筑波大学
University of Tsukuba

Single-Factor Experiments: Analysis of Variance (ANOVA)

Marco Antonio Florenzano Mollinetti[1]
[1]**University of Tsukuba, Systems Optimization Laboratory**
mollinetti@syou.cs.tsukuba.ac.jp

Before we Begin

- Go to the github repo:
  - https://github.com/Mollinetti/Statistics-R
- Download the script for this class! (in the ‘scripts’ folder, class_4.r!)
- Run the first lines to load/install the required libraries

Agenda

- Introduction
- Completely Randomized single-factor model
- Unbalanced Design
- Random Effects model
- Blocking design
- Model Validation
- Two way ANOVA

- Introduction
- Completely Randomized single-factor model
- Unbalanced Design
- Random Effects model
- Blocking design
- Model Validation
- Two way ANOVA

Introduction

- Many single-factor experiments require more than two levels of the factor to be considered
- Randomization of the experiments is now taken into account
- In the medical field, effects of medicines/treatments are verified for multiple samples of populations
- We will now call each level a treatment

Introduction

- Montgomery explains the steps for a experiment:

1. **Conjecture**: the original hypothesis that motivates the experiment.
2. **Experiment**: the test performed to investigate the conjecture.
3. **Analysis**: the statistical analysis of the data from the experiment.
4. **Conclusion**: what has been learned about the original conjecture from the experiment. Often the experiment will lead to a revised conjecture, and a new experiment, and so forth.

Introduction

- Factor levels can be chosen in two ways:
  - Fixed-effects model
  - Random effects/ Components of variance model

Introduction

- Factor levels can be chosen in two ways:
  - Fixed-effects model
    - Specifically choose the a levels
    - Conclusions cannot be extended to treatments that were not considered
  - Random effects/ Components of variance model

Introduction

- Factor levels can be chosen in two ways:
  - Fixed-effects model
  - Random effects/ Components of variance model
    - Random sample from a larger population of treatments
    - Extend the conclusion to all treatments
    - Knowledge about the treatments investigated is not important

- Introduction
- Completely Randomized single-factor model
- Unbalanced Design
- Random Effects model
- Blocking design
- Model Validation
- Two way ANOVA

Completely Randomized single-factor Model

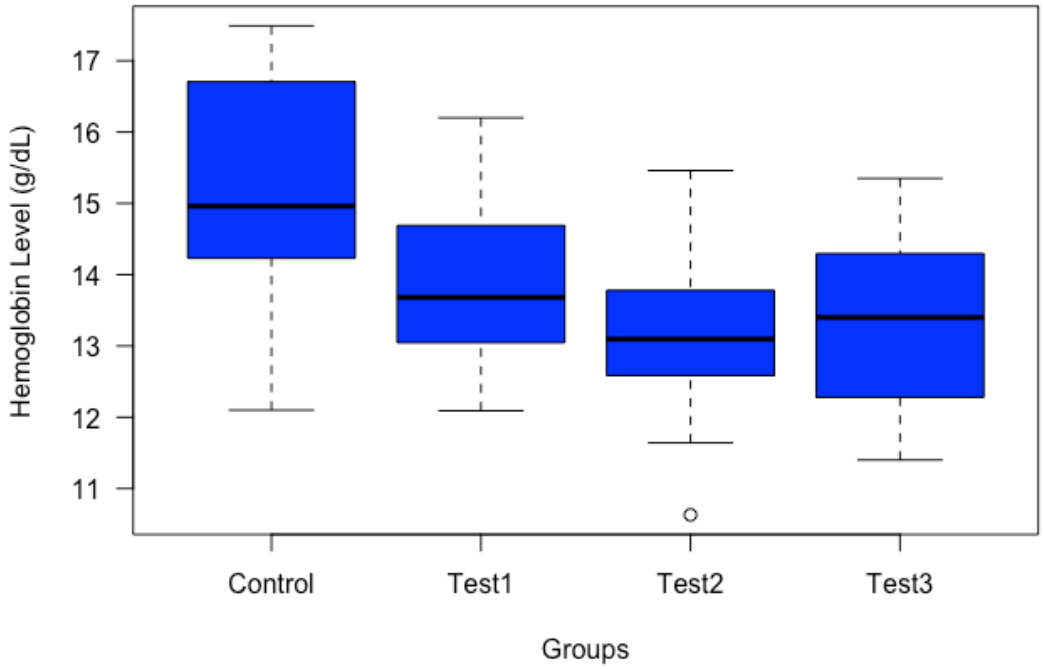
- Consider the following experiment: “We need to verify the effect of some medicine to anemic male patients. We have 4 groups: control, placebo and two variations of the medicine. Nominal hemoglobin levels for male are between 13.5 to 17.5g/dl. Sample size is 20. Age is disregarded

