

$$x_{ijklmn} = \mu + repl_i + block_j(repl_i) + plot_k + pop_l + seedlot_m(pop_l) + \varepsilon_n$$

Training session on Design of Experiments

Replications: 1-4

Block: 1-18 (by replication)

Experimental unit: 5 seedlings

Plot: 1-5

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Sketch out

- ❖ Introduction
- ❖ Stages
- ❖ Principles
- ❖ Designs and analysis theory
- ❖ Operational tools for design
- ❖ [Analysis of experiments]

OUTLINE

❖ Introduction

❖ Stages

❖ Principles

❖ Designs and analysis theory

❖ Operational tools for design

❖ [Analysis of experiments]

❖ DoE \leftrightarrow AoE

❖ Practical aspects

❖ Some statistics theory

❖ Operational tools for design

❖ Data collecting

❖ Preprocessing (screening, outliers)

❖ Checking assumptions

❖ [Analysis of experiments]

Introduction

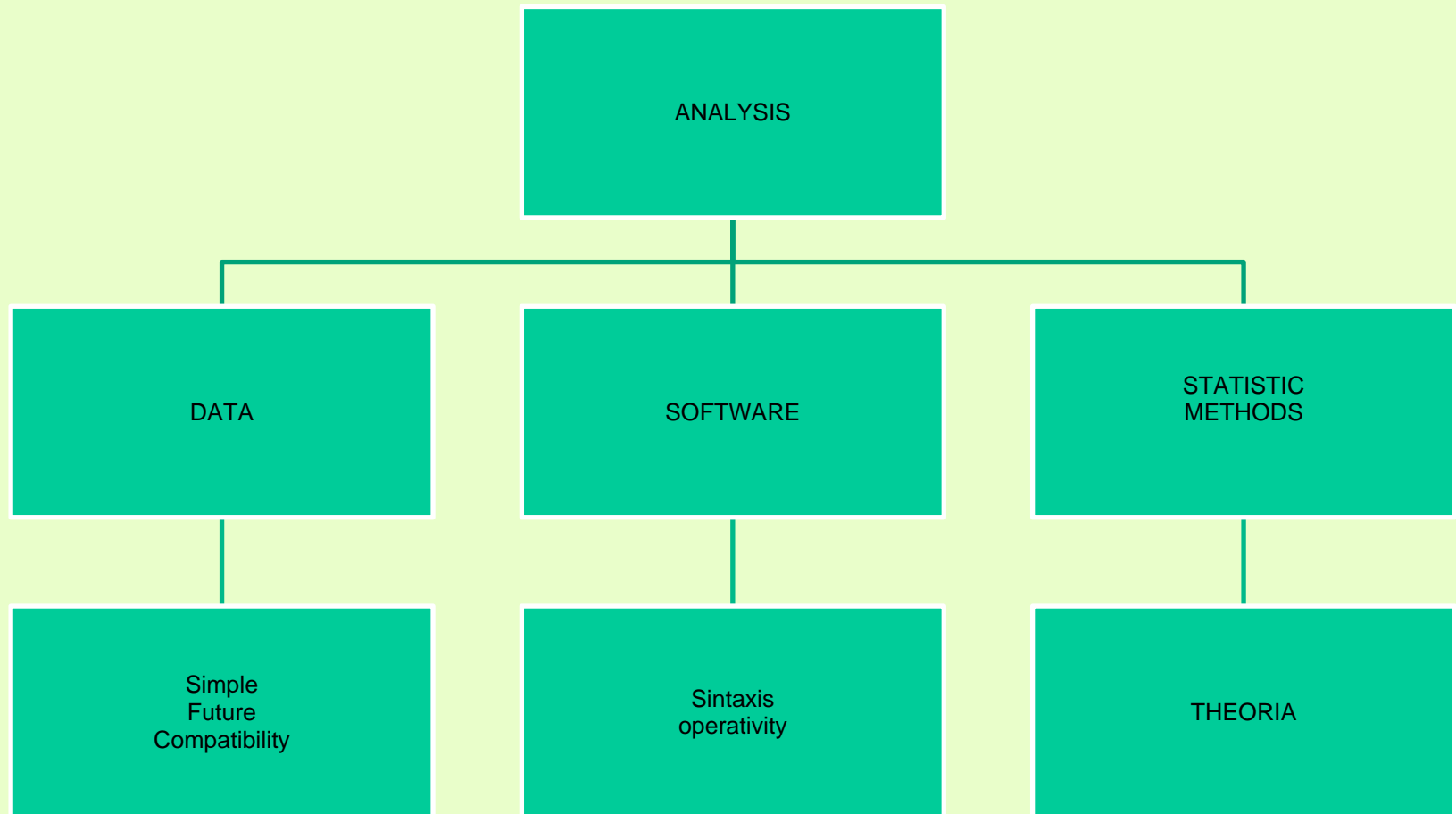
❖ Goal

Tool for addressing analytical problems without fixed laws

❖ Variability

- Existence
- Dealing and understanding
- Modeling and controlling

experimental error



Planning of an experiment (i)

- ❖ Definition of objectives
- ❖ Definition of all sources of variation
 - ❖ Treatments and their levels
 - ❖ Experimental units
 - ❖ Nuisance factors: blocking, noise & covs
- ❖ Setting up the experimental units & treatments

Planning of an experiment (ii)

- ❖ Definition of response variable, experimental process and issues foresight
- ❖ Set up the model
- ❖ Scheme of analysis steps
- ❖ Set up sampling size
- ❖ Review all foregoing points and modifying if necessary

Stages (i)

- ❖ Definition of the problem
- ❖ Definition of objectives
