Common Experimental Designs in Agronomic Research and their Analysis

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Conservation Agriculture Based Innovation Systems Course

June 04, 2018, Mexico City
Introduction

Statistics starts with a problem, continues with the collection of data, proceeds with the data analysis and finishes with conclusions.

It is a common mistake of inexperienced statisticians to plunge into a complex analysis without paying attention to what the objectives are or even whether the data are appropriate for the proposed analysis.

The formulation of a problem is often more essential than its solution itself, which may be merely a matter of mathematical or experimental skills, Albert Einstein.
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Formulation of the problem

- Understand the physical background
- Understand the Objective
- Make sure what the client wants
- Put the problem in statistical terms
- This is a challenge step and where irreparable errors are something made. Once that the problem is translated into the statistics language, the solution is often routine.
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Data collection

It is important to understand how the data was collected
1. Are the data observational or experimental
2. Are there missing values
3. How the data was coded
4. What are the units of measurement
5. Beware of data entry errors.

The last problem is all too common, almost a certainty in any real dataset of at least moderate size. Perform some data sanity check.
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- Numerical Summaries
  - means
  - Standard deviations
  - Standard deviations
  - five-number summaries
  - Correlations

- Graphical summaries
  - One variable - Boxplot, histograms, etc.
  - Two variables - scatterplots
  - Many variables - interactive graphics
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When doing an analysis: What can go wrong?

Many things, unfortunately

Source and quality of the data directly affects what conclusions we can draw

Look for outliers, data entry errors and skewed or unusual distributions

Are the data distributed as you expected?

Getting data into a suitable form for analysis by cleaning out mistakes and aberrations is often time consuming. It often takes more time than the data analysis itself.
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Histogram of pima$\text{diastolic}$

- Frequency
- $20, 50, 100, 200$
- $20, 40, 60, 80, 100, 120$

- pima$\text{diastolic}$

- diabetes
- $0.0, 0.5, 1.0, 1.5, 2.0, 2.5$
- $0.0, 40, 80, 120$

- diabetes
- $0.0, 50, 100, 150, 200, 2.5$
- $0.0, 40, 80, 120$

- negative
- positive

- test
Basic concepts on experimental designs

- The subject of statistics deals with variability and how control it.
- In the planning and conduction of field research, we can use different strategies to control the variability as:
  1. Selection of homogeneous material and/or environments
  2. Grouping (blocking, stratifying) material into homogeneous subgroups (blocks, strata), and
  3. Measurement of related variables and use of covariance analysis
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Basic concepts on experimental designs: The three Fisher basic principles

- **Replication**
- **Why?**
  - It is the only way in which we are able to get an estimate of the experimental error
- **How many replications?**
  - At least two. As higher number is better precision
  - Unfortunately, there are a compromise between precision and cost
  - Also, the number of replications to use depends of the response variable to be assessed
    - Continuous variables do not need too much replications
    - However for discrete variables (diseases, counts of insects), it is advisable to make more replications
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- **Blocking**

- Arrangement of experimental units (or experimental material) into similar groups reduces the sources of variation and allows greater precision

- The size, shape and orientation of the blocks affects the precision in the control of environmental noise sources
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- Randomization

  - Replication 1
  - Replication 2
Randomization

Replication 1

B10

B2  20  19  18  17  16  15  14  13  12  11
B1   1   2   3   4   5   6   7   8   9  10

Replication 2

B20

16   19
  6   14
  1   15
  2   9
  5
11   10
13   8
20

4   7   17
12   18

B11
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**Randomization**

- **Replication 1**
  - B10
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  - 13
  - 3
  - 8
  - 20
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  - 18
The three Fisher principles: Randomization

- Reduces the bias, avoiding to favor some treatments.
- The main assumption in all statistical linear models related to the experimental error is
  \[ \epsilon_{ij} \sim N(0, 1\sigma_{ij}^2) \]  
- Therefore, the randomization guarantee that experimental units (e.u.) are independent to each other, in a such way that is possible to use the classical parametric statistical methodologies.
- Randomization is one of the most important components of a well-designed experiments.
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Basic terms and concepts

