

Common Experimental Designs in Agronomic Research and their Analaysis

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Conservation Agriculture Based Innovation Systems Course

June 04, 2018, Mexico City

- 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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- Understand the Objective
- Make sure what the client wants
- Put the problem in statistical terms
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- 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 certainly in any real dataset of at least moderate size. Perform some data sanity check

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Numerical Summaries

- means
- Standard deviations
- Standard deviationsfive-number summaries
- Correlations
- Graphical summaries
 - One variable Boxplot, histograms, etc.
 - Two variables -scatterplots
 - Many variables interactive graphics

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- Many things, unfortunately
- Source and quality of the data directly affects what cocnlusions 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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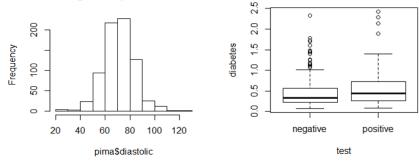
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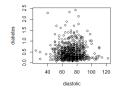
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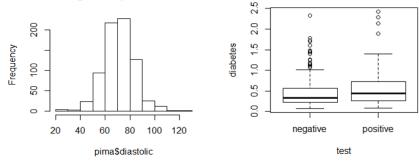
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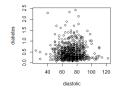
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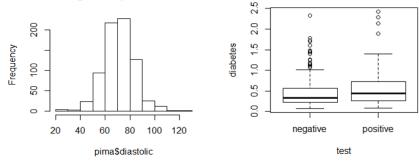
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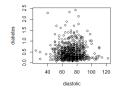


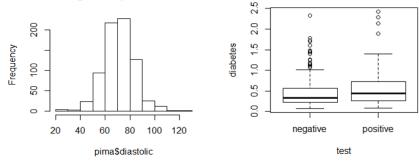


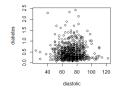












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- In the planning and conduction of field research, we can use different strategies to control the variability as:
 - 1. Selection of homogeneous material and/or environments
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- Why?
- It is the only 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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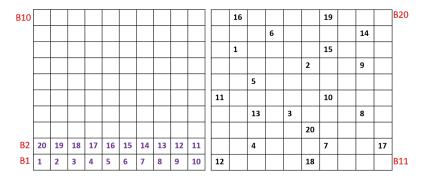
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Randomization

Replication 1

Replication 2

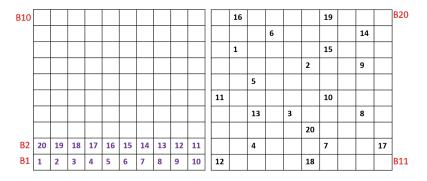


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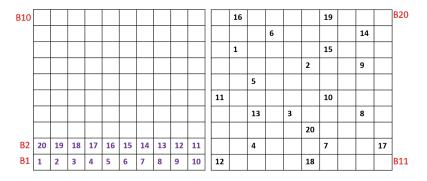


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$$\epsilon_{ij} \sim NI(0, 1\sigma_{ij}^2)$$
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- Factor: Are the explanatory variable (independent) variables that the researcher are interested in evaluate their effect.
- Levels: Are the different 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 thet we observe after applying a treatment to an experimental unit. Is a measure to judge what happened in the experiment.
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Experimental Designs: Completely Randomized Design (CRD)

A1	B1	C1	A2
D1	A3	D2	C2
B2	D3	C3	B 3
C4	A4	B4	D4



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$$y_{ij} = \mu + \tau_i + \epsilon_{ij} \tag{2}$$

- y_{ij} : Is the response associated with the effect of the *i*th treatment in the *j*th replication
- μ: Is the general grand mean common to all experimental units before applying the treatments
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- if $[Pr > F] \leqslant threshold$ then we reject H_0

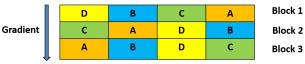
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Experimental Designs: Random Complete Block Designs (RCBD)

• 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

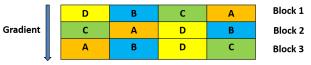


• In the first block, the *t* treatments are assigned randomly to g units; then are generated other independent randomizations, assigning treatments to units in each of the other blocks

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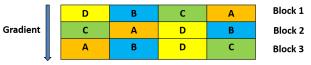


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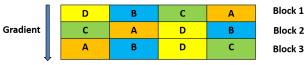