- ❖ Selection of treatments to test (interactions)
- ❖ Selection of the material to test
- ❖ Selection of the experimental design (simple)
- ❖ Selection of the experimental unit size and number of replications

Stages (ii)

- ❖ Control of “surroundings” effects
- ❖ Kind of data to be taken
- ❖ Selection of statistical tests
- ❖ Accomplishment of the experiment
- ❖ Analysis and interpretation of results
- ❖ Final reporting (conclusions)

Principles (i)

1. Replication **n**s. (experimental error basis)

Standard Error of Difference

Agronomic trials $SED < 1/3$ diff

Material selection $SED < 1/6$ diff

Knowing s^2 & $d \implies n$

$$SED = \sqrt{\frac{2\sigma^2}{n}}$$

2. Treatment (broad sense) **R**andomization

3. Local control of existing variation in trial site
(**B**locking or spatial analysis)

ANCOVA / SDA / Robust methods

“typical numbers & expressions”

4 replications
randomization
25 plants per plot
4 treatments
latinization
RCB
2 border lines
3 sites
single tree plot
5 x 5 m spacing
25 genotypes

Principles (ii)

Operational Limiting factors

- Number of available effectives
- Site constraints (topography, surface ...)
- Technical limitations (machinery,)
- Measurements
- Competence, specific needs,
- Future treatments, thinings,...
- Spacing, density

Experimental design

Initial assumptions or constraints:

Additivity

Normality

Homocedasticity.

Different treatment errors
are independent
& distributed $N(0, \sigma^2)$

Statistic tests:

N: Shapiro-Wilks, graphs distrib,
freq acum., res * pred

H: Barlett, Levenne, ratios variances

Transformations

No parametric methods

Elementary Designs

G.R.