- **Factor:** Are the explanatory variable (independent) variables that the researcher are interested in evaluate their effect.
- **Levels:** Are the different categories in which a factor can be divided.
- **Treatments:** Are the different procedures we want to compare. Sometimes correspond to the combination of factors and their levels.
- **Experimental Units (E.U.):** Are the smallest physical area in which we apply one and only one treatment.
- **Responses:** Are the outcomes that we observe after applying a treatment to an experimental unit. Is a measure to judge what happened in the experiment.
- **Control treatment:** is a standard treatment that is used as baseline to compare with other treatments.
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<td>D4</td>
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\[ y_{ij} = \mu + \tau_i + \epsilon_{ij} \quad (2) \]

- \( y_{ij} \): Is the response associated with the effect of the \( i^{th} \) treatment in the \( j^{th} \) replication
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CRD: Test of hypotheses and analysis of variance (ANOVA)

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- if $[Pr > F] \leq threshold$ then we reject $H_0$
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- The RCBD has as restriction that all the treatments are replicated once and only once in each block, using an unrestricted randomization independently in each block.

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- \( y_{ij} \): Is the response associated with the effect of the \( i^{th} \) treatment in the \( j^{th} \) replication
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RCBD: Test of hypotheses and analysis of variance

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CRD: Test of hypotheses and analysis of variance (ANOVA)

- With decision rule
- if $[Pr > F] \leq threshold$ then we reject $H_0$
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Experimental Designs: Latin Square Designs (LS)

- RCBD allows to block on a single source of variation in the responses.
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- The Latin Square (LS) blocks for two gradients of variability.
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- Row 1: A, B, C, D
- Row 2: B, C, D, A
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Fertility

pH
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<td>D</td>
<td>A</td>
</tr>
<tr>
<td>Row 3</td>
<td>C</td>
<td>D</td>
<td>A</td>
<td>B</td>
</tr>
<tr>
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Legend:
- **pH**
- **Fertility**

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RCBD: Test of hypotheses and analysis of variance

- We have the null hypotheses
  - $H_0: \tau_i = \tau_j$, for all $i \neq j$
  - $H_a: \tau_i \neq \tau_j$; for at least one $i \neq j$

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<td>$\sum_{i=1}^{t} \frac{(y_{i.})^2}{t} - \frac{(y_{..})^2}{tt}$</td>
<td>$\frac{ss \ treat}{(t - 1)}$</td>
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- With decision rule
- if \([Pr > F] \leq \text{threshold}\) then we reject \(H_0\)
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Experimental Designs: Factorial Designs

- When there are the suspect that two independent variables are correlated
  - The fertilization level applied to increase the performance of genotypes
  - The susceptibility/resistance of genotypes infested with some pest
  - The performance of genotypes in different environments
- Thus, the independent variables are considered as array of factors
- Therefore, this factors can be included in an classical experimental designs as CRD or RCBD or more sophisticated designs as Lattice or alpha-lattice
- If there are a levels of factor A, and b levels of factor B, then each replicate contains all ab treatment combinations.
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- The main effect of a factor is defined to be the change in response produced by a change in the level of a factor.
- However, in some experiments we may find that the difference in response between the levels of one factor is not the same at all levels of the other factor. When this occurs, there is an interaction between the factors.
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Example: 2 factors at 2 levels each, 4 replications

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Factorial Designs

- statistical Linear model

\[ y_{ijk} = \mu + \tau_i + \delta_j + (\tau\delta)_{ij} + \epsilon_{ijk} \]  

- \( \mu \): Is the general grand mean common to all experimental units before applying the treatments
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- Classical assumptions about the errors are: \( \epsilon_{ijk} \sim NI(0, 1\sigma_{ijk}^2) \)
Factorial Designs

- statistical Linear model

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Factorial Designs: Test of hypotheses and analysis of variance

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  - $H_0$: $\tau_i = \tau_{i'}$, for all $i \neq i'$
  - $H_a$: $\tau_i \neq \tau_{i'}$; for at least one $i \neq i'$