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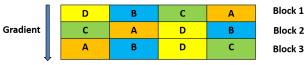


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Treatments	(t-1)	$\sum_{i=1}^{t} \frac{(y_{i.})^2}{r} - \frac{(y_{})^2}{t r}$	$\frac{ss\ treat}{(t-1)}$	$\frac{ms\ treat}{ms\ error}$	
Blocks	(t-1)(b-1)	$\sum_{j=1}^{b} \frac{(y_{.j})^2}{t} - \frac{(y_{})^2}{t r}$			
Error	t(r-1)		$\frac{ss\ error}{t(r-1)}$		
Total	tr -1	$\sum_{i=1}^{t} \sum_{j=1}^{r} (y_{ij})^2 - \frac{(y_{})^2}{t r}$			

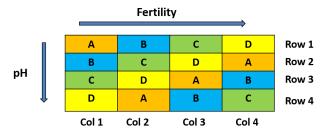
- With decision rule
- if $[Pr > F] \leqslant threshold$ then we reject H_0

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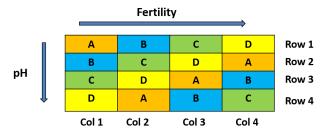
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- However, there are experimental situations with more than one source of extraneous variation
- The Latin Square (LS) blocks for two gradients of variability



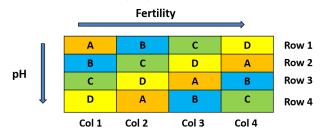
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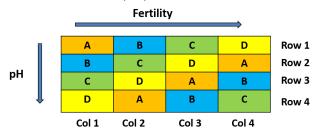
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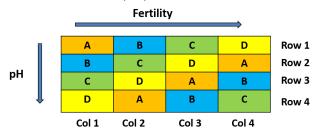


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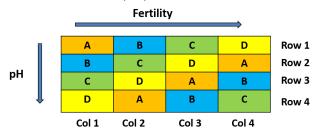
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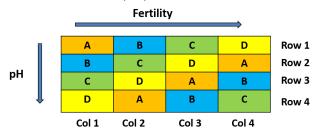
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$y_{ijk} = \mu + \tau_i + \gamma_j + \delta_k + \epsilon_{ijk} \tag{4}$

- y_{ijk}: Is the response associated with the effect of the *ith* treatment in the *jth* row and the *kth* column
- μ: Is the general grand mean common to all experimental units before applying the treatments
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- $H_0: \tau_i = \tau_j$, for all $i \neq j$
- H_a : $\tau_i \neq \tau_j$; for at least one i $\neq j$

Source of variation	Df	Sum of squares	mean squares	F value	Pr> F
Treatments	(t-1)	$\sum_{i=1}^{t} \frac{(y_{i})^2}{t} - \frac{(y_{})^2}{t t}$	$\frac{ss\ treat}{(t-1)}$	$\frac{ms\ treat}{ms\ error}$	
Rows	(t-1)	$\sum_{j=1}^{t} \frac{(y_{.j.})^2}{t} - \frac{(y_{})^2}{t t}$			
Columns	(t-1)	$\sum_{k=1}^{t} \frac{(y_{k})^2}{t} - \frac{(y_{})^2}{t t}$			
Error	(t-1)(t-2)		$\frac{ss \ error}{(t-1)(t-2)}$		
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 - 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
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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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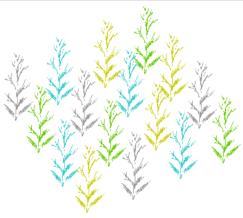
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> Example: 2 factors at 2 levels each, 4 replications

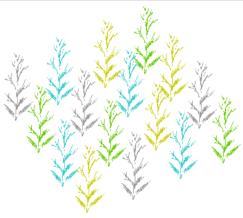
Ab	aB	ab	AB
AB	Ab	aB	ab
aB	AB	ab	Ab
ab	Ab	aB	AB





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aB	AB	ab	Ab
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$$y_{ijk} = \mu + \tau_i + \delta_j + (\tau \delta)_{ij} + \epsilon_{ijk}$$
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- μ: Is the general grand mean common to all experimental units before applying the treatments
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statistical Linear model

