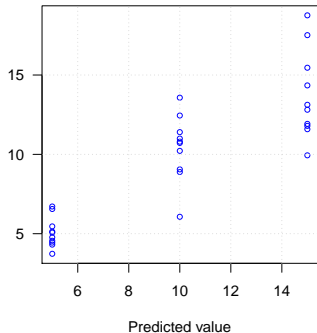
- Assessing normality
 - Formal tests (e.g., Shapiro–Wilk, Anderson–Darling) are often not very informative
 - Small samples: low power to detect non-normality
 - Large samples: trivial deviations may appear significant
 - Use QQ-plots and histograms for graphical assessment
- Handling non-normality
 - Use nonparametric methods such as the Kruskal–Wallis test
 - Apply transformations such as the Box–Cox transformation
- The ANOVA F -test is reasonably robust to moderate non-normality

- We can test for equal variance, but some tests rely heavily on normality assumption:
 - Hartley's test
 - Bartlett's test
 - Cochran's C test
- F -test is reasonably robust to unequal variance if n_i 's are equal **balanced design**, or nearly so
- *"If you have to test for equality of variances, your best bet is Levene's test."* – Gary Oehlert

- 1 Compute $r_{ij} = y_{ij} - \bar{y}_i$.
- 2 Treat the $|r_{ij}|$ as data and use the ANOVA F -test to test H_0 that the groups have the same average value of $|r_{ij}|$
- 3 If $\frac{MS_{TRT}}{MS_E} > F_{g-1, N-g-1; \alpha} \Rightarrow$ reject H_0
- 4 Modified Levene's (Brown-Forsythe) test: use $d_{ij} = |y_{ij} - \tilde{y}_i|$, the absolute deviations from the group medians instead of $|r_{ij}|$

Fairly robust to non-normality and unequal sample size

Diagnostic Plot for Non-Constant Variance



Residuals vs. fitted values plot

- Assess the constant variance assumption
- Identify possible outliers or unusual patterns

- **Assessing constant variance**

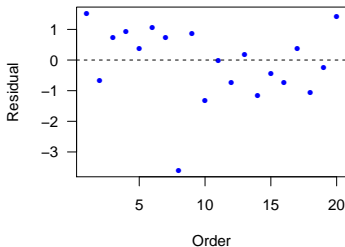
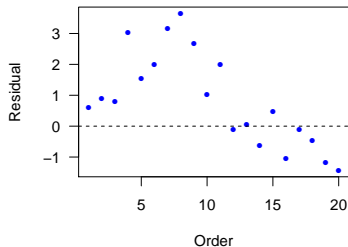
- Use residual plots for qualitative assessment
- Do not rely solely on formal tests

- **Handling unequal variance**

- Apply variance-stabilizing transformations
- Incorporate unequal variances into the model
- The ANOVA F -test is reasonably robust to unequal variances when the design is (nearly) balanced

Assessing Dependence

Randomization helps support independence. Residual plots against **run order** or **spatial location** can help detect possible dependence



Durbin-Watson Statistic

A simple diagnostic for serial dependence:

$$DW = \frac{\sum_{k=1}^{n-1} (r_k - r_{k+1})^2}{\sum_{k=1}^n r_k^2}$$

DW \approx 2 : independence

DW < 2 : positive dependence

DW > 2 : negative dependence

Example: Balloon Experiment (DAE 2017, Exercise 3.12)

An experiment was conducted to investigate whether balloon color affects the time required to inflate a balloon to a diameter of 7 inches.

- Four balloon colors from the same manufacturer were tested
- An assistant inflated the balloons
- Inflation time was recorded using a stopwatch
- Color codes:

1 = Pink, 2 = Yellow, 3 = Orange, 4 = Blue

Purpose of this example: Assess whether the experimental errors are independent.

⇒ See the accompanying R session for the full analysis

Table 3.13 Times (in seconds) for the balloon experiment

Time order	1	2	3	4	5	6	7	8
Coded color	1	3	1	4	3	2	2	2
Inflation time	22.0	24.6	20.3	19.8	24.3	22.2	28.5	25.7
Time order	9	10	11	12	13	14	15	16
Coded color	3	1	2	4	4	4	3	1
Inflation time	20.2	19.6	28.8	24.0	17.1	19.3	24.2	15.8
Time order	17	18	19	20	21	22	23	24
Coded color	2	1	4	3	1	4	4	2
Inflation time	18.3	17.5	18.7	22.9	16.3	14.0	16.6	18.1
Time order	25	26	27	28	29	30	31	32
Coded color	2	4	2	3	3	1	1	3
Inflation time	18.9	16.0	20.1	22.5	16.0	19.3	15.9	20.3

Topics Covered

- Completely Randomized Designs (CRD)
- ANOVA decomposition and the F -test
- Multiple comparisons
- Checking model assumptions

Completely
Randomized Designs

ANOVA & Multiple
Comparisons

Checking Model
Assumptions

R Functions to Know

- **Data preparation:** `as.factor`
- **ANOVA:** `aov`
- **Multiple comparisons:** `LSD.test` (`agricolae`),
`TukeyHSD`
- **Diagnostics:** `dwtest`, `levene.test`, `qqnorm`, `qqline`,
`hist`