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- The test of hypotheses for factor B
  - $H_0$: $\delta_j = \delta_{j'}$, for all $j \neq j'$
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- The test of hypotheses for interaction AB
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<thead>
<tr>
<th>Source of variation</th>
<th>Df</th>
<th>Sum of squares</th>
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<th>F value</th>
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</tr>
</thead>
<tbody>
<tr>
<td>A Treatments</td>
<td>(A-1)</td>
<td>$\sum_{i=1}^{t} \left( \frac{(y_{i.})^2}{n_a} - \frac{(y_{..})^2}{t} \right)$</td>
<td>$ss \ treat \ \frac{(A-1)}{ms \ AB}$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>B Treatments</td>
<td>(B-1)</td>
<td>$\sum_{i=1}^{t} \left( \frac{(y_{..j})^2}{n_b} - \frac{(y_{..})^2}{t} \right)$</td>
<td>$ss \ treat \ \frac{(B-1)}{ms \ AB}$</td>
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<tr>
<td>AB Treatments</td>
<td>(AB-1)</td>
<td>$\sum_{j=1}^{n_b} \sum_{i=1}^{n_a} \frac{(y_{ij})^2}{n_a n_b} - \sum_{i=1}^{n_a} \frac{(y_{i.})^2}{n_a} - \sum_{i=1}^{n_b} \frac{(y_{..j})^2}{n_b} - \frac{(y_{..})^2}{AB}$</td>
<td>$ss \ treat \ \frac{(AB-1)}{Error}$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Error</td>
<td>Tot-AB</td>
<td>$ss \ error \ \frac{1}{(t-1)(t-2)}$</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>Tot -1</td>
<td>$\sum_{i=1}^{t} \sum_{j=1}^{t} \sum_{k=1}^{t} \frac{(y_{ijk})^2}{t} - \frac{(y_{..})^2}{t}$</td>
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<td>$\sum_{i=1}^{t} \frac{(y_{.j})^2}{n_b} - \frac{(\bar{y})^2}{t}$</td>
<td>$ss \ treat$</td>
<td>$\frac{ms \ B \ treat}{ms \ AB}$</td>
<td></td>
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<td>(AB-1)</td>
<td>$\sum_{j=1}^{n_b} \sum_{i=1}^{n_a} \frac{(y_{ij.})^2}{n_an_b} - \sum_{i=1}^{n_a} \frac{(y_{i.})^2}{n_a} - \sum_{i=1}^{n_b} \frac{(y_{.j})^2}{n_b} - \frac{(\bar{y})^2}{AB}$</td>
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Factorial Design: Test of hypotheses and analysis of variance (ANOVA)

• With decision rule
• if $[Pr > F] \leq \text{threshold}$ then we reject $H_0$
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Experimental Designs: Split Plot Designs

- In some experimental situations there is not practical accommodate all treatments of a factorial experiment in one complete block.
- Thus, is necessary to use incomplete blocks, no all treatments are included in the blocks.
- We can do this by using the split plot designs, where each block is named as whole plot and the subdivisions into the plot are named as small plots.
- As example, suppose that we want test the effect of 3 irrigation methods (a1 = gravity, a2 = sprinkling, and a3 = drip) and 4 yield maize varieties b1, b2, b3 and b4.
- So, the list of treatments will be: a1b1 a1b2 a1b3 a1b4, a2b1 a2b2 a2b3 a2b4, a3b1 a3b2 a3b3 a3b4, a4b1 a4b2 a4b3 a4b4.
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- Due to the land conditions, it is necessary to use a RCBD, so the treatments can be assigned in the next way:

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</tr>
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<tr>
<td>a₁b₃</td>
<td>a₂b₃</td>
</tr>
<tr>
<td>a₃b₄</td>
<td>a₃b₂</td>
</tr>
<tr>
<td>a₂b₄</td>
<td>a₁b₄</td>
</tr>
</tbody>
</table>

This array is complicated of implementing in the field, because we cannot manage neighbor units with different irrigation method.
Experimental Designs: Split Plot Design

Due to the land conditions, it is necessary to use a RCBD, so the treatments can be assigned in the next way:

<table>
<thead>
<tr>
<th>Block 1</th>
<th>Block 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>a₁b₂</td>
<td>a₂b₂</td>
</tr>
<tr>
<td>a₂b₁</td>
<td>a₃b₁</td>
</tr>
<tr>
<td>a₃b₃</td>
<td>a₁b₁</td>
</tr>
<tr>
<td>a₁b₃</td>
<td>a₂b₃</td>
</tr>
<tr>
<td>a₃b₄</td>
<td>a₃b₂</td>
</tr>
<tr>
<td>a₂b₄</td>
<td>a₁b₄</td>
</tr>
<tr>
<td>a₂b₄</td>
<td>a₁b₄</td>
</tr>
<tr>
<td>a₃b₄</td>
<td>a₂b₃</td>
</tr>
<tr>
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<td>a₁b₂</td>
</tr>
<tr>
<td>a₃b₁</td>
<td>a₂b₁</td>
</tr>
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<td>a₂b₂</td>
<td>a₃b₃</td>
</tr>
</tbody>
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This array is complicated to implement in the field because we cannot manage neighbor units with different irrigation method.
Experimental Designs: Split Plot design

Therefore, the split plot array could be

By general the whole plot factors are generated by mean of a CRD, RCBD, or LS, whereas the small plots factors are generated by a CRD.
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Therefore, the split plot array could be

\[
\begin{array}{c|c|c}
\text{(R)₁} & \text{(R)₂} & \text{(R)₃} \\
a₁b₂ & a₂b₄ & a₃b₁ \\
a₁b₁ & a₂b₂ & a₃b₂ \\
a₁b₄ & a₂b₃ & a₃b₄ \\
a₁b₃ & a₂b₁ & a₃b₃ \\
\end{array}
\]

\[
\begin{array}{c|c|c}
\text{(R)₂} & \text{(R)₃} & \text{(R)₁} \\
A₂b₃ & a₃b₄ & A₁b₄ \\
A₂b₂ & a₃b₃ & A₁b₃ \\
A₂b₁ & a₃b₁ & A₁b₂ \\
A₂b₄ & a₃b₂ & A₁b₁ \\
\end{array}
\]

By general the whole plot factors are generated by mean of a CRD, RCBD, or LS, whereas the small plots factors are generated by a CRD.
The statistical linear model depends on the experimental design in which the whole and small plots are arranged.

For example, when the whole plot (WP) and the small plots are arranged in a CRD, the statistical linear model is given by:

\[ y_{ijk} = \mu + A_i + \epsilon_{a(i)} + B_j + (AB)_{ij} + \epsilon_{(b)ijk} \]  

(6)

where:
- \( y_{ijk} \) is the observed response in the \( i \)th whole plot, \( j \)th small plot, and \( k \)th replication.
- \( \mu \) is the overall mean.
- \( A_i \) is the effect of the \( i \)th whole plot.
- \( \epsilon_{a(i)} \) is the random error associated with the \( i \)th whole plot.
- \( B_j \) is the effect of the \( j \)th small plot.
- \( (AB)_{ij} \) is the interaction effect between the \( i \)th whole plot and the \( j \)th small plot.
- \( \epsilon_{(b)ijk} \) is the random error associated with the \( ijk \)th observation.
**Split Plot**

- **statistical Linear model**

  The statistical linear model depends on the experimental design in which the whole and small plots are arranged.

  For example, when the whole Plot (WP) and the small plots are arranged in a CRD

  \[ y_{ijk} = \mu + A_i + \epsilon_{a(i)} + B_j + (AB)_{ij} + \epsilon_{(b)ijk} \]  
  (6)
Split Plot

- statistical Linear model
- The statistical linear model depends on the experimental design in which the whole and small plots are arranged
- For example, when the whole Plot (WP) and the small plots are arranged in a CRD

\[ y_{ijk} = \mu + A_i + \epsilon_a(i) + B_j + (AB)_{ij} + \epsilon(b)_{ijk} \]  

(6)
Split Plot

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y_{ijk} = \mu + A_i + \epsilon_a(i) + B_j + (AB)_{ij} + \epsilon_b(ijk) \tag{6}
\]
statistical Linear model

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For example, when the whole Plot (WP) and the small plots are arranged in a CRD

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(6)
The statistical linear model depends on the experimental design in which the whole and small plots are arranged. For example, when the whole plot (WP) and the small plots are arranged in a CRD, the model can be expressed as:

\[ y_{ijk} = \mu + A_i + \epsilon_{a(i)} + B_j + (AB)_{ij} + \epsilon_{(b)ijk} \]  