Model: $y_{ij} = \mu + t_i + \varepsilon_{ij}$

	dof	SS	MS	F	EMS
Total	rt-1	a	a/rt-1		
Treat	t-1	b	b/t-1	MS_T / MS_E	$\sigma_e^2 + r \sigma_t^2$
Error	t(r-1)	c	c/t(r-1)		σ_e^2

Model $y = \text{treat};$

Elementary Designs

R.G.B

$$\text{Model: } y_{ijk} = \mu + t_i + b_j + \varepsilon_{ijk}$$

	dof	SS	MS	F	EMS
Total	rb-1	a	a/rb-1		
Treat	t-1	b	b/t-1	MS_T / MS_E	$\sigma_e^2 + b \sigma_t^2$
Blq	b-1	c	c/b-1	MS_B / MS_E	$\sigma_e^2 + t \sigma_b^2$
Error	t-1)(r-1)	d	d/t(r-1)		σ_e^2

Model $y = \text{treat blq};$

Experimental design

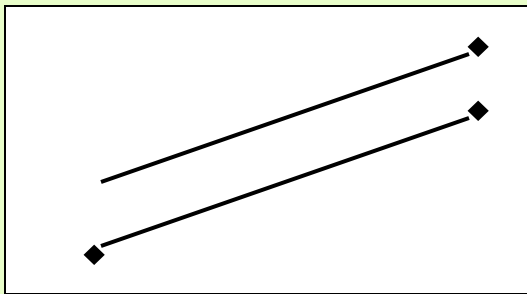
Possible structure of treatments

Factorial: total combination all x all

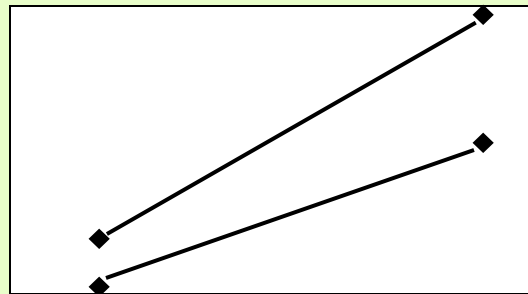
Possibility interactions study (GxE)

Reaction norms

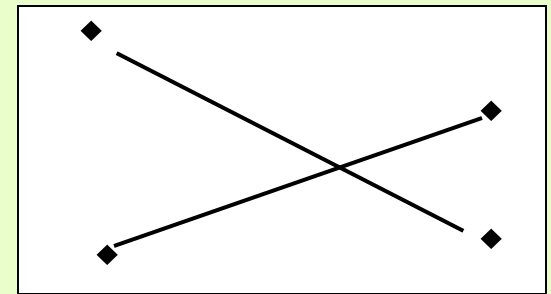
$$y_{ijk} = \mu + \alpha_i + \beta_j + \gamma_{ij} + \varepsilon_{ijk}$$



No interaction



quantitative
interaction



qualitative
interaction

Experimental design

Possible structure of treatments

Hierarchical or nested: Impossible combination

$$y_{ijk} = \mu + \alpha_i + \beta_j(\alpha_i) + \varepsilon_{ijk}$$

Model $y = \text{pop fam}(\text{pop});$

Is it important the treatment structure ?

F

E.M.S.

other structure + important.....

¿Fixed o Random?

F E.M.S.

1. Critic decision
2. Not well documented on texts
3. Usually based on subjective statistic agreements

Fixed: Levels of factor clearly targeted or selected

Results & conclusions from anova are for these levels

Main aim: Mean estimation of the variable for each level

(BLUE)

Random: Levels are a random sample from all posible.

Results & conclusions from anova can be extrapolated + levels

Main aim: Variability estimation of the variable or factor
or perhaps prediction at a given level

(BLUP)

	dof	MS	A y B fixed	A y B rand	A:fix B:rand
Total	abr-1				
A	a-1	MS_A	MS_A / MS_E	MS_A / MS_{AB}	MS_A / MS_{AB}
B	b-1	MS_B	MS_B / MS_E	MS_B / MS_{AB}	MS_B / MS_E
AxB	$(a-1)(b-1)$	MS_{AB}	MS_{AB} / MS_E	MS_{AB} / MS_E	MS_{AB} / MS_E
Error	$ab(r-1)$	MS_E			

$$\sigma_e^2 + c_1 \Phi_\alpha$$

$$\sigma_e^2 + n \sigma_{ab}^2 + nb \sigma_a^2$$

¿Fixed o Random?

