Sketch out

❖Introduction

❖Stages

❖Principles

❖Designs and analysis theory

❖Operational tools for design

❖[Analysis of experiments]

Introduction

❖ Goal

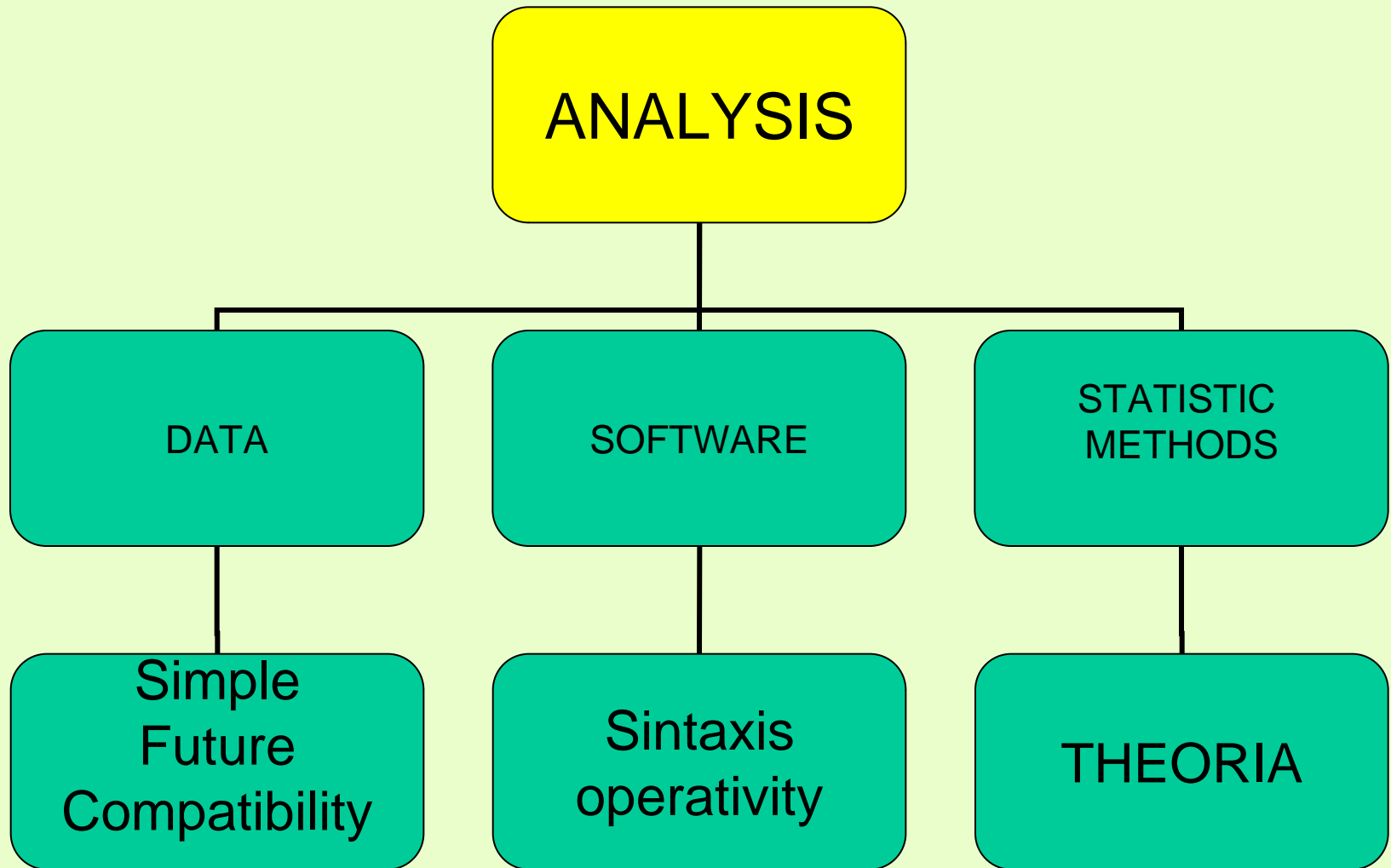Tool for addressing analytical problems without fixed laws

❖ Variability

- Existence

- Dealing and understanding

- Modeling and controlling

experimental error

Plant material or treatment evaluation

❖ Design of experiments

❖ Analysis of experiments

➢ Basic Principles

➢ Conventional and current (IB) designs

➢ Software

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**s**. (experimental error basis)
   Standard Error of Difference
   Agronomic trails SED<1/3 diff
   Material selection SED<1/6 diff
   Knowing s^2 & d ==> 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)

ANOVA / SDA / Robust methods

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"typical numbers & expressions"

4 replications

25 plants per plot

randomization

4 treatments

latinization

3 sites

2 border lines

RCB

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

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Experimental design

Initial hypotheses or constraints:

Aditive Model

Normality

Homocedasticity.

Different treatment errors
are independient
& 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

R.D.