Completely Randomized single-factor Model

- Blood samples are taken in a completely randomized fashion
- Need to reduce any nuisance variable in the experiment
- Human error x Machine error
- Graphical interpretation and statistic interpretation

Completely Randomized single-factor Model

- Let's observe the boxplot of our data



Completely Randomized single-factor Model

- Suppose we have a different levels of a single factor we wish to compare
- Observations follow the linear model:

$$Y_{ij} = \mu_i + \epsilon_{ij} \begin{cases} i = 1,2,\dots,a \\ j = 1,2,\dots,n \end{cases}$$

Where $\mu_i = \mu + \tau_i$

Completely Randomized single-factor Model

- Suppose we have a different levels of a single factor we wish to compare
- Observations follow the linear model:

Mean of the treatment

Random observation → $Y_{ij} = \mu_i + \epsilon_{ij}$ $\begin{cases} i = 1,2,\dots,a \\ j = 1,2,\dots,n \end{cases}$ ← Error

Where $\mu_i = \mu + \tau_i$ ← Effect factor

Mean of the population (overall mean)

Completely Randomized single-factor Model

- Each treatment can be thought of as a normal population with mean μ_i and variance σ^2
- Moreover, each treatment can be understood as a normally distributed variable with mean μ plus a perturbation τ_i

Completely Randomized single-factor Model

- For the fixed effect models, effects τ_i are considered as deviations from overall mean μ
- So the sum of τ_i is expected to be 0
- This is equivalent to testing the following hypotheses

$$H_0: \tau_1 = \tau_2 = \ ... = \tau_a = 0$$

$$H_1: \tau_i \neq 0 \text{ for at least one } i$$

Completely Randomized single-factor Model

- ANOVA partitions the variability into two parts
- Test the hypothesis based on a comparison of two independent estimates of the population variance
- We will consider the one-way ANOVA

Completely Randomized single-factor Model

- We have the following point estimators:
  - Total sum of squares: $SS_T = \sum_{i=1}^{a}\sum_{j=1}^{n} y_{ij}^2 - \frac{\bar{y}^2}{N}$
  - Sum square of treatments: $SS_{Tr} = \sum_{i=1}^{a} \frac{y_i^2}{n} - \frac{\bar{y}^2}{N}$
  - Mean square of treatments: $MS_{Tr} = \frac{SS_{Tr}}{(a-1)}$
  - Error sum of squares: $SS_E = SS_T - SS_{Tr}$
  - Error mean square: $MS_E = \frac{SS_E}{a(n-1)}$
  - F-statistic: $F_0 = \frac{MS_{Tr}}{MS_E}$