How to asses?
A PRIORI

Scientific Criteria :

- 1) is it possible to repeat the factor levels in other site or year?
- 2) has it meaning this replication?

Yes + Yes = Fixed

Statistic Criteria :

“Random” few levels (3-5) =>weak variance estimation,
Better setting as fixed and use the results only at these levels

“Fixed” with many levels (>10) without structure, better setting as random and estimating means by BLUPs

E.M.S. Numeric difficulty

¿Fixed o Random?

GLM

Model $y = \text{loc} \text{ blq}(\text{loc}) \text{ var} \text{ var}^* \text{ loc};$
Random $\text{loc} \text{ blq}(\text{loc}) \text{ var}^* \text{ loc} / \text{test};$

1^o Calculation as fixed

2^o Calculation EMS

3^o Repeat F-tests with proper denominators

MIXED MODELS

Incomplete Blocks

Evaluation : high n^0 genotypes
limited material

‘Many genotypes’ means huge blocks # no control

I.B. Not all treat by block, so several blocks are needed
for a complete replication

.	.	B	A	.	1
.	.	A	C	.	2
B	.	.	.	C	3

Based on

$$\begin{aligned} \text{Aditivity: } B-C &= (B-C)_3 \\ &= (B-A)_1 - (C-A)_2 \end{aligned}$$

Experimental error independent of treatment

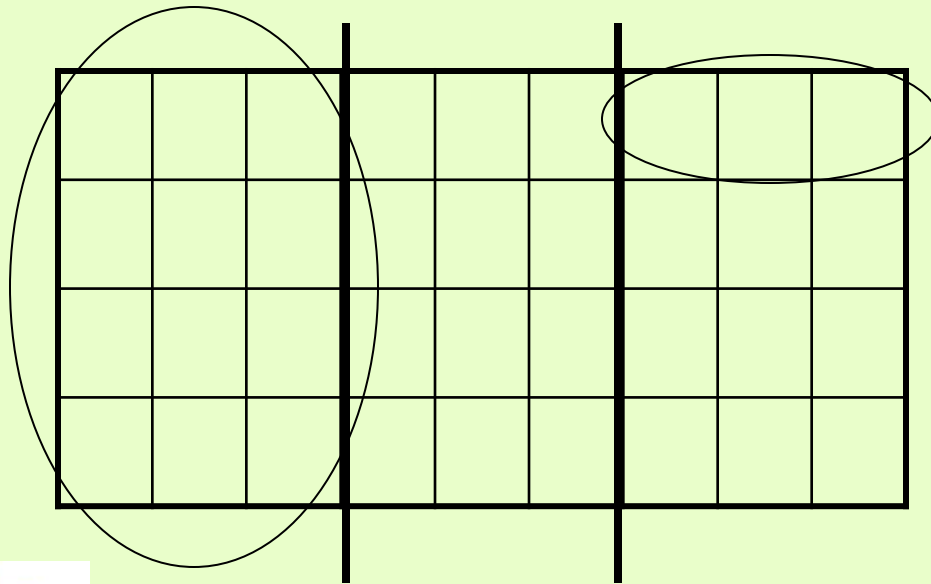
Incomplete Blocks

- Coexist direct & indirect comparisons
- Lost of accuracy on indirect comparisons but experimental error reduction