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	$\sigma^2_e + r\,\sigma^2_t$
Error	t(r-1)	c	c/t(r-1)		σ^2_e

SAS

Data.........;
Proc GLM;
     Class treat;
     Model y = treat;
Run;

Elementary Designs

R.C.B

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	$\sigma^2_e + b\, \sigma^2_t$
Blq	b-1	c	c/b-1	MS_B/ MS_E	$\sigma^2_e + t\, \sigma^2_b$
Error	t-1)(r-1)	d	d/t(r-1)		σ^2_e

SAS

Data.........;
Proc GLM;
    Class treat blq;
    Model y = treat blq;
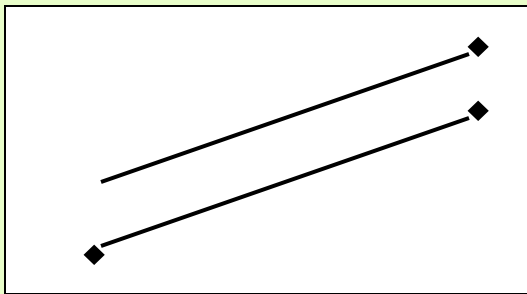Run;

Experimental design

Possible structure of treatments
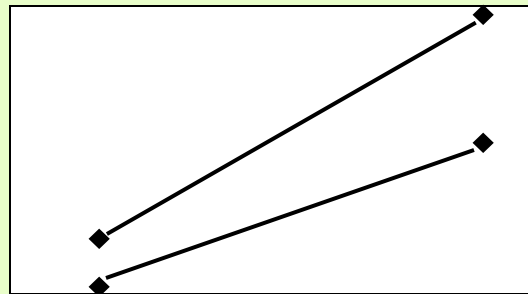
     Factorial: total combination all x all

          Possibility interactions study (GxE)
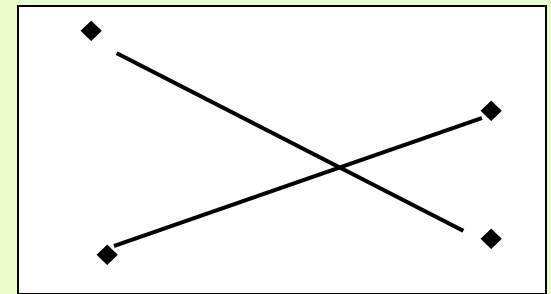
Reaction norms

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

No interaction

quantitative interaction

qualitative interaction

Experimental design

Possible structure of treatments

Hierarquical or nested: Impossible combination

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

SAS

Data.........;
Proc GLM;
     Class pop fam;
     Model y = pop fam(pop);
Run;

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			

$$\sigma^2_e + c_1 \Phi_\alpha \quad \mid \quad \sigma^2_e + n\,\sigma^2_{ab} + nb\,\sigma^2_a$$

¿Fixed o Random?

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 $\longrightarrow$ SAS

¿Fixed o Random?

```
Data.........;
Proc GLM;
        Class loc var blq;
        Model y =loc blq(loc) var var*loc;
        Random loc blq(loc) var*loc /test;
Run;
```

1º Calculation as fixed
2º Calculation EMS
3º Repeat F-tests with proper denominators

PROC MIXED

Incomplete Blocks

Evaluation : high nº 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
 Aditivity: $B-C = (B-C)_3$
$= (B-A)_1 - (C-A)_2$
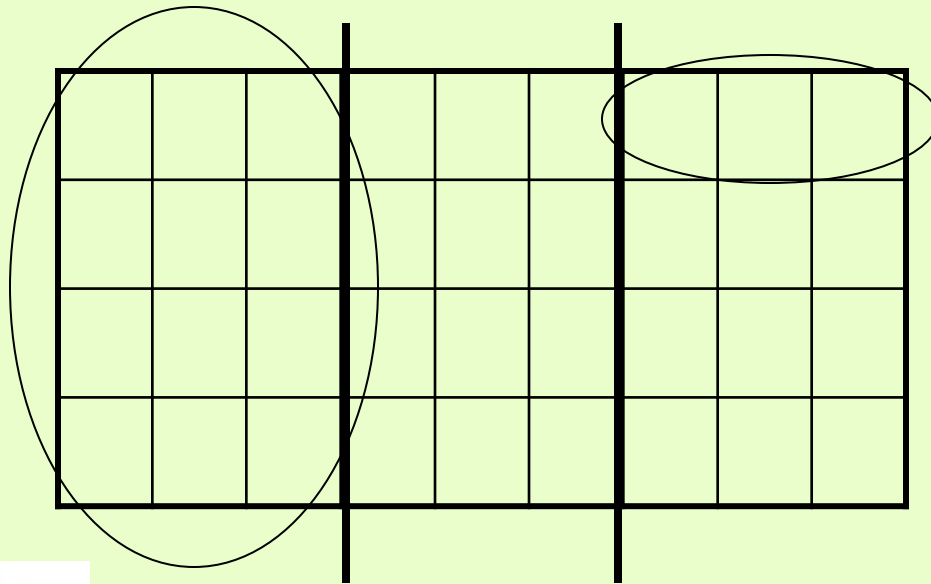Experimental error independent of treatment

Incomplete Blocks

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

Resolvable designs
i.e.: g=k bi
α-latice, latinized, row-columns,...