(6)
- $y_{ijk}$: Is the response for the whole plot $i$, small plot $j$, and the replicate $k$
- $\mu$: Is the general grand mean common to all experimental units before applying the treatments
- $A_i$: Is the effect of the treatment $i$ over the whole plot $i$
- $\epsilon_{a(i)}$: Are the random errors associated whole plot
- $B_j$: Is the effect of the sub-treatment $j$ over the small plot $j$
- $(AB)_{ij}$: represents the interaction effect between the treatment $i$ and the sub-treatment $j$
- $\epsilon_{ijk}$: Are the random errors associated to treatment $i$, subtreatment $j$ and replication $r$
- Classical assumptions about the errors are: $\epsilon_{ijk} \sim NI(0, 1\sigma_{ijk}^2)$
- \( y_{ijk} \): Is the response for the whole plot \( i \), small plot \( j \), and the replicate \( k \)
- \( \mu \): Is the general grand mean common to all experimental units before applying the treatments
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\[ y_{ijk} = \mu + B_i + A_i + \epsilon_{a(ij)} + B_k + (AB)_{jk} + \epsilon_{(b)ijk} \quad (7) \]

- Now
- \( B_i \): Is the effect of the \( i^{th} \) block
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Split Plot

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For example, when the whole Plot (WP) is a LS and the small plots are arranged in a CRD

\[ y_{ijkl} = \mu + \gamma_i + \delta_j + A_k + \epsilon_{a(ijk)} + B_l + (AB)_{kl} + \epsilon_{(b)ijkl} \]  (8)

- Now
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- \( \delta_j \): Is the effect of the \( j^{th} \) column
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### SPD: ANOVA, PG → RCBD, PCh → CRD

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>S.S</th>
<th>MS</th>
<th>Expected mean squares</th>
<th>F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bloque</td>
<td>(i-1)</td>
<td></td>
<td></td>
<td>-----</td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>(j-1)</td>
<td></td>
<td></td>
<td>(\sigma^2_b + (k)\sigma^2_a + (ik) \sum \frac{(A_j - \bar{A})^2}{(j-1)})</td>
<td>(F_{(A)})</td>
</tr>
<tr>
<td>E(a)=Bloq x A</td>
<td>(i-1)(j-1)</td>
<td></td>
<td></td>
<td>(\sigma^2_b + (k)\sigma^2_a)</td>
<td></td>
</tr>
<tr>
<td>B</td>
<td>(k-1)</td>
<td></td>
<td></td>
<td>(\sigma^2_b + (ij) \sum \frac{(B_k - \bar{B})^2}{(k-1)})</td>
<td>(F_{(B)})</td>
</tr>
<tr>
<td>AB</td>
<td>(j-1)(k-1)</td>
<td></td>
<td></td>
<td>(\sigma^2_b + (i) \sum \sum \frac{[AB_{jk} - \bar{AB}]^2}{(j-1)(k-1)})</td>
<td>(F_{(AB)})</td>
</tr>
<tr>
<td>E(b)=Residual</td>
<td>(i-1)j(k-1)</td>
<td></td>
<td></td>
<td>(\sigma^2_b)</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>ijk-1</td>
<td></td>
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<td></td>
<td></td>
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<td>(i-1)j(k-1)</td>
<td></td>
<td></td>
<td>(\sigma^2_b)</td>
<td></td>
</tr>
<tr>
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<td>ljk-1</td>
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Experimental Designs: Strip Plot Designs

- When a split plot with $i$ treatments $A$ in the whole plots, $j$ sub-treatments in $B$ in mean plots and, each each mean plot divided in $k$ small plots,
- then when this $k$ sub sub treatments $C$ are randomized, we are speaking about a strip plot
- Example
  - Whole plots: Tillage systems
  - Mean plots: Irrigation systems
  - Small plots: Fertilizer dosage
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Example
- Whole plots: Tillage systems
- Mean plots: Irrigation systems
- Small plots: Fertilizer dosage
Conservation tillage

Whole plots

Traditional tillage

<table>
<thead>
<tr>
<th>R₁D₂</th>
<th>R₁D₄</th>
<th>R₂D₁</th>
<th>R₂D₇</th>
</tr>
</thead>
<tbody>
<tr>
<td>R₁D₁</td>
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Sprinkling  drip