Completely Randomized single-factor Model

- Now let's run the ANOVA for our hemoglobin experiment

```
> summary(aov.ex1)
             Df Sum Sq Mean Sq F value   Pr(>F)
m.hemo$Group  3   50.8  16.935   10.97 4.57e-06 ***
Residuals    76  117.3   1.543
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Since P is considerably smaller than 0.1 we can safely reject H_0

Completely Randomized single-factor Model

- Since the Mean Squared error MS_E is an estimator of variance σ, we can build confidence intervals
- Let's verify the confidence interval for each mean μ_i

Completely Randomized single-factor Model

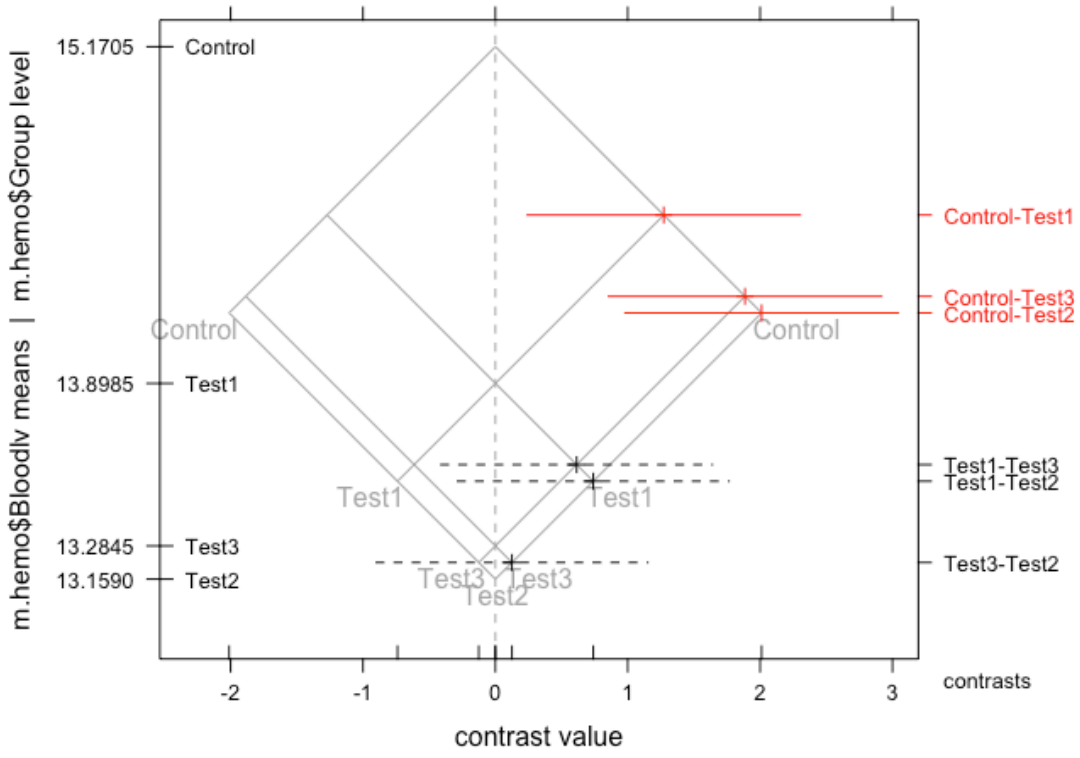
- Since we rejected H_0, we know that there is at least one factor that is different from the others
- How do we know what factor?
  - Fisher's least significant Difference (LSD)
  - Tukey's test
  - mmc
- We'll run a mean-mean multiple comparison (mmc)

Completely Randomized single-factor Model

- Tukey test
  - Post-hoc analysis of the ANOVA
  - H_0: no significance in the difference of means
  - H_1: significance in the difference of means

Completely Randomized single-factor Model

- Plotting the mmc we get a very straightforward answer:



- Introduction
- Completely Randomized single-factor model
- Unbalanced Design
- Random Effects model
- Blocking design
- Model Validation
- Two way ANOVA

Unbalanced Design

- In some cases, the number of observations taken under each treatment may be different
- We say the the design is unbalanced
- Disadvantages over balanced design:
  - Insensitive to small departures from the assumption of equality
  - More prone to Type-II errors, less power β

Unbalanced Design

- Load the assimetric_hemo_exp dataset