Complex
specific Software

interblock info

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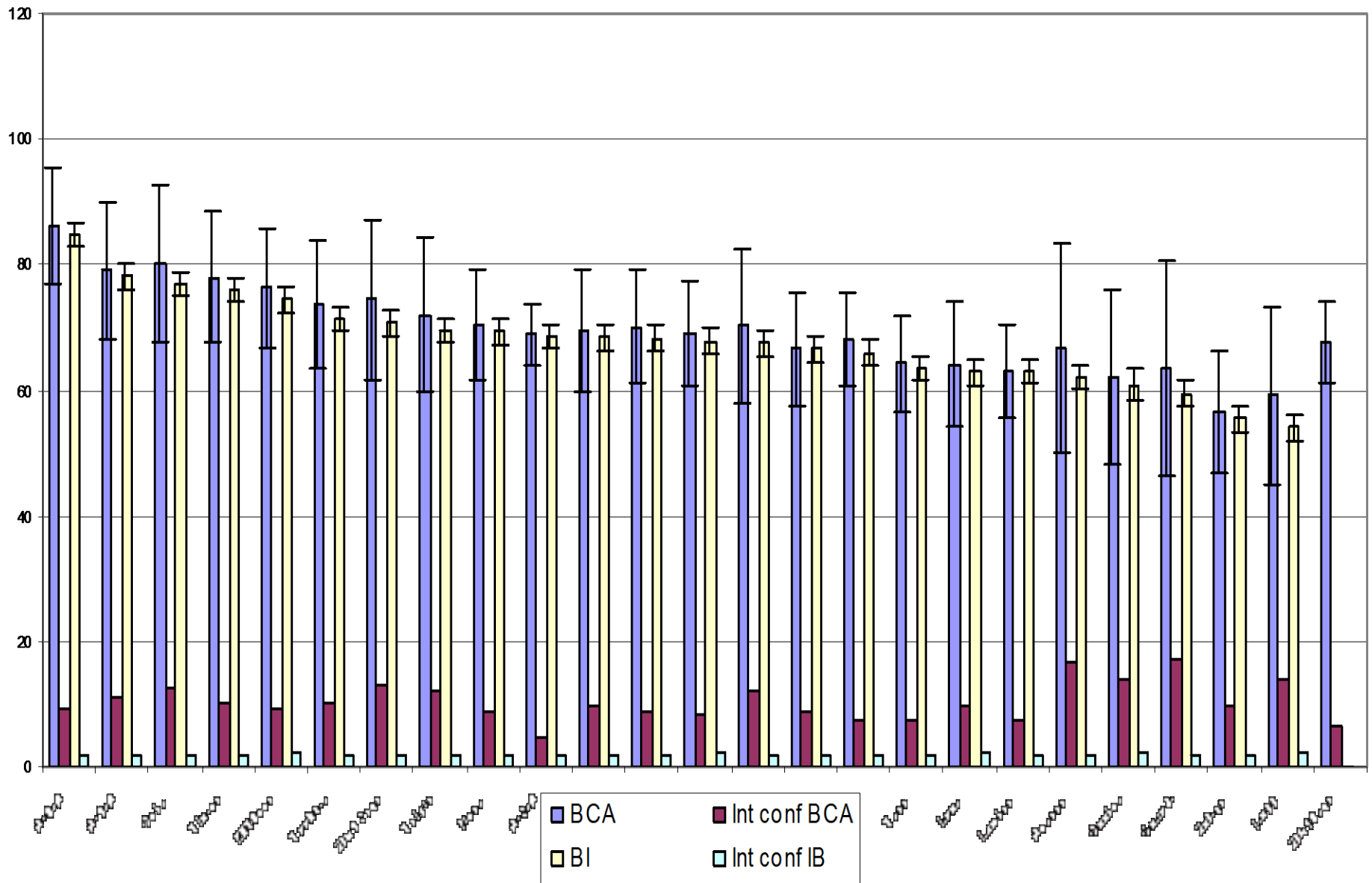
I.B. design Efficiency

Objetive: To compare genotypes con la mayor precisión

$E = (SED_{RCB}/ SED_{IB})^2$ nº of extra replications in a RCB
                    to get same accuracy level

$$\left(\frac{\sqrt{\left(\dfrac{2\sigma^2}{r}\right)}}{\sqrt{\left(\dfrac{2\sigma^2}{rxE}\right)}}\right)^2 = E$$

A IB with 4 reps y E=1.5 equals to a RCB with 4x1.5=6 CB

"Efficiency" ~ costs

Replications: 1-4

Block: 1-18 (by replication)