Mean plots

Small plots

Drip  sprinkling
### Conservation tillage

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### Traditional tillage

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</tr>
</tbody>
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#### Mean plots
- Sprinkling
- Drip

#### Small plots
- Drip
- Sprinkling
The linear model of Strip plot is:

\[ y_{ijkl} = \mu + \beta_i + A_j + \epsilon_{a(ij)} + B_k + (AB)_{jk} + \epsilon_{(b)ijk} + \\
C_l + (AC)_{jl} + (BC)_{kl} + (ABC)_{jkl} + \epsilon_{(c)ijkl} \]
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When a split plot with i treatments A in the whole plots, j sub-treatments in B in mean plots and, each each mean plot divided in k small plots,
then when this k sub sub treatments C are randomized, we are speaking about a strip plot

Example

- Whole plots: Tillage systems
- Mean plots: Irrigation systems
- Small plots: Fertilizer dosage
When a split plot with $i$ treatments $A$ in the whole plots, $j$ sub-treatments in $B$ in mean plots and, each each mean plot divided in $k$ small plots,

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After the ANOVA analyses what?

- The ANOVA hypothesis is quite little informative

- If we didn’t reject $H_0(\tau) : \tau_i = \tau_j \quad \forall \ i \neq j$ then the analysis ends here. In applied research the cheaper, more practical, more available treatments should be recommended

- If the ANOVA $H_0$ hypothesis is rejected, then that rejection could be due to different situations:
  
  - $\tau_1 = \tau_2 = \cdots = \tau_{t-1}$, but $\tau_{t-1} \neq \tau_t$
  
  - $\tau_1 = \tau_2 = \cdots = \tau_{t-2} = \tau_t$, but $\tau_{t-2} \neq \tau_{t-1}$
  
  etc., etc.

- So, additional method for inquiring about the structure of the differences among treatments are needed
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After rejecting the ANOVA hypothesis, what?

Is there a pre-planned treatment structure?

- No
  - Pairwise comparisons
    - LSD
    - Tukey
    - Scheffe
    - Duncan
    - Student - Newman – Keuls
  - Yes
    - Is there any control?
      - Yes
        - Comparison against the control.
          - Dunnett
      - No
        - Comparisons between groups
          - Non orthogonal contrasts
          - Orthogonal contrasts
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Pairwise comparisons methods: fundamentals

➢ Hypothesis:

\[ H_0_k: \tau_i = \tau_j \quad \text{vs} \quad H_{a_k}: \tau_i \neq \tau_j \]

where

\[ i = 1, 2, \ldots, t - 1; \quad j = i + 1, i + 2, \ldots, t \]

\[ k = 1, 2, \ldots, \frac{t(t-1)}{2} \quad \binom{t}{2} = \frac{t!}{2!(t-2)!} \]

➢ Example, for 4 treatments; the hypotheses to test are:

\[ \frac{t(t-1)}{2} = \frac{4(3)}{2} = 6, \]

1. \[ H_0: \tau_1 = \tau_2 \quad \text{vs} \quad H_0: \tau_1 \neq \tau_2 \]
2. \[ H_0: \tau_1 = \tau_3 \quad \text{vs} \quad H_0: \tau_1 \neq \tau_3 \]
3. \[ H_0: \tau_1 = \tau_4 \quad \text{vs} \quad H_0: \tau_1 \neq \tau_4 \]
4. \[ H_0: \tau_2 = \tau_3 \quad \text{vs} \quad H_0: \tau_2 \neq \tau_3 \]
5. \[ H_0: \tau_2 = \tau_4 \quad \text{vs} \quad H_0: \tau_2 \neq \tau_4 \]
6. \[ H_0: \tau_3 = \tau_4 \quad \text{vs} \quad H_0: \tau_3 \neq \tau_4 \]
Pairwise comparisons methods: fundamentals

- **Hypothesis:**
  \[ H_0_k: \tau_i = \tau_j \quad \text{versus} \quad H_{a_k}: \tau_i \neq \tau_j \]
  where \( i = 1, 2, ..., t - 1; \quad j = i + 1, i + 2, ..., t \)