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- The test of hypotheses for factor A
 - $H_0: \tau_i = \tau_{i'}$, for all $i \neq i'$
 - H_a : $\tau_i \neq \tau_{i'}$; for at least one i \neq i'
- The test of hypotheses for factor *B*
 - $H_0: \delta_j = \delta_{j'}$, for all $j \neq j'$
 - $H_a: \delta_j \neq \delta_{j'}$; for at least one $j \neq j'$
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 - H_a : $\tau \delta_{ij} = \tau \delta_{i'j'}$; for all $ij \neq i'j'$
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Source of variation	Df	Sum of squares	mean squares	F value	Pr > F
A Treatments	(A-1)	$\sum_{i=1}^{t} \frac{(y_{i})^2}{n_a} - \frac{(y_{})^2}{t t}$	$\frac{ss\ treat}{(A-1)}$	$\frac{ms \ A \ treat}{ms \ AB}$	
B Treatments	(B-1)	$\sum_{i=1}^{t} \frac{(y_{i,j})^2}{n_b} - \frac{(y_{})^2}{t t}$	$\frac{ss\ treat}{(B-1)}$	$\frac{ms B treat}{ms AB}$	
AB Treatments	(AB-1)	$\sum_{j=1}^{n_b} \sum_{i=1}^{n_a} \frac{(y_{ij.})^2}{n_a n_b} - \sum_{i=1}^{n_a} \frac{(y_{i})^2}{n_a} - \sum_{i=1}^{n_b} \frac{(y_{})^2}{n_b} - \frac{(y_{})^2}{AB}$	$\frac{ss treat}{(AB-1)}$	ss treat Error	
Error	Tot-AB		$\frac{ss \ error}{(t-1)(t-2)}$		
Total	Tot -1	$\sum_{i=1}^{t} \sum_{j=1}^{t} \sum_{k=1}^{t} (y_{ijk})^2 - \frac{(y_{})^2}{t t}$			

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AB Treatments	(AB-1)	$\sum_{j=1}^{n_b} \sum_{i=1}^{n_a} \frac{(y_{ij.})^2}{n_a n_b} - \sum_{i=1}^{n_a} \frac{(y_{i})^2}{n_a} - \sum_{i=1}^{n_b} \frac{(y_{})^2}{n_b} - \frac{(y_{})^2}{AB}$	$\frac{ss treat}{(AB-1)}$	ss treat Error	
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- if $[Pr > F] \leqslant threshold$ then we reject H_0

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- In some experimental situations there is not practical accomodate 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=sprinking, 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 that the land conditions, is neccesary to use a RCBD, so the treatments can be assigned in the next way:

Block 1		Bloo	ck 2 →
a ₁ b ₂	a ₂ b ₂	a ₂ b ₄	a₁b₄
a ₂ b ₁	a ₃ b ₁	a₁b₁	a ₃ b ₂
a ₃ b ₃	a₁b₁	a ₃ b ₄	a ₂ b ₃
a₁b₃	a ₂ b ₃	a ₁ b ₃	a ₁ b ₂
a ₃ b ₄	a ₃ b ₂	a ₃ b ₁	a ₂ b ₁
a ₂ b ₄	a₁b₄	a ₂ b ₂	a ₃ b ₃

 This array is complicated of implementing in the field, because we cannot manage neighbor units with different irrigation method

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Block 1			Bloc	k 2 →
a ₁ b ₂	a ₂ b ₂] a	2 b 4	a₁b₄
a ₂ b ₁	a ₃ b ₁	а	1 b 1	a ₃ b ₂
a ₃ b ₃	a₁b₁	a	3 b 4	a ₂ b ₃
a₁b₃	a ₂ b ₃	а	1 b 3	a ₁ b ₂
a ₃ b ₄	a ₃ b ₂	a	₃ b ₁	a ₂ b ₁
a ₂ b ₄	a₁b₄	a	2 b 2	a ₃ b ₃

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a ₃ b ₃	a₁b₁	a	3 b 4	a ₂ b ₃
a₁b₃	a ₂ b ₃	а	1 b 3	a ₁ b ₂
a ₃ b ₄	a ₃ b ₂	a	₃ b ₁	a ₂ b ₁
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a ₃ b ₃	a₁b₁	a ₃ b ₄	a ₂ b ₃
a ₁ b ₃	a ₂ b ₃	a ₁ b ₃	a ₁ b ₂
a ₃ b ₄	a ₃ b ₂	a ₃ b ₁	a ₂ b ₁
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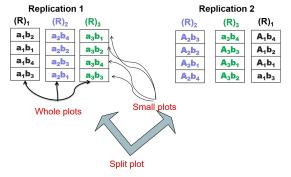
• Therefore, the split plot array could be