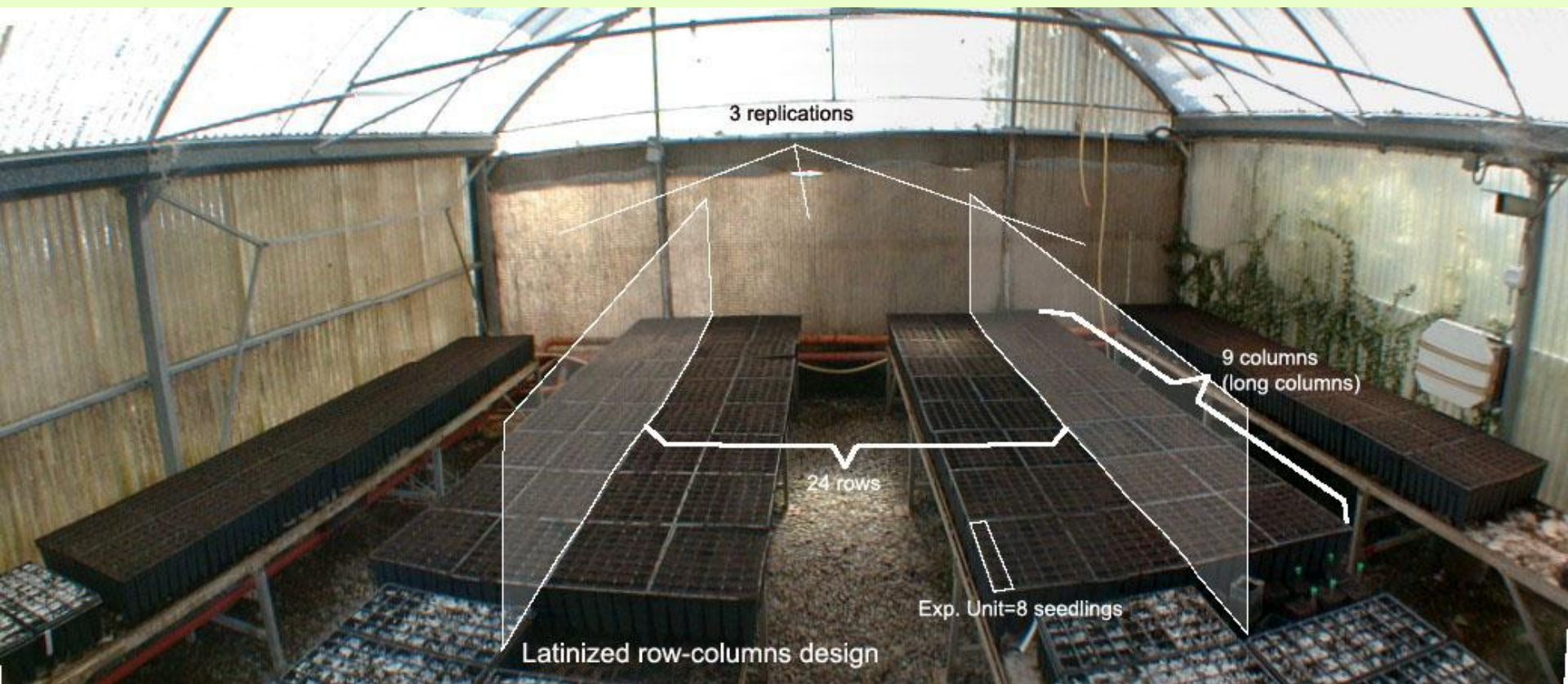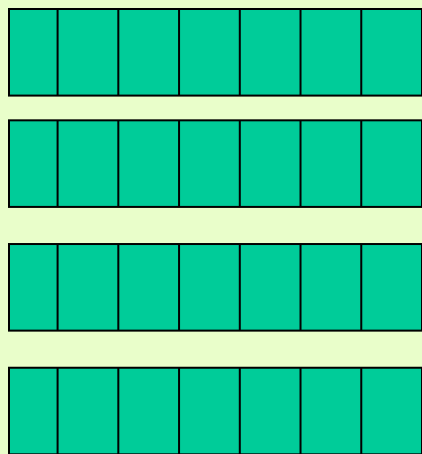Experimental unit: 5 seedlings

Plot: 1-5

$$x_{ijklmn} = \mu + repl_i + block_j(repl_i) + plot_k + pop_l + seedlot_m(pop_l) + \varepsilon_n$$
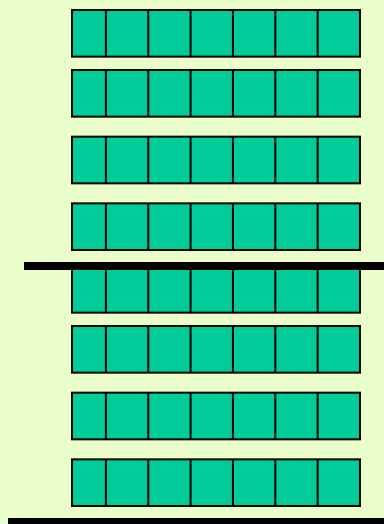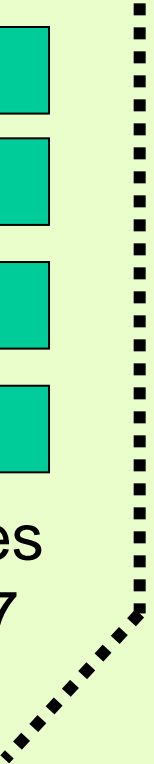
Mixed model REML BLUP & BLUE