- Run the ANOVA
- Run the mmc
- Verify the differences

- Introduction
- Completely Randomized single-factor model
- Unbalanced Design
- Random Effects model
- Blocking design
- Model Validation
- Two way ANOVA

Random Effects Model

- In many cases, the factor of interest has too many levels
- We want to draw conclusions for the entire population of factor levels
- a random factors are chosen

Random Effects Model

- Consider variance of the treatment effects τ_i to be σ_τ^2
- The variance of the response is $\sigma_\tau^2 + \sigma^2$
- So we test Hypotheses about σ_τ^2

$$H_0: \sigma_\tau^2 = 0$$
$$H_1: \sigma_\tau^2 \neq 0$$

Random Effects Model

- The computational procedure of the ANOVA table is the same as of the fixed-effects
- Conclusions, however apply for the entire population of treatments
- Load the 'Block_Hemo_exp.csv' dataset

Random Effects Model

- We will use a slightly different function rather than aov()
- Check the confidence intervals
- No mmc this time

- Introduction
- Completely Randomized single-factor model
- Unbalanced Design
- Random Effects model
- Blocking design
- Model Validation
- Two way ANOVA

Blocking Design

- Reduce the variability from a nuisance factor
- Extension of the paired t-test when more than two treatments must be compared
- Selection of b blocks and running a complete replicate of the experiment in each block
- A levels, b blocks

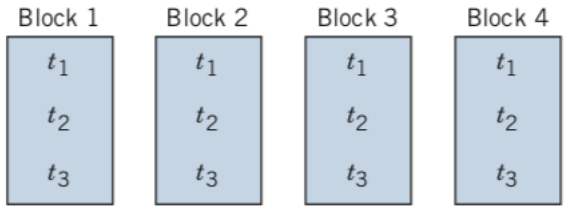


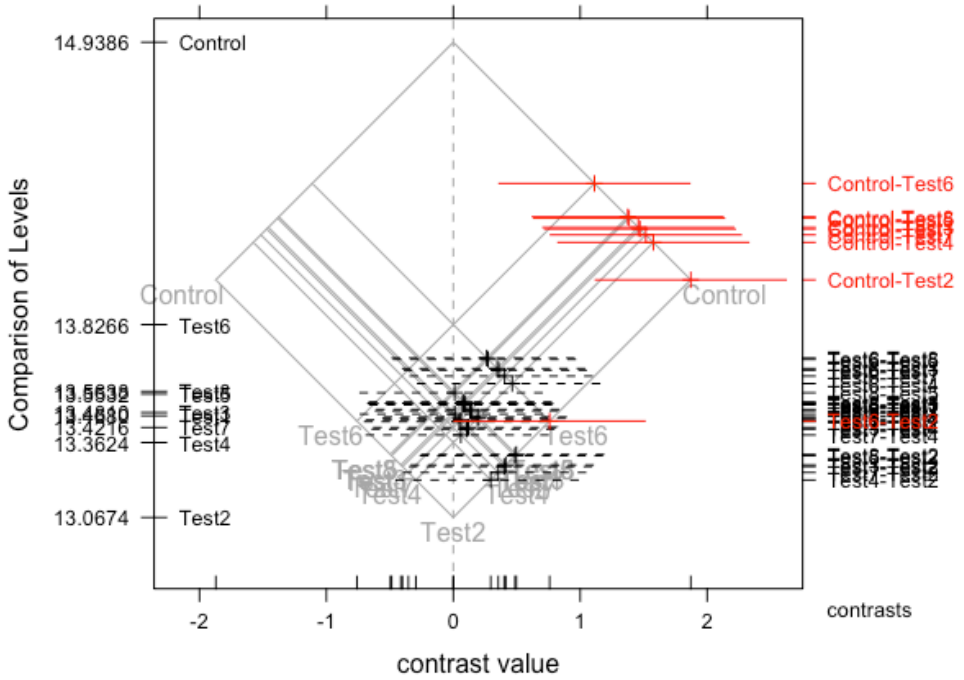
Figure 13-8 A randomized complete block design.

Blocking Design

- When to use block design?
  - When you want to reduce the MS_E
  - When doing a single factor experiment has much more degrees of freedom