Replication 1 Replication 2 (R)1 (R)₁ (R)₂ (R)₃ $(R)_3$ (R)₂ a_1b_2 a₂b₄ a₃b₁ a₃b₄ A₁b₄ A₂b₃ a₁b₁ a,b, a_3b_2 A₃b₃ A₁b₂ A₂b₂ a₁b₄ a₂b₃ a₃b₄ A₂b₁ A₃b₁ A₁b₁ a₁b₃ a₂b₁ a₃b₃ A₂b₄ A₃b₂ a₁b₃ Small plots Whole plots Split plot

• 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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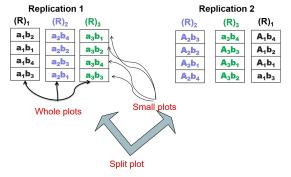
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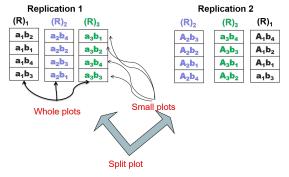
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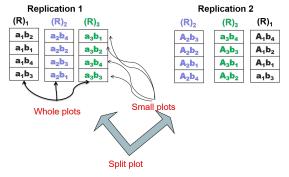
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Experimental Designs: Split Plot design

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- The statistical linear model depends of 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

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- *y_{ijk}*: Is the response for the whole plot i, small plot j, and the replicate k
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SPD: ANOVA, $PG \rightarrow RCBD$, $PCh \rightarrow CRD$

Source	DF	S.S	MS	Expected mean squares	F
Bloque	(i-1)				
Α	(j-1)			$\sigma_b^2 + (k) \sigma_a^2 + (ik) \sum \frac{(A_j - (\overline{A}))^2}{(j-1)}$	F _(A)
E(a)=Bloq x A	(i-1)(j-1)			$\sigma_b^2 + (k) \sigma_a^2$	
В	(k-1)			$\sigma^2_b + (ij) \sum \frac{(B_k - (\overline{B}))^2}{(k-1)}$	F _(B)
AB	(j-1)(k-1)			$\sigma_b^2 + (i) \sum \sum \frac{[AB_{jk} - \overline{AB}]2}{(j-1)(k-1)}$	F _(AB)
E(b)=Residual	(i-1)j(k-1)			σ_b^2	
Total	ljk-1				

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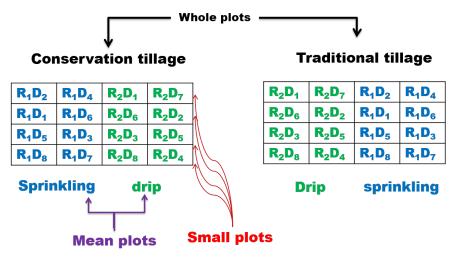
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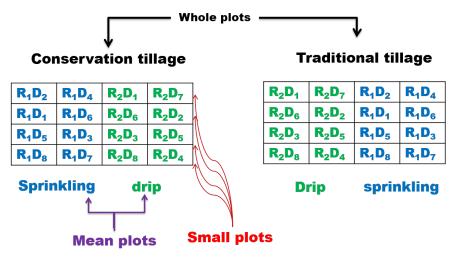




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After the ANOVA analyses what ?

- > 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 H₀ hypothesis is rejected, then that rejection could be due to different situations:
- $au_1 = au_2 = \dots = au_{t-1}$, but $au_{t-1} \neq au_t$ $au_1 = au_2 = \dots = au_{t-2} = au_t$, but $au_{t-2} \neq au_{t-1}$ etc., etc.
- So, additional method for inquiring about the structure of the differences among treatments are needed

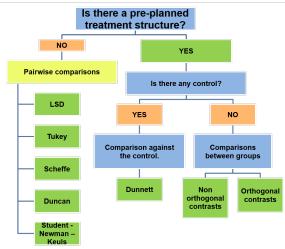


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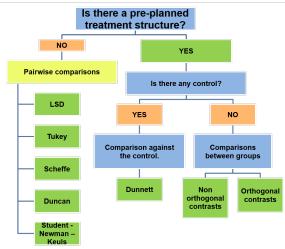
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Pairwise comparisons methods: fundaments

> Hypothesis:

 $\begin{array}{l} & \textbf{Example, for 4 treatments ; the hypotheses to test are:} \\ & \textbf{} \frac{t(t-1)}{2} = \frac{4(3)}{2} = 6, \\ & \textbf{1.} \quad H_0: \tau_1 = \tau_2 \quad vs \quad H_0: \tau_1 \neq \tau_2 \\ & \textbf{2.} \quad H_0: \tau_1 = \tau_3 \quad vs \quad H_0: \tau_1 \neq \tau_3 \\ & \textbf{3.} \quad H_0: \tau_1 = \tau_4 \quad vs \quad H_0: \tau_1 \neq \tau_4 \\ & \textbf{4.} \quad H_0: \tau_2 = \tau_3 \quad vs \quad H_0: \tau_2 \neq \tau_3 \\ & \textbf{5.} \quad H_0: \tau_2 = \tau_4 \quad vs \quad H_0: \tau_2 \neq \tau_4 \\ & \textbf{6.} \quad H_0: \tau_3 = \tau_4 \quad vs \quad H_0: \tau_3 \neq \tau_4 \end{array}$



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The Test Statistic is:

 $D_k = \left| \overline{y}_i - \overline{y}_j \right|; \qquad k = 1, 2, \dots, \frac{t(t-1)}{2}$

- 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):

 $MSD = [D'n_{dfe,\alpha/2}]$ [Standard Error]

With Decision Rule :

If $|\overline{y}_i - \overline{y}_j| \ge MSD \to Reject Ho_k$



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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)

$$LSD_{k} = \left[t_{dfe,\alpha/2}\right] \left[\sqrt[2]{MSE\left(\frac{1}{r_{i}} + \frac{1}{r_{j}}\right)}\right]$$

> For $r_i = r_j = r$ (balanced designs)

$$LSD = \left[t_{dfe,\alpha/2} \right] \left[\sqrt[2]{\frac{2 MSE}{r}} \right]$$



Least Significant Difference (LSD) method > It is based on the Student's t distribution

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Comparisonwise error rate vs Experimentwise error rate

Pr (type I error) = Pr (rejecting H0 / H0 is true) = Pr (declaring differences that not exist) = Pr (False Positive) Experimentwise error rate: $Pr(False Positive) = 1 - (1 - \alpha)^k$ where k = number of comparisons realized $= \frac{t(t-1)}{2}$

For
$$\alpha = 0.05$$

If t = 4; k=6; $Pr(False\ Positive) = 1 - (1 - 0.05)^6 = 0.4012$
t = 5; k=10; $Pr(False\ Positive) = 1 - (1 - 0.05)^{10} = 0.9005$
t = 10; k=45; $Pr(False\ Positive) = 1 - (1 - 0.05)^{45} = 0.999$

While for $\alpha = 0.01$ If t = 4; k=6; $Pr(False\ Positive) = 1 - (1 - 0.01)^6 = 0.0585$ t = 5; k=10; $Pr(False\ Positive) = 1 - (1 - 0.01)^{10} = 0.0956$ t = 10; k=45; $Pr(False\ Positive) = 1 - (1 - 0.01)^{45} = 0.3638$



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Tukey's method (Honestly Significant Difference)

- It is based on the Studentized or Standardized Range Distribution
- > For $r_i \neq r_j$ (unbalanced designs)

$$HSD_{k} = \left[q_{dfe,\alpha}^{t}\right] \left[\sqrt[2]{\frac{MSE}{2}\left(\frac{1}{r_{i}} + \frac{1}{r_{j}}\right)}\right]$$

> For $r_i = r_j = r$ (balanced designs)

$$HSD = \left[q^t_{dfe,\alpha}\right] \left[\sqrt[2]{\frac{MSE}{r}}\right]$$

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)

$$S_k = \sqrt[2]{(t-1)\left[F\frac{(t-1)}{dfe,\alpha}\right]} \quad [MSE\left(\frac{1}{r_i}+\frac{1}{r_j}\right)]$$

> While for $r_i = r_j = r$ (balanced designs)

$$S = \sqrt[2]{\left[\frac{2(t-1)}{r}\right]} \left[F\frac{(t-1)}{dfe,\alpha}\right] \quad [MSE]$$



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Comparing methods

For alpha = 0.05 we got:

LSD(0.6268) < Tukey(0.8705) < Scheffe(0.9494)

While for alpha = 0.01 was gotten:

LSD(0.9121) < Tukey(1.1924) < Scheffe(1.2972)

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