Ethiopia-Spain PCI project Training session on design of experiments. Madrid 25-26/04/2012
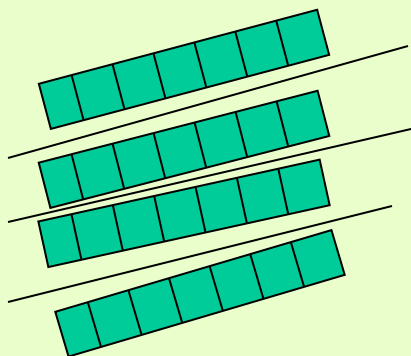
Layout software: CyCDesigN
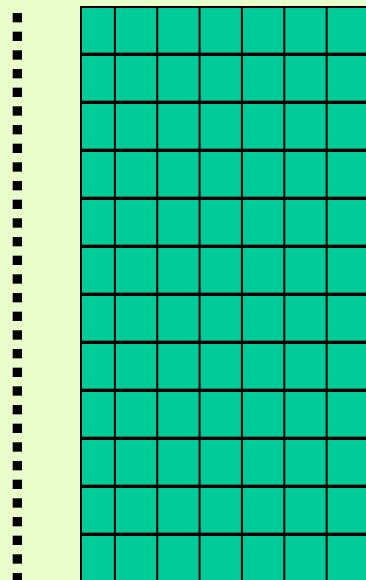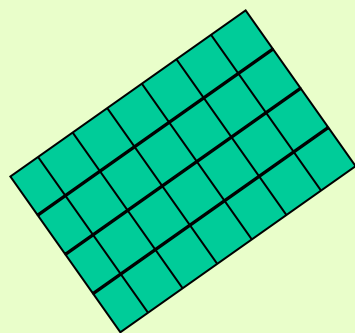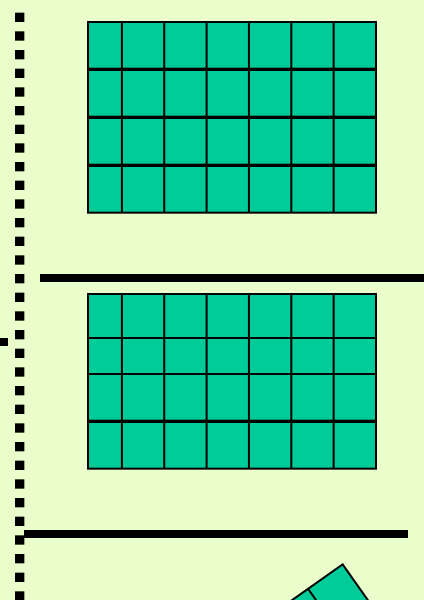
RCB azar.exe

28 genotypes
4 blocks of 7

3 rep α-lattice

Row-Column

Latinized
Row-column

CycDesigN 4.0

Home

What's New

CycDesigN

CycXOver

CycAnalysis

F.A.Q.

CycDesigN 4.0 is a computer package for the generation of optimal or near-optimal experimental designs. It comprises three modules:

CycDesigN provides a comprehensive design generation module for experimenters; particularly those involved in plant breeding, horticulture, agriculture, forestry and market research and for all field, glasshouse and laboratory trials.

CycXover provides a wide choice of designs for experiments that involve sequences of treatments (such as stimuli, diets or drugs) applied to subjects over successive time periods. Known as crossover (or changeover) experiments, they are used in such areas as clinical trials, sensory perception experiments, psychological testing and dietary experiments.

CycAnalysis allows you to tailor your output from a **CycDesigN** or **CycXOver** session into a form ready for analysis. It also gives you the option to generate either **GenStat** or **SAS** code for the analysis of the design you have chosen.

CycDesigN 4.0 is written in Visual C++ and runs under Windows 95, 98, NT, 2000, XP, Vista and Windows 7.

CSIRO Forestry and Forest Products
Canberra
Australia

The University of Waikato
Hamilton
New Zealand

CycDesigN

Version 2.0

CycDesigN Version 2.0

Setup   View   Help

CycDesigN

Block design — Kind of design: Incomp. Block or row-column

Resolvable — Resolvable, if v=ks v treats=s blocks of k treats

Design parameters [24,4,4] — Parameters: nºreps, nº i.b., nº treats

Single factor.. [1] — Factorial or nested

Alpha design

Not latinized

Not spatial — Latinization and spatial restrictions

Seed: clock

< Back   Next >

Generation of algorithms
(starting point)

Choose your design

Working directory: C:\Archivos de programa\DataPlus\pruebas   NUM

Block design

Block design

Resolvable

Design parameters [24,4,4]

Single factor.. [1]

Alpha design

Not latinized

Not spatial

Seed: clock

< Back   Next >

Row-column design

Row-column design

Resolvable

Design parameters [30,6,5,3]

Single factor.. [1]

Alpha design

Not latinized

Spatial: Integer

Seed: clock

Two stage

< Back   Next >

No operative differences for user

Design parameters [120,10,3]

Block design

Row-column design

Design parameters [?] [X]

Number of treatments 120

Number of units/block 10

Number of replicates 3

< Back   Next >

Design parameters [?] [X]

Number of treatments 120

Number of rows 10

Number of columns 12

Number of replicates 3

< Back   Next >

12 I.B. of 10 treat.
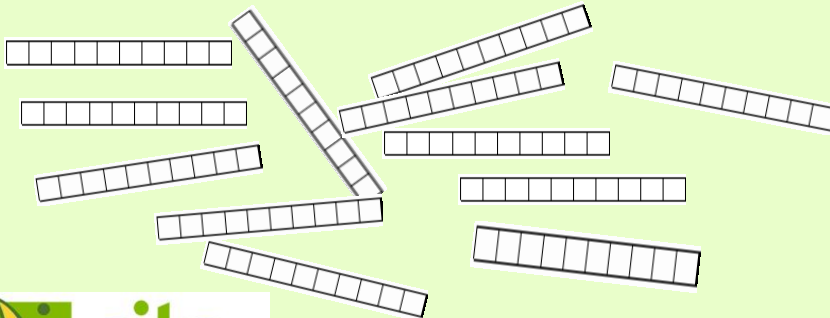
1 REP
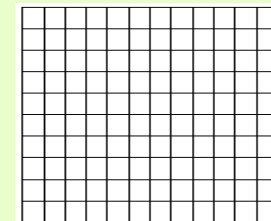
Single factor.. [5]

NESTED
5 POPULATIONS:
30, 20, 24, 26 y 20
Families respectiv.