Resolvable designs

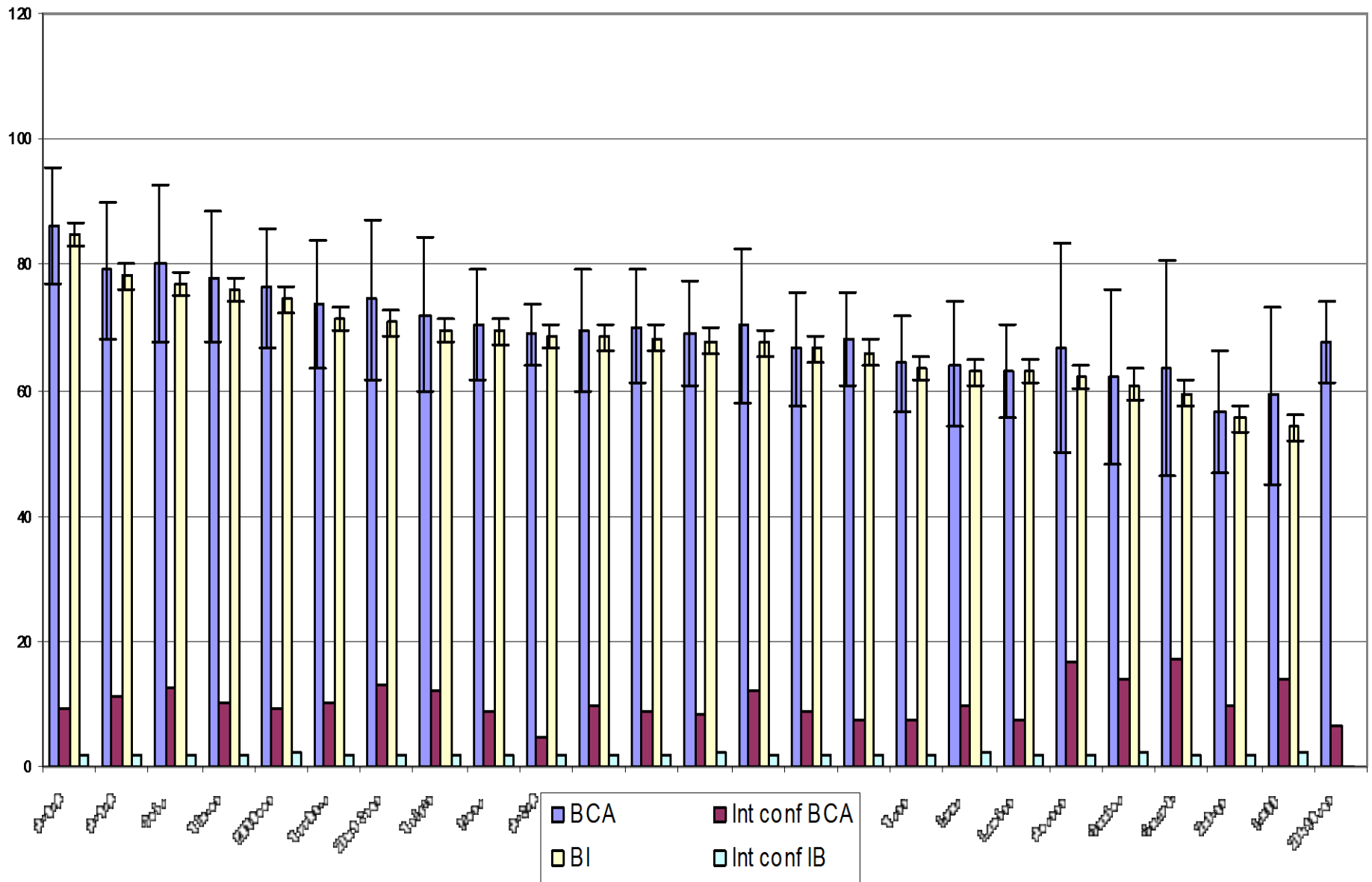
i.e.: $g = k \cdot b_i$

α -lattice, latinized, row-columns,...



Complex
specific Software

interblock info





$$x_{ijklmn} = \mu + repl_i + block_j(repl_i) + plot_k + pop_l + seedlot_m(pop_l) + \varepsilon_n$$

Mixed model REML BLUP & BLUE

ACGVELA Project Training session on DoE. CTFC-Solsona (Spain) 11-12/05/2016