- Generally, it is based on trial and error

Blocking Design

- Run the ANOVA with block design at R
- Do the mmc
- Check the plot



- Introduction
- Completely Randomized single-factor model
- Unbalanced Design
- Random Effects model
- Blocking design
- Model Validation
- Two way ANOVA

Model Validation

- Like the t-test, we must test our model for:
  - Normality
  - Independence
  - Heteroscedascity

Model Validation

- Like the t-test, we must test our model for:
  - Normality
  - Independence
  - Heteroscedascity
- Unlike the t-test, all of them are based on plots:
  - Normal Probability plot of residuals
  - Plotting the residuals against time
- Fortunately, we can obtain that by simply using plot() on our ANOVA model!

- Introduction
- Completely Randomized single-factor model
- Unbalanced Design
- Random Effects model
- Blocking design
- Model Validation
- Two way ANOVA

Two-way ANOVA

- Suppose now we want to analyze the effect of two factors
- Two-way ANOVA is the answer
- Hypothesis is still:

$$H_0: \tau_1 = \tau_2 = \ ... = \tau_a = 0$$

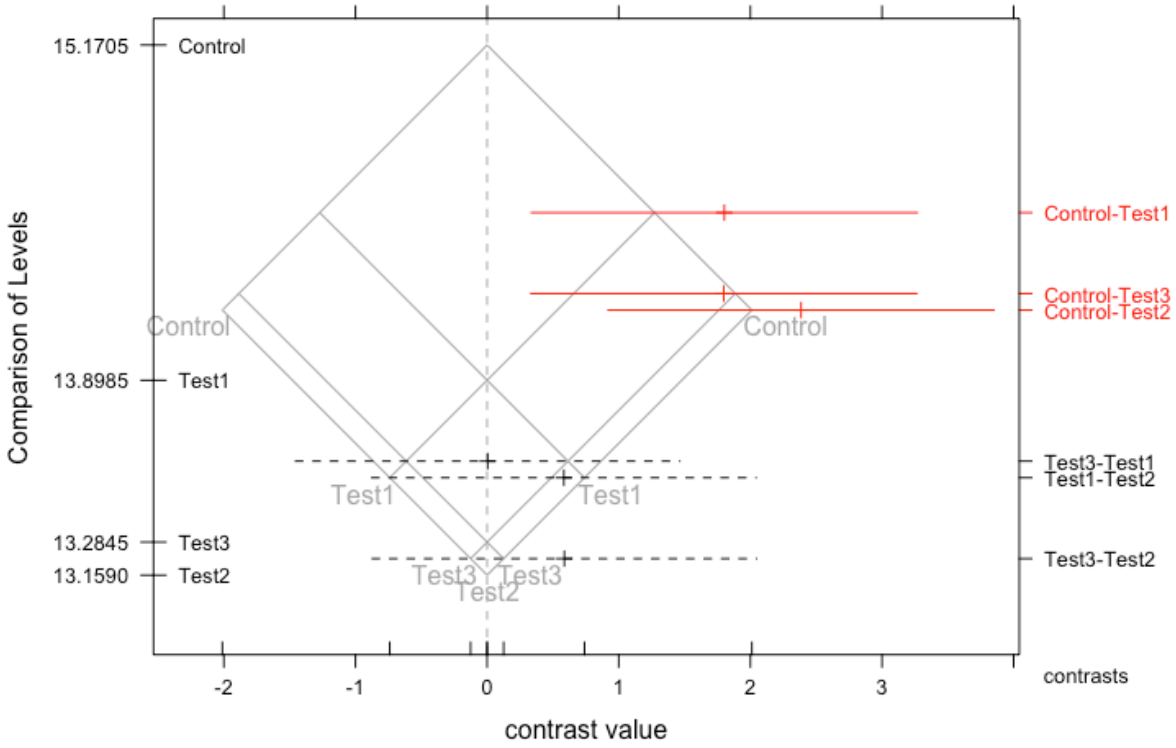
$H_1: \tau_i \neq 0$ for at least one i

Two-way ANOVA

- In R, we just add another factor to the equation in the aov()
- Same procedure as before
- Mmc and tukey test is also conducted

Two-way ANOVA

- Let's take a look at the mmc plot:



Next Episode

- ANOVA is not over yet! We will talk about ANOVA with multiple factors
- Non parametric tests for “non punchable” data

筑波大学
University of Tsukuba

Single-Factor Experiments: Analysis of Variance (ANOVA)

Marco Antonio Florenzano Mollinetti[1]
[1]**University of Tsukuba, Systems Optimization Laboratory**
mollinetti@syou.cs.tsukuba.ac.jp