Treatment structure

Single factor

Number of treatment groups 5

Factorial

< Back   Next >

Treatment group sizes

1 30   2 26
3 20   4 20
5 24

< Back   Next >

FACTORIAL:

2 Factors
10 levels in factor 1
12 levels in factor 2
10 x 12= 120 treat.

Treatment structure

Single factor

Factorial

Number of factors 2

< Back   Next >

Factor levels

1 10   2 12

< Back   Next >

28 genotypes
4 blocks of 7
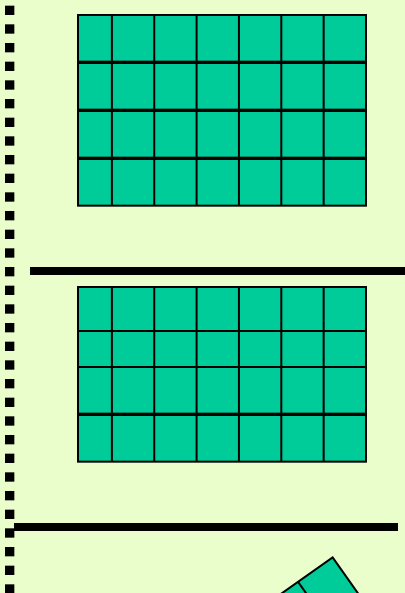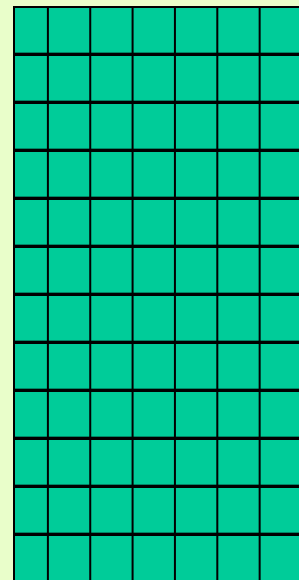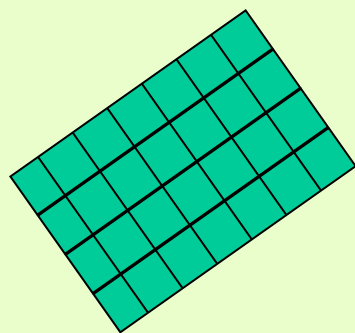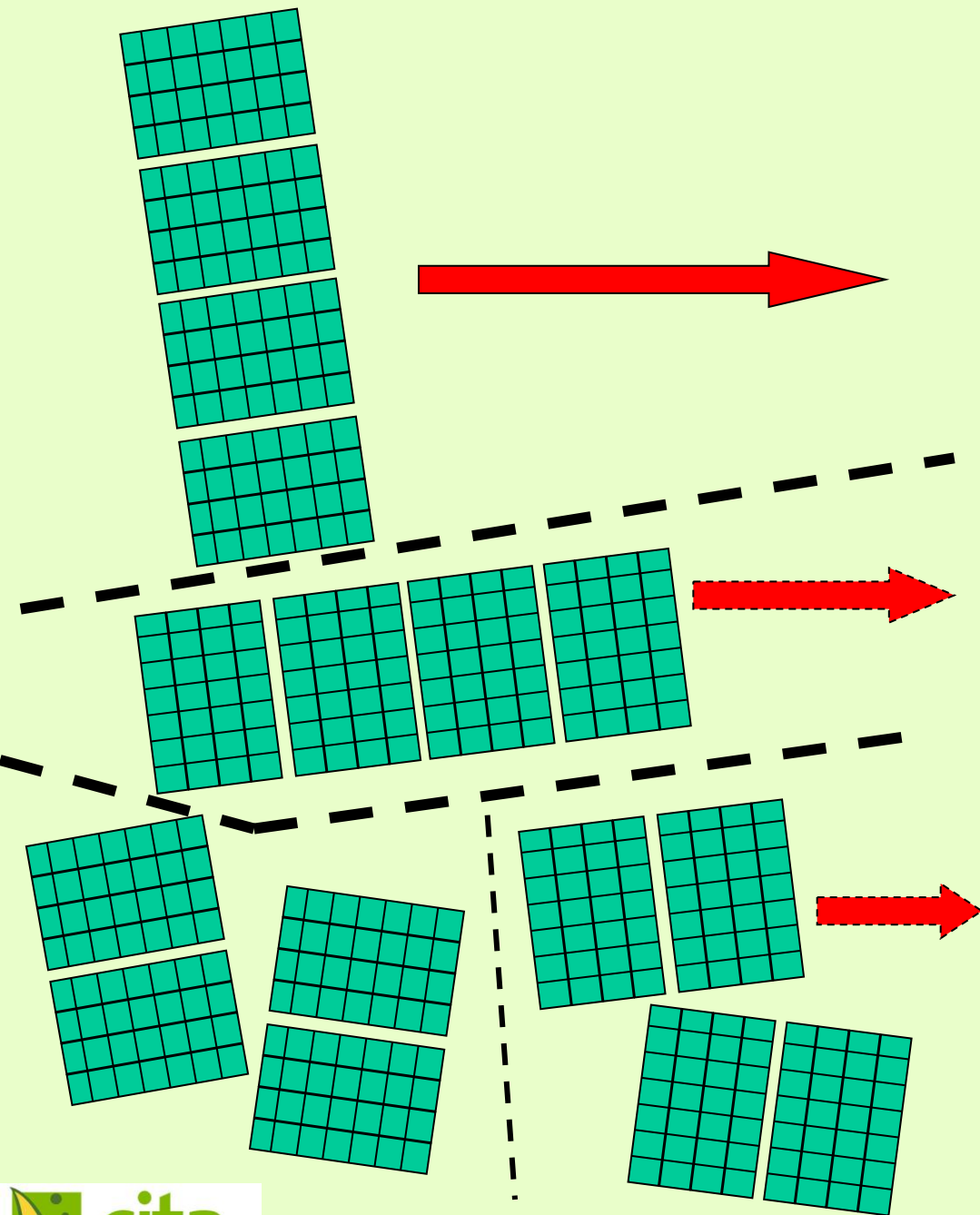
3 rep α-lattice