- \( k = 1, 2, ..., \frac{t(t-1)}{2} \)

\[ \binom{t}{2} = \frac{t!}{2!(t-2)!} \]

- **Example, for 4 treatments:** the hypotheses to test are:

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  4. \( H_0: \tau_2 = \tau_3 \quad \text{vs} \quad H_0: \tau_2 \neq \tau_3 \)
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**Pairwise comparisons methods: fundamentals**

- **The Test Statistic is:**
  \[ D_k = |\bar{y}_i - \bar{y}_j| ; \quad k = 1, 2, \ldots, \frac{t(t-1)}{2} \]

- The number of differences to calculate is equal to the number of hypothesis to test, using the means of the treatments involved in the corresponding hypothesis.

- So, for the above example its necessary to calculate 6 differences

- **Critical Value (Threshold):**
  \[ MSD = [D' n_{df, \epsilon/2}] \text{[Standard Error]} \]

- **With Decision Rule:**
  \[ \text{If } |\bar{y}_i - \bar{y}_j| \geq MSD \rightarrow \text{Reject } H_{0k} \]
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Least Significant Difference (LSD) method

- It is based on the Student’s t distribution

- For \( r_i \neq r_j \) (unbalanced designs)

\[
LSD_k = \left[ t_{dfe, \alpha/2} \right] \sqrt{2 \cdot MSE \left( \frac{1}{r_i} + \frac{1}{r_j} \right)}
\]

- For \( r_i = r_j = r \) (balanced designs)

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Comparisonwise error rate vs Experimentwise error rate

\[ Pr(\text{type I error}) = Pr(\text{rejecting } H_0 / \text{ } H_0 \text{ is true}) \]
\[ = Pr(\text{declaring differences that not exist}) \]
\[ = Pr(\text{False Positive}) \]

Experimentwise error rate:

\[ Pr(\text{False Positive}) = 1 - (1 - \alpha)^k \]

where \( k \) = number of comparisons realized = \( \frac{t(t-1)}{2} \)

For \( \alpha = 0.05 \)

If \( t = 4; k=6; \) \( Pr(\text{False Positive}) = 1 - (1 - 0.05)^6 = 0.4012 \)

\( t = 5; k=10; \) \( Pr(\text{False Positive}) = 1 - (1 - 0.05)^{10} = 0.9005 \)

\( t = 10; k=45; \) \( Pr(\text{False Positive}) = 1 - (1 - 0.05)^{45} = 0.9999 \)

While for \( \alpha = 0.01 \)

If \( t = 4; k=6; \) \( Pr(\text{False Positive}) = 1 - (1 - 0.01)^6 = 0.0585 \)

\( t = 5; k=10; \) \( Pr(\text{False Positive}) = 1 - (1 - 0.01)^{10} = 0.0956 \)

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Tukey’s method (Honesty Significant Difference)

- It is based on the Studentized or Standardized Range Distribution
- For \( r_i \neq r_j \) (unbalanced designs)
  \[
  HSD_k = \left[ q_{df_e,\alpha}^t \right] \left[ \sqrt{\frac{MSE}{2}} \left( \frac{1}{r_i} + \frac{1}{r_j} \right) \right]
  \]
- For \( r_i = r_j = r \) (balanced designs)
  \[
  HSD = \left[ q_{df_e,\alpha}^t \right] \left[ \sqrt{\frac{MSE}{r}} \right]
  \]
- The hypothesis, test statistic and decision rule, are the same as the LSD test
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Scheffe’s method

- Like ANOVA, it is based on the Snedecor’s F distribution
- Because is a general method for both pairwise and groups comparisons is more strict than LSD and Tukey
- For \( r_i \neq r_j \) (unbalanced designs)

\[
S_k = \sqrt{\frac{2}{(t-1) \left[ F_{df e, \alpha}^{(t-1)} \right]} \left[ MSE \left( \frac{1}{r_i} + \frac{1}{r_j} \right) \right]}
\]

- While for \( r_i = r_j = r \) (balanced designs)

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\]
Comparing methods

- For alpha = 0.05 we got:
  \[ \text{LSD (0.6268)} < \text{Tukey (0.8705)} < \text{Scheffe (0.9494)} \]

- While for alpha = 0.01 was gotten:
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