Row-Column

Latinized
Row-column

CycDesigN Version 2.0

Setup   View   Help

CycDesigN

Row-column design

Resolvable

Design parameters [120,10,12,3]

Single factor.. [1]

Alpha design

Latinized...[1,0,1]

Not spatial

Seed: clock

Two stage

< Back   Next >

Working directory

Enter your new working directory

C:\Archivos de programa\DataPlus\pr   Browse

Cancel   OK

Randomization/Output

☑ Randomize

Number of randomizations   1

Seed: clock

Default levels

Rows by columns

Index file: design.ind

Design file: design.out

Log file: design.log

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Possibility of recoding our levels (treats o genotypes)

Choose your design   Working directory: C:\Archivos de programa\DataPlus\pruebas   NUM

```
Date and time are: Mon Aug 08 14:00:44 2005
Row-column design
Resolvable
Design parameters
      Number of treatments   =    120
      Number of rows         =     10
      Number of columns      =     12
      Number of replicates   =      3

Latinized by columns


Random number seed for design generation = 46


Two stage


Average efficiency factors  (Upper bounds)
    Row           0.895737   (0.896446)
    Column        0.875536   (0.875563)
    Row-Column    0.789671   (0.795142)



Concurrence            Row           Column
      0               5229            5520
      1               1842            1620
      2                 69               0


Randomization 1


Random number seed for randomization = 203


Treatment randomization:
Group  1:
  98 100 102   97 103   36 105 108 110 112 115   70  39  25  67
  63  77  74   10  72   78 116  88  90  93  19   57 114  28 117
  30  26    8 118 119   21  40  24  64  91 104    5  23  81  47
  82  60    9  79  14   94   6  80  34  84  86   59   4  95  41
  20  46 101  38  37  111  65  52 107  17  32   56  76  92  12
  55  11 106    2  69   29   7  15  53  87  43   71  99  66 109
 113  62 120  18  31   42  49   3  16  54  27    1  61  48  75
  83  45  50  44  51   85  89  33  22  35  68   73  96  13  58


Replicate randomization:
    3   1   2


Column randomization:
  11   4   8  12   1  10   2   3   5   6   7   9


Row randomization:
   2   9   8  10   3   4   5   6   1   7
   6   4   2   8   5   3   1   9   7  10
  10   6   7   9   8   2   5   4   1   3
```

```
rep  1 -----------------------------------------------
column    1    2    3    4    5    6    7    8    9   10   11   12
row    +-------------------------------------------------------------
  1    |   86   70   92   54  107   96    6  106  101   20   13  114
  2    |  113   12    4    9  115   93   82   14   94   18  103   60
  3    |    2   59  102   53   15   71  116   76   78   77   75    1
  4    |   49   72   73   89   50   43    5   51   87   22    8   79
  5    |   67   28   85   68   84   21   46   80   11   64  105   23
  6    |  110  104   37   40    3   98  100   33  117  111   57   16
  7    |   58   48   47  119   52  108   10   99   27   26   30   95
  8    |   90   55   31   42   66   88   62   91   19   29   61   97
  9    |   38   32   36  109   44  112   83   45  118  120   81   17
 10    |   24    7   34   63   74   39   25   41   65   69   56   35


rep  2 -----------------------------------------------
column    1    2    3    4    5    6    7    8    9   10   11   12
row    +-------------------------------------------------------------
  1    |   17   58   18   70  102   63   67   61  116   80  117   50
  2    |    9   15   81   85   54   19   26   24  106   43   12  100
  3    |   92   97   33   75   49  111   53   28   74   30   82  118
  4    |   71   36   35   21   94   90   57   89   32   52   51   20
  5    |    3   40   86   27   23   76  115   47    8   25   29   93
  6    |   72   14   59   16  120  107   65    6  108  110   68   31
  7    |   56   11  119   45  104   83   79   64   37   60   96    2
  8    |   77   46   87   66   41  103  112   98  114   55   34  109
  9    |   62   13   84    5   39   95   91   78   22    4   38   48
 10    |   99   69   88  113   10   73    7   44   42  101    1  105


rep  3 -----------------------------------------------
column    1    2    3    4    5    6    7    8    9   10   11   12
row    +-------------------------------------------------------------
  1    |   10   85   17   96   86   78  109   55   57   14   73   74
  2    |   98   30   50  100   76   66   11   54   18   38   32    7
  3    |   84  117   41   59   42   20  113   56   43   47   97   83
  4    |  103   89  108   92  118   25    1   67   15  104    5   29
  5    |   69   62   75   94   28   79  106  107   23  112  119  110
  6    |   70  120   40   91   71   37   52   82   63  105   24   87
  7    |   53    2   12    8   16   99   39   36    6   19   80   21
  8    |   60   33   90   44   26   68   72   27   34  116   93   13
  9    |   51  114   64   58    4   81  111   88   48    3   65  102
 10    |   31  115  101   95   46   49   61   22   45   35   77    9
```
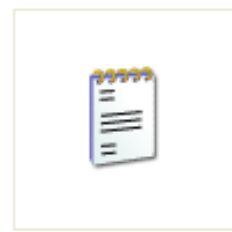
design.log

design.ind - Bloc de notas

Archivo Edición Formato Ver Ayuda

Rnd	rep	row	col	trt
1	1	1	1	86
1	1	1	2	70
1	1	1	3	92
1	1	1	4	54
1	1	1	5	107
1	1	1	6	96
1	1	1	7	6
1	1	1	8	106
1	1	1	9	101
1	1	1	10	20
1	1	1	11	13
1	1	1	12	114
1	1	2	1	113
1	1	2	2	12
1	1	2	3	4
1	1	2	4	9
1	1	2	5	115
1	1	2	6	93
1	1	2	7	82
1	1	2	8	14
1	1	2	9	94
1	1	2	10	18
1	1	2	11	103
1	1	2	12	60
1	1	3	1	2
1	1	3	2	59
1	1	3	3	102
1	1	3	4	53
1	1	3	5	15
1	1	3	6	71
1	1	3	7	116
1	1	3	8	76
1	1	3	9	78
1	1	3	10	77
1	1	3	11	75
1	1	3	12	1
1	1	4	1	49
1	1	4	2	72
1	1	4	3	73
1	1	4	4	89
1	1	4	5	50
1	1	4	6	43
1	1	4	7	5
1	1	4	8	51
1	1	4	9	87
1	1	4	10	22
1	1	4	11	8
1	1	4	12	79
1	1	5	1	67
1	1	5	2	28
1	1	5	3	85
1	1	5	4	68
1	1	5	5	84
1	1	5	6	21
1	1	5	7	46
1	1	5	8	80
1	1	5	9	11
1	1	5	10	64
1	1	5	11	105
1	1	5	12	23

design.ind

design.ind   design.out   design.log

design.out - Bloc de notas

Archivo Edición Formato Ver Ayuda

```
Row-column design
Resolvable
Design parameters
        Number of treatments    =    120
        Number of rows          =     10
        Number of columns       =     12
        Number of replicates    =      3

Latinized by columns

Randomization 1


rep  1 ------------------------------
column    1    2    3    4    5    6    7    8    9
row    +------------------------------
  1    |   86   70   92   54  107   96    6  106  101
  2    |  113   12    4    9  115   93   82   94
  3    |    2   59  102   53   15   71  116   76   78
  4    |   49   72   73   89   50   43    5   51   87
  5    |   67   28   85   68   84   21   46   80   11   64  105   23
  6    |  110  104   37   40    3   98  100   33  117  111   57   16
  7    |   58   48   47  119   52  108   10   99   27   26   30   95
  8    |   90   55   31   42   66   88   62   91   19   29   61   97
  9    |   38   32   36  109   44  112   83   45  118  120   81   17
 10    |   24    7   34   63   74   39   25   41   65   69   56   35

rep  2 ------------------------------
column    1    2    3    4    5    6    7    8    9   10   11   12
row    +------------------------------
  1    |   17   58   18   70  102   63   67   61  116   80  117   50
  2    |    9   15   81   85   54   19   26   24  106   43   12  100
  3    |   92   97   33   75   49  111   53   28   74   30   82  118
  4    |   71   36   35   21   94   90   57   89   32   52   51   20
  5    |    3   40   86   27   23   76  115   47    8   25   29   93
  6    |   72   14   59   16  120  107   65    6  108  110   68   31
  7    |   56   11  119   45  104   83   79   64   37   60   96    2
  8    |   77   46   87   66   41  103  112   98  114   55   34  109
  9    |   62   13   84    5   39   95   91   78   22    4   38   48
 10    |   99   69   88  113   10   73    7   44   42  101    1  105

rep  3 ------------------------------
column    1    2    3    4    5    6    7    8    9   10   11   12
row    +------------------------------
  1    |   10   85   17   96   86   78  109   55   57   14   73   74
  2    |   98   30   50  100   76   66   11   54   18   38   32    7
  3    |   84  117   41   59   42   20  113   56   43   47   97   83
  4    |  103   89  108   92  118   25    1   67   15  104    5   29
  5    |   69   62   75   94   28   79  106  107   23  112  119  110
  6    |   70  120   40   91   71   37   52   82   63  105   24   87
  7    |   53    2   12    8   16   99   39   36    6   19   80   21
  8    |   60   33   90   44   26   68   72   27   34  116   93   13
  9    |   51  114   64   58    4   81  111   88   48    3   65  102
 10    |   31  115  101   95   46   49   61   22   45   35   77    9
```
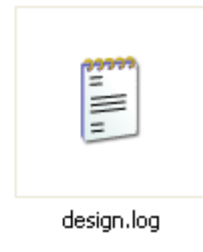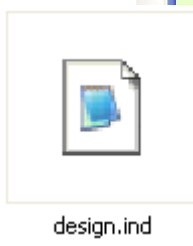
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CENTRO DE INVESTIGACIÓN Y TECNOLOGÍA
AGROALIMENTARIA DE ARAGÓN